

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
24 August 2006 (24.08.2006)

PCT

(10) International Publication Number
WO 2006/087334 A1

(51) International Patent Classification:

C12P 3/00 (2006.01) *C12N 15/01* (2006.01)
C12N 9/02 (2006.01) *C02F 3/34* (2006.01)

(21) International Application Number:

PCT/EP2006/050942

(22) International Filing Date:

15 February 2006 (15.02.2006)

(25) Filing Language:

English

(26) Publication Language:

English

(30) Priority Data:

05290387.9 21 February 2005 (21.02.2005) EP

(71) Applicant (for all designated States except US): **CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE** [FR/FR]; 3, Rue Michel-Ange, F-75794 Paris Cedex 16 (FR).

(72) Inventors; and

(75) Inventors/Applicants (for US only): **ROUSSET, Marc** [FR/FR]; 3 Rotonde De Roussargue, F-13420 Gemenos (FR). **CASALOT, Laurence** [FR/FR]; 16 Boulevard Georges Clémenceau, F-13004 Marseille (FR). **DE PHILIP, Pascale** [FR/FR]; 52 Rue d'Algésiras, F-13010 Marseille (FR). **BELAICH, Anne** [FR/FR]; 33 Rue Floralie, F-13009 Marseille (FR).

(74) Agent: **GROSSET, Chantal, Catherine**; GROSSET-FOURNIER & DEMACHY, 54 Rue Saint-lazare, F-75009 Paris (FR).

(81) Designated States (unless otherwise indicated, for every kind of national protection available): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KN, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, LY, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NG, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SM, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(84) Designated States (unless otherwise indicated, for every kind of regional protection available): ARIPO (BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LT, LU, LV, MC, NL, PL, PT, RO, SE, SI, SK, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:

- with international search report
- with sequence listing part of description published separately in electronic form and available upon request from the International Bureau

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

(54) Title: USE OF BACTERIUM STRAINS FOR THE PREPARATION OF METALLIC BIOCATALYSTS, IN PARTICULAR FOR THE PREPARATION OF PALLADIUM BIOCATALYSTS

(57) Abstract: The present invention relates to the use of a bacterium strain characterized in that its genome contains at least a gene coding for a membrane-bound [NiFe] hydrogenase, or of membrane extracts containing said membrane-bound [NiFe] hydrogenase of said bacterium strain, for the preparation of metallic biocatalysts, provided that in the case of the use of a bacterium strain the genome of which contains one or several genes coding for a soluble periplasmic hydrogenase, then said strain is transformed by inactivation, repression or deletion of at least one of said genes coding for a soluble periplasmic hydrogenase, the corresponding soluble periplasmic hydrogenase being then non produced or absent.



WO 2006/087334 A1

USE OF BACTERIUM STRAINS FOR THE PREPARATION OF METALLIC BIOCATALYSTS, IN PARTICULAR FOR THE PREPARATION OF PALLADIUM BIOCATALYSTS

5

The present invention concerns the use of bacterium strains for the preparation of metallic biocatalysts, in particular for the preparation of palladium biocatalysts.

10

15

20

Palladium is one of the most expensive metals; the highest consumer worldwide is the automobile industry where this metal, together with other platinum group metals (PGM), is used in automobile catalytic converters to reduce the toxicity of vehicle exhaust gases. Palladium is also extensively used in the electronics industry and in chemical manufacturing and processing (Platinum, 2003). Palladium is a highly valuable metal with only limited world resources reported before the widespread implementation of automotive catalyst (Hoffman, 1988). The existing methods of Pd recovery from scrap, e.g. hydro- and pyrometallurgical routes, are either energy demanding or harmful to the environment, or both. Therefore alternative, clean methods of recovery are very important. It was shown by Lloyd *et al.*, (1998), that palladium can be effectively recovered from solution by resting cells of *Desulfovibrio desulfuricans* at ambient temperature. As an alternative approach, Mertig, et al. (1998) and Wahl et al. (2001) described abiotic reduction of Pd(II) to Pd(0) onto a protein surface under H₂, but, unlike the use of bacteria (Yong et al., 2003) this has not been applied to the development of a flow-through metal recovery process.

25

Desulfovibrio sp. and other sulphate-reducing bacteria (SRB) are well-known as metal reducers (Lovely & Philips, 1992; Tucker et al., 1998; Ganesh et al. 1999; Spear et al., 1999; Lloyd et al., 1998, 1999, 1999a, 2001). Yong et al. (2002) showed that Pd(II) can be reduced by *D. desulfuricans* over a wide pH range and this organism was effectively used to recover Pd from chemical processing waste (Yong, et al., 2002a) and leachates from spent automotive catalysts (Yong et al., 2003).

30

The biomineralised palladium (Bio-Pd) identified as Pd(0) by X-ray powder diffraction analysis (Lloyd *et al.*, 1998) was found to have catalytic properties not seen in Pd(0) prepared by simple chemical reduction of Pd(II) salts under H₂. For example, Bio-Pd catalysed the reduction of Cr(VI) to Cr(III) (Mabett *et al.*, 2001), the reductive dehalogenation of chlorophenol and polychlorinated biphenyls (Baxter-Plant et al., 2003) and effected the hydrogenation of methylene succinic acid at rates comparable to

a commercial supported palladium catalyst. The properties of a supported metal catalyst depend critically on both the size of the metal clusters (Henry, 1998) and the ability of supporting material to prevent their coalescence (Henry, 1998). Bacteria have both biomanufacturing and templating/supporting functions.

5 It has been reported that *Escherichia coli*, like *D. desulfuricans*, possesses significant metal reducing capability (Lloyd et al., 1997, 1997a, 1999a). The physiology and genetics of this organism are well investigated (Menon et al., 1991; Sauter et al., 1992; Lloyd et al., 1997, 1999a) and, using these approaches, involvement of hydrogenase activity in Tc(VII) reduction by *E. coli* was attributed to the hydrogenase
10 III component of the formate hydrogenlyase (FHL) complex (Lloyd et al., 1997), a rudimentary form of which has been proposed to exist in *D. desulfuricans* (Peck, 1993).

The aim of the present invention is to provide a new process for the preparation of metallic biocatalysts, which implementation is easier and cheaper than industrial processes.

15 The aim of the present invention is to provide a new process for the preparation of metallic biocatalysts, which comprises the use of transformed bacterium strains, in particular of transformed *Desulfovibrio fructosovorans* strains.

The aim of the present invention is to provide a metallic biocatalyst of smaller particle size than the catalysts of the prior art, said metallic biocatalyst thus having a
20 higher catalytic activity.

The present invention relates to the use

– of a bacterium strain characterized in that its genome contains at least a gene coding for a membrane-bound [NiFe] hydrogenase, or

– of membrane extracts containing said membrane-bound [NiFe]

25 hydrogenase of said bacterium strain,
for the preparation of metallic biocatalysts,

provided that in the case of the use of a bacterium strain the genome of which contains one or several genes coding for a soluble periplasmic hydrogenase, then said strain is transformed by inactivation, repression or deletion of at least one of said genes
30 coding for a soluble periplasmic hydrogenase, the corresponding soluble periplasmic hydrogenase being then non produced or absent.

The expression “membrane-bound hydrogenase” designates any enzyme, attached directly or by an anchoring subunit to the membrane, which catalyses hydrogen production or oxidation. Membrane-bound hydrogenases are closely related to the

proton-pumping NADH:quinone oxidoreductase (complex I): the small subunit is considerably smaller than that of other [NiFe]hydrogenases and contains only the cysteine ligands for the proximal [4Fe-4S] cluster (Classification and phylogeny of hydrogenases, Vignais et al., 2001). The corresponding hydrogenase activity is measured according to the method described in Fernandez et al. (1985).

The expression "soluble periplasmic hydrogenase" designates any enzyme containing iron and nickel or only iron, which catalyses hydrogen production or oxydation (Vignais et al., 2001). The corresponding hydrogenase activity is measured according to the method described in Fernandez et al. (1985).

The expression "inactivation of said gene coding for a soluble periplasmic hydrogenase" corresponds to an insertion of a DNA fragment into said gene or to a mutation of the coding sequence of said gene resulting in the absence of expression or to the expression of a truncated or aberrant protein.

The expression "repression of said gene coding for a soluble periplasmic hydrogenase" corresponds to the absence of production of the corresponding protein due to growth conditions under which said gene is under the control of a regulatory element that prevents synthesis of the corresponding messenger RNA or the production of the translated protein.

The expression "deletion of said gene coding for a soluble periplasmic hydrogenase" corresponds to the total or partial removal of the coding sequence of said gene from its natural locus.

The present invention relates to the above-mentioned use of a bacterium strain, or of membrane extracts thereof, the genome of which contains a gene, represented by SEQ ID NO: 1, coding for a membrane-bound [NiFe] hydrogenase represented by the sequence SEQ ID NO: 2, or contains a gene coding for a sequence having at least 30% of identity with sequence SEQ ID NO: 2.

The present invention relates to the above-mentioned use of a bacterium strain, or of membrane extracts thereof, chosen among Eubacteria or Archaeobacteria.

According to an advantageous embodiment, the use according to the present invention is characterized in that the bacterium strain, or the membrane extracts thereof, is chosen among:

* the following Eubacteria:

– *Desulfovibrio vulgaris*, the genome of which contains a gene represented by SEQ ID NO: 1 coding for a membrane-bound [NiFe] hydrogenase represented by SEQ

ID NO: 2, and a gene represented by SEQ ID NO: 3 coding for a membrane-bound [NiFe] hydrogenase represented by SEQ ID NO: 4,

– *Desulfovibrio fructosovorans*, the genome of which contains a gene represented by SEQ ID NO: 5 coding for a membrane-bound [NiFe] hydrogenase having 70% of identity with sequence SEQ ID NO: 2, said hydrogenase being represented by SEQ ID NO: 6,

– *Desulfovibrio gigas*, the genome of which contains a gene represented by SEQ ID NO: 7 coding for a membrane-bound [NiFe] hydrogenase having 74% of identity with sequence SEQ ID NO: 2, said hydrogenase being represented by SEQ ID NO: 8,

– *Thermoanaerobacter tengcongensis*, the genome of which contains a gene represented by SEQ ID NO: 9 coding for a membrane-bound [NiFe] hydrogenase having 63% of identity with sequence SEQ ID NO: 2, said hydrogenase being represented by SEQ ID NO: 10, and contains a gene represented by SEQ ID NO: 11 coding for a membrane-bound [NiFe] hydrogenase having 38% of identity with sequence SEQ ID NO: 2, said hydrogenase being represented by SEQ ID NO: 12,

– *Rhodospirillum rubrum*, the genome of which contains a gene represented by SEQ ID NO: 13 coding for a membrane-bound [NiFe] hydrogenase having 41% of identity with sequence SEQ ID NO: 2, said hydrogenase being represented by SEQ ID NO: 14,

– *Escherichia coli*, the genome of which contains a gene represented by SEQ ID NO: 15 coding for a membrane-bound [NiFe] hydrogenase having 37% of identity with sequence SEQ ID NO: 2, said hydrogenase being represented by SEQ ID NO: 16, and contains a gene represented by SEQ ID NO: 17 coding for a membrane-bound [NiFe] hydrogenase having 35% of identity with sequence SEQ ID NO: 2, said hydrogenase being represented by SEQ ID NO: 18,

– *Erwinia carotovora*, the genome of which contains a gene represented by SEQ ID NO: 19 coding for a membrane-bound [NiFe] hydrogenase having 36% of identity with sequence SEQ ID NO: 2, said hydrogenase being represented by SEQ ID NO: 20,

– *Salmonella typhi*, the genome of which contains a gene represented by SEQ ID NO: 21 coding for a membrane-bound [NiFe] hydrogenase having 36% of identity with sequence SEQ ID NO: 2, said hydrogenase being represented by SEQ ID NO: 22,

– *Salmonella typhimurium*, the genome of which contains a gene represented by SEQ ID NO: 23 coding for a membrane-bound [NiFe] hydrogenase having 36% of

identity with sequence SEQ ID NO: 2, said hydrogenase being represented by SEQ ID NO: 24,

– *Shigella flexneri*, the genome of which contains a gene represented by SEQ ID NO: 25 coding for a membrane-bound [NiFe] hydrogenase having 35% of identity with sequence SEQ ID NO: 2, said hydrogenase being represented by SEQ ID NO: 26,

– *Wolinella succinogenes*, the genome of which contains a gene represented by SEQ ID NO: 27 coding for a membrane-bound [NiFe] hydrogenase having 35% of identity with sequence SEQ ID NO: 2, said hydrogenase being represented by SEQ ID NO: 28,

* the following Archaeobacteria:

– *Methanosarcina mazei*, the genome of which contains a gene represented by SEQ ID NO: 29 coding for a membrane-bound [NiFe] hydrogenase having 54% of identity with sequence SEQ ID NO: 2, said hydrogenase being represented by SEQ ID NO: 30,

– *Methanosarcina barkeri*, the genome of which contains a gene represented by SEQ ID NO: 31 coding for a membrane-bound [NiFe] hydrogenase having 53% of identity with sequence SEQ ID NO: 2, said hydrogenase being represented by SEQ ID NO: 32,

– *Pyrococcus abyssi*, the genome of which contains a gene represented by SEQ ID NO: 33 coding for a membrane-bound [NiFe] hydrogenase having 40% of identity with sequence SEQ ID NO: 2, said hydrogenase being represented by SEQ ID NO: 34, and contains a gene represented by SEQ ID NO: 35 coding for a membrane-bound [NiFe] hydrogenase having 38% of identity with sequence SEQ ID NO: 2, said hydrogenase being represented by SEQ ID NO: 36,

– *Pyrococcus horikoshii*, the genome of which contains a gene represented by SEQ ID NO: 37 coding for a membrane-bound [NiFe] hydrogenase having 39% of identity with sequence SEQ ID NO: 2, said hydrogenase being represented by SEQ ID NO: 38,

– *Pyrococcus furiosus*, the genome of which containing a gene represented by SEQ ID NO: 39 coding for a membrane-bound [NiFe] hydrogenase having 39% of identity with sequence SEQ ID NO: 2, said hydrogenase being represented by SEQ ID NO: 40,

– *Methanococcus jannaschii*, the genome of which contains a gene represented by SEQ ID NO: 41 coding for a membrane-bound [NiFe] hydrogenase having 36% of

identity with sequence SEQ ID NO: 2, said hydrogenase being represented by SEQ ID NO: 42,

– *Methanococcus maripuladis*, the genome of which contains a gene represented by SEQ ID NO: 43 coding for a membrane-bound [NiFe] hydrogenase having 36% of identity with sequence SEQ ID NO: 1, and represented by SEQ ID NO: 44,

– *Methanopyrus kandleri*, the genome of which contains a gene represented by SEQ ID NO: 45 coding for a membrane-bound [NiFe] hydrogenase having 36% of identity with sequence SEQ ID NO: 2, said hydrogenase being represented by SEQ ID NO: 46,

– *Methanobacterium thermoautotrophicum*, the genome of which contains a gene represented by SEQ ID NO: 47 coding for a membrane-bound [NiFe] hydrogenase having 37% of identity with sequence SEQ ID NO: 2, said hydrogenase being represented by SEQ ID NO: 48,

– *Methanobacterium thermoformicium*, the genome of which contains a gene represented by SEQ ID NO: 49 coding for a membrane-bound [NiFe] hydrogenase having 37% of identity with sequence SEQ ID NO: 2, said hydrogenase being represented by SEQ ID NO: 50, and contains a gene represented by SEQ ID NO: 51 coding for a membrane-bound [NiFe] hydrogenase having 33% of identity with sequence SEQ ID NO: 2, said hydrogenase being represented by SEQ ID NO: 52.

The present invention relates to the above-mentioned use of a bacterium strain characterized in that its genome contains at least a gene coding for a membrane-bound [NiFe] hydrogenase, but does not contain genes coding for a soluble periplasmic hydrogenase.

According to an advantageous embodiment, the present invention relates to the use of a bacterium strain whose genome contains at least a gene coding for a membrane-bound [NiFe] hydrogenase, but does not contain genes coding for a soluble periplasmic hydrogenase, said bacterium strain being in particular *E. coli*.

The present invention also relates to the above-mentioned use, of a bacterium strain characterized in that its genome contains at least a gene coding for a membrane-bound [NiFe] hydrogenase, and one or several genes coding for a soluble periplasmic hydrogenase, said strain being transformed by inactivation or deletion of at least one of said genes coding for a soluble periplasmic hydrogenase, the corresponding soluble periplasmic hydrogenase being then inactivated or deleted.

According to an advantageous embodiment, said gene is mutated by the use of a chemical agent such as acridine orange or nitomycine or by the insertion of a mobile element (transposons - insertion sequences) or by recombination, or by the use of ionising radiations (UV radiations).

5 The present invention also relates to the above-mentioned use, of a bacterium strain characterized in that its genome contains at least a gene coding for a membrane-bound [NiFe] hydrogenase, and one or several genes coding for a soluble periplasmic hydrogenase, said strain being cultivated in such conditions that at least one of said genes coding for a soluble periplasmic hydrogenase is repressed, the corresponding
10 soluble periplasmic hydrogenase being then not produced.

According to an advantageous embodiment, repression of some hydrogenase genes is observed under non-nitrogen fixing conditions, in aerobiosis or in the absence of formate or molecular hydrogen in the growth medium.

The present invention also relates to the use such as defined above, of a
15 transformed bacterium strain chosen among *Desulfovibrio vulgaris*, *Desulfovibrio fructosovorans*, *Desulfovibrio gigas*, or *Desulfovibrio desulfuricans*, the genome of which being transformed by inactivation or deletion of at least one of said genes coding for a soluble periplasmic hydrogenase.

The present invention also relates to the use such as defined above, of a bacterium
20 strain the genome of which being transformed by deletion of at least one of said genes coding for a soluble periplasmic hydrogenase.

The present invention also relates to the use as defined above, of a *Desulfovibrio fructosovorans* strain transformed in such way that the gene represented by SEQ ID NO: 53 coding for the soluble periplasmic [NiFe] hydrogenase represented by SEQ ID
25 NO: 54, and/or the gene represented by SEQ ID NO: 55 coding for the soluble periplasmic [Fe] hydrogenase represented by SEQ ID NO: 56, are deleted.

According to an advantageous embodiment, the present invention relates to the use of a transformed *Desulfovibrio fructosovorans* strain wherein the gene represented by SEQ ID NO: 53 is deleted.

30 According to an advantageous embodiment, the present invention relates to the use of the transformed *Desulfovibrio fructosovorans* strain MR400, which was deposited on the January 11th, 2005, at the Collection Nationale de Cultures de Microorganismes (CNCM) of the Institut Pasteur under the number I-3349.

According to an advantageous embodiment, the present invention relates to the use of a transformed *Desulfovibrio fructosovorans* strain wherein the genes represented by SEQ ID NO: 53 and SEQ ID NO: 55 are both deleted.

According to an advantageous embodiment, the present invention relates to the use of the transformed *Desulfovibrio fructosovorans* strain DF400, which was deposited on the January 11th, 2005, at the Collection Nationale de Cultures de Microorganismes (CNCM) of the Institut Pasteur under the number I-3350.

The present invention also relates to the above-mentioned use, of a bacterium strain, the genome of which being transformed by inactivation of at least one of said genes coding for a soluble periplasmic hydrogenase.

According to an advantageous embodiment, the present invention relates to the use of a bacterium strain, the genome of which being transformed by inactivation of at least one of said genes coding for a soluble periplasmic hydrogenase, said inactivation being obtained by mutation of at least one amino acid of said genes, and selection of the corresponding mutated proteins encoded by said mutated genes exhibiting from 0.1% to 30% of the native soluble periplasmic hydrogenase activity.

The periplasmic hydrogenase activity is measured according to the method described in Activity measurements (Fernandez et al., 1985). H₂ uptake activity was measured with 1mM methyl viologen as described in Fernandez et al. (1985). Briefly, oxygen was removed under vacuum and the cuvette was flushed with Ar. Enzyme (10 µg for wt (wild-type) and E25D mutated form and 1 mg for E25Q, and E25V mutated forms) was allowed to activate for 1h under H₂ in 20mM Tris/Hcl buffer at pH 8. The activity was then measured in an H₂-flushed UV-cuvette, containing 1 mL of the buffer, in which residual oxygen was eliminated by adding 1 µL of a 100g.L⁻¹ dithionite solution. The reaction was started by the addition of 5 to 30 µL of activated enzyme and the kinetics of the reduction of methyl viologen was measured at 604 nm in a UV 1601 spectrophotometer (Shimadzu) at 30°C.

According to an advantageous embodiment, the genome of *Desulfovibrio fructosovorans* strain is transformed by inactivation of the gene represented by SEQ ID NO: 53 coding for the soluble periplasmic [NiFe] hydrogenase represented by SEQ ID NO: 54, and/or of the gene represented by SEQ ID NO: 55 coding for the soluble periplasmic [Fe] hydrogenase represented by SEQ ID NO: 56.

According to an advantageous embodiment, the invention relates to the use of a transformed *Desulfovibrio fructosovorans* strain wherein the gene represented by SEQ ID NO: 53 is inactivated by:

– mutation of the nucleotide(s) GAA in position 264 of SEQ ID NO: 53 by substitution of said nucleotide by GAC, leading to a mutated gene represented by SEQ ID NO: 57 encoding a mutated soluble periplasmic [NiFe] hydrogenase represented by SEQ ID NO: 58 and corresponding to the native sequence SEQ ID NO: 54 wherein the glutamate in position 25 is substituted by an aspartate, said mutated soluble periplasmic [NiFe] hydrogenase SEQ ID NO: 58 exhibiting from 30% to 60%, more particularly 45%, of the native soluble periplasmic hydrogenase SEQ ID NO: 54 activity,

– and/or mutation of the nucleotide(s) GAA in position 264 of SEQ ID NO: 53 by substitution of said nucleotide by CAG, leading to a mutated gene represented by SEQ ID NO: 59 encoding a mutated soluble periplasmic [NiFe] hydrogenase represented by SEQ ID NO: 60 and corresponding to the native sequence SEQ ID NO: 54 wherein the glutamate in position 25 is substituted by a glutamine, said mutated soluble periplasmic [NiFe] hydrogenase SEQ ID NO: 60 exhibiting from 0.05% to 0.2%, more particularly 0.1%, of the native soluble periplasmic hydrogenase SEQ ID NO: 54 activity,

– and/or mutation of the nucleotide(s) GAA in position 264 of SEQ ID NO: 53 by substitution of said nucleotide by GTC, leading to a mutated gene represented by SEQ ID NO: 61 encoding a mutated soluble periplasmic [NiFe] hydrogenase represented by SEQ ID NO: 62 and corresponding to the native sequence SEQ ID NO: 54 wherein the glutamate in position 25 is substituted by a valine, said mutated soluble periplasmic [NiFe] hydrogenase SEQ ID NO: 62 exhibiting from 8% to 15%, more particularly 10%, of the native soluble periplasmic hydrogenase SEQ ID NO: 54 activity.

The present invention also relates to the above-mentioned use, of membrane extracts containing at least one membrane-bound [NiFe] hydrogenase of bacterium strains as defined above.

The present invention also relates to the use of membrane extracts such as obtained according to the following method, which comprises the following steps:

– centrifugation of fully grown cells and washing of these cells, in order to obtain a cell suspension,

– breaking of said cell suspension to obtain a crude extract, which is centrifuged at low speed to collect the bacterial debris, and then centrifuged for two hours at 50,000 rpm, in order to obtain a supernatant and a membrane pellet,

– discarding of said supernatant containing soluble proteins, and resuspension of said membrane pellet.

Fully grown cells are harvested by centrifugation at 8000 rpm and washed twice in Tris/HCl buffer pH = 8. The cell suspension is then broken using a French pressure cell. The crude extract is first centrifuged at low speed (500 rpm for ten minutes) to collect the bacterial debris, and then centrifuged for two hours at 50,000 rpm. The supernatant containing soluble proteins is discarded, and the membrane pellet is resuspended and tested for hydrogenase activity and palladisation experiments.

According to an advantageous embodiment, the present invention relates to the use of membrane extracts of *Desulfovibrio fructosovorans* such as obtained according to the method such as defined above.

The present invention also relates to the use as defined above, for the preparation of metallic biocatalysts chosen among the following precious metals: palladium, platinum, ruthenium, rhodium and iridium.

The present invention also relates to a process for the preparation of metallic biocatalysts comprising the following steps:

– bringing together bacterium strains, or transformed bacterium strains, or membrane extracts such as defined above, with a solution of a metal in oxidized form, for a time period sufficient to allow the initial sorption of the metal in oxidized form in said, bacterium strains, or transformed bacterium strains, or membrane extracts,

– bubbling of hydrogen gas through the solution such as obtained in the previous step, in order to allow the formation of a metal precipitate corresponding to the metal in reduced form, and recovering of said metal in reduced form.

The expression “for a time period sufficient to allow the initial sorption of the metal in oxidized form” corresponds to a duration of a few minutes to about one hour.

According to an advantageous embodiment, the process of the invention is used for the preparation of metallic biocatalysts chosen among the following precious metals: palladium, platinum, ruthenium, rhodium and iridium.

The present invention also relates to a process for the preparation of palladium biocatalyst comprising the following steps:

- bringing together the DF400 strain such as defined above with a solution of palladium in oxidized form Pd(II), especially a solution of Na₂PdCl₄, for a time period sufficient to allow the initial sorption of Pd(II) in said strain,
- bubbling of hydrogen gas through the solution such as obtained in the previous step, in order to allow the formation of a palladium precipitate corresponding to the metal in reduced form Pd(0), and recovering of said palladium.

DESCRIPTION OF FIGURES

Figure 1A represents the deletion of the [NiFe] hydrogenase encoding genes and construction of the MR400 strain and derivatives. *hynA,B,C* corresponds to the [NiFe] hydrogenase operon and *npt* to the fragment containing the Kn^r gene.

Figure 1B represents the deletion of the [Fe] hydrogenase encoding genes and construction of the DF400 strain and derivatives. *hydA,B* corresponds to the [Fe] hydrogenase operon and *accI* to a gentamicin resistance gene.

Figure 2 - Reduction of Pd(II) by *D. fructosovorans*, wild type (white circles ○); [Fe]-only hydrogenase negative mutant (white lozenges ◇); [NiFe] hydrogenase negative mutant (black circles ●); double [Fe]-[NiFe] hydrogenase negative mutant (black triangles ▲); control, no cells (black squares ■); control, heat-killed cells (white squares □). The mass ratio Pd(II) dry biomass was 1:3; the test solution was 2 mM Na₂PdCl₄, in 0.1 M HNO₃; the electron donor 0.25 mM sodium formate. The final pH of the mixture after adding electron donor and the sample was 2.3. The cells were suspended in the mixture for 1 h prior to formate addition: the difference between the dosed Pd (II) and that analysed at the time of formate addition was contributable to biosorption by the biomass and remained constant in the heat-killed cells.

Figure 3 - TEM micrograph of initial stages of Pd(0) clusters growth within the periplasm of *D. fructosovorans* wild type cell (a), [Fe]-only hydrogenase negative mutant cell (b), [NiFe] hydrogenase negative mutant cell (c) and double [Fe]-[NiFe] hydrogenase negative mutant cell (d). The reaction stopped after 5 min of hydrogen

supply into the cell suspensions preincubated with 2 mM Na₂PdCl₄, pH 2.3. The magnification is 120 000[×].

Figure 4 - TEM micrograph of palladised 'periplasmically treated' wild type (a) and double mutant (b) *D. fructosovorans* cells. Pd(II) was reduced from 2 mM Na₂PdCl₄, pH 2.3 with hydrogen. The magnification is 120 000[×].

EXPERIMENTAL PART

The ability of sulphate-reducing bacteria (SRB) to reduce metallic ion species is a well-investigated phenomenon, and the involvement of microbial enzymes in this process has been established for many metals. Microbial enzyme-mediated reduction of Cr(VI), Se(VI), As(V), Tc(VII) and other metals has been reported for several species of bacteria during the last decade.

The growth of anaerobic sulphate-reducing *Desulfovibrio* species is based on the reduction of sulphate as the terminal electron acceptor and these organisms can utilise hydrogen as the sole source of electrons and energy (Brandis et al., 1981). Hydrogen metabolism plays a central role in the energy-generating mechanisms of the SRB. The key enzymes in hydrogen metabolism are hydrogenases which catalyse the reversible redox reaction: $H_2 \leftrightarrow 2H^+ + 2e^-$ (Fauque et al., 1988).

Three types of hydrogenase have been isolated from various *Desulfovibrio* species and have been characterised in detail (Casalot et al., 2002; Fauque et al., 1988). The presence of one periplasmic [NiFe] hydrogenase, which represents about 1 % of the total periplasmic proteins, one periplasmic [Fe] hydrogenase and one cytoplasmic heterotetrameric NADP-reducing hydrogenase (Malki et al., 1995) was previously established in *D. fructosovorans*.

In order to elucidate the importance of these hydrogenases in the energy-generating metabolism of *D. fructosovorans*, mutant strains were produced by marker exchange mutagenesis of the genes encoding [NiFe] hydrogenase (Rousset et al., 1991) and the NADP-reducing hydrogenase (Malki et al., 1997). It was demonstrated that the single- and double- mutants were able to grow on organic substrates and on medium containing hydrogen as the sole energy source (Malki et al., 1997). It was suggested that

growth under these conditions was possible due to the presence of the periplasmic [Fe]-only hydrogenase. Later a strain of *D. fructosovorans* lacking all three hydrogenases was constructed using marker exchange mutagenesis (Casalot et al., 2002). The triple hydrogenase negative mutant grew more slowly than the wild type although there were
5 no major differences in growth compared to the double mutant strain (Malki et al., 1997). The growth of the triple mutant in medium with H₂ as the sole electron donor can only be explained by the presence of an enzyme able to split hydrogen. This helped to establish the presence of a fourth hydrogenase in *D. fructosovorans*.

A focus of the present invention is to investigate the hydrogenase-dependent
10 reduction of Pd(II) under acidic conditions using wild type *D. fructosovorans* and to study the involvement of hydrogenase in Pd(II) reduction using specific periplasmic hydrogenase-negative mutant strains ([Fe]-hydrogenase, [NiFe]-hydrogenase and double [Fe]-[NiFe] negative mutant).

MATERIAL AND METHODS

15

Preparation of the mutant strains

1) Deletion of the [NiFe] hydrogenase encoding genes and construction of the MR400 strain and derivatives (Figure 1A)

The 7-kb fragment that contains the [NiFe] hydrogenase operon (*hynA,B,C*), was
20 digested with *MluI*, blunt-end repaired and ligated with the *SmaI*-digested 1.4-kb fragment containing the Kn^r gene (*npt*). The resulting construction was cloned into a suicide vector and introduced into *Desulfovibrio fructosovorans* wild-type strain (DSM3604). Recombinant strains were selected on culture medium containing
25 Kanamycin. One clone, named MR400, has been isolated and characterised.

2) Deletion of the [Fe] hydrogenase encoding genes and construction of the DF400 strain and derivatives (Figure 1B)

The gentamicin resistance gene (*accI*) was obtained by PCR amplification
30 performed on using two oligonucleotides designed to introduce the *BspEI* and *BstEII* restriction sites. The 5-kb fragment that contains the [Fe] hydrogenase operon (*hydA,B*), was digested with *BspEI* and *BstEII* and ligated with the *BspEI/BstEII*-digested 1.4-kb fragment containing the Gm^r gene (*accI*). The resulting construction was cloned into a suicide vector and introduced into *D. fructosovorans* wild-type strain (DSM3604) and

D. fructosovorans MR400 strain described above. Recombinant strains were selected on culture medium containing Genatamicin. One clone, named SF, deriving from the wild-type strain has been isolated and characterised. Another clone, named DF400, deriving from the MR400 strain has been isolated and characterised.

5

Bacterial Strains and Growth Conditions

Mutants of *D. fructosovorans* were constructed using marker exchange mutagenesis (Rousset et al., 1991). *D. fructosovorans* wild type and strains carrying a deletion in the [NiFe] hydrogenase operon (Rousset et al., 1991) and [Fe] hydrogenase operon and the double [Fe]-[NiFe] hydrogenase-negative mutant were grown
10 anaerobically at 37°C in SOS medium (Rousset et al., 1998). Cells were grown in 2 litre septum-stoppered serum bottles.

Preparation of resting cells

The cells were harvested at 48 hours after inoculation ($OD_{600} = 2.100$) by centrifugation in air (8000 rpm, Beckman G2-21M/E centrifuge, 20 min). The obtained pellet was washed in 20 mM N-morpholinopropanesulfonic acid (MOPS)-NaOH buffer, pH 7.0, three times. After the final wash the cells were centrifuged as before and the pellets were resuspended in 50 ml of 20 mM MOPS-NaOH buffer, pH 7.0. Aliquots of
20 the suspension were used for assay of hydrogenase activity, Pd(II) reduction tests and for preparation of "periplasmically treated cells" (see below).

Pd(II) assay

Pd(II) concentration in solutions was estimated spectrophotometrically by measuring the concentration of the yellow coloured $[PdCl_4]^{2-}$ complex ion at A_{420} . The maximum height of the specific absorption peak of $[PdCl_4]^{2-}$ at 420 nm is proportional to the palladium concentration. This method was confirmed using an assay based on $SnCl_2/HCl$ (Dasages, 1978) with the latter method in turn cross-checked using polarographic analysis (Yong et al., 2002). The three methods gave identical results.
25

30

Pd(II) reduction

A solution of Na_2PdCl_4 (10 ml of 2 mM in 0.01 M HNO_3 , pH 2.2) was degassed under oxygen free nitrogen (OFN) in butyl rubber septum-sealed vials. Resting cell suspensions of each strain were added anaerobically to the Pd(II) solution in the ratio of

3 parts dry weight of biomass (estimated by a pre-determined conversion from the OD₆₀₀ of the suspension) to 1 one part of Pd(II) by mass and left to biosorb Pd(II) at 30°C. After one hour, aliquots of the cell suspensions in the Pd(II) solution were withdrawn and centrifuged (13000 rpm for 3 min, Heraeus Biofuge pico). The supernatants were analysed to quantify Pd(II) remaining in solution after biosorption but prior to reduction. Pd(II) bioreduction was initiated via addition of the electron donor (20 mM sodium formate solution, pH 7.0). The final pH of the reaction mixture was 2.3. The reaction was carried out anaerobically at 30°C with samples withdrawn at 20 min intervals. The residual concentration of Pd in the supernatant was measured and plotted as a function of time. All experiments were done in triplicate; the experimental error was within 5% of the mean throughout.

Preparation of 'periplasmically-treated' (PT) cells

In order to prepare the wild type *D. fructosovorans* cells containing only membrane-bound hydrogenase, the periplasmic proteins were extracted from the cells using a modification of the procedure developed by Badzoin and Thauer as described in Hatchikian et al. (1990). Cells of wild type *D. fructosovorans* and the double mutant, used as a reference strain, were treated simultaneously. Approximately 1 g wet weight of freshly harvested cells (by centrifugation: 8 000 rpm at 4°C, 25 min Beckman G2-21M/E centrifuge) was resuspended in 100 ml of 50 mM Tris-HCl buffer, pH 9, containing 50 mM EDTA and 170 mM Na₂CO₃. The ratio of wet cell mass to the volume of the buffer was 10 times higher compared to the original method to ensure maximum extraction of periplasmic proteins. The suspensions were stirred gently for 30 min at 35°C and then centrifuged at 25 000 g for 30 min. The cells were resuspended in the same buffer and the treatment was repeated. The periplasmic proteins were retained in the combined supernatants (Hatchikian et al., 1990). The periplasmically-treated cells were resuspended in 20 mM MOPS buffer, pH 7.0, and used to reduce palladium (II) in parallel with untreated controls. The supernatants were concentrated (from 200 ml to 5 ml) using Millipore ultrafiltration polyethersulfone 76 mm diameter membranes (nominal molecular weight cut-off 30 000) under nitrogen pressure for estimation of extracted periplasmic hydrogenase activity. The hydrogenase activity of suspensions of 'periplasmically' treated cells was also measured.

Preparation of membrane extracts

Freshly thawed cells were passed twice in a French pressure cell at 1,000 lb/in² pressure in the presence of a few crystals of DNase. Cell debris were removed by centrifugation at 4,000 x g for 30min, and the supernatant (crude extract) was then centrifuged at 120,000 x g for 2 h. The membrane fraction that was collected in the pellet was used to reduce palladium (II).

Assay of Hydrogenase Activity

The total hydrogenase activity (as H₂ uptake) of *D. fructosovorans* resting cell suspension was quantified by spectrophotometric measurement of the reduction of methyl viologen at 30°C (Fernandez et al., 1985). One ml of 1 mM methyl viologen in 50 mM Tris-HCl buffer, pH 8.0, containing 1 mM EDTA (to render the cell outer membrane permeable) was degassed in an air-tight quartz cuvette. The solution was then saturated with H₂ and 1 µl of sodium dithionite saturated aqueous solution was added to eliminate the traces of O₂. The reaction was initiated by adding 2 µl of sample and the reaction was followed at A₆₀₄. One unit of hydrogenase activity is the amount of enzyme which catalyses the reduction of 2 µM methyl viologen per minute. Alternatively, in the case where hydrogenase activity of the cell suspension was estimated, enzyme activity was expressed in µM H₂ consumed per minute per 10⁹ cells. In order to establish whether the periplasmic [NiFe] hydrogenase from *D. fructosovorans* retains its activity at low pH, a purified (following the procedure reported previously (Rousset et al., 1998) periplasmic [NiFe] hydrogenase was used in the following experiments. A solution of purified enzyme (initial protein concentration 26 mg/ml) was mixed with 20 mM glycine-HCl buffer, pH 2.2, in a 1:10 (v/v) ratio, degassed, and left to stand. After one hour, the hydrogenase activity was measured with 1 mM methyl viologen as above in 50 mM Tris-NCl buffer, pH 8.0. Hydrogenase activity was also measured in the 20 mM glycine-HCl buffer, pH 2.2. In this case, reduction of the high-potential compound phenazine methosulfate was used instead of low-potential methyl viologen, and reduction was monitored spectrophotometrically at 387 nm.

Electron microscopy and Energy dispersive X-ray (EDS) analysis

Samples of Pd-loaded bacteria were fixed in 2.5% (wt/vol) aqueous glutaraldehyde and were resin-embedded following a standard dehydration procedure

(Yong et al., 2002a). Microtome-cut sections 100-150 nm thick were placed on copper grids and viewed with a JEOL 120CX2 transmission electron microscope fitted with a Link ISI EDX system for Pd detection (Lloyd et al., 1999).

5

RESULTS

Stability of hydrogenase activity at acidic pH

10 Biorecovery of Pd(II) from solution was shown previously to be optimal if an initial biosorption step at pH 2-3 (30-60 min) preceded hydrogenase mediated metal reduction (Yong et al., 2002). The conditions for biosorption were defined by de Vargas et al. (2004), but the stability of the bacterial hydrogenase to exposure to acidic pH has not been established previously.

15 Measurement of hydrogen consumption by purified periplasmic [NiFe] hydrogenase from *D. fructosovorans* (pre-incubated in 20 mM glycine-HCl buffer, pH 2.2, for 1 hour) showed that the enzyme retained approximately 32 % of its initial activity following exposure to acidic conditions, but no enzyme activity was detected following 2 hours of pre-incubation in the acidic buffer. The enzyme activity in this case was estimated via reduction of methyl viologen in Tris-HCl buffer, pH 8.0.

20 The purified hydrogenase was also active in the test with 25 μ M phenazine methosulfate in 20 mM glycine-HCl buffer pH 2.2, where the activity was 8.23 ± 0.21 mA₃₈₇/min/mg protein.

Hydrogenase activity of periplasmic extracts and 'periplasmically treated' cells

25

The hydrogenase activity of the periplasmic protein extracted from the wild type cells was 0.416 μ M H₂ consumed/min/mg protein whereas that of the extract from the double mutant was zero, confirming the lack of contamination of the periplasmic extract by the membrane-bound enzyme and confirming maintenance of cellular integrity. The hydrogenase activity of wild type and double mutant cell suspensions after extraction of periplasmic proteins ('periplasmically treated cells') was 0.00701 ± 0.0015 and 0.00661 ± 0.0018 respectively, which is comparable with the activity of untreated double mutant cell suspension (0.00684 ± 0.0004).

30

Hydrogenase activity and Pd(II) reduction by parent and mutant strains

The total hydrogenase activity of resting cell suspensions of the wild type and mutant strains was estimated (Table 1).

Table 1

The hydrogenase activity of *D. fructosovorans* resting cell suspensions used for Bio-Pd reduction (H₂ uptake methyl viologen test).

Strain	Wild type	[Fe] hydrogenase negative mutant	[Ni-Fe] hydrogenase negative mutant	[Fe] – [Ni-Fe] hydrogenase negative mutant
A_{HD} , $\mu\text{M H}_2$ consumpt/min. 10^9 cells $\pm$ SEM, (% of wild type catalytic activity)	0.202 ± 0.014 (100%)	0.169 ± 0.013 (83.7%)	0.0273 ± 0.0026 (13.5%)	$0.00684 \pm 4.46.10^{-4}$ (3.4%)

Hydrogenase activity $A_{HD} = \mu\text{mol H}_2$ consumed/min/ 10^9 cells. $OD_{600} = 1.00$ corresponds to 10^8 cells/ml.

The enzyme activity was consistent with the amount of enzyme expressed according to the genetic structure of the strains. The total hydrogenase activity of [Fe]- and [NiFe]-hydrogenase negative mutants was, accordingly, 83.7 % and 13.5 % of the hydrogenase activity of wild type cell suspension. The hydrogenase activity of the double mutant suspension, attributable to cytoplasmic-bound hydrogenase, comprised 3.4 % of that of wild type strain and agreed with residual amount in 'periplasmically treated' cells.

The bioreduction of Pd(II) by the parental strain of *D. fructosovorans* and its [Fe]-only, [NiFe]- and double [Fe]-[NiFe]-hydrogenase negative was compared using Na₂PdCl₄ at pH 2.3 (Figure 2). Reduction of Pd by sodium formate alone was used as a control. Figure 2 shows that the wild type and all mutant strains initially reduced Pd(II) at approximately the same rate but after approximately 40 minutes Pd(II) reduction by the [NiFe]- and double mutant strains was slightly higher. Identical results were obtained using cell suspension sparged with H₂. Sodium formate was used in order to quantify the amount of reducing agent in the reaction mixture, which was more difficult to achieve using hydrogen.

Examination of palladised cells

Palladised biomass was obtained by reducing palladium (II) using the wild type and [Fe]-, [NiFe]- and [Fe]-[NiFe] double hydrogenase negative mutants under acidic conditions (mimicking the pH of industrial waste solutions) from 2 mM Na₂PdCl₄ at pH 2, with hydrogen as a reducing agent. In order to observe the initial stage of Pd(0) cluster growth in the wild type and double mutant cells Pd(II) reduction was stopped after 5 minutes via termination of hydrogen supply through the solution and substituting with N₂. Pd(0) was visible within the periplasmic space of the parent and [Fe] hydrogenase mutant strains (Fig. 3a,b). EDX analyses of all preparations confirmed that the black precipitate associated with the cells was Pd(0) (Lloyd et al., 1998). Pd(0) clusters were distributed randomly through the whole width of the periplasm in the wild type and [Fe]-hydrogenase negative mutant cells (Fig. 3a, 3b), whereas in the [NiFe]-hydrogenase negative mutant (Fig. 3c) and double mutant cells (Fig. 3d) they were localised on the cytoplasmic membrane.

In both the double mutant and the wild type “periplasmically-treated” cells, from which soluble periplasmic hydrogenases had been extracted, Pd(0) clusters were associated with the inner cytoplasmic membrane (Fig. 4). These are similar to the Pd(0) deposits observed on the inner cytoplasmic membrane of intact double mutant cells (Fig. 3d).

DISCUSSION

Microbial Pd(II) reduction is not only of theoretical interest but also has a potential application in palladium recovery from waste solutions. Industrial Pd(II)-containing waste solutions are usually fairly acidic since in many cases they are prepared using aqua regia (mixture of hydrochloric acid and nitric acid) for precious metal leaching from solid wastes (Yong et al., 2002). This study showed that 30% of the activity of purified [NiFe] hydrogenase from *D. fructosovorans* is retained after one hour preincubation at pH 2.2; although whether the similar decreasing of activity under the same conditions was attributable equally to other two hydrogenases was not tested (Table 1 shows the relative activities of the three hydrogenases in untreated cells).

The fact that purified [Ni-Fe] hydrogenase was exposed to glycine-HCl buffer, pH 2.2, for one hour and remained active demonstrated in principle its resistance to acidic

conditions; the enzymes could be more pH-stable in their cellular locations. The one hour period was chosen because it was estimated to be the optimal time for pre-incubation of the resting cells with Pd(II)-containing industrial waste solution (pH about 2) to achieve biosorption of the $[\text{PdCl}_4]^{2-}$ complex onto the protonated biomass prior to bio-reduction (Yong et al., 2002). The working pH 2.2 is consistent the usual pH of precious metal wastes. According to de Vargas et al. (2004), biosorption of Pd (II) onto *D. desulfuricans* at pH 0.1-3.0 in HNO_3 background was achieved after 30 min, the time taken to reach equilibrium. During the pre-incubation period, the hydrogenase retained its structure, which was monitored visually as the brown colour of the enzyme solution (the denaturated enzyme loses Fe atoms and becomes colourless). After two hours exposure, the enzyme demonstrated no hydrogenase activity, possibly due to degradation. The residual activity (if to assume that hydrogenase was affected by low pH within the resting cell) after one hour was sufficient to achieve good Pd(II) removal.

The purified [Ni-Fe] hydrogenase was also active at pH 2.2 when its activity was measured using the high potential phenazine-methosulfate. In all cases prior to activity measurements the enzyme was activated with hydrogen as in Hatchikian et al. (1990). These results suggest that periplasmic hydrogenases *in vivo* within resting cells remain active during pre-incubation of the biomass with low pH palladium-containing solutions and can work effectively at pH 2.3.

Comparison of Pd(II) bioreduction by wild type *D. fructosovorans* and the [Fe]-only, [NiFe]- and double [Fe]-[NiFe]-hydrogenase negative mutants after pre-incubation at low pH showed that the initial rate of Pd(II) reduction was similar. After approximately 1 hour in the presence of formate, Pd(II) reduction by [NiFe]- and double mutants was slightly higher (Figure 2) than that by the wild type and [Fe]-only negative mutant. No correlation was observed between the initial hydrogenase activity of the strains and their Pd(II) reducing activity. This to be expected since only nucleation and initiation of the palladium crystals is dependent on hydrogenase activity whereas subsequent crystal growth is due to auto-catalytic reduction of palladium (Yong et al., 2002).

Electron microscopy of the initial stage of cellular palladisation revealed peculiarities of palladium deposition onto the cell surface depending on the mutant used. The most obvious difference was between wild type and [NiFe]-hydrogenase negative mutant and double mutant. In the wild type cells, Pd(0) clusters were distributed randomly throughout the periplasm (Fig. 3a) whereas in the double mutant

cells, which lack soluble periplasmic hydrogenases and contain only a single cytoplasmic membrane bound [NiFe]-hydrogenase (Casalot et al., 2002), Pd clusters were clearly associated with the inner cytoplasmic membrane (Fig. 3d). A similar pattern of Pd crystal distribution was observed in the [NiFe] hydrogenase negative mutant (Fig. 3c), which retained only 13.5 % of its periplasmic hydrogenase activity compared to the parental strain. Removal of the minor periplasmic [Fe]-only hydrogenase appeared to have little effect on the localisation of Pd(0), probably attributable to the predominance of the periplasmic [NiFe] hydrogenase, but quantitative assays were not attempted since the retention of activity of each of the enzymes at pH 2.2 was not attempted.

The localisation of palladium crystals on the inner cytoplasmic membrane is coincident with the localisation of this hydrogenase suggesting that the enzyme serves as a nucleation site for palladium particle growth, probably by supplying the electrons for the initial Pd(II) reduction.

In order to verify this suggestion, 'periplasmically-treated' cells of the wild type and double mutant were used for palladisation. These cells were depleted of periplasmic soluble proteins and left with only membrane-bound periplasmic hydrogenase. Analysis of hydrogenase activity of the soluble proteins extract from the parental strain demonstrated hydrogenase activity whereas the double mutant extract did not. This indicated that the inner cytoplasmic membrane remained intact and prevented extraction of cytoplasmic hydrogenase and membrane-bound hydrogenases.

Periplasmically-treated cells were palladised at pH 2.3 and the distribution of Pd clusters was observed using TEM. In periplasmically-treated cells of both the wild type and the double mutant Pd(0) clusters were associated with the inner cytoplasmic membrane (Fig. 4), similar to the pattern observed in intact double mutant cells (Fig. 3d). This again suggests that the localisation of Pd(II) reduction is associated with the localisation of membrane-bound hydrogenase in the double mutant cells and the periplasmically treated wild type cells.

In conclusion, the data obtained show that in the parent strain Pd(0) nucleation could occur at both membrane and periplasmic loci, whereas in the double mutant the nucleation sites would be confined to the cytoplasmic membrane (Fig. 3a,d).

REFERENCES

- 5 – Baxter-Plant VS, Mikheenko IP, Macaskie LE (2003) Sulphate reducing bacteria, palladium and reductive dehalogenation of chlorinated aromatic compounds. *Biodegradation* **14**: 83-90,
- Brandis A , and Thauer RK (1981) Growth of *Desulfovibrio* species on hydrogen and sulfate as sole energy source. *J.Gen. Microbiol.* **126**: 249–252,
- 10 – Casalot L, de Luca G, Dermoun Z, Rousset M and de Philip P (2002) Evidence for a fourth hydrogenase in *Desulfovibrio fructosovorans*. *J. Bacteriol.* **184**: 853–856,
- Dasages GC (1978) Absorptiometriques des elements mineraux. Masson Ed. Paris,
- de Vargas I, Macaskie LE and Guibal E (2004) Biosorption of palladium and platinum by sulfate-reducing bacteria. *J. Chem. Technol. Biotechnol.* **79**: 49-56,
- 15 – Fauque G, Peck DH, Huynh BH, Berlier Y, Dervatanian DV, Texeira M, Przybyla AE, Lespinat PA, Moura I and LeGall J (1988) The three classes of hydrogenases from sulfate-reducing bacteria of the genus *Desulfovibrio*. *FEMS Microbiol. Rev.* **54**: 299–344,
- 20 – Fernandez VM, Hatchikian EC and Cammack R (1985) Properties and reactivation of two different deactivated forms of *Desulfovibrio gigas* hydrogenase. *Biochim. Biophys. Acta.* **832**: 69-79,
- Ganesh R, Robinson KG, Chu L, Kucsmas D, Reed GD (1999) Reductive precipitation of uranium by *Desulfovibrio desulfuricans*: Evaluation of contaminant effects and elective removal. *Water Research* **33**: 3447-3458,
- 25 – Hatchikian CE, Traore A, Fernandez VM and Cammack R (1990) Characterization of the nickel-iron periplasmic hydrogenase from *Desulfovibrio fructosovorans*. *Europ. J. of Biochem.* **187**: 635-643,
- Hatchikian CE, Traore A, Fernandez VM and Cammack R (1990). Characterization of the nickel-iron periplasmic hydrogenase from *Desulfovibrio fructosovorans*. *Europ. J. of Biochem.* **187**: 635-643,
- 30

- Henry CR (1998) Surface studies of supported model catalysts. *Surf Science Reports* **31**:235-325,
- Hoffman JE (1988) Recovering platinum-group metals from auto catalysts. *J Metals* **88**: 40-44,
- 5 – Lloyd JR, Cole JA, Macaskie LE (1997) Reduction and removal of heptavalent technetium from solution by *Escherichia coli*. *J. Bacteriol* **179**: 2014 –2021,
- Lloyd JR, Harding CL, Macaskie LE (1997a) Reduction and accumulation of Tc(VII) by immobilized cells of *Escherichia coli* in a hollow fibre reactor. *Biotechnol Bioeng* **55**: 505-510,
- 10 – Lloyd JR, Nolting HF, Sole VA, Bosecker K, Macaskie LE (1998) Technetium reduction and precipitation by sulphate-reducing bacteria. *Geomicrobiol J* **15**: 43-58,
- Lloyd JR, Yong P, Macaskie LE (1998) Enzymatic recovery of elemental palladium by using sulfate-reducing bacteria. *Appl Environ Microbiol* **64**: 4607-4609,
- Lloyd JR, Ridley J, Khizniak T, Lyalikova NN, Macaskie LE (1999) Reduction
15 of technetium by *Desulfovibrio desulfuricans*: biocatalyst characterization and use in a flowthrough bioreactor. *Appl Environ Microbiol* **65**: 2691-2696,
- Lloyd JR, Thomas GH, Finlay JA, Cole JA, Macaskie LE (1999a) Microbial reduction of technetium by *Escherichia coli* and *Desulfovibrio desulfuricans*: enhancement via the use of high-activity strains and effect of process parameters.
20 *Biotechnol Bioeng* **66**: 122-130,
- Lloyd JR, Mabbett AN, Williams DR, Macaskie LE (2001) Metal reduction by sulphate-reducing bacteria: physiological diversity and metal specificity. *Hydrometallurgy* **59**: 327-337.
- Lovely DR, Phillips EJP (1992) Reduction of uranium by *Desulfovibrio desulfuricans*. *Appl Environ Microbiol* **54**:1472-1480,
25
- Mabbett NA (2001) The reduction and recovery of Cr(VI) from industrially polluted waste waters using sulphate-reducing bacteria, PhD Thesis, University of Birmingham, UK,
- Malki S, Saimmaime I, De Luca G, Rousset M, Dermoun Z and Bélaich J-P
30 (1995) Characterization of an operon encoding a NADP-reducing hydrogenase in *Desulfovibrio fructosovorans*. *J. Bacteriol.* **177**: 2628-2636,
- Malki S, de Luca G, Fardeau ML, Rousset M, Belaich J-P and Dermoun Z (1997) Physiological characteristics and growth behavior of single and double hydrogenase mutants of *Desulfovibrio fructosovorans*. *Arch. of Microbiol.* **167**: 38-45,

– Menon NK, Robbins J, Wendt JC, Shanmugam, KT, Przybyla AE (1991) Mutational analysis and characterization of *Escherichia coli* *hya* operon, which encodes [NiFe] hydrogenase 1. *J Bacteriol* **173**: 4851-4861,

– Mertig M, Kirsch R, Pompe W (1998) Biomolecular approach to nanotube fadrication. *Appl Phys A* **66**: S723-727,

– Peck HD (1993) Bioenergetic strategies of the sulphate-reducing bacteria. In Odom JM, Singleton R. (eds.). *Sulfate-Reducing Bacteria: Contemporary Perspectives*. New York: Springer-Verlag,

– Platinum (2003) Interim Review. Johnson Matthey. November, 2003,

– Postgate JR (1979) *The Sulphate-Reducing Bacteria*. Cambridge, UK: University Press,

– Rousset M, Dermoun Z, Chippaux M and Bélaich J-P (1991) Marker exchange mutagenesis of the *hydN* genes in *Desulfovibrio fructosovorans*. *Molec. Microbiol.* **5**: 1735-1740,

– Rousset M, Casalot L, Rapp-Giles BJ, Dermoun Z, de Philip P, Be'laich J-P and Wall JD (1998) New shuttle vectors for the introduction of cloned DNA in *Desulfovibrio*. *Plasmid*. **39**: 114-122,

– Sauter M, Bohm R, Bock A (1992) Mutation analysis of the operon (*hyc*) determining hydrogenase 3 formation in *Escherichia coli*. *Mol Microbiol* **6**: 1523–1532,

– Spear JR, Figueroa LA, Honeyman BD (1999) Modelling the removal of uranium U(VI) from aqueous solutions in the presence of sulphate-reducing bacteria. *Environ Science Technol* **33**: 2667-2675,

– Tucker MD, Barton LL, Thomson BM (1998) Reduction of Cr, Mo, Se and U by *Desulfovibrio desulfuricans* immobilized in polyacrylamide gels. *J of Industrial Microbiol Biotechnol* **20**: 13-19,

– Vignais PM, Billoud B, Meyer M (2001) Classification and phylogeny of hydrogenases. *FEMS Microbiol. Rev.* **25**: 455-501,

– Wahl R, Mertig M, Raff J, Selenska-Pobell S, Pompe W (2001) Electron-beam induced formation of highly ordered palladium and platinum nanoparticle arrays on the S layer of *Bacillus sphaericus* NCTC 9602. *Adv Mater* **13**: 736–74025,

– Yong P, Rowson NA, Farr J.P, Harris IR, Macaskie LE (2002) Bioaccumulation of palladium by *Desulfovibrio desulfuricans*. *J Chem Technol Biotechnol* **77**:1-9,

– Yong P, Farr JPG, Harris IR, Macaskie LE (2002a) Palladium recovery by immobilized cells of *Desulfovibrio desulfuricans* using hydrogen as the electron donor in a novel electrobioreactor. *Biotechnol Lett* **4**: 205-212,

5 – Yong P, Rowson NA, Farr J.P, Harris IR, Macaskie LE (2002b) Bioreduction and bio-crystallisation of palladium by *Desulfovibrio desulfuricans* NCIMB 8307. *Biotechnol Bioeng* **80**: 369-379,

– Yong P, Rowson NA, Farr J.P, Harris IR, Macaskie LE (2003) A novel biotechnology for the recovery of precious metals from spent automotive catalyst. *Environ Technol* **24**:289-297.

CLAIMS

1. The use of a bacterium strain characterized in that its genome contains at least a gene coding for a membrane-bound [NiFe] hydrogenase, or of membrane extracts containing said membrane-bound [NiFe] hydrogenase of said bacterium strain, for the preparation of metallic biocatalysts, provided that in the case of the use of a bacterium strain the genome of which contains one or several genes coding for a soluble periplasmic hydrogenase, then said strain is transformed by inactivation, repression or deletion of at least one of said genes coding for a soluble periplasmic hydrogenase, the corresponding soluble periplasmic hydrogenase being then non produced or absent.

2. The use according to claim 1, of a bacterium strain, or of membrane extracts thereof, the genome of which containing a gene, represented by SEQ ID NO: 1, coding for a membrane-bound [NiFe] hydrogenase represented by the sequence SEQ ID NO: 2, or containing a gene coding for a sequence having at least 30% of identity with sequence SEQ ID NO: 2.

3. The use according to claim 1 or 2, of a bacterium strain, or of membrane extracts thereof, chosen among Eubacteria or Archaeobacteria.

4. The use according to any of claims 1 to 3, of a bacterium strain, or of membrane extracts thereof, chosen among:

* the following Eubacteria:

– *Desulfovibrio vulgaris*, the genome of which contains a gene represented by SEQ ID NO: 1 coding for a membrane-bound [NiFe] hydrogenase represented by SEQ ID NO: 2, and a gene represented by SEQ ID NO: 3 coding for a membrane-bound [NiFe] hydrogenase represented by SEQ ID NO: 4,

– *Desulfovibrio fructosovorans*, the genome of which contains a gene represented by SEQ ID NO: 5 coding for a membrane-bound [NiFe] hydrogenase having 70% of identity with sequence SEQ ID NO: 2, said hydrogenase being represented by SEQ ID NO: 6,

– *Desulfovibrio gigas*, the genome of which contains a gene represented by SEQ ID NO: 7 coding for a membrane-bound [NiFe] hydrogenase having 74% of identity with sequence SEQ ID NO: 2, said hydrogenase being represented by SEQ ID NO: 8,

– *Thermoanaerobacter tengcongensis*, the genome of which contains a gene represented by SEQ ID NO: 9 coding for a membrane-bound [NiFe] hydrogenase having 63% of identity with sequence SEQ ID NO: 2, said hydrogenase being represented by SEQ ID NO: 10, and contains a gene represented by SEQ ID NO: 11 coding for a membrane-bound [NiFe] hydrogenase having 38% of identity with sequence SEQ ID NO: 2, said hydrogenase being represented by SEQ ID NO: 12,

– *Rhodospirillum rubrum*, the genome of which contains a gene represented by SEQ ID NO: 13 coding for a membrane-bound [NiFe] hydrogenase having 41% of identity with sequence SEQ ID NO: 2, said hydrogenase being represented by SEQ ID NO: 14,

– *Escherichia coli*, the genome of which contains a gene represented by SEQ ID NO: 15 coding for a membrane-bound [NiFe] hydrogenase having 37% of identity with sequence SEQ ID NO: 2, said hydrogenase being represented by SEQ ID NO: 16, and contains a gene represented by SEQ ID NO: 17 coding for a membrane-bound [NiFe] hydrogenase having 35% of identity with sequence SEQ ID NO: 2, said hydrogenase being represented by SEQ ID NO: 18,

– *Erwinia carotovora*, the genome of which contains a gene represented by SEQ ID NO: 19 coding for a membrane-bound [NiFe] hydrogenase having 36% of identity with sequence SEQ ID NO: 2, said hydrogenase being represented by SEQ ID NO: 20,

– *Salmonella typhi*, the genome of which contains a gene represented by SEQ ID NO: 21 coding for a membrane-bound [NiFe] hydrogenase having 36% of identity with sequence SEQ ID NO: 2, said hydrogenase being represented by SEQ ID NO: 22,

– *Salmonella typhimurium*, the genome of which contains a gene represented by SEQ ID NO: 23 coding for a membrane-bound [NiFe] hydrogenase having 36% of identity with sequence SEQ ID NO: 2, said hydrogenase being represented by SEQ ID NO: 24,

– *Shigella flexneri*, the genome of which contains a gene represented by SEQ ID NO: 25 coding for a membrane-bound [NiFe] hydrogenase having 35% of identity with sequence SEQ ID NO: 2, said hydrogenase being represented by SEQ ID NO: 26,

– *Wolinella succinogenes*, the genome of which contains a gene represented by SEQ ID NO: 27 coding for a membrane-bound [NiFe] hydrogenase having 35% of

identity with sequence SEQ ID NO: 2, said hydrogenase being represented by SEQ ID NO: 28,

* the following Archaeobacteria:

– *Methanosarcina mazei*, the genome of which contains a gene represented by SEQ ID NO: 29 coding for a membrane-bound [NiFe] hydrogenase having 54% of identity with sequence SEQ ID NO: 2, said hydrogenase being represented by SEQ ID NO: 30,

– *Methanosarcina barkeri*, the genome of which contains a gene represented by SEQ ID NO: 31 coding for a membrane-bound [NiFe] hydrogenase having 53% of identity with sequence SEQ ID NO: 2, said hydrogenase being represented by SEQ ID NO: 32,

– *Pyrococcus abyssi*, the genome of which contains a gene represented by SEQ ID NO: 33 coding for a membrane-bound [NiFe] hydrogenase having 40% of identity with sequence SEQ ID NO: 2, said hydrogenase being represented by SEQ ID NO: 34, and contains a gene represented by SEQ ID NO: 35 coding for a membrane-bound [NiFe] hydrogenase having 38% of identity with sequence SEQ ID NO: 2, said hydrogenase being represented by SEQ ID NO: 36,

– *Pyrococcus horikoshii*, the genome of which contains a gene represented by SEQ ID NO: 37 coding for a membrane-bound [NiFe] hydrogenase having 39% of identity with sequence SEQ ID NO: 2, said hydrogenase being represented by SEQ ID NO: 38,

– *Pyrococcus furiosus*, the genome of which containing a gene represented by SEQ ID NO: 39 coding for a membrane-bound [NiFe] hydrogenase having 39% of identity with sequence SEQ ID NO: 2, said hydrogenase being represented by SEQ ID NO: 40,

– *Methanococcus jannaschii*, the genome of which contains a gene represented by SEQ ID NO: 41 coding for a membrane-bound [NiFe] hydrogenase having 36% of identity with sequence SEQ ID NO: 2, said hydrogenase being represented by SEQ ID NO: 42,

– *Methanococcus maripuladis*, the genome of which contains a gene represented by SEQ ID NO: 43 coding for a membrane-bound [NiFe] hydrogenase having 36% of identity with sequence SEQ ID NO: 1, and represented by SEQ ID NO: 44,

– *Methanopyrus kandleri*, the genome of which contains a gene represented by SEQ ID NO: 45 coding for a membrane-bound [NiFe] hydrogenase having 36% of identity with sequence SEQ ID NO: 2, said hydrogenase being represented by SEQ ID NO: 46,

5 – *Methanobacterium thermoautotrophicum*, the genome of which contains a gene represented by SEQ ID NO: 47 coding for a membrane-bound [NiFe] hydrogenase having 37% of identity with sequence SEQ ID NO: 2, said hydrogenase being represented by SEQ ID NO: 48,

10 – *Methanobacterium thermoformicium*, the genome of which contains a gene represented by SEQ ID NO: 49 coding for a membrane-bound [NiFe] hydrogenase having 37% of identity with sequence SEQ ID NO: 2, said hydrogenase being represented by SEQ ID NO: 50, and contains a gene represented by SEQ ID NO: 51 coding for a membrane-bound [NiFe] hydrogenase having 33% of identity with sequence SEQ ID NO: 2, said hydrogenase being represented by SEQ ID NO: 52.

15 5. The use according to any of claims 1 to 4, of a bacterium strain characterized in that its genome contains at least a gene coding for a membrane-bound [NiFe] hydrogenase, but does not contain genes coding for a soluble periplasmic hydrogenase.

20 6. The use according to claim 5, of *E. coli*.

25 7. The use according to any of claims 1 to 4, of a bacterium strain characterized in that its genome contains at least a gene coding for a membrane-bound [NiFe] hydrogenase, and one or several genes coding for a soluble periplasmic hydrogenase, said strain being transformed by inactivation or deletion of at least one of said genes coding for a soluble periplasmic hydrogenase, the corresponding soluble periplasmic hydrogenase being then inactivated or deleted.

30 8. The use according to any of claims 1 to 4, of a bacterium strain characterized in that its genome contains at least a gene coding for a membrane-bound [NiFe] hydrogenase, and one or several genes coding for a soluble periplasmic hydrogenase, said strain being cultivated in such conditions that at least one of said

genes coding for a soluble periplasmic hydrogenase is repressed, the corresponding soluble periplasmic hydrogenase being then not produced.

9. The use according to claim 7, of a transformed bacterium strain chosen among *Desulfovibrio vulgaris*, *Desulfovibrio fructosovorans*, *Desulfovibrio gigas*, or *Desulfovibrio desulfuricans*, the genome of which being transformed by inactivation or deletion of at least one of said genes coding for a soluble periplasmic hydrogenase.

10. The use according to any of claims 7 to 9, of a bacterium strain the genome of which being transformed by deletion of at least one of said genes coding for a soluble periplasmic hydrogenase.

11. The use according to any of claims 7 to 10, of a *Desulfovibrio fructosovorans* strain transformed in such way that the gene represented by SEQ ID NO: 53 coding for the soluble periplasmic [NiFe] hydrogenase represented by SEQ ID NO: 54, and/or the gene represented by SEQ ID NO: 55 coding for the soluble periplasmic [Fe] hydrogenase represented by SEQ ID NO: 56, are deleted.

12. The use according to any of claims 7 to 11, of a transformed *Desulfovibrio fructosovorans* strain wherein the gene represented by SEQ ID NO: 53 is deleted.

13. The use according to claim 12, of the transformed *Desulfovibrio fructosovorans* strain MR400, which was deposited on the January 11th, 2005 at the Collection Nationale de Cultures de Microorganismes (CNCM) of the Institut Pasteur under the number I-3349.

14. The use according to any of claims 7 to 11, of a transformed *Desulfovibrio fructosovorans* strain wherein the genes represented by SEQ ID NO: 53 and SEQ ID NO: 55 are both deleted.

15. The use according to claim 14, of the transformed *Desulfovibrio fructosovorans* strain DF400, which was deposited on the January 11th, 2005 at the Collection Nationale de Cultures de Microorganismes (CNCM) of the Institut Pasteur under the number I-3350.

16. The use according to claims 7 to 9, of a bacterium strain the genome of which being transformed by inactivation of at least one of said genes coding for a soluble periplasmic hydrogenase.

17. The use according to claim 16, of a bacterium strain the genome of which being transformed by inactivation of at least one of said genes coding for a soluble periplasmic hydrogenase, said inactivation being obtained by mutation of at least one amino acid of said genes, and selection of the corresponding mutated proteins encoded by said mutated genes exhibiting from 0.1% to 30% of the native soluble periplasmic hydrogenase activity.

18. The use according to claim 16 or 17, of a *Desulfovibrio fructosovorans* strain the genome of which being transformed by inactivation of the gene represented by SEQ ID NO: 53 coding for the soluble periplasmic [NiFe] hydrogenase represented by SEQ ID NO: 54, and/or of the gene represented by SEQ ID NO: 55 coding for the soluble periplasmic [Fe] hydrogenase represented by SEQ ID NO: 56.

19. The use according to any of claims 16 to 18, of a transformed *Desulfovibrio fructosovorans* strain wherein the gene represented by SEQ ID NO: 53 is inactivated by:

– mutation of the nucleotide(s) GAA in position 264 of SEQ ID NO: 53 by substitution of said nucleotide by GAC, leading to a mutated gene represented by SEQ ID NO: 57 encoding a mutated soluble periplasmic [NiFe] hydrogenase represented by SEQ ID NO: 58 and corresponding to the native sequence SEQ ID NO: 54 wherein the glutamate in position 25 is substituted by an aspartate, said mutated soluble periplasmic [NiFe] hydrogenase SEQ ID NO: 58 exhibiting from 30% to 60%, more particularly 45%, of the native soluble periplasmic hydrogenase SEQ ID NO: 54 activity,

– and/or mutation of the nucleotide(s) GAA in position 264 of SEQ ID NO: 53 by substitution of said nucleotide by CAG, leading to a mutated gene represented by SEQ ID NO: 59 encoding a mutated soluble periplasmic [NiFe] hydrogenase represented by SEQ ID NO: 60 and corresponding to the native sequence SEQ ID NO: 54 wherein the glutamate in position 25 is substituted by a glutamine, said mutated soluble periplasmic [NiFe] hydrogenase SEQ ID NO: 60 exhibiting from 0.05% to

0.2%, more particularly 0.1%, of the native soluble periplasmic hydrogenase SEQ ID NO: 54 activity,

– and/or mutation of the nucleotide(s) GAA in position 264 of SEQ ID NO: 53 by substitution of said nucleotide by GTC, leading to a mutated gene represented by SEQ ID NO: 61 encoding a mutated soluble periplasmic [NiFe] hydrogenase represented by SEQ ID NO: 62 and corresponding to the native sequence SEQ ID NO: 54 wherein the glutamate in position 25 is substituted by a valine, said mutated soluble periplasmic [NiFe] hydrogenase SEQ ID NO: 62 exhibiting from 8% to 15%, more particularly 10%, of the native soluble periplasmic hydrogenase SEQ ID NO: 54 activity.

20. The use according to any of claims 1 to 4, of membrane extracts containing at least one membrane-bound [NiFe] hydrogenase of bacterium strains as defined in claims 1 to 4.

21. The use according to claim 20, of membrane extracts such as obtained according to the following method, which comprises the following steps:

- centrifugation of fully grown cells and washing of these cells, in order to obtain a cell suspension,
- breaking of said cell suspension to obtain a crude extract, which is centrifuged at low speed to collect the bacterial debris, and then centrifuged for two hours at 50,000 rpm, in order to obtain a supernatant and a membrane pellet,
- discarding of said supernatant containing soluble proteins, and resuspension of said membrane pellet.

22. The use according to claim 20 or 21, of membrane extracts of *Desulfovibrio fructosovorans* such as obtained according to the method defined in claim 21.

23. The use according to any of claims 1 to 22, for the preparation of metallic biocatalysts chosen among the following precious metals: palladium, platinum, ruthenium, rhodium and iridium.

24. A process for the preparation of metallic biocatalysts comprising the following steps:

– bringing together bacterium strains, or transformed bacterium strains, or membrane extracts such as defined in any of claims 1 to 22, with a solution of a metal in oxidized form, for a time period sufficient to allow the initial sorption of the metal in oxidized form in said, bacterium strains, or transformed bacterium strains, or membrane extracts,

– bubbling of hydrogen gas through the solution such as obtained in the previous step, in order to allow the formation of a metal precipitate corresponding to the metal in reduced form, and recovering of said metal in reduced form.

25. A process according to claim 24, for the preparation of metallic biocatalysts chosen among the following precious metals: palladium, platinum, ruthenium, rhodium and iridium.

26. A process according to claim 24 or 25, for the preparation of palladium biocatalyst comprising the following steps:

– bringing together the DF400 strain such as defined in claim 15 with a solution of palladium in oxidized form Pd(II), especially a solution of Na_2PdCl_4 , for a time period sufficient to allow the initial sorption of Pd(II) in said strain,

– bubbling of hydrogen gas through the solution such as obtained in the previous step, in order to allow the formation of a palladium precipitate corresponding to the metal in reduced form Pd(0), and recovering of said palladium.

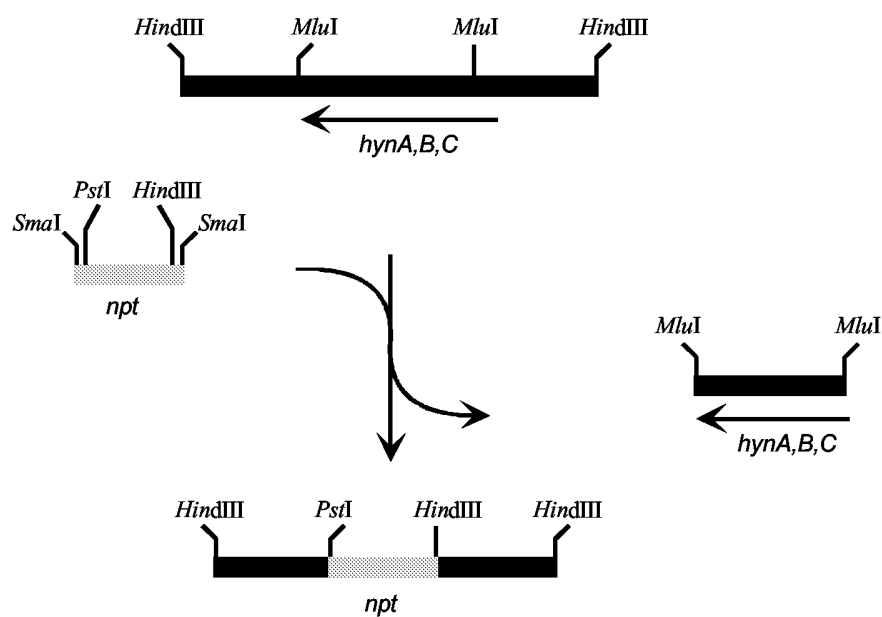


FIGURE 1A

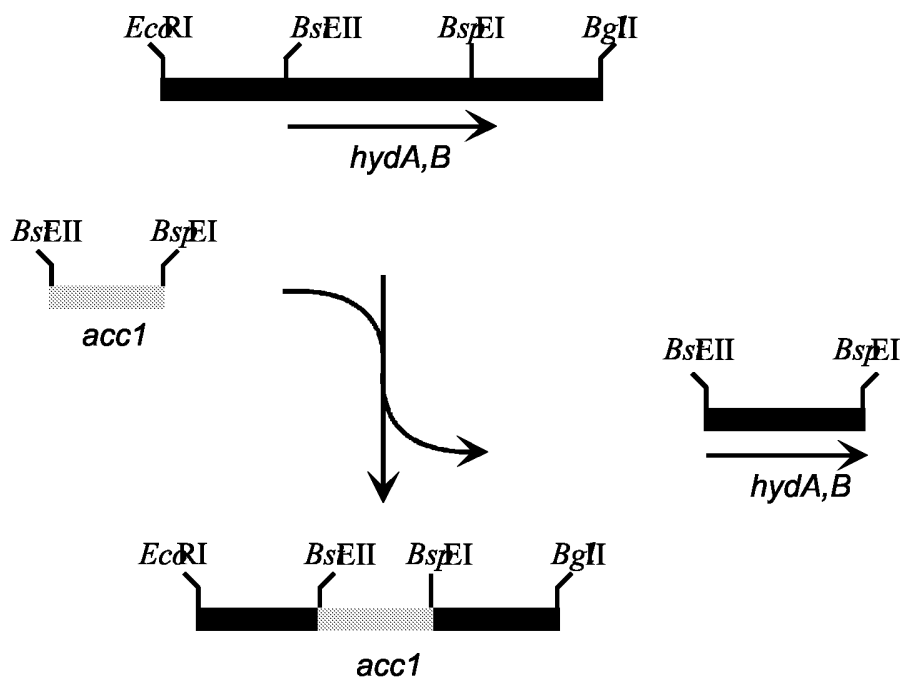


FIGURE 1B

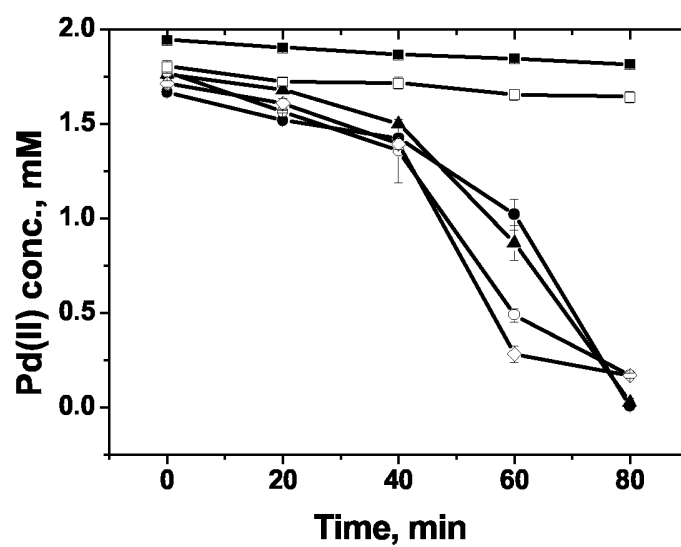


FIGURE 2

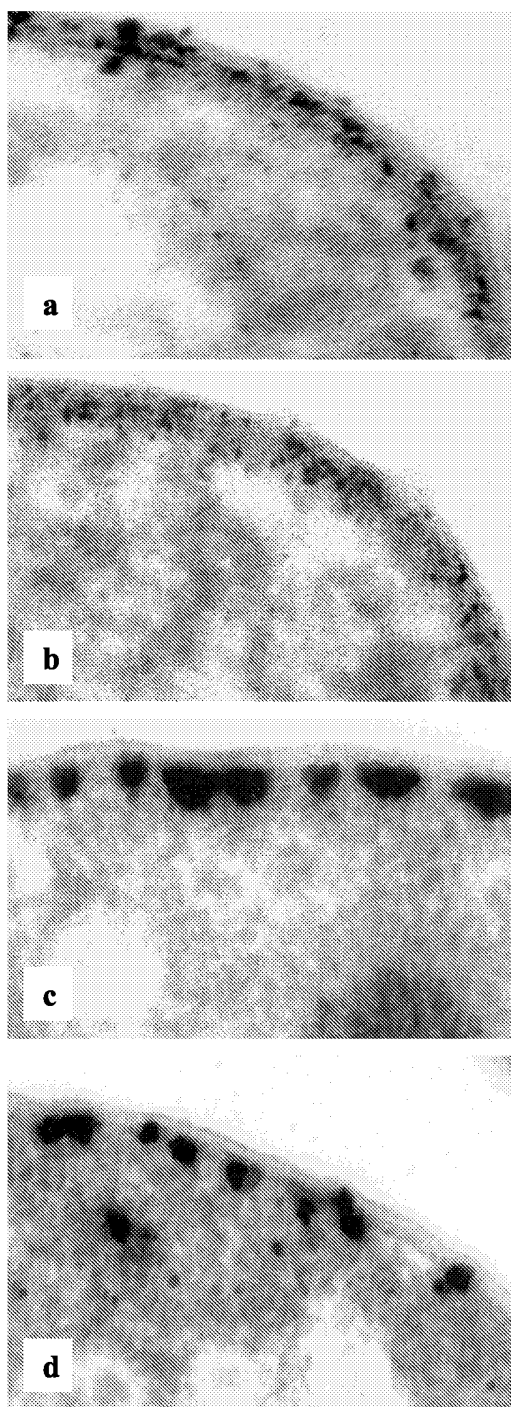


FIGURE 3

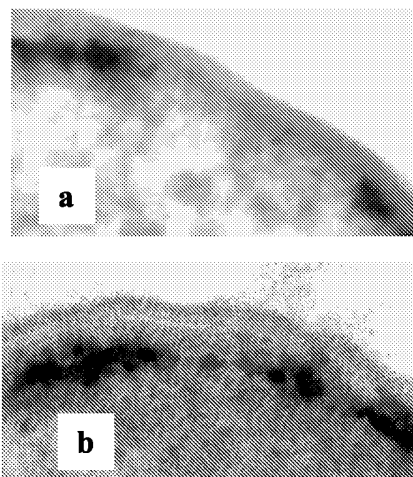


FIGURE 4

DESUanglais-seql.txt

SEQUENCE LISTING

<110> CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE

<120> USE OF BACTERIUM STRAINS FOR THE PREPARATION OF METALLIC BIOCATALYSTS, IN PARTICULAR FOR THE PREPARATION OF PALLADIUM BIOCATALYSTS

<130> IOB 04 CU CNR DESU

<160> 62

<170> PatentIn version 3.1

<210> 1

<211> 1077

<212> DNA

<213> Desulfovibrio vulgaris

<220>

<221> CDS

<222> (1)..(1077)

<223>

<400> 1

atg tcc cgc acc atc att cct ttc ggc ccg cag cat ccg gtt ctg ccg	48
Met Ser Arg Thr Ile Pro Phe Gly Pro Gln His Pro Val Leu Pro	
1 5 10 15	
gag ccc ctg cac ctg aag ctg gtc gtc gag gac gag acc gtg gtc gaa	96
Glu Pro Leu His Leu Lys Leu Val Val Glu Asp Glu Thr Val Val Glu	
20 25 30	
gcc att ccg gcc ctc ggc tac gtc cac cgc ggc ctc gag acc ctc gcc	144
Ala Ile Pro Ala Leu Gly Tyr Val His Arg Gly Leu Thr Leu Ala	
35 40 45	
tcc atc cgc gac tac aac cag atg gtc tac gtg gtc cgc gtg tgc	192
Ser Ile Arg Asp Tyr Asn Gln Met Val Tyr Val Val Glu Arg Val Cys	
50 55 60	
ggc atc tgc tcg tgc atc cac gcc atg tgc tac tgc cag tcg ctc gag	240
Gly Ile Cys Ser Cys Ile His Ala Met Cys Tyr Cys Gln Ser Leu Glu	
65 70 75 80	
tgc atg atg aac gtc gaa gtg ccc cgt cgc gcc aag gtc ctg cgc acc	288
Cys Met Met Asn Val Glu Val Pro Arg Arg Ala Lys Val Leu Arg Thr	
85 90 95	
atc tgg tcg gaa ctg cac cgt atc cac agc cac ctg ctg tgg ctc ggt	336
Ile Trp Ser Glu Leu His Arg Ile His Ser His Leu Leu Trp Leu Gly	
100 105 110	
ctc ttc gcc gac ggc ttc ggc ttc gag agc ctg ttc atg cag ttc tgg	384
Leu Phe Ala Asp Gly Phe Gly Phe Glu Ser Leu Phe Met Gln Phe Trp	
115 120 125	
aaa gtg cgc gag cgc gtc atg gac atc aac gaa gcc aca gcg ggc aac	432
Lys Val Arg Glu Arg Val Met Asp Ile Asn Glu Ala Thr Ala Gly Asn	
130 135 140	
cgc gtg gtc atc tcc acc aac atc gtg ggt ggt gtg cgc cgc gac ctg	480
Arg Val Val Ile Ser Thr Asn Ile Val Gly Val Val Arg Arg Asp Leu	
145 150 155 160	
tcg cct gaa cac cag aag tgg att ctc gac gag atg aac cac ctc gaa	528
Ser Pro Glu His Gln Lys Trp Ile Leu Asp Glu Met Asn His Leu Glu	
165 170 175	
cgc gaa atc cgt gcc ctg atg acc acc atc ctc gac gac tac acc gtg	576
Arg Glu Ile Arg Ala Leu Met Thr Thr Ile Leu Asp Asp Tyr Thr Val	
180 185 190	
tgc aag cgc acc aag ggt gtg ggc gta ctc acc gca cag cag gcc atc	624
Cys Lys Arg Thr Lys Gly Val Gly Val Leu Thr Ala Gln Ala Ile	
195 200 205	
cag ctt ggt gcc gtc ggc ccc atg ctg cgc ggc agc ggc gtg gcg cag	672
Gln Leu Gly Ala Val Gly Pro Met Leu Arg Gly Ser Gly Val Ala Gln	
210 215 220	
gac gcc cgc cag ctg cag tac gcg gcc ttc gac gaa ctc gac ttc gaa	720
Asp Ala Arg Gln Leu Gln Tyr Ala Ala Phe Asp Glu Leu Asp Phe Glu	
225 230 235 240	
ccc atc gcc gta ccc gac ggc gac tcg tgg gca cgc tgc aag gtg cgc	768

DESUanglais-seql.txt
Pro Ile Ala Val Pro Asp Gly Asp Ser Trp Ala Arg Cys Lys Val Arg
245 250 255
ttc ctc gaa gtg ctc cag tcg gta gac ctc gtg cgt cag gcc atc tcc 816
Phe Leu Glu Val Leu Gln Ser Val Asp Leu Val Arg Gln Ala Ile Ser
260 265 270
aag ctt ccg gac acc gaa ctc tcc gtg aag gtt ccc ggc aag ccg gaa 864
Lys Leu Pro Asp Thr Glu Leu Ser Val Lys Val Pro Gly Lys Pro Glu
275 280 285
ggt gaa gtc gtg gcg cgt gtg gaa cag ccg cgt ggc gag ctc atg tac 912
Gly Glu Val Val Ala Arg Val Glu Gln Pro Arg Gly Glu Leu Met Tyr
290 295 300
tac gtc aag ggt aac ggc tcg aag cac ctt gaa cgt gta cgc atc cgc 960
Tyr Val Lys Gly Asn Gly Ser Lys His Leu Glu Arg Val Arg Ile Arg
305 310 315 320
act ccc aca ttc gcc aac atc ccg ccg ctg ctc gcc atc atg ggc ggt 1008
Thr Pro Thr Phe Ala Asn Ile Pro Pro Leu Ala Ile Met Gly Gly
325 330 335
ctg caa ctg gcg gac gtg ccc gtg gcg gta ctg tcc atc gac ccg tgc 1056
Leu Gln Leu Ala Asp Val Pro Val Ala Val Leu Ser Ile Asp Pro Cys
340 345 350
atc agc tgc aca gag cgc tag 1077
Ile Ser Cys Thr Glu Arg
355

<210> 2
<211> 358
<212> PRT
<213> Desulfovibrio vulgaris

<400> 2
Met Ser Arg Thr Ile Ile Pro Phe Gly Pro Gln His Pro Val Leu Pro
1 5 10 15
Glu Pro Leu His Leu Lys Leu Val Val Glu Asp Glu Thr Val Val Glu
20 25 30
Ala Ile Pro Ala Leu Gly Tyr Val His Arg Gly Leu Glu Thr Leu Ala
35 40 45
Ser Ile Arg Asp Tyr Asn Gln Met Val Tyr Val Val Glu Arg Val Cys
50 55 60
Gly Ile Cys Ser Cys Ile His Ala Met Cys Tyr Cys Gln Ser Leu Glu
65 70 75 80
Cys Met Met Asn Val Glu Val Pro Arg Arg Ala Lys Val Leu Arg Thr
85 90 95
Ile Trp Ser Glu Leu His Arg Ile His Ser His Leu Leu Trp Leu Gly
100 105 110
Leu Phe Ala Asp Gly Phe Gly Phe Glu Ser Leu Phe Met Gln Phe Trp
115 120 125
Lys Val Arg Glu Arg Val Met Asp Ile Asn Glu Ala Thr Ala Gly Asn
130 135 140
Arg Val Val Ile Ser Thr Asn Ile Val Gly Gly Val Arg Arg Asp Leu
145 150 155 160
Ser Pro Glu His Gln Lys Trp Ile Leu Asp Glu Met Asn His Leu Glu
165 170 175
Arg Glu Ile Arg Ala Leu Met Thr Thr Ile Leu Asp Asp Tyr Thr Val
180 185 190
Cys Lys Arg Thr Lys Gly Val Gly Val Leu Thr Ala Gln Gln Ala Ile
195 200 205
Gln Leu Gly Ala Val Gly Pro Met Leu Arg Gly Ser Gly Val Ala Gln
210 215 220
Asp Ala Arg Gln Leu Gln Tyr Ala Ala Phe Asp Glu Leu Asp Phe Glu
225 230 235 240
Pro Ile Ala Val Pro Asp Gly Asp Ser Trp Ala Arg Cys Lys Val Arg
245 250 255

DESUanglais-seq1.txt

Phe Leu Glu Val Leu Gln Ser Val Asp Leu Val Arg Gln Ala Ile Ser
 260 265 270

Lys Leu Pro Asp Thr Glu Leu Ser Val Lys Val Pro Gly Lys Pro Glu
 275 280 285

Gly Glu Val Val Ala Arg Val Glu Gln Pro Arg Gly Glu Leu Met Tyr
 290 295 300

Tyr Val Lys Gly Asn Gly Ser Lys His Leu Glu Arg Val Arg Ile Arg
 305 310 315 320

Thr Pro Thr Phe Ala Asn Ile Pro Pro Leu Leu Ala Ile Met Gly Gly
 325 330 335

Leu Gln Leu Ala Asp Val Pro Val Ala Val Leu Ser Ile Asp Pro Cys
 340 345 350

Ile Ser Cys Thr Glu Arg
 355

<210> 3
 <211> 1101
 <212> DNA
 <213> *Desulfovibrio vulgaris*

<220>
 <221> CDS
 <222> (1)..(1101)
 <223>

<400> 3
 atg agc act ccc gac agc acg acg cag aca tgg acg ctg ccc gta ggc 48
 Met Ser Thr Pro Asp Ser Thr Thr Gln Thr Trp Thr Leu Pro Val Gly
 1 5 10 15

ccg ctg cat gtg gcc ctt gaa gag ccc atg tac ttc aag ctg gat gtc 96
 Pro Leu His Val Ala Leu Glu Glu Pro Met Tyr Phe Lys Leu Asp Val
 20 25 30

gac ggc gaa atc gtc cgc aac gtg gaa atc acc gcc gga cat gtc cac 144
 Asp Gly Glu Ile Val Arg Asn Val 40 Glu Ile Thr Ala Gly His Val His
 35 40 45

cgg ggc atg gag gcg ctg gcc atg cgc cgc aac ctg ttc cag aac atc 192
 Arg Gly Met Glu Ala Leu Ala Met Arg Arg Asn Leu Phe Gln Asn Ile
 50 55 60

gtg ctc acc gaa cgc gtg tgc tcg ctg tgc tcg aac agc cat ccc ttc 240
 Val Leu Thr Glu Arg Val Cys Ser Leu Cys Ser Asn Ser His Pro Phe
 65 70 75 80

acc tac tgc atg gca gtc gag cac ctc gcg ggc atc gaa gtg ccc gcc 288
 Thr Tyr Cys Met Ala Val Glu His Leu Ala Gly Ile Glu Val Pro Ala
 85 90 95

cgc gcc gac cat ctg cgt gtg gtg gcg gag gag ata aag cgc acg gcc 336
 Arg Ala Asp His Leu Arg Val Val Ala 105 Glu Glu Ile Lys Arg Thr Ala
 100 105 110

tcg cac ctg ttc aac gtc gcc atc ctc gcg cac atc atc ggc ttc aag 384
 Ser His Leu Phe Asn Val Ala Ile Leu Ala His Ile Ile Gly Phe Lys
 115 120 125

tcg ctg ttc atg cat gtg atg gaa gtg cgt gag atc atg cag gac atc 432
 Ser Leu Phe Met His Val Met 135 Glu Val Arg Glu Ile Met Gln Asp Ile
 130 135 140

aag gag acg gtg tac gcc aac cgc atg gac ctc gcc gcc aac tgc atc 480
 Lys Glu Thr Val Tyr Gly Asn Arg Met Asp Leu Ala Ala Asn Cys Ile
 145 150 155 160

ggc ggc gtg aag tac gac gtg gac gcc gaa ctg ctg gcc atg ctg ctt 528
 Gly Gly Val Lys Tyr Asp Val Asp Ala 170 Leu Leu Ala Met Leu Leu
 165 170 175

gcc ggt ctc gac aag gtg gaa cgt aac gcc cgc gag ata tac cgc atc 576
 Ala Gly Leu Asp Lys Val Glu Arg Asn Ala Arg Glu Ile Tyr Arg Ile
 180 185 190

tac gcc tcc gac ccc atg gtc aca ggg cgc acc acc ggc atc ggc gta 624
 Tyr Ala Ser Asp Pro Met Val Thr 200 Gly Arg Thr Thr Gly Ile Gly Val
 195 200 205

DESUanglais-seq1.txt

ctg ccc ccc gac gag gca cgc cgc ttc ggc gtg gtg ggc ccc gtg gcg 672
 Leu Pro Pro Asp Glu Ala Arg Arg Phe Gly Val Val Gly Pro Val Ala
 210 215 220
 cga ggt tcc ggc ctt gcc gtc gac gtg cgc cgc gac gtg ccc tat gcc 720
 Arg Gly Ser Gly Leu Ala Val Asp Val Arg Arg Asp Val Pro Tyr Ala
 225 230 235 240
 gcc tac ccg caa ctc tcg ttc gat gtg atc acc gaa gag ggc tgc gac 768
 Ala Tyr Pro Gln Leu Ser Phe Asp Val Ile Thr Glu Glu Gly Cys Asp
 245 250 255
 gtg cgc gcc cgc gcc ctc gta cgt ctg cgc gag gtg ttc gag tcc atc 816
 Val Arg Ala Arg Ala Leu Val Arg Leu Arg Glu Val Phe Glu Ser Ile
 260 265 270
 tcc atc atc cgc cag tgc gtg gcg acc ctg ccc gaa ggc gcc atg acg 864
 Ser Ile Ile Arg Gln Cys Val Ala Thr Leu Pro Glu Gly Ala Met Thr
 275 280 285
 gtc atc atg ccg gag ata ccc gcc ggc cag tcg gtg gca cgt agc gaa 912
 Val Ile Met Pro Glu Ile Pro Ala Gly Gln Ser Val Ala Arg Ser Glu
 290 295 300
 gcc ccc cgc ggc gag ctc atg tac tac ctg cgc acc gac ggc acc gac 960
 Ala Pro Arg Gly Glu Leu Met Tyr Tyr Leu Arg Thr Asp Gly Thr Asp
 305 310 315 320
 atc ccc aac cgg ctc aag tgg cgc gtc ccg tcc tac atg aac tgg gac 1008
 Ile Pro Asn Arg Leu Lys Trp Arg Val Pro Ser Tyr Met Asn Trp Asp
 325 330 335
 gcc ctc ggc gtg atg atg cgc gac gcc aac gtc gcc gac atc ccg ctc 1056
 Ala Leu Gly Val Met Met Arg Asp Ala Asn Val Ala Asp Ile Pro Leu
 340 345 350
 atc gtg aac agc atc gac ccc tgc atc tcc tgc acg gag cgt tag 1101
 Ile Val Asn Ser Ile Asp Pro Cys Ile Ser Cys Thr Glu Arg
 355 360 365

<210> 4

<211> 366

<212> PRT

<213> Desulfovibrio vulgaris

<400> 4

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

DESUanglais-seq1.txt

Leu Pro Pro Asp Glu Ala Arg Arg Phe Gly Val Val Gly Pro Val Ala
 210 215 220
 Arg Gly Ser Gly Leu Ala Val Asp Val Arg Arg Asp Val Pro Tyr Ala
 225 230 235 240
 Ala Tyr Pro Gln Leu Ser Phe Asp Val Ile Thr Glu Glu Gly Cys Asp
 245 250 255
 Val Arg Ala Arg Ala Leu Val Arg Leu Arg Glu Val Phe Glu Ser Ile
 260 265 270
 Ser Ile Ile Arg Gln Cys Val Ala Thr Leu Pro Glu Gly Ala Met Thr
 275 280 285
 Val Ile Met Pro Glu Ile Pro Ala Gly Gln Ser Val Ala Arg Ser Glu
 290 295 300
 Ala Pro Arg Gly Glu Leu Met Tyr Tyr Leu Arg Thr Asp Gly Thr Asp
 305 310 315 320
 Ile Pro Asn Arg Leu Lys Trp Arg Val Pro Ser Tyr Met Asn Trp Asp
 325 330 335
 Ala Leu Gly Val Met Met Arg Asp Ala Asn Val Ala Asp Ile Pro Leu
 340 345 350
 Ile Val Asn Ser Ile Asp Pro Cys Ile Ser Cys Thr Glu Arg
 355 360 365

<210> 5
 <211> 543
 <212> DNA
 <213> Desulfovibrio fructosovorans

<220>
 <221> CDS
 <222> (1)..(543)
 <223>

<400> 5
 cgc gcc aag gtc ctg cgc acc atc tgg ggc gag ctg cac cgc atg cac 48
 Arg Ala Lys Val Leu Arg Thr Ile Trp Gly Glu Leu His Arg Met His
 1 5 10 15
 tcc cac ctg ctg tgg ctg ggg ctt ttc gcc gac gcc ttc ggc ttc gag 96
 Ser His Leu Leu Trp Leu Gly Leu Phe Ala Asp Ala Phe Gly Phe Glu
 20 25 30
 agc ctg ttc atg cag ttc tgg cgg att cgc gag cgc atc atg gac atc 144
 Ser Leu Phe Met Gln Phe Trp Arg Ile Arg Glu Arg Ile Met Asp Ile
 35 40 45
 atg gaa gcc acc tgc ggc aac cgc gtc gtc gtt tcc gtc aac gtc atc 192
 Met Glu Ala Thr Cys Gly Asn Arg Val Val Val Ser Val Asn Val Ile
 50 55 60
 ggc ggc acg cgc cgt gac ctc tcc ccc gaa cag tgc cag tgg atc gaa 240
 Gly Gly Thr Arg Arg Asp Leu Ser Pro Glu Gln Cys Gln Trp Ile Glu
 65 70 75 80
 cag cag ctg gcg atc tcc gaa aag gag ctc aag cag ctt tcg agc acc 288
 Gln Gln Leu Ala Ile Ser Glu Lys Glu Leu Lys Gln Leu Ser Ser Thr
 85 90 95
 atc tta aac gac tac acc gtg aaa aag cgc acc gtg ggc aag ggc gtg 336
 Ile Leu Asn Asp Tyr Thr Val Lys Lys Arg Thr Val Gly Lys Gly Val
 100 105 110
 ctg acc aag gag cag gcc tac cag ctc ggc gcg gct ggc ccc acg ctt 384
 Leu Thr Lys Glu Gln Ala Tyr Gln Leu Gly Ala Ala Gly Pro Thr Leu
 115 120 125
 cgc ggc tcg ggc tgg gcc cag gac gcc cgg cag acc ggc tat gcg gcc 432
 Arg Gly Ser Gly Trp Ala Gln Asp Ala Arg Gln Thr Gly Tyr Ala Ala
 130 135 140
 ttc ggc gaa ctc ggc ttc gat ccc atc gtc gaa tac gac ggc gat tcc 480
 Phe Gly Glu Leu Gly Phe Asp Pro Ile Val Glu Tyr Asp Gly Asp Ser
 145 150 155 160
 tac gcc cgc tcg gcc gtg cgc ttt cgg gag acg ctc cag tcc atc gac 528

DESUanglais-seql.txt
 Tyr Ala Arg Ser Ala Val Arg Phe Arg Glu Thr Leu Gln Ser Ile Asp
 165 170 175

ctc gtg cgc cag gcc
 Leu Val Arg Gln Ala
 180

543

<210> 6
 <211> 181
 <212> PRT
 <213> Desulfovibrio fructosovorans

<400> 6
 Arg Ala Lys Val Leu Arg Thr Ile Trp Gly Glu Leu His Arg Met His
 1 5 10 15
 Ser His Leu Leu Trp Leu Gly Leu Phe Ala Asp Ala Phe Gly Phe Glu
 20 25 30
 Ser Leu Phe Met Gln Phe Trp Arg Ile Arg Glu Arg Ile Met Asp Ile
 35 40 45
 Met Glu Ala Thr Cys Gly Asn Arg Val Val Val Ser Val Asn Val Ile
 50 55 60
 Gly Gly Thr Arg Arg Asp Leu Ser Pro Glu Gln Cys Gln Trp Ile Glu
 65 70 75 80
 Gln Gln Leu Ala Ile Ser Glu Lys Glu Leu Lys Gln Leu Ser Ser Thr
 85 90 95
 Ile Leu Asn Asp Tyr Thr Val Lys Lys Arg Thr Val Gly Lys Gly Val
 100 105 110
 Leu Thr Lys Glu Gln Ala Tyr Gln Leu Gly Ala Ala Gly Pro Thr Leu
 115 120 125
 Arg Gly Ser Gly Trp Ala Gln Asp Ala Arg Gln Thr Gly Tyr Ala Ala
 130 135 140
 Phe Gly Glu Leu Gly Phe Asp Pro Ile Val Glu Tyr Asp Gly Asp Ser
 145 150 155 160
 Tyr Ala Arg Ser Ala Val Arg Phe Arg Glu Thr Leu Gln Ser Ile Asp
 165 170 175
 Leu Val Arg Gln Ala
 180

<210> 7
 <211> 1077
 <212> DNA
 <213> Desulfovibrio gigas

<220>
 <221> CDS
 <222> (1)..(1077)
 <223>

<400> 7
 atg gct cag act att ctg cct ttc ggc ccg cag cac ccc gtg ttg ccc
 Met Ala Gln Thr Ile Leu Pro Phe Gly Pro Gln His Pro Val Leu Pro
 1 5 10 15
 gaa ccc atc cat ctg aag ctc acc gtg gag gat gaa atc gtc gtc gat
 Glu Pro Ile His Leu Lys Leu Thr Val Glu Asp Glu Ile Val Val Asp
 20 25 30
 gcg ctg ccc gca ctc ggc tac gtc cac cgc ggc ctg gaa aaa ctc tgc
 Ala Leu Pro Ala Leu Gly Tyr Val His Arg Gly Leu Glu Lys Leu Cys
 35 40 45
 gat atc cgt gat tac aac cag atg gtg cag att gtg gaa cgc gtc tgc
 Asp Ile Arg Asp Tyr Asn Gln Met Val Gln Ile Val Glu Arg Val Cys
 50 55 60
 ggc atc tgc tcc aaa atc cac gcc atg tgc tac tgc cag ggc atc gaa
 Gly Ile Cys Ser Lys Ile His Ala Met Cys Tyr Cys Gln Gly Ile Glu
 65 70 75 80
 gag atg atg ggc gtg caa gtg ccg gac cgc gcc aag gtc ctg cgc gtg
 85 90
 Glu Met Met Gly Val Gln Val Pro Asp Arg Ala Lys Val Leu Arg Val
 95

48

96

144

192

240

288

DESUanglais-seql.txt

gtc tgg agc gag ctg cac cgc gtg cac tcc cac ctg ctc tgg ctc ggc 336
 Val Trp Ser Glu Leu His Arg Val His Ser His Leu Leu Trp Leu Gly
 100 105 110
 ctc ttt gcc gac gcc ttc ggc ttc gaa gcg ctg ttc tac cag ttc tgg 384
 Leu Phe Ala Asp Ala Phe Gly Phe Glu Ala Leu Phe Tyr 125 Gln Phe Trp
 115 120
 aag att cgt gaa aag gtg atg gac atc aac gaa gcc acc acc ggc aac 432
 Lys Ile Arg Glu Lys Val Met Asp Ile Asn Glu Ala Thr Thr Gly Asn
 130 135 140
 cgc gtc atc gtt tcc gtg aac gaa gtg ggc ggc gta cgg cgc gat ctc 480
 Arg Val Ile Val Ser Val Asn Glu Val Gly Val Val Arg Arg Asp Leu
 145 150 155
 tcc gcc gag cag atc cgc tgg atc gaa gct gaa ctc aag gtg gtg gaa 528
 Ser Ala Glu Gln Ile Arg Trp Ile Glu Ala Glu Leu Lys Val Val Val Glu
 165 170 175
 aag cag gtc cgc gaa ctg cgc tcc acc att ctg gac gac tac acc gtg 576
 Lys Gln Val Arg Glu Leu Arg Ser Thr Ile Leu Asp Asp Tyr Thr Val
 180 185 190
 aaa aag cgc acc gtg ggc aag ggc gtg ctc acc ggt gcc cag gcc ctg 624
 Lys Lys Arg Thr Val Gly Lys Gly Val Leu Thr Gly Ala Gln Ala Leu
 195 200 205
 gag ctt gcc gcc gtg ggc ccc acc ctg cgc ggc agc gcc gtc ttc cag 672
 Glu Leu Gly Ala Val Gly Pro Thr Leu Arg Gly Ser Gly Val Phe Gln
 210 215 220
 gat gcc cgc cag ctt aag tac gct gcc ttc gac cgc atc gac ttc cag 720
 Asp Ala Arg Gln Leu Lys Tyr Ala Ala Phe Asp Arg Ile Asp Phe Gln
 225 230 235 240
 ccc atc gcc tat ccc aat ggc gac agc tgg tcc cgc tgc gcc gtg cgc 768
 Pro Ile Ala Tyr Pro Asn Gly Asp Ser Trp Ser Arg Cys Ala Val Arg
 245 250 255
 tac gac gag acc ctg cag tcc atc gac ctc gtg cgc cag gcc ctg gcc 816
 Tyr Asp Glu Thr Leu Gln Ser Ile Asp Leu Val Arg Gln Ala Leu Ala
 260 265 270
 cgg ctg ccc gaa ggc gag ctg agc acc aag gtg aag gcc aag ccg gaa 864
 Arg Leu Pro Glu Gly Glu Leu Ser Thr Lys Val Lys Gly Lys Pro Glu
 275 280 285
 ggc gaa gtc gtc acc cgc gtg gaa cag ccc cgc ggc gag ctg ctg tac 912
 Gly Glu Val Val Thr Arg Val Glu Gln Pro Arg Gly Glu Leu Leu Tyr
 290 295 300
 tac ctc aag ggc aat ggc acc aac aac ctg gac cgc tgc cgc atc cgc 960
 Tyr Leu Lys Gly Asn Thr Thr Asn Asn Leu Asp Arg Cys Arg Ile Gln
 305 310 315 320
 acc ccc acg ttc tcc aac atc ccg ccg ctg gtg gtc atg ctg ccc ggc 1008
 Thr Pro Thr Phe Ser Asn Ile Pro Pro Leu Val Val Met Leu Pro Gly
 325 330 335
 ctg gaa ctg gcc gac gtg cct gtg gtt gtg ctg tcc atc gac ccc tgc 1056
 Leu Glu Leu Ala Asp Val Pro Val Val Val Leu Ser Ile Asp Pro Cys
 340 345 350
 atc agc tgc acc gaa cgc taa 1077
 Ile Ser Cys Thr Glu Arg
 355

<210> 8
 <211> 358
 <212> PRT
 <213> Desulfovibrio gigas

<400> 8
 Met Ala Gln Thr Ile Leu Pro Phe Gly Pro Gln His Pro Val Leu Pro
 1 5 10 15
 Glu Pro Ile His Leu Lys Leu Thr Val Glu Asp Glu Ile Val Val Asp
 20 25 30
 Ala Leu Pro Ala Leu Gly Tyr Val His Arg Gly Leu Glu Lys Leu Cys
 35 40 45

DESUanglais-seq1.txt

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

<210> 9
 <211> 1083
 <212> DNA
 <213> thermoanaerobacter tengcongensis

<220>
 <221> CDS
 <222> (1)..(1083)
 <223>

<400> 9
 atg agt gag aag agc aca ata cct ttt ggg cca cag cat cct gtt ttg 48
 Met Ser Glu Lys Ser Thr Ile Pro Phe Gly Pro Gln His Pro Val Leu
 1 5 10 15
 cct gag cct ata cat ctt aaa ctg ata gta gaa gac gaa aag gta gta 96
 Pro Glu Pro Ile His Leu Lys Leu Ile Val Glu Asp Glu Lys Val Val
 20 25 30
 gaa gcg tat cct gct ttt ggc tat gtt cac aga ggt tta gaa ctt ctt 144
 Glu Ala Tyr Pro Ala Phe Gly Tyr Val His Arg Gly Leu Glu Leu Leu
 35 40 45
 gtg aaa aaa agg gac ttt aat cag atg gtt tat gta gtt gac cac ata 192
 page 8

DESUanglais-seql.txt

Val	Lys	Lys	Arg	Asp	Phe	Asn	Gln	Met	Val	Tyr	Val	Val	Asp	His	Ile		
50						55				60							
tgc	ggc	att	tgc	agt	gct	ata	cat	gga	gag	act	tat	tgc	cag	gca	gtg	240	
Cys	Gly	Ile	Cys	Ser	Ala	Ile	His	Gly	Glu	Thr	Tyr	Cys	Gln	Ala	Val		
65					70				75						80		
gag	aaa	ttg	att	ggg	att	gac	gtt	ccg	gaa	agg	gca	aag	ttt	ttg	aga	288	
Glu	Lys	Leu	Ile	Gly	Ile	Asp	Val	Pro	Glu	Arg	Ala	Lys	Phe	Leu	Arg		
				85				90					95				
gtc	atc	tgg	gct	gaa	att	cac	agg	att	cac	agc	cat	ctt	ttg	tgg	ttt	336	
Val	Ile	Trp	Ala	Glu	Ile	His	Arg	Ile	His	Ser	His	Leu	Leu	Trp	Phe		
			100				105					110					
ggc	ctt	tta	gca	gat	gct	ttt	ggg	ttt	gaa	aac	ctg	ttt	atg	ctt	tct	384	
Gly	Leu	Leu	Ala	Asp	Ala	Phe	Gly	Phe	Glu	Asn	Leu	Phe	Met	Leu	Ser		
	115					120					125						
tgg	aga	ata	agg	gag	aag	gta	atg	gac	ata	ttg	gag	gct	acg	gct	ggc	432	
Trp	Arg	Ile	Arg	Glu	Lys	Val	Met	Asp	Ile	Leu	Glu	Ala	Thr	Ala	Gly		
	130					135					140						
aat	aga	gtt	gtg	att	tct	gtc	aat	att	gta	ggc	ggt	gtg	aga	aga	gat	480	
Asn	Arg	Val	Val	Ile	Ser	Val	Asn	Ile	Val	Gly	Gly	Val	Arg	Arg	Asp		
145					150				155						160		
att	gac	agt	gag	cag	gcc	aaa	tgg	gtg	ctt	gcc	cag	ctt	aaa	gag	gta	528	
Ile	Asp	Ser	Glu	Gln	Ala	Lys	Trp	Val	Leu	Ala	Gln	Leu	Lys	Glu	Val		
				165				170					175				
gag	gaa	ggg	cta	aaa	gag	att	gaa	aag	ata	gta	aga	gat	aac	tac	act	576	
Glu	Glu	Gly	Leu	Lys	Glu	Ile	Glu	Lys	Ile	Val	Arg	Asp	Asn	Tyr	Thr		
			180					185				190					
ttg	aaa	aag	aga	act	gta	ggg	ata	gga	gtc	ctt	tca	aaa	gaa	gag	gct	624	
Leu	Lys	Lys	Arg	Thr	Val	Gly	Ile	Gly	Val	Leu	Ser	Lys	Glu	Glu	Ala		
		195				200						205					
tat	atg	ctg	gga	gca	gta	ggg	cct	act	ttg	aga	gga	agt	gga	gtt	cca	672	
Tyr	Met	Leu	Gly	Ala	Val	Gly	Pro	Thr	Leu	Arg	Gly	Ser	Gly	Val	Pro		
	210					215					220						
ata	gat	act	aga	acc	ttg	gga	tat	gct	gct	tac	aaa	tat	tta	gac	ttt	720	
Ile	Asp	Thr	Arg	Thr	Leu	Gly	Tyr	Ala	Ala	Tyr	Lys	Tyr	Leu	Asp	Phe		
	225				230					235					240		
gaa	cca	gtt	gtt	gaa	aaa	gat	ggg	gat	acc	tat	gca	aga	act	ctc	gtc	768	
Glu	Pro	Val	Val	Glu	Lys	Asp	Gly	Asp	Thr	Tyr	Ala	Arg	Thr	Leu	Val		
				245				250						255			
aga	cta	agg	gag	atg	ttc	cag	tct	att	gac	ctt	gtg	agg	caa	gct	ata	816	
Arg	Leu	Arg	Glu	Met	Phe	Gln	Ser	Ile	Asp	Leu	Val	Arg	Gln	Ala	Ile		
			260				265						270				
agc	aag	atg	cca	gaa	ggt	gaa	ata	aat	gtc	aaa	gta	aaa	ccc	aat	ttg	864	
Ser	Lys	Met	Pro	Glu	Gly	Glu	Ile	Asn	Val	Lys	Val	Lys	Pro	Asn	Leu		
		275					280					285					
cca	gca	gga	gag	gtc	ata	gaa	agg	gct	gag	cag	ccc	aga	gga	gaa	gta	912	
Pro	Ala	Gly	Glu	Val	Ile	Glu	Arg	Ala	Glu	Gln	Pro	Arg	Gly	Glu	Val		
	290					295					300						
ttt	tac	tat	atc	aag	tca	aat	gga	ggc	aaa	tac	ttg	gat	aga	ttg	agg	960	
Phe	Tyr	Tyr	Ile	Lys	Ser	Asn	Gly	Gly	Lys	Tyr	Leu	Asp	Arg	Leu	Arg		
	305				310					315				320			
ata	agg	act	ccc	act	ttt	gcg	aat	ctg	gct	gct	ctt	ctg	cac	atg	cta	1008	
Ile	Arg	Thr	Pro	Thr	Phe	Ala	Asn	Leu	Ala	Ala	Leu	Leu	His	Met	Leu		
				325				330						335			
ccg	ggc	tgt	act	ttg	gca	gac	gtg	cct	gtt	ctg	gtt	ctg	acg	att	gac	1056	
Pro	Gly	Cys	Thr	Leu	Ala	Asp	Val	Pro	Val	Leu	Val	Leu	Thr	Ile	Asp		
			340				345						350				
cca	tgt	atc	agc	tgt	acg	gaa	agg	tag								1083	
Pro	Cys	Ile	Ser	Cys	Thr	Glu	Arg										
		355					360										

<210> 10
 <211> 360
 <212> PRT
 <213> thermoanaerobacter tengcongensis

<400> 10

DESUanglais-seql.txt
 Met Ser Glu Lys Ser Thr Ile Pro Phe Gly Pro Gln His Pro Val Leu
 1 5 10 15
 Pro Glu Pro Ile His Leu Lys Leu Ile Val Glu Asp Glu Lys Val Val
 20 25 30
 Glu Ala Tyr Pro Ala Phe Gly Tyr Val His Arg Gly Leu Glu Leu Leu
 35 40 45
 Val Lys Lys Arg Asp Phe Asn Gln Met Val Tyr Val Val Asp His Ile
 50 55 60
 Cys Gly Ile Cys Ser Ala Ile His Gly Glu Thr Tyr Cys Gln Ala Val
 65 70 75 80
 Glu Lys Leu Ile Gly Ile Asp Val Pro Glu Arg Ala Lys Phe Leu Arg
 85 90 95
 Val Ile Trp Ala Glu Ile His Arg Ile His Ser His Leu Leu Trp Phe
 100 105 110
 Gly Leu Leu Ala Asp Ala Phe Gly Phe Glu Asn Leu Phe Met Leu Ser
 115 120 125
 Trp Arg Ile Arg Glu Lys Val Met Asp Ile Leu Glu Ala Thr Ala Gly
 130 135 140
 Asn Arg Val Val Ile Ser Val Asn Ile Val Gly Gly Val Arg Arg Asp
 145 150 155 160
 Ile Asp Ser Glu Gln Ala Lys Trp Val Leu Ala Gln Leu Lys Glu Val
 165 170 175
 Glu Glu Gly Leu Lys Glu Ile Glu Lys Ile Val Arg Asp Asn Tyr Thr
 180 185 190
 Leu Lys Lys Arg Thr Val Gly Ile Gly Val Leu Ser Lys Glu Glu Ala
 195 200 205
 Tyr Met Leu Gly Ala Val Gly Pro Thr Leu Arg Gly Ser Gly Val Pro
 210 215 220
 Ile Asp Thr Arg Thr Leu Gly Tyr Ala Ala Tyr Lys Tyr Leu Asp Phe
 225 230 235 240
 Glu Pro Val Val Glu Lys Asp Gly Asp Thr Tyr Ala Arg Thr Leu Val
 245 250 255
 Arg Leu Arg Glu Met Phe Gln Ser Ile Asp Leu Val Arg Gln Ala Ile
 260 265 270
 Ser Lys Met Pro Glu Gly Glu Ile Asn Val Lys Val Lys Pro Asn Leu
 275 280 285
 Pro Ala Gly Glu Val Ile Glu Arg Ala Glu Gln Pro Arg Gly Glu Val
 290 295 300
 Phe Tyr Tyr Ile Lys Ser Asn Gly Gly Lys Tyr Leu Asp Arg Leu Arg
 305 310 315 320
 Ile Arg Thr Pro Thr Phe Ala Asn Leu Ala Ala Leu Leu His Met Leu
 325 330 335
 Pro Gly Cys Thr Leu Ala Asp Val Pro Val Leu Val Leu Thr Ile Asp
 340 345 350
 Pro Cys Ile Ser Cys Thr Glu Arg
 355 360

<210> 11
 <211> 1731
 <212> DNA
 <213> thermoanaerobacter tengcongensis

<220>
 <221> CDS
 <222> (1)..(1731)
 <223>

<400> 11
 gtg gag aat gaa ata aag gca caa caa gac aga aaa aaa tat gtt agg 48
 Val Glu Asn Glu Ile Lys Ala Gln Gln Asp Arg Lys Lys Tyr Val Arg
 1 5 10 15

gct ttg tac tca aag ttt ggt gcg agc atc ctt gaa gag aag tgg caa 96
 Page 10

DESUanglais-seq1.txt																	
Ala	Leu	Tyr	Ser	Lys	Phe	Gly	Ala	Ser	Ile	Leu	Glu	Glu	Lys	Trp	Gln		
			20					25					30				
aca	ccg	gat	caa	gtg	act	ctg	aca	gta	aag	cta	aat	ata	ctc	cca	gaa	144	
Thr	Pro	Asp	Gln	Val	Thr	Leu	Thr	Val	Lys	Leu	Asn	Ile	Leu	Pro	Glu		
		35					40				45						
att	gta	gaa	gag	gca	tat	tac	gga	cag	gga	ggg	tgg	ctg	tca	aat	gtt	192	
Ile	Val	Glu	Glu	Ala	Tyr	Tyr	Gly	Gln	Gly	Gly	Trp	Leu	Ser	Asn	Val		
	50					55					60						
atc	ggg	aac	gat	gag	cgc	agc	ata	aac	gga	cat	ttt	gcg	gta	tac	tat	240	
Ile	Gly	Asn	Asp	Glu	Arg	Ser	Ile	Asn	Gly	His	Phe	Ala	Val	Tyr	Tyr		
	65				70					75					80		
gtt	tta	tcc	att	gag	gca	gaa	aaa	gac	ccg	gat	aaa	aac	ctt	tgg	ctg	288	
Val	Leu	Ser	Ile	Glu	Ala	Glu	Lys	Asp	Pro	Asp	Lys	Asn	Leu	Trp	Leu		
				85					90				95				
aca	gtt	aag	gct	ttg	gtt	cct	gct	gac	aaa	cca	gag	ttt	cct	tcg	gta	336	
Thr	Val	Lys	Ala	Leu	Val	Pro	Ala	Asp	Lys	Pro	Glu	Phe	Pro	Ser	Val		
			100					105					110				
gcg	cct	cgt	gtg	ccg	gca	gct	gta	tgg	tac	gaa	cgg	gag	gtg	cgg	gat	384	
Ala	Pro	Arg	Val	Pro	Ala	Ala	Val	Trp	Tyr	Glu	Arg	Glu	Val	Arg	Asp		
		115				120						125					
atg	ctg	ggg	ttg	gag	ccg	gtg	ggg	ctt	cca	gat	gcg	aga	aga	ctt	gtg	432	
Met	Leu	Gly	Leu	Glu	Pro	Val	Gly	Leu	Pro	Asp	Ala	Arg	Arg	Leu	Val		
	130					135					140						
ttg	ccc	gat	gac	tgg	cca	gat	aac	ctt	tat	cct	ttg	cga	aag	gat	atg	480	
Leu	Pro	Asp	Asp	Trp	Pro	Asp	Asn	Leu	Tyr	Pro	Leu	Arg	Lys	Asp	Met		
	145				150					155					160		
gat	tat	cgt	cta	cgc	cct	gag	ccg	gca	gcg	gaa	gaa	gaa	aat	tat	gag	528	
Asp	Tyr	Arg	Leu	Arg	Pro	Glu	Pro	Ala	Ala	Glu	Glu	Glu	Asn	Tyr	Glu		
				165				170						175			
ttt	atc	gaa	gta	aaa	gga	gaa	ggt	att	gta	gaa	gta	cca	ctg	gga	ccg	576	
Phe	Ile	Glu	Val	Lys	Gly	Glu	Gly	Ile	Val	Glu	Val	Pro	Leu	Gly	Pro		
			180					185					190				
ctt	cac	att	act	tct	gac	gag	cct	gga	cat	ttc	cga	ctc	tat	gtc	gac	624	
Leu	His	Ile	Thr	Ser	Asp	Glu	Pro	Gly	His	Phe	Arg	Leu	Tyr	Val	Asp		
		195					200					205					
ggc	gaa	tat	atc	gtt	gat	gcc	gac	tac	cgc	ctt	ttc	tat	gtg	cat	cga	672	
Gly	Glu	Tyr	Ile	Val	Asp	Ala	Asp	Tyr	Arg	Leu	Phe	Tyr	Val	His	Arg		
	210					215					220						
ggc	ctt	gaa	aaa	ctt	gct	gaa	agt	cgc	atg	gac	tat	aac	cag	gtt	act	720	
Gly	Leu	Glu	Lys	Leu	Ala	Glu	Ser	Arg	Met	Asp	Tyr	Asn	Gln	Val	Thr		
	225				230					235					240		
ttt	tta	gcg	gag	cga	att	tgt	gga	att	tgt	ggt	tat	gca	cac	agc	gtg	768	
Phe	Leu	Ala	Glu	Arg	Ile	Cys	Gly	Ile	Cys	Gly	Tyr	Ala	His	Ser	Val		
				245					250					255			
gcg	tat	gcc	atg	gca	gta	gaa	gca	gcc	aac	aga	att	gaa	gtc	cct	ctg	816	
Ala	Tyr	Ala	Met	Ala	Val	Glu	Ala	Ala	Asn	Arg	Ile	Glu	Val	Pro	Leu		
		260					265						270				
cgg	gcc	cag	tat	att	cga	act	att	cta	tta	gag	gta	gag	agg	ata	cac	864	
Arg	Ala	Gln	Tyr	Ile	Arg	Thr	Ile	Leu	Leu	Glu	Val	Glu	Arg	Ile	His		
		275					280					285					
agc	cac	ctt	ttg	aat	ata	ggg	tta	gcg	gct	cac	tta	gtg	ggt	ttt	gat	912	
Ser	His	Leu	Leu	Asn	Ile	Gly	Leu	Ala	Ala	His	Leu	Val	Gly	Phe	Asp		
	290					295					300						
tcg	ggc	ttt	atg	cat	ttc	ttt	aga	ata	aga	gaa	aag	gct	atg	cag	atg	960	
Ser	Gly	Phe	Met	His	Phe	Phe	Arg	Ile	Arg	Glu	Lys	Ala	Met	Gln	Met		
	305				310					315					320		
gcg	gaa	att	ctt	aca	ggt	ggt	cga	aaa	act	tat	gga	atg	aac	ctc	ata	1008	
Ala	Glu	Ile	Leu	Thr	Gly	Gly	Arg	Lys	Thr	Tyr	Gly	Met	Asn	Leu	Ile		
				325					330					335			
gga	ggt	gta	cga	cgt	gat	att	tta	aaa	gag	gag	aag	gtt	cag	gcc	ttg	1056	
Gly	Gly	Val	Arg	Arg	Asp	Ile	Leu	Lys	Glu	Glu	Lys	Val	Gln	Ala	Leu		
			340					345					350				
cga	tta	att	tct	gag	att	cga	tct	gaa	ctt	aaa	gaa	ctt	atc	gat	atg	1104	
Arg	Leu	Ile	Ser	Glu	Ile	Arg	Ser	Glu	Leu	Lys	Glu	Leu	Ile	Asp	Met		

DESUanglais-seql.txt

355	360	365	1152
ttg cta aat acc ccc aac ttt att tcg cga aca cag gga gtt ggg cgt			
Leu Leu Asn Thr Pro Asn Phe Ile Ser Arg Thr Gln Gly Val Gly Arg			
370	375	380	
ctg gac cct aag gta gct cga aac ttt gga tcg gtt ggc ccc aat ctg			1200
Leu Asp Pro Lys Val Ala Arg Asn Phe Gly Ser Val Gly Pro Asn Leu			
385	390	395	400
aga ggt tct gga tat gga cga gat aca cga gcg gac cat ccc tat tgt			1248
Arg Gly Ser Gly Tyr Gly Arg Asp Thr Arg Ala Asp His Pro Tyr Cys			
405	410	415	
gcc tac aaa cat gta tct tgg aat gtt atc tcc aag gag gga tgt gat			1296
Ala Tyr Lys His Val Ser Trp Asn Val Ile Ser Lys Glu Gly Cys Asp			
420	425	430	
gtt ttg tct aga gta tta gta cga gcg gaa gag ctt ttt gag tct tta			1344
Val Leu Ser Arg Val Leu Val Arg Ala Glu Glu Leu Phe Glu Ser Leu			
435	440	445	
gat ata att gaa aga tgt ttg tct gat ttg cct cct ggt cct atc ctt			1392
Asp Ile Ile Glu Arg Cys Leu Ser Asp Leu Pro Pro Gly Pro Ile Leu			
450	455	460	
cat gaa ggg ttt acc tat aca cct tat act ttt gca ctt gga tat acg			1440
His Glu Gly Phe Thr Tyr Thr Pro Tyr Thr Phe Ala Leu Gly Tyr Thr			
465	470	475	480
gaa gct cct agg gga gaa aat gtc cat tgg gtg atg aca gct aat caa			1488
Glu Ala Pro Arg Gly Glu Asn Val His Trp Val Met Thr Ala Asn Gln			
485	490	495	
cat cag gtg tac cgg tgg cga gta cgg gcc tct act tat aat aat tgg			1536
His Gln Val Tyr Arg Trp Arg Val Arg Ala Ser Thr Tyr Asn Asn Trp			
500	505	510	
cca gtc ctt cgt tat atg ttt tac ggt aat act gtg gcc gat gca cct			1584
Pro Val Leu Arg Tyr Met Phe Tyr Gly Asn Thr Val Ala Asp Ala Pro			
515	520	525	
ttg att gtg gca agt att gac cct tgt tac tct tgc gct gaa aga gtt			1632
Leu Ile Val Ala Ser Ile Asp Pro Cys Tyr Ser Cys Ala Glu Arg Val			
530	535	540	
aca ttg gtc gat gtg cgt aaa aag agg gca aaa act gtc caa tat caa			1680
Thr Leu Val Asp Val Arg Lys Lys Arg Ala Lys Thr Val Gln Tyr Gln			
545	550	555	560
gaa ttg gaa caa tac tgt cgc gaa aga aaa tat tca cca ctg aaa aat			1728
Glu Leu Glu Gln Tyr Cys Arg Glu Arg Lys Tyr Ser Pro Leu Lys Asn			
565	570	575	
tag			1731
<210> 12 <211> 576 <212> PRT <213> thermoanaerobacter tengcongensis			
<400> 12 Val Glu Asn Glu Ile Lys Ala Gln Gln Asp Arg Lys Lys Tyr Val Arg 1 5 10 15 Ala Leu Tyr Ser Lys Phe Gly Ala Ser Ile Leu Glu Glu Lys Trp Gln 20 25 30 Thr Pro Asp Gln Val Thr Leu Thr Val Lys Leu Asn Ile Leu Pro Glu 35 40 45 Ile Val Glu Glu Ala Tyr Tyr Gly Gln Gly Gly Trp Leu Ser Asn Val 50 55 60 Ile Gly Asn Asp Glu Arg Ser Ile Asn Gly His Phe Ala Val Tyr Tyr 65 70 75 80 Val Leu Ser Ile Glu Ala Glu Lys Asp Pro Asp Lys Asn Leu Trp Leu 85 90 95 Thr Val Lys Ala Leu Val Pro Ala Asp Lys Pro Glu Phe Pro Ser Val 100 105 110 Ala Pro Arg Val Pro Ala Ala Val Trp Tyr Glu Arg Glu Val Arg Asp			

DESUanglais-seq1.txt

115 Met Leu Gly Leu Glu Pro Val Gly Leu Pro Asp Ala Arg Arg Leu Val 130 135 Leu Pro Asp Asp Trp Pro Asp Asn Leu Tyr Pro Leu Arg Lys Asp Met 145 150 Asp Tyr Arg Leu Arg Pro Glu Pro Ala Ala Glu Glu Glu Asn Tyr Glu 165 170 175 Phe Ile Glu Val Lys Gly Glu Gly Ile Val Glu Val Pro Leu Gly Pro 180 185 190 Leu His Ile Thr Ser Asp Glu Pro Gly His Phe Arg Leu Tyr Val Asp 195 200 205 Gly Glu Tyr Ile Val Asp Ala Asp Tyr Arg Leu Phe Tyr Val His Arg 210 215 220 Gly Leu Glu Lys Leu Ala Glu Ser Arg Met Asp Tyr Asn Gln Val Thr 225 230 235 240 Phe Leu Ala Glu Arg Ile Cys Gly Ile Cys Gly Tyr Ala His Ser Val 245 250 255 Ala Tyr Ala Met Ala Val Glu Ala Ala Asn Arg Ile Glu Val Pro Leu 260 265 270 Arg Ala Gln Tyr Ile Arg Thr Ile Leu Leu Glu Val Glu Arg Ile His 275 280 285 Ser His Leu Leu Asn Ile Gly Leu Ala Ala His Leu Val Gly Phe Asp 290 295 300 Ser Gly Phe Met His Phe Phe Arg Ile Arg Glu Lys Ala Met Gln Met 305 310 315 320 Ala Glu Ile Leu Thr Gly Gly Arg Lys Thr Tyr Gly Met Asn Leu Ile 325 330 335 Gly Gly Val Arg Arg Asp Ile Leu Lys Glu Glu Lys Val Gln Ala Leu 340 345 350 Arg Leu Ile Ser Glu Ile Arg Ser Glu Leu Lys Glu Leu Ile Asp Met 355 360 365 Leu Leu Asn Thr Pro Asn Phe Ile Ser Arg Thr Gln Gly Val Gly Arg 370 375 380 Leu Asp Pro Lys Val Ala Arg Asn Phe Gly Ser Val Gly Pro Asn Leu 385 390 395 400 Arg Gly Ser Gly Tyr Gly Arg Asp Thr Arg Ala Asp His Pro Tyr Cys 405 410 415 Ala Tyr Lys His Val Ser Trp Asn Val Ile Ser Lys Glu Gly Cys Asp 420 425 430 Val Leu Ser Arg Val Leu Val Arg Ala Glu Glu Leu Phe Glu Ser Leu 435 440 445 Asp Ile Ile Glu Arg Cys Leu Ser Asp Leu Pro Pro Gly Pro Ile Leu 450 455 460 His Glu Gly Phe Thr Tyr Thr Pro Tyr Thr Phe Ala Leu Gly Tyr Thr 465 470 475 480 Glu Ala Pro Arg Gly Glu Asn Val His Trp Val Met Thr Ala Asn Gln 485 490 495 His Gln Val Tyr Arg Trp Arg Val Arg Ala Ser Thr Tyr Asn Asn Trp 500 505 510 Pro Val Leu Arg Tyr Met Phe Tyr Gly Asn Thr Val Ala Asp Ala Pro 515 520 525 Leu Ile Val Ala Ser Ile Asp Pro Cys Tyr Ser Cys Ala Glu Arg Val 530 535 540 Thr Leu Val Asp Val Arg Lys Lys Arg Ala Lys Thr Val Gln Tyr Gln 545 550 555 560 Glu Leu Glu Gln Tyr Cys Arg Glu Arg Lys Tyr Ser Pro Leu Lys Asn 565 570 575	120
--	------------

DESUanglais-seql.txt

```

<210> 13
<211> 1086
<212> DNA
<213> Rhodospirillum rubrum

<220>
<221> CDS
<222> (1)..(1086)
<223>

<400> 13
atg agc acc tat acc att ccc gtc ggc ccg ctg cat gtg gcc ctt gaa 48
Met Ser Thr Tyr Thr Ile Pro Val Gly Pro Leu His Val Ala Leu Glu
1 5 10 15

gag ccg atg tac ttc cgc atc gag gtc gat ggc gag aag gtg gtc agc 96
Glu Pro Met Tyr Phe Arg Ile Glu Val Asp Gly Glu Lys Val Val Ser
20 25 30

gtc gat atc acc gcc ggc cat gtc cat cgc ggc atc gaa tac ctg gcg 144
Val Asp Ile Thr Ala Gly His Val His Arg Gly Ile Glu Tyr Leu Ala
35 40 45

acc aag cgc aac atc tat caa aat atc gtg ctg acc gag cgc gtc tgc 192
Thr Lys 50 Arg Asn Ile Tyr 55 Asn Ile Val Leu Thr 60 Glu Arg Val Cys

tcg ctc tgc tcc aac agc cat ccg caa act tat tgc atg gcc ctg gaa 240
Ser Leu Cys Ser Asn Ser His Pro Gln Thr Tyr Cys Met Ala Leu Glu
65 70 75 80

agc atc acc ggc atg gtg gtg ccg ccg cgc gcc caa tat ctg cgg gtg 288
Ser Ile Thr Gly Met 85 Val Val Pro Pro Arg Ala Gln Tyr Leu Arg Val
90 95

atc gcc gac gag acc aag cgc gtc gcc tcg cat atg ttc aac gtc gcc 336
Ile Ala Asp 100 Thr Lys Arg Val Ala 105 Ser His Met Phe Asn Val Ala
110

atc ctt gcc cat atc gtc ggt ttt gat tcg ctg ttc atg cat gtc atg 384
Ile Leu Ala His Ile Val Gly Phe Asp Ser Leu Phe Met His Val Met
115 120 125

gaa gcc cgc gag atc atg caa gac acc aag gaa gcg gtc ttt ggc aat 432
Glu Ala Arg Glu Ile Met Gln Asp Thr Lys Glu Ala Val Phe Gly Asn
130 135 140

cgc atg gac atc gcc gcc atg gcg atc ggc ggg gtc aaa tac gat ctt 480
Arg Met Asp Ile Ala 150 Met Ala Ile Gly Gly Val Lys Tyr Asp Leu
145 155 160

gat aag gac ggg cgc gat tat ttc atc ggt cag ctc gat aag ctt gaa 528
Asp Lys Asp Gly Arg Asp Tyr Phe Ile Gly Gln Leu Asp Lys Leu Glu
165 170 175

cca acg ctg cgc gac gag atc atc ccg ctt tat cag acc aac ccg tcg 576
Pro Thr Leu Arg Asp Glu Ile Ile Pro 185 Leu Tyr Gln Thr Asn Pro Ser
180 190

atc gtt gat cgc acc cgg ggc att ggc gtt ctg agc gcg gcc gat tgc 624
Ile Val Asp Arg Thr Arg Gly Ile Gly Val Leu Ser Ala Ala Asp Cys
195 200 205

gtg gac tat ggc ctg atg ggg ccg gtg gcg cgc ggc tcg ggc cat gcc 672
Val Asp Tyr Gly Leu Met Gly Pro Val Ala Arg Gly Ser Gly His Ala
210 215 220

tat gac gtg cgc aag cag gcg ccc tat gcg gtt tat gat cgt ctg gac 720
Tyr Asp Val Arg Lys Gln Ala Pro Tyr Ala Val Tyr Asp Arg Leu Asp
225 230 235 240

ttc gag atg gcc ctg ggc gag cac ggc gat gtg tgg tcg cgc gcc atg 768
Phe Glu Met Ala Leu Gly Glu His Gly Asp Val Trp Ser Arg Ala Met
245 250 255

gtg cgc tgg caa gag gcc ctg acc tcg atc ggg ctg atc cgc caa tgc 816
Val Arg Trp 260 Glu Ala Leu Thr 265 Ile Gly Leu Ile Arg 270 Gln Cys

ctg cgc gac atg ccc gac ggt ccg acg aag gcg ggg ccg gtg ccg ccc 864
Leu Arg Asp Met Pro Asp Gly Pro Thr Lys Ala Gly Pro Val Pro Pro
275 280 285

```

DESUanglais-seq1.txt
 att ccc gct ggc gag gcg gtc gcc aag acc gag gcg ccg cgc ggc gag 912
 Ile Pro Ala Gly Glu Ala Val Ala Lys Thr Glu Ala Pro Arg Gly Glu
 290 295 300
 ttg atc tat tac ctg aag acc aac ggc acc gac cgg ccc gaa cgc ctg 960
 Leu Ile Tyr Tyr Leu Lys Thr Asn Gly Thr Asp Arg Pro Glu Arg Leu
 305 310 315
 aaa tgg cgc gtt ccc acc tat atg aac tgg gat gcg ctc aat gtg atg 1008
 Lys Trp Arg Val Pro Thr Tyr Met Asn Trp Asp Ala Leu Asn Val Met
 325 330 335
 atg gcc ggg gcg cgg att tcc gat atc ccg ctg atc gtc aac agc atc 1056
 Met Ala Gly Ala Arg Ile Ser Asp Ile Pro Leu Ile Val Asn Ser Ile
 340 345 350
 gat ccc tgc atc tcc tgt acg gaa cgc tga 1086
 Asp Pro Cys Ile Ser Cys Thr Glu Arg
 355 360

<210> 14
 <211> 361
 <212> PRT
 <213> Rhodospirillum rubrum

<400> 14
 Met Ser Thr Tyr Thr Ile Pro Val Gly Pro Leu His Val Ala Leu Glu
 1 5 10 15
 Glu Pro Met Tyr Phe Arg Ile Glu Val Asp Gly Glu Lys Val Val Ser
 20 25 30
 Val Asp Ile Thr Ala Gly His Val His Arg Gly Ile Glu Tyr Leu Ala
 35 40 45
 Thr Lys Arg Asn Ile Tyr Gln Asn Ile Val Leu Thr Glu Arg Val Cys
 50 55 60
 Ser Leu Cys Ser Asn Ser His Pro Gln Thr Tyr Cys Met Ala Leu Glu
 65 70 75 80
 Ser Ile Thr Gly Met Val Val Pro Pro Arg Ala Gln Tyr Leu Arg Val
 85 90 95
 Ile Ala Asp Glu Thr Lys Arg Val Ala Ser His Met Phe Asn Val Ala
 100 105 110
 Ile Leu Ala His Ile Val Gly Phe Asp Ser Leu Phe Met His Val Met
 115 120 125
 Glu Ala Arg Glu Ile Met Gln Asp Thr Lys Glu Ala Val Phe Gly Asn
 130 135 140
 Arg Met Asp Ile Ala Ala Met Ala Ile Gly Gly Val Lys Tyr Asp Leu
 145 150 155 160
 Asp Lys Asp Gly Arg Asp Tyr Phe Ile Gly Gln Leu Asp Lys Leu Glu
 165 170 175
 Pro Thr Leu Arg Asp Glu Ile Ile Pro Leu Tyr Gln Thr Asn Pro Ser
 180 185 190
 Ile Val Asp Arg Thr Arg Gly Ile Gly Val Leu Ser Ala Ala Asp Cys
 195 200 205
 Val Asp Tyr Gly Leu Met Gly Pro Val Ala Arg Gly Ser Gly His Ala
 210 215 220
 Tyr Asp Val Arg Lys Gln Ala Pro Tyr Ala Val Tyr Asp Arg Leu Asp
 225 230 235 240
 Phe Glu Met Ala Leu Gly Glu His Gly Asp Val Trp Ser Arg Ala Met
 245 250 255
 Val Arg Trp Gln Glu Ala Leu Thr Ser Ile Gly Leu Ile Arg Gln Cys
 260 265 270
 Leu Arg Asp Met Pro Asp Gly Pro Thr Lys Ala Gly Pro Val Pro Pro
 275 280 285
 Ile Pro Ala Gly Glu Ala Val Ala Lys Thr Glu Ala Pro Arg Gly Glu
 290 295 300

DESUanglais-seql.txt
 Leu Ile Tyr Tyr Leu Lys Thr Asn Gly Thr Asp Arg Pro Glu Arg Leu
 305 310 315 320
 Lys Trp Arg Val Pro Thr Tyr Met Asn Trp Asp Ala Leu Asn Val Met
 325 330 335
 Met Ala Gly Ala Arg Ile Ser Asp Ile Pro Leu Ile Val Asn Ser Ile
 340 345 350
 Asp Pro Cys Ile Ser Cys Thr Glu Arg
 355 360

<210> 15
 <211> 1716
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)..(1716)
 <223>

<400> 15
 gtg aac gtt aat tca tca tca aat cgt ggc gaa gcg att ctc gcc gcc 48
 Val Asn Val Asn Ser Ser Ser Asn Arg Gly Glu Ala Ile Leu Ala Ala
 1 5 10 15
 ctg aaa acg cag ttc ccc ggc gcg gtg ctg gat gaa gag cga caa acg 96
 Leu Lys Thr Gln Phe Pro Gly Ala Val Leu Asp Glu Glu Arg Gln Thr
 20 25 30
 cct gaa cag gtc acc att acg gtg aaa atc aat ctg ctg cct gac gtt 144
 Pro Glu Gln Val Thr Ile Thr Val Lys Ile Asn Leu Leu Pro Asp Val
 35 40 45
 gta cag tat ctt tat tat caa cat gat ggc tgg ctt ccg gtc ctg ttt 192
 Val Gln Tyr Leu Tyr Tyr Gln His Asp Gly Trp Leu Pro Val Leu Phe
 50 55 60
 ggc aac gac gag cgg aca ctt aac ggt cat tac gcg gtt tat tat gcc 240
 Gly Asn Asp Glu Arg Thr Leu Asn Gly His Tyr Ala Val Tyr Tyr Ala
 65 70 75 80
 ctt tca atg gaa ggg gcc gaa aaa tgc tgg att gtg gtg aag gcg ctg 288
 Leu Ser Met Glu Gln Ala Glu Lys Cys Trp Ile Val Val Lys Ala Leu
 85 90 95
 gtc gat gcc gac agt cgg gag ttt ccg tca gtc aca ccg cgc gtc cct 336
 Val Asp Ala Asp Ser Arg Glu Phe Pro Ser Val Thr Pro Arg Val Pro
 100 105 110
 gcc gcg gtc tgg ggc gag cga gaa att cgt gat atg tac ggg ctg att 384
 Ala Ala Val Trp Gly Glu Arg Glu Ile Arg Asp Met Tyr Gly Leu Ile
 115 120 125
 ccg gtt ggc ctg ccg gat cag cgt cgc ctg gtg ttg ccc gat gac tgg 432
 Pro Val Gly Leu Pro Asp Gln Arg Arg Leu Val Leu Pro Asp Asp Trp
 130 135 140
 ccg gaa gat atg cat ccg ctg cgc aaa gat gcg atg gat tat cga ctg 480
 Pro Glu Asp Met His Pro Leu Arg Lys Asp Ala Met Asp Tyr Arg Leu
 145 150 155 160
 cgc cct gaa ccg acg act gat tcc gaa acg tat ccg ttt atc aat gag 528
 Arg Pro Glu Pro Thr Thr Asp Ser Glu Thr Tyr Pro Phe Ile Asn Glu
 165 170 175
 ggc aac agc ggt gcg cgg gtg atc cct gtc ggc ccg ctg cat atc acc 576
 Gly Asn Ser Gly Ala Arg Val Ile Pro Val Gly Pro Leu His Ile Thr
 180 185 190
 tcc gat gaa ccg ggt cac ttc cgc ttg ttt gtg gat ggc gag caa att 624
 Ser Asp Glu Pro Gly His Phe Arg Leu Phe Val Asp Gly Glu Gln Ile
 195 200 205
 gtc gat gct gat tac cgt ctg ttt tat gtc cat cgc ggc atg gag aaa 672
 Val Asp Ala Asp Tyr Arg Leu Phe Tyr Val His Arg Gly Met Glu Lys
 210 215 220
 ctg gca gaa acg cgg atg ggc tac aac gaa gtg acc ttc tta tcg gac 720
 Leu Ala Glu Thr Arg Met Gly Tyr Asn Glu Val Thr Phe Leu Ser Asp
 225 230 235 240
 cgc gtg tgt ggg att tgc ggt ttt gcc cac agt gtg gcc tat acc aac 768

DESUanglais-seq1.txt

Arg Val Cys Gly Ile Cys Gly Phe Ala His Ser Val Ala Tyr Thr Asn	
245 250 255	
tcg gtt gaa aat gca ctg ggg att gag gtg ccg caa cga gcg cat acc	816
Ser Val Glu Asn Ala Leu Gly Ile Glu Val Pro Gln Arg Ala His Thr	
260 265 270	
att cgc tcg att ctg ctg gaa gtc gaa cgg cta cac agt cat ttg ctc	864
Ile Arg Ser Ile Leu Leu Glu Val Glu Arg Leu His Ser His Leu Leu	
275 280 285	
aac ctt ggc ctc tcc tgc cat ttt gtt gga ttt gat acc ggc ttt atg	912
Asn Leu Gly Leu Ser Cys His Phe Val Gly Phe Asp Thr Gly Phe Met	
290 295 300	
caa ttt ttc cgc gtg cgg gaa aag tcg atg aca atg gcg gaa ttg ctg	960
Gln Phe Phe Arg Val Arg Glu Lys Ser Met Thr Met Ala Glu Leu Leu	
305 310 315 320	
acc ggg tcg cgt aaa acc tac ggt ctg aat ctg att ggt ggt gtt cgc	1008
Thr Gly Ser Arg Thr Tyr Gly Leu Asn Leu Ile Gly Gly Val Arg	
325 330 335	
cgc gat att ctc aaa gag caa cgt ctg caa acg ctg aaa ctg gtg cgc	1056
Arg Asp Ile Leu Lys Glu Gln Arg Leu Gln Thr Leu Lys Leu Val Arg	
340 345 350	
gag atg cgc gcc gac gtg tcg gag ctg gta gaa atg ctg ctt gcc acg	1104
Glu Met Arg Ala Asp Val Ser Glu Leu Val Glu Met Leu Leu Ala Thr	
355 360 365	
ccg aat atg gaa caa cgc act cag ggc att ggc att ctc gac cga caa	1152
Pro Asn Met Glu Gln Arg Thr Gln Gly Ile Gly Ile Leu Asp Arg Gln	
370 375 380	
atc gcc cgt gat tat agc cct gta ggg ccg ctg atc cgc ggc agt ggt	1200
Ile Ala Arg Asp Tyr Ser Pro Val Gly Pro Ile Arg Gly Ser Gly	
385 390 395 400	
ttt gcc cgt gat ttg cgc ttt gat cac ccc tac gcc gac tac ggc aat	1248
Phe Ala Arg Asp Leu Arg Phe Asp His Pro Tyr Ala Asp Tyr Gly Asn	
405 410 415	
att cca aaa aca ctg ttt acc ttc acc ggc ggc gat gtt ttc tcc cgc	1296
Ile Pro Lys Thr Leu Phe Thr Phe Thr Gly Gly Asp Val Phe Ser Arg	
420 425 430	
gtg atg gtc cgt gtc aaa gag acg ttt gat tcg ctg gca atg ctg gaa	1344
Val Met Val Arg Val Lys Glu Thr Phe Asp Ser Leu Ala Met Leu Glu	
435 440 445	
ttt gct ctc gac aac atg ccg gat acc cca ctg ctg acc gaa ggc ttt	1392
Phe Ala Leu Asp Asn Met Asp Thr Pro Leu Leu Thr Glu Gly Phe	
450 455 460	
agc tat aaa cct cac gca ttc gcg ctc ggc ttt gtt gaa gcg cca cgc	1440
Ser Tyr Lys Pro His Ala Phe Ala Leu Gly Phe Val Glu Ala Pro Arg	
465 470 475 480	
ggt gaa gac gtg cac tgg agc atg ctc ggt gat aac caa aaa ttg ttc	1488
Gly Glu Asp Val His Trp Ser Met Leu Gly Asp Asn Gln Lys Leu Phe	
485 490 495	
cgc tgg cgc tgc cgt gcc gcc acc tac gcc aac tgg ccg gtg ttg cgt	1536
Arg Trp Arg Cys Arg Ala Ala Thr Tyr Ala Asn Trp Pro Val Leu Arg	
500 505 510	
tac atg ctg cgc ggc aat acc gtt tct gac gca ccg ctg att atc ggt	1584
Tyr Met Leu Arg Gly Asn Thr Val Ser Asp Ala Pro Leu Ile Ile Gly	
515 520 525	
agc ctt gat ccc tgc tac tcc tgt acc gac cgt gtg acg ctg gtt gat	1632
Ser Leu Asp Pro Cys Tyr Ser Cys Thr Asp Arg Val Thr Leu Val Asp	
530 535 540	
gtg cgc aag cgc cag tca aaa acc gtg ccg tat aaa gag atc gaa cgc	1680
Val Arg Lys Arg Gln Ser Lys Thr Val Pro Tyr Lys Glu Ile Glu Arg	
545 550 555 560	
tac ggc att gat cgt aac cgt tcg ccg ctg aag taa	1716
Tyr Gly Ile Asp Arg Asn Arg Ser Pro Leu Lys	
565 570	

DESUanglais-seq1.txt

<211> 571

<212> PRT

<213> Escherichia coli

<400> 16

Val Asn Val Asn Ser Ser Asn Arg Gly Glu Ala Ile Leu Ala Ala
 1 5 10 15
 Leu Lys Thr Gln Phe Pro Gly Ala Val Leu Asp Glu Glu Arg Gln Thr
 20 25 30
 Pro Glu Gln Val Thr Ile Thr Val Lys Ile Asn Leu Leu Pro Asp Val
 35 40 45
 Val Gln Tyr Leu Tyr Tyr Gln His Asp Gly Trp Leu Pro Val Leu Phe
 50 55 60
 Gly Asn Asp Glu Arg Thr Leu Asn Gly His Tyr Ala Val Tyr Tyr Ala
 65 70 75 80
 Leu Ser Met Glu Gly Ala Glu Lys Cys Trp Ile Val Val Lys Ala Leu
 85 90 95
 Val Asp Ala Asp Ser Arg Glu Phe Pro Ser Val Thr Pro Arg Val Pro
 100 105 110
 Ala Ala Val Trp Gly Glu Arg Glu Ile Arg Asp Met Tyr Gly Leu Ile
 115 120 125
 Pro Val Gly Leu Pro Asp Gln Arg Arg Leu Val Leu Pro Asp Asp Trp
 130 135 140
 Pro Glu Asp Met His Pro Leu Arg Lys Asp Ala Met Asp Tyr Arg Leu
 145 150 155 160
 Arg Pro Glu Pro Thr Thr Asp Ser Glu Thr Tyr Pro Phe Ile Asn Glu
 165 170 175
 Gly Asn Ser Gly Ala Arg Val Ile Pro Val Gly Pro Leu His Ile Thr
 180 185 190
 Ser Asp Glu Pro Gly His Phe Arg Leu Phe Val Asp Gly Glu Gln Ile
 195 200 205
 Val Asp Ala Asp Tyr Arg Leu Phe Tyr Val His Arg Gly Met Glu Lys
 210 215 220
 Leu Ala Glu Thr Arg Met Gly Tyr Asn Glu Val Thr Phe Leu Ser Asp
 225 230 235 240
 Arg Val Cys Gly Ile Cys Gly Phe Ala His Ser Val Ala Tyr Thr Asn
 245 250 255
 Ser Val Glu Asn Ala Leu Gly Ile Glu Val Pro Gln Arg Ala His Thr
 260 265 270
 Ile Arg Ser Ile Leu Leu Glu Val Glu Arg Leu His Ser His Leu Leu
 275 280 285
 Asn Leu Gly Leu Ser Cys His Phe Val Gly Phe Asp Thr Gly Phe Met
 290 295 300
 Gln Phe Phe Arg Val Arg Glu Lys Ser Met Thr Met Ala Glu Leu Leu
 305 310 315 320
 Thr Gly Ser Arg Lys Thr Tyr Gly Leu Asn Leu Ile Gly Gly Val Arg
 325 330 335
 Arg Asp Ile Leu Lys Glu Gln Arg Leu Gln Thr Leu Lys Leu Val Arg
 340 345 350
 Glu Met Arg Ala Asp Val Ser Glu Leu Val Glu Met Leu Leu Ala Thr
 355 360 365
 Pro Asn Met Glu Gln Arg Thr Gln Gly Ile Gly Ile Leu Asp Arg Gln
 370 375 380
 Ile Ala Arg Asp Tyr Ser Pro Val Gly Pro Leu Ile Arg Gly Ser Gly
 385 390 395 400
 Phe Ala Arg Asp Leu Arg Phe Asp His Pro Tyr Ala Asp Tyr Gly Asn
 405 410 415
 Ile Pro Lys Thr Leu Phe Thr Phe Thr Gly Gly Asp Val Phe Ser Arg
 420 425 430

DESUanglais-seql.txt

Val Met Val Arg Val Lys Glu Thr Phe Asp Ser Leu Ala Met Leu Glu
 435 440 445
 Phe Ala Leu Asp Asn Met Pro Asp Thr Pro Leu Leu Thr Glu Gly Phe
 450 455 460
 Ser Tyr Lys Pro His Ala Phe Ala Leu Gly Phe Val Glu Ala Pro Arg
 465 470 475 480
 Gly Glu Asp Val His Trp Ser Met Leu Gly Asp Asn Gln Lys Leu Phe
 485 490 495
 Arg Trp Arg Cys Arg Ala Ala Thr Tyr Ala Asn Trp Pro Val Leu Arg
 500 505 510
 Tyr Met Leu Arg Gly Asn Thr Val Ser Asp Ala Pro Leu Ile Ile Gly
 515 520 525
 Ser Leu Asp Pro Cys Tyr Ser Cys Thr Asp Arg Val Thr Leu Val Asp
 530 535 540
 Val Arg Lys Arg Gln Ser Lys Thr Val Pro Tyr Lys Glu Ile Glu Arg
 545 550 555 560
 Tyr Gly Ile Asp Arg Asn Arg Ser Pro Leu Lys
 565 570

<210> 17
 <211> 1710
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)..(1710)
 <223>

<400> 17
 atg tct gaa gaa aaa tta ggt caa cat tat ctc gcc gcg ctg aat gag 48
 Met Ser Glu Glu Lys Leu Gly Gln His Tyr Leu Ala Ala Leu Asn Glu
 1 5 10 15
 gca ttt ccg ggc gtc gtg ctg gac cac gcc tgg cag acc aaa gat cag 96
 Ala Phe Pro Gly Val Val Leu Asp His Ala Trp Gln Thr Lys Asp Gln
 20 25 30
 ctg act gtc acc gta aag gtg aac tat ctg ccg gaa gtg gtg gag ttt 144
 Leu Thr Val Thr Val Lys Val Asn Tyr Leu Pro Glu Val Val Glu Phe
 35 40 45
 ctc tac tac aag cag ggg ggc tgg ctg tcg gtg ctt ttt ggt aac gac 192
 Leu Tyr Tyr Lys Gln Gly Gly Trp Leu Ser Val Leu Phe Gly Asn Asp
 50 55 60
 gaa cgc aaa ctg aat ggt cat tac gcc gtt tac tac gtg ctg tcg atg 240
 Glu Arg Lys Leu Asn Gly His Tyr Ala Val Tyr Tyr Val Leu Ser Met
 65 70 75 80
 gag aag ggg act aag tgc tgg gta acg gtt cgc gtc gaa gtt gat gcc 288
 Glu Lys Gly Thr Lys Cys Trp Val Thr Val Arg Val Glu Val Asp Ala
 85 90 95
 aac aaa ccg gag tat cct tcc gtg acg ccg cgc gtt ccg gct gcg gtg 336
 Asn Lys Pro Glu Tyr Pro Ser Val Thr Pro Arg Val Pro Ala Ala Val
 100 105 110
 tgg ggc gag cgt gaa gta cgt gat atg tac ggt ttg att ccg gtt ggt 384
 Trp Gly Glu Arg Glu Val Arg Asp Met Tyr Gly Leu Ile Pro Val Gly
 115 120 125
 ttg ccg gat gaa cgt cgt ctg gtg ctg ccg gat gac tgg ccg gat gaa 432
 Leu Pro Asp Glu Arg Arg Leu Val Leu Pro Asp Trp Pro Asp Glu
 130 135 140
 ctt tat ccg ctg cgt aaa gac agc atg gat tat cgt cag cgt ccg gca 480
 Leu Tyr Pro Leu Arg Lys Asp Ser Met Asp Tyr Arg Gln Arg Pro Ala
 145 150 155 160
 ccg acc acc gat gct gaa acc tac gag ttc atc aac gaa ctg ggc gac 528
 Pro Thr Thr Asp Ala Glu Thr Tyr Glu Phe Ile Asn Glu Leu Gly Asp
 165 170 175
 aag aaa aac aac gtc gtg ccg att ggt ccg ctg cac gtc act tct gac 576
 Lys Lys Asn Asn Val Val Pro Ile Gly Pro Leu His Val Thr Ser Asp

DESUanglais-seq1.txt																	
180						185						190					
gaa Glu	ccg Pro	ggc Gly 195	cac His	ttc Phe	cgt Arg	ctg Leu	ttc Phe 200	gtc Val	gat Asp	ggc Gly	gaa Glu	aac Asn 205	att Ile	atc Ile	gac Asp		624
gcc Ala	gac Asp 210	tac Tyr	cgc Arg	ctg Leu	ttc Phe	tat Tyr 215	gtc Val	cat His	cgc Arg	ggc Gly	atg Met 220	gaa Glu	aaa Lys	ctg Leu	gca Ala		672
gaa Glu 225	acc Thr	cgc Arg	atg Met	ggt Gly	tat Tyr 230	aac Asn	gaa Glu	gtg Val	acc Thr	ttc Phe 235	ctc Leu	tct Ser	gac Asp	cgt Arg	gtg Val 240		720
tgc Cys	ggg Gly	atc Ile	tgc Cys	ggt Gly 245	ttt Phe	gct Ala	cac His	agc Ser	acc Thr 250	gcc Ala	tac Tyr	acc Thr	acg Thr	tcg Ser 255	gtg Val		768
gaa Glu	aac Asn	gcg Ala	atg Met 260	ggt Gly	att Ile	cag Gln	gtg Val	cca Pro 265	gaa Glu	cgt Arg	gcg Ala	cag Gln	atg Met 270	atc Ile	cgc Arg		816
gcc Ala	att Ile	ctg Leu 275	ctg Leu	gag Glu	gta Val	gaa Glu	cgt Arg 280	ctg Leu	cac His	tcg Ser	cat His	ctg Leu 285	ctc Leu	aac Asn	ctc Leu		864
ggc Gly 290	ctc Leu	gcc Ala	tgt Cys	cac His	ttt Phe	acc Thr 295	ggc Gly	ttt Phe	gac Asp	tcc Ser	ggc Gly 300	ttt Phe	atg Met	cag Gln	ttc Phe		912
ttc Phe 305	cgc Arg	gtg Val	cgt Arg	gaa Glu	acc Thr 310	tcc Ser	atg Met	aaa Lys	atg Met	gca Ala 315	gag Glu	atc Ile	ctt Leu	acc Thr	ggt Gly 320		960
gcg Ala	cgt Arg	aaa Lys	acc Thr 325	tac Tyr	ggc Gly	ctg Leu	aac Asn	ctg Leu	atc Ile 330	ggc Gly	ggg Gly	att Ile	cgt Arg	cgc Arg 335	gat Asp		1008
ctg Leu	ctg Leu	aaa Lys	gat Asp 340	gac Asp	atg Met	atc Ile	cag Gln	acc Thr 345	cgt Arg	caa Gln	ctg Leu	gcg Ala	caa Gln 350	cag Gln	atg Met		1056
cgt Arg	cgt Arg	gaa Glu 355	gtg Val	cag Gln	gag Glu	ctg Leu	gtg Val 360	gat Asp	gtg Val	ctg Leu	ctg Leu	agt Ser 365	acg Thr	ccg Pro	aac Asn		1104
atg Met 370	gaa Glu	cag Gln	cgc Arg	act Thr	gtc Val	ggc Gly 375	att Ile	ggt Gly	cgt Arg	ctg Leu	gac Asp 380	ccg Pro	gaa Glu	atc Ile	gct Ala		1152
cgc Arg 385	gac Asp	ttc Phe	agt Ser	aac Asn	gtc Val 390	ggc Gly	ccg Pro	atg Met	gtc Val	cgt Arg 395	gcc Ala	agc Ser	ggt Gly	cac His	gcc Ala 400		1200
cgc Arg	gat Asp	acc Thr	cgc Arg	gcc Ala 405	gat Asp	cac His	ccg Pro	ttt Phe	gtt Val 410	ggt Gly	tat Tyr	ggc Gly	ctg Leu	ctg Leu 415	cca Pro		1248
atg Met	gaa Glu	gtc Val	cac His 420	agc Ser	gag Glu	cag Gln	ggc Gly 425	tgc Cys	gac Asp	gtt Val	att Ile	tcg Ser	cgt Arg 430	ctg Leu	aaa Lys		1296
gtg Val	cgt Arg	att Ile 435	aac Asn	gaa Glu	gtc Val	tat Tyr 440	acc Thr	gcg Ala	ctg Leu	aac Asn	atg Met	atc Ile 445	gac Asp	tac Tyr	ggt Gly		1344
ctg Leu	gat Asp 450	aac Asn	ctg Leu	ccg Pro	ggc Gly 455	ggc Gly	ccg Pro	ctg Leu	atg Met	gtg Val	gaa Glu 460	ggc Gly	ttt Phe	acc Thr	tac Tyr		1392
att Ile 465	ccg Pro	cac His	cgt Arg	ttt Phe	gcg Ala 470	ctg Leu	ggc Gly	ttt Phe	gcc Ala	gaa Glu 475	gcg Ala	ccg Pro	cgc Arg	ggc Gly	gat Asp 480		1440
gat Asp	atc Ile	cac His	tgg Trp 485	agc Ser	atg Met	acc Thr	ggc Gly	gac Asp	aac Asn 490	cag Gln	aag Lys	ctg Leu	tac Tyr	cgc Arg 495	tgg Trp		1488
cgc Arg	tgc Cys	cgt Arg	gcc Ala 500	gcg Ala	acc Thr	tac Tyr	gcg Ala	aac Asn 505	tgg Trp	ccg Pro	acc Thr	ctg Leu	cgc Arg 510	tac Tyr	atg Met		1536
ctg Leu	cgc Arg	ggc Gly 515	aac Asn	acc Thr	gtt Val	tct Ser	gat Asp 520	gcg Ala	ccg Pro	ctg Leu	att Ile	atc Ile 525	ggt Gly	agt Ser	ctg Leu		1584

DESUanglais-seql.txt
 gac cct tgc tac tcc tgt acc gac cgc atg acc gtg gtc gat gtg cgt 1632
 Asp Pro Cys Tyr Ser Cys Thr Asp Arg Met Thr Val Val Asp Val Arg
 530 535 540
 aag aaa aag agc aaa gtg gtg ccg tac aaa gaa ctc gag cgt tac agc 1680
 Lys Lys Lys Ser Lys Val Val Pro Tyr Lys Glu Leu Glu Arg Tyr Ser
 545 550 555 560
 att gag cgt aaa aac tcg ccg ctg aaa taa 1710
 Ile Glu Arg Lys Asn Ser Pro Leu Lys
 565

<210> 18
 <211> 569
 <212> PRT
 <213> Escherichia coli

<400> 18
 Met Ser Glu Glu Lys Leu Gly Gln His Tyr Leu Ala Ala Leu Asn Glu
 1 5 10 15
 Ala Phe Pro Gly Val Val Leu Asp His Ala Trp Gln Thr Lys Asp Gln
 20 25 30
 Leu Thr Val Thr Val Lys Val Asn Tyr Leu Pro Glu Val Val Glu Phe
 35 40 45
 Leu Tyr Tyr Lys Gln Gly Gly Trp Leu Ser Val Leu Phe Gly Asn Asp
 50 55 60
 Glu Arg Lys Leu Asn Gly His Tyr Ala Val Tyr Tyr Val Leu Ser Met
 65 70 75 80
 Glu Lys Gly Thr Lys Cys Trp Val Thr Val Arg Val Glu Val Asp Ala
 85 90 95
 Asn Lys Pro Glu Tyr Pro Ser Val Thr Pro Arg Val Pro Ala Ala Val
 100 105 110
 Trp Gly Glu Arg Glu Val Arg Asp Met Tyr Gly Leu Ile Pro Val Gly
 115 120 125
 Leu Pro Asp Glu Arg Arg Leu Val Leu Pro Asp Asp Trp Pro Asp Glu
 130 135 140
 Leu Tyr Pro Leu Arg Lys Asp Ser Met Asp Tyr Arg Gln Arg Pro Ala
 145 150 155 160
 Pro Thr Thr Asp Ala Glu Thr Tyr Glu Phe Ile Asn Glu Leu Gly Asp
 165 170 175
 Lys Lys Asn Asn Val Val Pro Ile Gly Pro Leu His Val Thr Ser Asp
 180 185 190
 Glu Pro Gly His Phe Arg Leu Phe Val Asp Gly Glu Asn Ile Ile Asp
 195 200 205
 Ala Asp Tyr Arg Leu Phe Tyr Val His Arg Gly Met Glu Lys Leu Ala
 210 215 220
 Glu Thr Arg Met Gly Tyr Asn Glu Val Thr Phe Leu Ser Asp Arg Val
 225 230 235 240
 Cys Gly Ile Cys Gly Phe Ala His Ser Thr Ala Tyr Thr Thr Ser Val
 245 250 255
 Glu Asn Ala Met Gly Ile Gln Val Pro Glu Arg Ala Gln Met Ile Arg
 260 265 270
 Ala Ile Leu Leu Glu Val Glu Arg Leu His Ser His Leu Leu Asn Leu
 275 280 285
 Gly Leu Ala Cys His Phe Thr Gly Phe Asp Ser Gly Phe Met Gln Phe
 290 295 300
 Phe Arg Val Arg Glu Thr Ser Met Lys Met Ala Glu Ile Leu Thr Gly
 305 310 315 320
 Ala Arg Lys Thr Tyr Gly Leu Asn Leu Ile Gly Gly Ile Arg Arg Asp
 325 330 335
 Leu Leu Lys Asp Asp Met Ile Gln Thr Arg Gln Leu Ala Gln Gln Met
 340 345 350
 Arg Arg Glu Val Gln Glu Leu Val Asp Val Leu Leu Ser Thr Pro Asn

DESUanglais-seql.txt

355 360 365

Met Glu Gln Arg Thr Val Gly Ile Gly Arg Leu Asp Pro Glu Ile Ala
 370 375 380

Arg Asp Phe Ser Asn Val Gly Pro Met Val Arg Ala Ser Gly His Ala
 385 390 395 400

Arg Asp Thr Arg Ala Asp His Pro Phe Val Gly Tyr Gly Leu Leu Pro
 405 410 415

Met Glu Val His Ser Glu Gln Gly Cys Asp Val Ile Ser Arg Leu Lys
 420 425 430

Val Arg Ile Asn Glu Val Tyr Thr Ala Leu Asn Met Ile Asp Tyr Gly
 435 440 445

Leu Asp Asn Leu Pro Gly Gly Pro Leu Met Val Glu Gly Phe Thr Tyr
 450 455 460

Ile Pro His Arg Phe Ala Leu Gly Phe Ala Glu Ala Pro Arg Gly Asp
 465 470 475 480

Asp Ile His Trp Ser Met Thr Gly Asp Asn Gln Lys Leu Tyr Arg Trp
 485 490 495

Arg Cys Arg Ala Ala Thr Tyr Ala Asn Trp Pro Thr Leu Arg Tyr Met
 500 505 510

Leu Arg Gly Asn Thr Val Ser Asp Ala Pro Leu Ile Ile Gly Ser Leu
 515 520 525

Asp Pro Cys Tyr Ser Cys Thr Asp Arg Met Thr Val Val Asp Val Arg
 530 535 540

Lys Lys Lys Ser Lys Val Val Pro Tyr Lys Glu Leu Glu Arg Tyr Ser
 545 550 555 560

Ile Glu Arg Lys Asn Ser Pro Leu Lys
 565

<210> 19
 <211> 1737
 <212> DNA
 <213> *Erwinia carotovora*

<220>
 <221> CDS
 <222> (1)..(1737)
 <223>

<400> 19
 gtg act tac gat aat cac gtc agg gcc att cag agc gac caa aaa ctg 48
 Val Thr Tyr Asp Asn His Val Arg Ala Ile Gln Ser Asp Gln Lys Leu
 1 5 10 15

ggg ggg aac tac ctg gca caa att cgc caa aaa ttc ccg gcg gcg gta 96
 Gly Gly Asn Tyr Leu Ala Gln Ile Arg Gln Lys Phe Pro Ala Ala Val
 20 25 30

ctc gat gag gag tgg caa act cac gat caa ctg act att acg ata aaa 144
 Leu Asp Glu Glu Trp Gln Thr His Asp Gln Leu Thr Ile Thr Ile Lys
 35 40 45

acc gag tcg ctg cca gac gtc gta gag ttt att tat tac ccg tta ggc 192
 Thr Glu Ser Leu Pro Asp Val Val Glu Phe Ile Tyr Tyr Pro Leu Gly
 50 55 60

ggc tgg ctg ccg gtc ctg ttt ggc aac gac gaa cga aca tta aac ggt 240
 Gly Trp Leu Pro Val Leu Phe Gly Asn Asp Glu Arg Thr Leu Asn Gly
 65 70 75 80

aat tac gcg gtc tat tat gcg ctc tcc atg gaa cag ggc gag aag tgc 288
 Asn Tyr Ala Val Tyr Tyr Ala Leu Ser Met Glu Gln Gly Glu Lys Cys
 85 90 95

tgg atc gtg gtt aag gcg tat gtg gat ccc ctg acg ctg gaa ttc ccc 336
 Trp Ile Val Val Lys Ala Tyr Val Asp Pro Leu Thr Leu Glu Phe Pro
 100 105 110

tcc gtc acc ccg cga gtt ccc gcc gcc gtc tgg ggg gag cgc gaa att 384
 Ser Val Thr Pro Arg Val Pro Ala Val Trp Gly Glu Arg Glu Ile
 115 120 125

cga gac atg tac ggc ctg ata ccc gtc ggg cta ccg gat gag cgc cgt 432

DESUanglais-seql.txt															
Arg	Asp	Met	Tyr	Gly	Leu	Ile	Pro	Val	Gly	Leu	Pro	Asp	Glu	Arg	Arg
130	130					135				140					
ctg	gtg	ctg	ccg	gat	gac	tgg	ccc	gac	gat	ctc	tac	ccg	ctg	cgt	aaa
Leu	Val	Leu	Pro	Asp	Asp	Trp	Pro	Asp	Asp	Leu	Tyr	Pro	Leu	Arg	Lys
145					150					155					160
gac	acc	atg	gac	tat	cgg	cta	cgc	cca	gag	cca	acg	acc	caa	att	gaa
Asp	Thr	Met	Asp	Tyr	Arg	Leu	Arg	Pro	Glu	Pro	Thr	Thr	Gln	Ile	Glu
				165					170					175	
acc	tat	cag	ttt	aaa	aat	gaa	ggc	ggc	agc	gag	gca	cgg	atc	gtc	ccc
Thr	Tyr	Gln	Phe	Lys	Asn	Glu	Gly	Gly	Ser	Glu	Ala	Arg	Ile	Val	Pro
			180					185					190		
gtc	ggt	ccg	ctg	cac	att	acc	tca	gat	gaa	ccg	ggc	cac	ttc	cgc	ctg
Val	Gly	Pro	Leu	His	Ile	Thr	Ser	Asp	Glu	Pro	Gly	His	Phe	Arg	Leu
		195					200					205			
ttt	ggt	gac	gga	gaa	cgt	att	gtc	gat	gcg	gac	tac	cgc	cta	ttc	tat
Phe	Val	Asp	Gly	Glu	Arg	Ile	Val	Asp	Ala	Asp	Tyr	Arg	Leu	Phe	Tyr
	210					215					220				
gtc	cac	cgc	ggc	atg	gaa	aaa	ctg	gcg	gaa	acc	cgc	atg	ggc	tat	aac
Val	His	Arg	Gly	Met	Glu	Lys	Leu	Ala	Glu	Thr	Arg	Met	Gly	Tyr	Asn
225					230					235					240
gaa	gtg	acc	ttc	ctg	tct	gat	cgg	gta	tgt	ggg	atc	tgt	ggt	ttc	gcg
Glu	Val	Thr	Phe	Leu	Ser	Asp	Arg	Val	Cys	Gly	Ile	Cys	Gly	Phe	Ala
				245					250					255	
cac	agc	gtg	gct	tat	acc	tcc	tcg	gtg	gag	aac	gca	ctg	ggc	atc	tac
His	Ser	Val	Ala	Tyr	Thr	Ser	Ser	Val	Glu	Asn	Ala	Leu	Gly	Ile	Tyr
			260					265					270		
gtg	cca	ccg	cgc	gct	cac	gct	atc	cgc	agt	ata	ttg	ctg	gaa	gtg	gag
Val	Pro	Arg	Ala	His	Ala	Ile	Arg	Ser	Ile	Ile	Leu	Leu	Glu	Val	Glu
		275					280					285			
cgc	ctg	cac	agc	cac	ctg	ctc	aat	atc	ggg	ttg	tcc	agc	cac	ttt	att
Arg	Leu	His	Ser	His	Leu	Leu	Asn	Ile	Gly	Leu	Ser	Ser	His	Phe	Ile
	290					295					300				
ggc	ttc	gat	act	ggg	ttt	atg	cag	ttc	ttc	cga	gtc	aga	gag	aaa	tcc
Gly	Phe	Asp	Thr	Gly	Phe	Met	Gln	Phe	Phe	Arg	Val	Arg	Glu	Lys	Ser
305					310					315					320
atg	gcg	ctg	gcg	gag	ttg	cta	act	ggc	gcg	agg	aaa	acc	tac	gga	ctc
Met	Ala	Leu	Ala	Glu	Leu	Leu	Thr	Gly	Ala	Arg	Lys	Thr	Tyr	Gly	Leu
				325					330					335	
aat	ttg	atc	ggc	ggt	atc	cgc	cgc	gac	atc	ctg	aaa	gaa	cag	cgt	cag
Asn	Leu	Ile	Gly	Gly	Ile	Arg	Arg	Asp	Ile	Leu	Lys	Glu	Gln	Arg	Gln
			340					345					350		
aaa	ggg	atc	aaa	ctg	gtc	cag	gaa	atg	cgg	gcc	gaa	gtg	acc	caa	ctg
Lys	Gly	Ile	Lys	Leu	Val	Gln	Glu	Met	Arg	Ala	Glu	Val	Thr	Gln	Leu
		355					360					365			
gtc	gat	atg	ctg	ctc	aac	aca	ccc	aat	atg	gag	caa	cgt	acc	cag	ggc
Val	Asp	Met	Leu	Leu	Asn	Thr	Pro	Asn	Met	Glu	Gln	Arg	Thr	Gln	Gly
	370					375					380				
atc	ggc	ctg	ctg	gat	cgt	aag	atc	gcg	cgt	gac	tac	agc	ccg	ggt	ggc
Ile	Gly	Leu	Leu	Asp	Arg	Lys	Ile	Ala	Arg	Asp	Tyr	Ser	Pro	Val	Gly
	385				390					395					400
ccg	atg	att	cgc	ggc	agt	ggt	ttt	gcc	cgc	gat	atg	cgt	ttc	gac	cat
Pro	Met	Ile	Arg	Gly	Ser	Gly	Phe	Ala	Arg	Asp	Met	Arg	Phe	Asp	His
				405					410					415	
gat	tac	gcc	ggc	tac	agc	gca	ctg	ccg	aaa	acg	ctg	ttc	aca	ctg	gac
Asp	Tyr	Ala	Gly	Tyr	Ser	Ala	Leu	Pro	Lys	Thr	Leu	Phe	Thr	Leu	Asp
			420					425					430		
ggc	tgc	gat	gtg	ttc	tcc	cgc	gta	atg	gta	cgg	gtg	caa	gag	acg	ctg
Gly	Cys	Asp	Val	Phe	Ser	Arg	Val	Met	Val	Arg	Val	Gln	Glu	Thr	Leu
		435					440					445			
gaa	tct	ttg	tcc	atg	gtg	gag	ttc	ggt	ctg	gat	cac	ctg	ccg	gaa	ggt
Glu	Ser	Leu	Ser	Met	Val	Glu	Phe	Gly	Leu	Asp	His	Leu	Pro	Glu	Gly
	450					455					460				
ccc	ctg	tta	acc	gaa	gga	ttt	acc	tac	cga	ccg	tat	aag	ttc	gca	ctg
Pro	Leu	Leu	Thr	Glu	Gly	Phe	Thr	Tyr	Arg	Pro	Tyr	Lys	Phe	Ala	Leu

DESUanglais-seql.txt

465	470	475	480	
ggc tat acc gaa gcc ccg cgc gga gaa gac gtg cac tgg agc atg cta				1488
Gly Tyr Thr Glu Ala Pro Arg Gly Glu Asp Val His Trp Ser Met Leu	485	490	495	
ggc gac aac cag aaa ctg ttc cgc tgg cgc tgc cgc gcg gca act tac				1536
Gly Asp Asn Gln Lys Leu Phe Arg Trp Arg Cys Arg Ala Ala Thr Tyr	500	505	510	
gcc aac tgg ccg gta ctg cgc tat atg ctg cgc ggt aac acc atc tcc				1584
Ala Asn Trp Pro Val Leu Arg Tyr Met Leu Arg Gly Asn Thr Ile Ser	515	520	525	
gat gcg ccg ctt att atc ggt agt ctc gat ccc tgc tat tca tgc acc				1632
Asp Ala Pro Leu Ile Ile Gly Ser Leu Asp Pro Cys Tyr Ser Cys Thr	530	535	540	
gac cgc gtt acg ctg gtg gac att aaa aaa cgc aaa tcc act acg gtg				1680
Asp Arg Val Thr Leu Val Asp Ile Lys Lys Arg Lys Ser Thr Thr Val	545	550	555	560
cct tac aaa gag atc gag cgt tac agc att gag cgt aag aat tcg ccg				1728
Pro Tyr Lys Glu Ile Glu Arg Tyr Ser Ile Glu Arg Lys Asn Ser Pro	565	570	575	
ctg aaa tga				1737
Leu Lys				

<210> 20
 <211> 578
 <212> PRT
 <213> Erwinia carotovora

<400> 20
 Val Thr Tyr Asp Asn His Val Arg Ala Ile Gln Ser Asp Gln Lys Leu
 1 5 10 15
 Gly Gly Asn Tyr Leu Ala Gln Ile Arg Gln Lys Phe Pro Ala Ala Val
 20 25 30
 Leu Asp Glu Glu Trp Gln Thr His Asp Gln Leu Thr Ile Thr Ile Lys
 35 40 45
 Thr Glu Ser Leu Pro Asp Val Val Glu Phe Ile Tyr Tyr Pro Leu Gly
 50 55 60
 Gly Trp Leu Pro Val Leu Phe Gly Asn Asp Glu Arg Thr Leu Asn Gly
 65 70 75 80
 Asn Tyr Ala Val Tyr Tyr Ala Leu Ser Met Glu Gln Gly Glu Lys Cys
 85 90 95
 Trp Ile Val Val Lys Ala Tyr Val Asp Pro Leu Thr Leu Glu Phe Pro
 100 105 110
 Ser Val Thr Pro Arg Val Pro Ala Ala Val Trp Gly Glu Arg Glu Ile
 115 120 125
 Arg Asp Met Tyr Gly Leu Ile Pro Val Gly Leu Pro Asp Glu Arg Arg
 130 135 140
 Leu Val Leu Pro Asp Asp Trp Pro Asp Asp Leu Tyr Pro Leu Arg Lys
 145 150 155 160
 Asp Thr Met Asp Tyr Arg Leu Arg Pro Glu Pro Thr Thr Gln Ile Glu
 165 170 175
 Thr Tyr Gln Phe Lys Asn Glu Gly Gly Ser Glu Ala Arg Ile Val Pro
 180 185 190
 Val Gly Pro Leu His Ile Thr Ser Asp Glu Pro Gly His Phe Arg Leu
 195 200 205
 Phe Val Asp Gly Glu Arg Ile Val Asp Ala Asp Tyr Arg Leu Phe Tyr
 210 215 220
 Val His Arg Gly Met Glu Lys Leu Ala Glu Thr Arg Met Gly Tyr Asn
 225 230 235 240
 Glu Val Thr Phe Leu Ser Asp Arg Val Cys Gly Ile Cys Gly Phe Ala
 245 250 255
 His Ser Val Ala Tyr Thr Ser Ser Val Glu Asn Ala Leu Gly Ile Tyr

DESUanglais-seql.txt

260 265 270

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

Arg Leu His Ser His Leu Leu Asn Ile Gly Leu Ser Ser His Phe Ile
 290 295 300

Gly Phe Asp Thr Gly Phe Met Gln Phe Phe Arg Val Arg Glu Lys Ser
 305 310 315 320

Met Ala Leu Ala Glu Leu Leu Thr Gly Ala Arg Lys Thr Tyr Gly Leu
 325 330 335

Asn Leu Ile Gly Gly Ile Arg Arg Asp Ile Leu Lys Glu Gln Arg Gln
 340 345 350

Lys Gly Ile Lys Leu Val Gln Glu Met Arg Ala Glu Val Thr Gln Leu
 355 360 365

Val Asp Met Leu Leu Asn Thr Pro Asn Met Glu Gln Arg Thr Gln Gly
 370 375 380

Ile Gly Leu Leu Asp Arg Lys Ile Ala Arg Asp Tyr Ser Pro Val Gly
 385 390 395 400

Pro Met Ile Arg Gly Ser Gly Phe Ala Arg Asp Met Arg Phe Asp His
 405 410 415

Asp Tyr Ala Gly Tyr Ser Ala Leu Pro Lys Thr Leu Phe Thr Leu Asp
 420 425 430

Gly Cys Asp Val Phe Ser Arg Val Met Val Arg Val Gln Glu Thr Leu
 435 440 445

Glu Ser Leu Ser Met Val Glu Phe Gly Leu Asp His Leu Pro Glu Gly
 450 455 460

Pro Leu Leu Thr Glu Gly Phe Thr Tyr Arg Pro Tyr Lys Phe Ala Leu
 465 470 475 480

Gly Tyr Thr Glu Ala Pro Arg Gly Glu Asp Val His Trp Ser Met Leu
 485 490 495

Gly Asp Asn Gln Lys Leu Phe Arg Trp Arg Cys Arg Ala Ala Thr Tyr
 500 505 510

Ala Asn Trp Pro Val Leu Arg Tyr Met Leu Arg Gly Asn Thr Ile Ser
 515 520 525

Asp Ala Pro Leu Ile Ile Gly Ser Leu Asp Pro Cys Tyr Ser Cys Thr
 530 535 540

Asp Arg Val Thr Leu Val Asp Ile Lys Lys Arg Lys Ser Thr Thr Val
 545 550 555 560

Pro Tyr Lys Glu Ile Glu Arg Tyr Ser Ile Glu Arg Lys Asn Ser Pro
 565 570 575

Leu Lys

<210> 21
 <211> 1710
 <212> DNA
 <213> Salmonella typhi

<220>
 <221> CDS
 <222> (1)..(1710)
 <223>

<400> 21
 atg ttt gaa gaa aaa tta ggt caa caa tac ctt gcg gcg ctg cac cag 48
 Met Phe Glu Glu Lys Leu Gly Gln Gln Tyr 10 Leu Ala Ala Leu His Gln 15
 1

gcg ttt ccg ggc gtc gtg atg gac gaa gcc tgg cag acc aaa gat cag 96
 Ala Phe Pro Gly Val Val Met Asp Glu Ala Trp Gln Thr Lys Asp Gln 20 25 30

ctg act att acg gta aaa gtg aac tat ctg ccg gaa gtg gtg gag ttt 144
 Leu Thr Ile Thr Val Lys Val Asn Tyr Leu Pro Glu Val Val Glu Phe 35 40 45

DESUanglais-seql.txt

ctt tac tac cag cag ggt ggg tgg ctg tcg gtg ctg ttc ggt aat gac	192
Leu Tyr Tyr Gln Gln Gly Gly Trp Leu Ser Val Leu Phe Gly Asn Asp	
50 55 60	
gaa cgc cag ttg tgc ggc cac tat gcc gtt tat tac gtg ctg tcg atg	240
Glu Arg Gln Leu Cys Gly His Tyr Ala Val Tyr Val Leu Ser Met	
65 70 75 80	
gag cag ggc acc aag tgc tgg att acc gtc cgt gtt gaa gtg gat gcc	288
Glu Gln Gly Thr Lys Cys Trp Ile Thr Val Arg Val Glu Val Asp Ala	
85 90 95	
aat aag ctg gaa ttc cca tcc gtt acg ccg cgc gtg ccg gct gcc gtg	336
Asn Lys Leu Glu Phe Pro Ser Val Thr Pro Arg Val Pro Ala Ala Val	
100 105 110	
tgg ggt gag cgc gaa gta cgc gac atg tac ggt tta atc ccg gtc ggt	384
Trp Gly Glu Arg Glu Val Arg Asp Met Tyr Gly Leu Ile Pro Val Gly	
115 120 125	
ctg ccg gac gag cgc cgt ctg gtg ctg ccg gac gac tgg ccg gat gaa	432
Leu Pro Asp Glu Arg Arg Leu Val Leu Pro Asp Asp Trp Pro Asp Glu	
130 135 140	
ctc tat ccg ctg cgt aaa gac agc atg gat tat cgt cag cgc ccg gcg	480
Leu Tyr Pro Leu Arg Lys Asp Ser Met Asp Tyr Arg Gln Arg Pro Ala	
145 150 155 160	
ccg acc acc gat gcg gaa acc tac gag ttc att aac gag ctg ggt gac	528
Pro Thr Thr Asp Ala Glu Thr Tyr Glu Phe Ile Asn Glu Leu Gly Asp	
165 170 175	
aag aaa aat aac gtg gtg ccg att ggc ccg ctg cat gtc act tcc gat	576
Lys Lys Asn Asn Val Val Pro Ile Gly Pro Leu His Val Thr Ser Asp	
180 185 190	
gaa ccg ggc cac ttc cgt ctg ttc gtc gat ggc gaa aac att atc gat	624
Glu Pro Gly His Phe Arg Leu Phe Val Asp Gly Glu Asn Ile Ile Asp	
195 200 205	
gcc gac tac cgc ctg ttc tac gtc cac cgt ggt atg gaa aaa ctg gcg	672
Ala Asp Tyr Arg Leu Phe Tyr Val His Arg Gly Met Glu Lys Leu Ala	
210 215 220	
gaa acc cgc atg ggt tat aac gaa gtc acc ttc ctg tcg gat cgc gtg	720
Glu Thr Arg Met Gly Tyr Asn Glu Val Thr Phe Leu Ser Asp Arg Val	
225 230 235 240	
tgt gga atc tgc ggt ttc gcg cac agc act gcc tac acc act tcc gtg	768
Cys Gly Ile Cys Gly Phe Ala His Ser Thr Ala Tyr Thr Thr Ser Val	
245 250 255	
gaa aac gcg atg ggc att cag gtg ccg gag cgt gcg cag atg atc cgc	816
Glu Asn Ala Met Gly Ile Gln Val Pro Glu Arg Ala Gln Met Ile Arg	
260 265 270	
gcc att ctg ctg gaa gtg gag cgt ctg cac tcg cac ctg ctg aac cta	864
Ala Ile Leu Leu Glu Val Glu Arg Leu His Ser His Leu Leu Asn Leu	
275 280 285	
ggc ctc gcc tgc cac ttt acc ggc ttt gac tcc ggc ttt atg cag ttc	912
Gly Leu Ala Cys His Phe Thr Gly Phe Asp Ser Gly Phe Met Gln Phe	
290 295 300	
ttc cgc gtg cgt gaa acc tcc atg aag atg gcg gaa ata ctg acc ggg	960
Phe Arg Val Arg Glu Thr Ser Met Lys Met Ala Glu Ile Leu Thr Gly	
305 310 315 320	
gcg cgc aaa act tac ggt ctg aac ctg atc ggc ggg att cgc cgc gat	1008
Ala Arg Lys Thr Tyr Gly Leu Asn Leu Ile Gly Gly Ile Arg Arg Asp	
325 330 335	
ctg ctc aaa gag gac atg atc cag acc cgt caa ctg gcg cag cag atg	1056
Leu Leu Lys Glu Asp Met Ile Gln Thr Arg Gln Leu Ala Gln Gln Met	
340 345 350	
cgt cgt gac gtg cag gag ctg gtg gac atg ctg ctg agc acg ccg aat	1104
Arg Arg Asp Val Gln Glu Leu Val Asp Met Leu Leu Ser Thr Pro Asn	
355 360 365	
atg gaa cag cgt acc gtg ggt atc ggc cgt ctg gac ccg gaa att gcc	1152
Met Glu Gln Arg Thr Val Gly Ile Gly Arg Leu Asp Pro Glu Ile Ala	
370 375 380	

DESUanglais-seq1.txt
 cgc gac ttc agt aat gtc ggc ccg atg gtg cgc gcc agc ggt cac gcc 1200
 Arg Asp Phe Ser Asn Val Gly Pro Met Val Arg Ala Ser Gly His Ala 400
 385 390 395 400
 cgc gac acc cgc gcc gac cac ccg ttt gtc ggc tac ggt ctg ctg ccg 1248
 Arg Asp Thr Arg Ala Asp His Pro Phe Val Gly Tyr Gly Leu Leu Pro 415
 405 410 415
 atg gaa gta cat agc gag cag ggc tgc gac gtg att tct cgt ctg aaa 1296
 Met Glu Val His Ser Glu Gln Gly Cys Asp Val Ile Ser Arg Leu Lys 430
 420 425 430
 gtc cgt atc aac gaa gtc tac acc tcg ctg aat atg atc gat ttc ggt 1344
 Val Arg Ile Asn Glu Val Tyr Thr Ser Leu Asn Met Ile Asp Phe Gly 445
 435 440 445
 ctg gat aat cta ccg ggc ggc ccg ctg atg gtg gaa ggc ttt acc tat 1392
 Leu Asp Asn Leu Pro Gly Gly Pro Leu Met Val Glu Gly Phe Thr Tyr 460
 450 455 460
 att ccg cac cgt ttt gcg ctc ggc ttc gct gaa gcg ccg cgt ggt gac 1440
 Ile Pro His Arg Phe Ala Leu Gly Phe Ala Glu Ala Pro Arg Gly Asp 480
 465 470 475 480
 gat atc cac tgg agc atg acc ggc gac aac cag aag ctt tac cgc tgg 1488
 Asp Ile His Trp Ser Met Thr Gly Asp Asn Gln Lys Leu Tyr Arg Trp 495
 485 490 495
 cgc tgc cgt gcg gca acc tac gcc aac tgg ccg acc ctg cgt tat atg 1536
 Arg Cys Arg Ala Ala Thr Tyr Ala Asn Trp Pro Thr Leu Arg Tyr Met 510
 500 505 510
 ctg cgt ggc aac acc gtc tcc gac gcg ccg ctg atc atc ggt agc ctc 1584
 Leu Arg Gly Asn Thr Val Ser Asp Ala Pro Leu Ile Ile Gly Ser Leu 525
 515 520 525
 gat cct tgc tac tcc tgt acc gac cgg atg acc gtg gtc gat gta cgt 1632
 Asp Pro Cys Tyr Ser Cys Thr Asp Arg Met Thr Val Val Asp Val Arg 540
 530 535 540
 aag aag aag agc aaa gtc gtg ccg tac aaa gaa ctt gag cgc tac agc 1680
 Lys Lys Lys Ser Lys Val Val Pro Tyr Lys Glu Leu Glu Arg Tyr Ser 560
 545 550 555 560
 att gag cgt aaa aac tcg ccg ctg aaa taa 1710
 Ile Glu Arg Lys Asn Ser Pro Leu Lys 565

<210> 22
 <211> 569
 <212> PRT
 <213> Salmonella typhi

<400> 22
 Met Phe Glu Glu Lys Leu Gly Gln Gln Tyr Leu Ala Ala Leu His Gln
 1 5 10 15
 Ala Phe Pro Gly Val Val Met Asp Glu Ala Trp Gln Thr Lys Asp Gln
 20 25 30
 Leu Thr Ile Thr Val Lys Val Asn Tyr Leu Pro Glu Val Val Glu Phe
 35 40 45
 Leu Tyr Tyr Gln Gln Gly Gly Trp Leu Ser Val Leu Phe Gly Asn Asp
 50 55 60
 Glu Arg Gln Leu Cys Gly His Tyr Ala Val Tyr Tyr Val Leu Ser Met
 65 70 75 80
 Glu Gln Gly Thr Lys Cys Trp Ile Thr Val Arg Val Glu Val Asp Ala
 85 90 95
 Asn Lys Leu Glu Phe Pro Ser Val Thr Pro Arg Val Pro Ala Ala Val
 100 105 110
 Trp Gly Glu Arg Glu Val Arg Asp Met Tyr Gly Leu Ile Pro Val Gly
 115 120 125
 Leu Pro Asp Glu Arg Arg Leu Val Leu Pro Asp Asp Trp Pro Asp Glu
 130 135 140
 Leu Tyr Pro Leu Arg Lys Asp Ser Met Asp Tyr Arg Gln Arg Pro Ala
 145 150 155 160

DESUanglais-seql.txt

Pro Thr Thr Asp Ala Glu Thr Tyr Glu Phe Ile Asn Glu Leu Gly Asp
 165 170 175

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

Glu Pro Gly His Phe Arg Leu Phe Val Asp Gly Glu Asn Ile Ile Asp
 195 200 205

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

Glu Thr Arg Met Gly Tyr Asn Glu Val Thr Phe Leu Ser Asp Arg Val
 225 230 235 240

Cys Gly Ile Cys Gly Phe Ala His Ser Thr Ala Tyr Thr Thr Ser Val
 245 250 255

Glu Asn Ala Met Gly Ile Gln Val Pro Glu Arg Ala Gln Met Ile Arg
 260 265 270

Ala Ile Leu Leu Glu Val Glu Arg Leu His Ser His Leu Leu Asn Leu
 275 280 285

Gly Leu Ala Cys His Phe Thr Gly Phe Asp Ser Gly Phe Met Gln Phe
 290 295 300

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

Ala Arg Lys Thr Tyr Gly Leu Asn Leu Ile Gly Gly Ile Arg Arg Asp
 325 330 335

Leu Leu Lys Glu Asp Met Ile Gln Thr Arg Gln Leu Ala Gln Gln Met
 340 345 350

Arg Arg Asp Val Gln Glu Leu Val Asp Met Leu Leu Ser Thr Pro Asn
 355 360 365

Met Glu Gln Arg Thr Val Gly Ile Gly Arg Leu Asp Pro Glu Ile Ala
 370 375 380

Arg Asp Phe Ser Asn Val Gly Pro Met Val Arg Ala Ser Gly His Ala
 385 390 395 400

Arg Asp Thr Arg Ala Asp His Pro Phe Val Gly Tyr Gly Leu Leu Pro
 405 410 415

Met Glu Val His Ser Glu Gln Gly Cys Asp Val Ile Ser Arg Leu Lys
 420 425 430

Val Arg Ile Asn Glu Val Tyr Thr Ser Leu Asn Met Ile Asp Phe Gly
 435 440 445

Leu Asp Asn Leu Pro Gly Gly Pro Leu Met Val Glu Gly Phe Thr Tyr
 450 455 460

Ile Pro His Arg Phe Ala Leu Gly Phe Ala Glu Ala Pro Arg Gly Asp
 465 470 475 480

Asp Ile His Trp Ser Met Thr Gly Asp Asn Gln Lys Leu Tyr Arg Trp
 485 490 495

Arg Cys Arg Ala Ala Thr Tyr Ala Asn Trp Pro Thr Leu Arg Tyr Met
 500 505 510

Leu Arg Gly Asn Thr Val Ser Asp Ala Pro Leu Ile Ile Gly Ser Leu
 515 520 525

Asp Pro Cys Tyr Ser Cys Thr Asp Arg Met Thr Val Val Asp Val Arg
 530 535 540

Lys Lys Lys Ser Lys Val Val Pro Tyr Lys Glu Leu Glu Arg Tyr Ser
 545 550 555 560

Ile Glu Arg Lys Asn Ser Pro Leu Lys
 565

<210> 23
 <211> 1710
 <212> DNA
 <213> Salmonella typhimurium
 <220>

DESUanglais-seql.txt

<221> CDS

<222> (1)..(1710)

<223>

<400> 23

atg tct gaa gaa aaa tta ggt caa caa tac ctt gcg gcg ctg cac cag 48
Met Ser Glu Glu Lys Leu Gly Gln Gln Tyr 10 Leu Ala Ala Leu His Gln 15
1

gcg ttt ccg ggc gtc gtg ctg gac gaa gcc tgg cag acc aaa gat cag 96
Ala Phe Pro Gly Val Val Leu Asp Glu Ala Trp Gln Thr Lys Asp Gln 20 25 30

ctg act att acg gtg aaa gta aac tat ctg ccg gaa gtg gtg gag ttt 144
Leu Thr Ile Thr Val Lys Val Asn Tyr Leu Pro Glu Val Val Glu Phe 35 40 45

ctt tac tac cag cag ggt ggg tgg ctg tcg gtg ctg ttc ggt aat gac 192
Leu Tyr Tyr Gln Gln Gly Gly Trp Leu Ser Val Leu Phe Gly Asn Asp 50 55 60

gaa cgc cag ttg tgc ggc cac tat gcc gtt tat tac gtg ctg tcg atg 240
Glu Arg Gln Leu Cys Gly His Tyr Ala Val Tyr Tyr Val Leu Ser Met 65 70 75 80

gag cag ggc acg aag tgc tgg att acc gtt cgc gtt gaa gtg gat gcc 288
Glu Gln Gly Thr Lys Cys Trp Ile Thr Val Arg Val Glu Val Asp Ala 85 90 95

aat aag ctg gaa ttc cca tcc gtt acg ccg cgc gtg ccg gct gcc gtg 336
Asn Lys Leu Glu Phe Pro Ser Val Thr Pro Arg Val Pro Ala Ala Val 100 105 110

tgg ggt gag cgc gaa gta cgc gac atg tac ggt tta atc ccg gtc ggt 384
Trp Gly Glu Arg Glu Val Arg Asp Met Tyr Gly Leu Ile Pro Val Gly 115 120 125

ctg ccg gac gag cgc cgt ctg gtg ctg ccg gac gac tgg ccg gat gaa 432
Leu Pro Asp Glu Arg Arg Leu Val Leu Pro Asp Asp Trp Pro Asp Glu 130 135 140

ctc tat ccg ctg cgt aaa gac agt atg gat tat cgt cag cgc ccg gcg 480
Leu Tyr Pro Leu Arg Lys Asp Ser Met Asp Tyr Arg Gln Arg Pro Ala 145 150 155 160

ccg acc acc gat gcg gaa acc tac gag ttc att aac gag ctg ggt gac 528
Pro Thr Thr Asp Ala Glu Thr Tyr Glu Phe Ile Asn Glu Leu Gly Asp 165 170 175

aag aaa aat aac gtg gtg ccg att ggc ccg ctg cat gtc acc tcc gat 576
Lys Lys Asn Asn Val Val Pro Ile Gly Pro Leu His Val Thr Ser Asp 180 185 190

gaa ccg ggc cac ttc cgt ctg ttc gtc gat ggc gaa aac att atc gac 624
Glu Pro Gly His Phe Arg Leu Val Asp Gly Glu Asn Ile Ile Asp 195 200 205

gcc gac tac cgc ctg ttc tac gtc cac cgt ggt atg gaa aaa ctg gcg 672
Ala Asp Tyr Arg Leu Phe Tyr Val His Arg Gly Met Glu Lys Leu Ala 210 215 220

gaa acc cgc atg ggt tat aac gaa gtc acc ttc ctg tcg gat cgc gtg 720
Glu Thr Arg Met Gly Tyr Asn Glu Val Thr Phe Leu Ser Asp Arg Val 225 230 235 240

tgt ggt atc tgc ggc ttc gcg cac agc act gcc tac acc act tcc gtg 768
Cys Gly Ile Cys Gly Phe Ala His Ser Thr Ala Tyr Thr Thr Ser Val 245 250 255

gaa aac gcg atg ggc att cag gtg ccg gag cgt gcg cag atg atc cgc 816
Glu Asn Ala Met Gly Ile Gln Val Pro Glu Arg Ala Gln Met Ile Arg 260 265 270

gcc att ctg ctg gaa gtg gag cgt ctg cac tcg cac ctg ctg aac cta 864
Ala Ile Leu Leu Glu Val Glu Arg Leu His Ser His Leu Asn Leu 275 280 285

ggc ctc gcc tgc cac ttt acc ggt ttt gac tcc ggc ttt atg cag ttc 912
Gly Leu Ala Cys His Phe Thr Gly Phe Asp Ser Gly Phe Met Gln Phe 290 295 300

ttc cgc gtg cgt gaa acc tcc atg aaa atg gca gag atc ctt acc ggc 960
Phe Arg Val Arg Glu Thr Ser Met Lys Met Ala Glu Ile Leu Thr Gly 305 310 315 320

DESUanglais-seql.txt

gcg cgc aaa act tac gga ctg aac ctg atc ggc ggc att cgc cgc gat 1008
Ala Arg Lys Thr Tyr Gly Leu Asn Leu Ile 330 Gly Gly Ile Arg Arg Asp 335

ctg ctc aaa gag gac atg atc cag acc cgt caa ctg ggc cag cag atg 1056
Leu Leu Lys Glu Asp Met Ile Gln Thr Arg Gln Leu Ala Gln Gln Met 340 345 350

cgt cgt gac gtg cag gag ctg gtg gac atg ctg ctg agc acg ccg aat 1104
Arg Arg Asp Val Gln Glu Leu Val 360 Asp Met Leu Leu Ser Thr Pro Asn 365

atg gaa cag cgt acc gtg ggt atc ggc cgt ctg gac ccg gaa att gcc 1152
Met Glu Gln Arg Thr Val Gly Ile Gly Arg Leu Asp Pro Glu Ile Ala 370 375 380

cgt gac ttc agt aat gtc ggc ccg atg gtg cgc gcc agc ggt cac gcc 1200
Arg Asp Phe Ser Asn Val Gly Pro Met Val Arg Ala Ser Gly His Ala 385 390 395 400

cgc gac acc cgc gcc gac cac ccg ttt gtg ggc tat ggc ctg ctg ccg 1248
Arg Asp Thr Arg Ala Asp His Pro Phe Val Gly Tyr Gly Leu Leu Pro 405 410 415

atg gaa gtg cac agc gag cag ggc tgc gat gtg att tct cgt ctg aaa 1296
Met Glu Val His Ser Glu Gln Gly Cys Asp Val Ile Ser Arg Leu Lys 420 425 430

gtc cgt atc aac gaa gtt tac acc tgc ctg aat atg atc gat ttc ggt 1344
Val Arg Ile Asn Glu Val Tyr Thr 440 Ser Leu Asn Met Ile 445 Asp Phe Gly 445

ctg gat aat ctg ccg ggc ggc ccg ctg atg gtg gaa ggc ttt acc tat 1392
Leu Asp Asn Leu Pro Gly Gly Pro Leu Met Val Glu Gly Phe Thr Tyr 450 455 460

att ccg cac cgt ttt gcg ctc ggc ttc gct gaa gcg ccg cgt ggt gac 1440
Ile Pro His Arg Phe Ala Leu Gly Phe Ala Glu Ala Pro Arg Gly Asp 465 470 475 480

gat atc cac tgg agc atg acc ggc gac aac cag aag ctg tac cgc tgg 1488
Asp Ile His Trp Ser Met Thr Gly Asp Asn Gln Lys Leu Tyr Arg Trp 485 490 495

cgc tgc cgt gcg gcg acc tac gcc aac tgg ccg acg ctg cgc tat atg 1536
Arg Cys Arg Ala Ala Thr Tyr Ala Asn Trp Pro Thr Leu Arg Tyr Met 500 505 510

ctg cgc ggc aac acc gtc tcc gac gcg ccg ctg att atc ggc agc ctc 1584
Leu Arg Gly Asn Thr Val Ser Asp Ala Pro Leu Ile Ile Gly Ser Leu 515 520 525

gac ccg tgc tac tcc tgt acc gac gcg atg acc gtg gtc gat gtg cgt 1632
Asp Pro Cys Tyr Ser Cys Thr Asp Arg Met Thr Val Val Asp Val Arg 530 535 540

aag aag aag agc aaa gtc gtg ccg tac aaa gaa ctt gag cgc tac agc 1680
Lys Lys Lys Ser Lys Val Val Pro Tyr Lys Glu Leu Glu Arg Tyr Ser 545 550 555 560

att gag cgt aaa aac tgc ccg ctg aaa taa 1710
Ile Glu Arg Lys Asn Ser Pro Leu Lys 565

<210> 24
<211> 569
<212> PRT
<213> Salmonella typhimurium

<400> 24
Met Ser Glu Glu Lys Leu Gly Gln Gln Tyr Leu Ala Ala Leu His Gln 1 5 10 15
Ala Phe Pro Gly Val Val Leu Asp Glu Ala Trp Gln Thr Lys Asp Gln 20 25 30
Leu Thr Ile Thr Val Lys Val Asn Tyr Leu Pro Glu Val Val Glu Phe 35 40 45
Leu Tyr Tyr Gln Gln Gly Gly Trp Leu Ser Val Leu Phe Gly Asn Asp 50 55 60

Glu Arg Gln Leu Cys Gly His Tyr Ala Val Tyr Tyr Val Leu Ser Met
 65 70 75 80
 Glu Gln Gly Thr Lys Cys Trp Ile Thr Val Arg Val Glu Val Asp Ala
 85 90 95
 Asn Lys Leu Glu Phe Pro Ser Val Thr Pro Arg Val Pro Ala Ala Val
 100 105 110
 Trp Gly Glu Arg Glu Val Arg Asp Met Tyr Gly Leu Ile Pro Val Gly
 115 120 125
 Leu Pro Asp Glu Arg Arg Leu Val Leu Pro Asp Asp Trp Pro Asp Glu
 130 135 140
 Leu Tyr Pro Leu Arg Lys Asp Ser Met Asp Tyr Arg Gln Arg Pro Ala
 145 150 155 160
 Pro Thr Thr Asp Ala Glu Thr Tyr Glu Phe Ile Asn Glu Leu Gly Asp
 165 170 175
 Lys Lys Asn Asn Val Val Pro Ile Gly Pro Leu His Val Thr Ser Asp
 180 185 190
 Glu Pro Gly His Phe Arg Leu Phe Val Asp Gly Glu Asn Ile Ile Asp
 195 200 205
 Ala Asp Tyr Arg Leu Phe Tyr Val His Arg Gly Met Glu Lys Leu Ala
 210 215 220
 Glu Thr Arg Met Gly Tyr Asn Glu Val Thr Phe Leu Ser Asp Arg Val
 225 230 235 240
 Cys Gly Ile Cys Gly Phe Ala His Ser Thr Ala Tyr Thr Thr Ser Val
 245 250 255
 Glu Asn Ala Met Gly Ile Gln Val Pro Glu Arg Ala Gln Met Ile Arg
 260 265 270
 Ala Ile Leu Leu Glu Val Glu Arg Leu His Ser His Leu Leu Asn Leu
 275 280 285
 Gly Leu Ala Cys His Phe Thr Gly Phe Asp Ser Gly Phe Met Gln Phe
 290 295 300
 Phe Arg Val Arg Glu Thr Ser Met Lys Met Ala Glu Ile Leu Thr Gly
 305 310 315 320
 Ala Arg Lys Thr Tyr Gly Leu Asn Leu Ile Gly Gly Ile Arg Arg Asp
 325 330 335
 Leu Leu Lys Glu Asp Met Ile Gln Thr Arg Gln Leu Ala Gln Gln Met
 340 345 350
 Arg Arg Asp Val Gln Glu Leu Val Asp Met Leu Leu Ser Thr Pro Asn
 355 360 365
 Met Glu Gln Arg Thr Val Gly Ile Gly Arg Leu Asp Pro Glu Ile Ala
 370 375 380
 Arg Asp Phe Ser Asn Val Gly Pro Met Val Arg Ala Ser Gly His Ala
 385 390 395 400
 Arg Asp Thr Arg Ala Asp His Pro Phe Val Gly Tyr Gly Leu Leu Pro
 405 410 415
 Met Glu Val His Ser Glu Gln Gly Cys Asp Val Ile Ser Arg Leu Lys
 420 425 430
 Val Arg Ile Asn Glu Val Tyr Thr Ser Leu Asn Met Ile Asp Phe Gly
 435 440 445
 Leu Asp Asn Leu Pro Gly Gly Pro Leu Met Val Glu Gly Phe Thr Tyr
 450 455 460
 Ile Pro His Arg Phe Ala Leu Gly Phe Ala Glu Ala Pro Arg Gly Asp
 465 470 475 480
 Asp Ile His Trp Ser Met Thr Gly Asp Asn Gln Lys Leu Tyr Arg Trp
 485 490 495
 Arg Cys Arg Ala Ala Thr Tyr Ala Asn Trp Pro Thr Leu Arg Tyr Met
 500 505 510
 Leu Arg Gly Asn Thr Val Ser Asp Ala Pro Leu Ile Ile Gly Ser Leu
 515 520 525

DESUanglais-seql.txt

Asp Pro Cys Tyr Ser Cys Thr Asp Arg Met Thr Val Val Asp Val Arg
 530 535 540
 Lys Lys Lys Ser Lys Val Val Pro Tyr Lys Glu Leu Glu Arg Tyr Ser
 545 550 555 560
 Ile Glu Arg Lys Asn Ser Pro Leu Lys
 565
 <210> 25
 <211> 1710
 <212> DNA
 <213> *Shigella flexneri*
 <220>
 <221> CDS
 <222> (1)..(1710)
 <223>
 <400> 25
 atg tct gaa gaa aaa tta ggt caa cat tat ctc gcc gcg ctg aat gag 48
 Met Ser Glu Glu Lys Leu Gly Gln His Tyr 10 Leu Ala Ala Leu Asn Glu 15
 1
 gca ttt cta ggc gtc gtg ctg gac cac gcc tgg cag acc aaa gat cag 96
 Ala Phe Leu Gly Val Val Leu Asp His Ala Trp Gln Thr Lys Asp Gln 20 25 30
 ctg act gtc acc gta aag gtg aac tat ctg ccg gaa gtg gtg gag ttt 144
 Leu Thr Val Thr Val Lys Val Asn Tyr Leu Pro Glu Val Val Glu Phe 35 40 45
 ctc tac tac aag cag ggt ggc tgg ctg tcg gtg ctg ttt ggt aac gac 192
 Leu Tyr Tyr Lys Gln Gly Gly Trp Leu Ser Val Leu Phe Gly Asn Asp 50 55 60
 gaa cgc aaa ctg aat ggt cat tac gcc gtt tat tac gtg ctg tcg atg 240
 Glu Arg Lys Leu Asn Gly His Tyr Ala Val Tyr Tyr Val Leu Ser Met 65 70 75 80
 gag aag ggc acc aag tgt tgg gta acg gtt cgc gtc gaa gtt gac gcc 288
 Glu Lys Gly Thr Lys Cys Trp Val Thr Val Arg Val Glu Val Asp Ala 85 90 95
 aac aaa ccg gag tat ccg tcc gtg acg ccg cgc gtt ccg gcg gcg gtg 336
 Asn Lys Pro Glu Tyr Pro Ser Val Thr Pro Arg Val Pro Ala Ala Val 100 105 110
 tgg ggc gag cgc gaa gtg cgc gat atg tac ggt ttg att ccg gtt ggt 384
 Trp Gly Glu Arg Glu Val Arg Asp Met Tyr Gly Leu Ile Pro Val Gly 115 120 125
 ctg ccg gat gaa cgt cgt ctg gtg ctg ccg gat gac tgg ccg gat gaa 432
 Leu Pro Asp Glu Arg Arg Leu Val Leu Pro Asp Asp Trp Pro Asp Glu 130 135 140
 ctt tat ccg ctg cgt aaa gac agc atg gat tat cgt cag cgt ccg gca 480
 Leu Tyr Pro Leu Arg Lys Asp Ser Met Asp Tyr Arg Gln Arg Pro Ala 145 150 155 160
 ccg act acc gat gct gaa acc tac gag ttc atc aac gaa ctg ggc gac 528
 Pro Thr Thr Asp Ala Glu Thr Tyr Glu Phe Ile Asn Glu Leu Gly Asp 165 170 175
 aag aaa aac aac gtc gtg ccg att ggt ccg ctg cac gtc act tct gac 576
 Lys Lys Asn Asn Val Val Pro Ile Gly Pro Leu His Val Thr Ser Asp 180 185 190
 gaa ccg ggt cac his ttc cgt ctg ttc gtc cat cgc ggt atg gaa aaa ctg gcg 624
 Glu Pro Gly His Phe Arg Leu Phe Val Val Asp Gly Glu Asn Ile Ile Asp 195 200 205
 gcc gac tac cgt ctg ttc tac gtc cat cgc ggt atg gaa aaa ctg gcg 672
 Ala Asp Tyr Arg Leu Phe Tyr Val His Arg Gly Met Glu Lys Leu Ala 210 215 220
 gaa acc cgc atg ggt tat aac gaa gtg acc ttc ctc tct gac cgt gtg 720
 Glu Thr Arg Met Gly Tyr 230 Asn Glu Val Thr Phe Thr Leu Ser Asp Arg Val 225 235 240
 tgc ggc atc tgc ggc ttt gcc cac agc acc gcc tac acc acg tcg gtg 768
 Cys Gly Ile Cys Gly Phe Ala His Ser Thr Ala Tyr Thr Thr Ser Val 245 250 255

DESUanglais-seq1.txt															
gaa Glu	aac Asn	gcg Ala	atg Met	ggt Gly	att Ile	cag Gln	gtg Val	cca Pro	gaa Glu	cgc Arg	gag Ala	atg Gln	atc Met	cgc Ile	816
gcc Ala	att Ile	ctg Leu	ctg Leu	gag Glu	gtg Val	gaa Glu	cgc Arg	ctg Leu	cac His	ccg Pro	cat His	ctg Leu	ctc Leu	aac Asn	864
ggc Gly	ctc Leu	gac Ala	tgt Cys	cac His	ttt Phe	acc Thr	ggc Gly	ttc Phe	gac Asp	tcc Ser	ggc Gly	ttt Phe	atg Met	cag Gln	912
ttc Phe	cgc Arg	gtg Val	cgt Arg	gaa Glu	acc Thr	tcc Ser	atg Met	aaa Lys	atg Met	gca Ala	gag Glu	atc Ile	ctt Leu	acc Thr	960
gag Ala	cgt Arg	aaa Lys	acc Thr	tac Tyr	ggc Gly	ctg Leu	aac Asn	ctg Leu	atc Ile	ggc Gly	ggg Gly	att Ile	cgt Arg	cgc Arg	1008
ctg Leu	ctg Leu	aaa Lys	gat Asp	gac Asp	atg Met	atc Ile	cag Gln	acc Thr	cgc Arg	cag Gln	ctg Leu	gag Ala	caa Gln	caa Gln	1056
cgt Arg	cgt Arg	gaa Glu	gtg Val	cag Gln	gag Glu	ctg Leu	gtg Val	gat Asp	gtg Val	ctg Leu	ctg Leu	agt Ser	acg Thr	ccg Pro	1104
atg Met	gaa Glu	caa Gln	cgc Arg	acc Thr	gtc Val	ggc Gly	att Ile	ggt Gly	cgt Arg	ctg Leu	gac Asp	ccg Pro	gaa Glu	atc Ile	1152
cgc Arg	gat Asp	ttc Phe	agt Ser	aac Asn	gtt Val	ggc Gly	ccg Pro	atg Met	gtt Val	cgc Arg	gcc Ala	agc Ser	ggt Gly	ctc Leu	1200
cgc Arg	gat Asp	act Thr	cgc Arg	gcc Ala	gat Asp	cac His	ccg Pro	ttt Phe	gtc Val	ggt Gly	tat Tyr	ggc Gly	ctg Leu	ctg Leu	1248
atg Met	gaa Glu	gtc Val	cac His	agc Ser	gag Glu	cag Gln	ggc Gly	tgc Cys	gac Asp	gtt Val	att Ile	tcc Ser	cgt Arg	ctg Leu	1296
gtg Val	cga Arg	atc Ile	aac Asn	gag Glu	gtc Val	tat Tyr	acc Thr	gag Ala	ctg Leu	aat Asn	atg Met	atc Ile	gac Asp	tac Tyr	1344
ctg Leu	gat Asp	aac Asn	ctg Leu	ccg Pro	ggc Gly	ggt Gly	ccg Pro	ctg Leu	atg Met	gtg Val	gaa Glu	ggc Gly	ttt Phe	acc Thr	1392
att Ile	ccg Pro	cac His	cgt Arg	ttc Phe	gag Ala	ctg Leu	ggc Gly	ttt Phe	gcc Ala	gaa Glu	gag Ala	ccg Pro	cgc Arg	ggc Gly	1440
gat Asp	atc Ile	cac His	tgg Trp	agc Ser	atg Met	acc Thr	ggc Gly	gac Asp	aac Asn	cag Gln	aag Lys	ctg Leu	tac Tyr	cgc Arg	1488
cgc Arg	tgc Cys	cgt Arg	gac Ala	gag Ala	acc Thr	tac Tyr	gag Ala	aac Asn	tgg Trp	ccg Pro	acc Thr	ctg Leu	cgc Arg	tac Tyr	1536
ctg Leu	cgt Arg	ggc Gly	aat Asn	acc Thr	gtt Val	tcc Ser	tat Tyr	gtg Val	ccg Pro	ctg Leu	att Ile	atc Ile	ggt Gly	agc Ser	1584
gac Asp	cct Pro	tgc Cys	tac Tyr	tcc Ser	tgt Cys	acc Thr	gac Asp	cgc Arg	atg Met	acc Thr	gta Val	gtc Val	gat Asp	gtg Val	1632
aag Lys	aag Lys	aag Lys	agc Ser	aaa Lys	gtg Val	gtg Val	ccg Pro	tac Tyr	aaa Lys	gaa Glu	ctc Leu	gag Glu	cgt Arg	tac Tyr	1680
att Ile	gag Glu	cgt Arg	aaa Lys	aac Asn	tgc Ser	ccg Pro	ctg Leu	aaa Lys	taa						1710

<210> 26
 <211> 569
 <212> PRT
 <213> Shigella flexneri

DESUanglais-seql.txt

```

<400> 26
Met Ser Glu Glu Lys Leu Gly Gln His Tyr Leu Ala Ala Leu Asn Glu
1      5      10      15
Ala Phe Leu Gly Val Val Leu Asp His Ala Trp Gln Thr Lys Asp Gln
20      25      30
Leu Thr Val Thr Val Lys Val Asn Tyr Leu Pro Glu Val Val Glu Phe
35      40      45
Leu Tyr Tyr Lys Gln Gly Gly Trp Leu Ser Val Leu Phe Gly Asn Asp
50      55      60
Glu Arg Lys Leu Asn Gly His Tyr Ala Val Tyr Tyr Val Leu Ser Met
65      70      75      80
Glu Lys Gly Thr Lys Cys Trp Val Thr Val Arg Val Glu Val Asp Ala
85      90      95
Asn Lys Pro Glu Tyr Pro Ser Val Thr Pro Arg Val Pro Ala Ala Val
100     105     110
Trp Gly Glu Arg Glu Val Arg Asp Met Tyr Gly Leu Ile Pro Val Gly
115     120     125
Leu Pro Asp Glu Arg Arg Leu Val Leu Pro Asp Asp Trp Pro Asp Glu
130     135     140
Leu Tyr Pro Leu Arg Lys Asp Ser Met Asp Tyr Arg Gln Arg Pro Ala
145     150     155     160
Pro Thr Thr Asp Ala Glu Thr Tyr Glu Phe Ile Asn Glu Leu Gly Asp
165     170     175
Lys Lys Asn Asn Val Val Pro Ile Gly Pro Leu His Val Thr Ser Asp
180     185     190
Glu Pro Gly His Phe Arg Leu Phe Val Asp Gly Glu Asn Ile Ile Asp
195     200     205
Ala Asp Tyr Arg Leu Phe Tyr Val His Arg Gly Met Glu Lys Leu Ala
210     215     220
Glu Thr Arg Met Gly Tyr Asn Glu Val Thr Phe Leu Ser Asp Arg Val
225     230     235     240
Cys Gly Ile Cys Gly Phe Ala His Ser Thr Ala Tyr Thr Thr Ser Val
245     250     255
Glu Asn Ala Met Gly Ile Gln Val Pro Glu Arg Ala Gln Met Ile Arg
260     265     270
Ala Ile Leu Leu Glu Val Glu Arg Leu His Pro His Leu Leu Asn Leu
275     280     285
Gly Leu Ala Cys His Phe Thr Gly Phe Asp Ser Gly Phe Met Gln Phe
290     295     300
Phe Arg Val Arg Glu Thr Ser Met Lys Met Ala Glu Ile Leu Thr Gly
305     310     315     320
Ala Arg Lys Thr Tyr Gly Leu Asn Leu Ile Gly Gly Ile Arg Arg Asp
325     330     335
Leu Leu Lys Asp Asp Met Ile Gln Thr Arg Gln Leu Ala Gln Gln Met
340     345     350
Arg Arg Glu Val Gln Glu Leu Val Asp Val Leu Leu Ser Thr Pro Asn
355     360     365
Met Glu Gln Arg Thr Val Gly Ile Gly Arg Leu Asp Pro Glu Ile Ala
370     375     380
Arg Asp Phe Ser Asn Val Gly Pro Met Val Arg Ala Ser Gly Leu Ala
385     390     395     400
Arg Asp Thr Arg Ala Asp His Pro Phe Val Gly Tyr Gly Leu Leu Pro
405     410     415
Met Glu Val His Ser Glu Gln Gly Cys Asp Val Ile Ser Arg Leu Lys
420     425     430
Val Arg Ile Asn Glu Val Tyr Thr Ala Leu Asn Met Ile Asp Tyr Gly

```

DESUanglais-seq1.txt

435 440 445
 Leu Asp Asn Leu Pro Gly Gly Pro Leu Met Val Glu Gly Phe Thr Tyr
 450 455 460
 Ile Pro His Arg Phe Ala Leu Gly Phe Ala Glu Ala Pro Arg Gly Asp
 465 470 475 480
 Asp Ile His Trp Ser Met Thr Gly Asp Asn Gln Lys Leu Tyr Arg Trp
 485 490 495
 Arg Cys Arg Ala Ala Thr Tyr Ala Asn Trp Pro Thr Leu Arg Tyr Met
 500 505 510
 Leu Arg Gly Asn Thr Val Ser Tyr Val Pro Leu Ile Ile Gly Ser Leu
 515 520 525
 Asp Pro Cys Tyr Ser Cys Thr Asp Arg Met Thr Val Val Asp Val Arg
 530 535 540
 Lys Lys Lys Ser Lys Val Val Pro Tyr Lys Glu Leu Glu Arg Tyr Ser
 545 550 555 560
 Ile Glu Arg Lys Asn Ser Pro Leu Lys
 565

<210> 27
 <211> 1740
 <212> DNA
 <213> Wolinella succinogenes

<220>
 <221> CDS
 <222> (1)..(1740)
 <223>

<400> 27
 atg aaa tgt gat agc ttg att gag gcg cta agc caa agg gtg aaa gtc 48
 Met Lys Cys Asp Ser Leu Ile Glu Ala Leu Ser Gln Arg Val Lys Val
 1 5 10 15
 tta gag gtc acc cga caa tac gaa gac caa gtg aca gcg ctc gtg gag 96
 Leu Glu Val Thr Arg Gln Tyr Glu Asp Gln Val Thr Ala Leu Val Glu
 20 25 30
 ctc aat gat ctc cct gag gca gtc tcc ttt tta tac tat gga aaa ggc 144
 Leu Asn Asp Leu Pro Glu Ala Val Ser Phe Leu Tyr Tyr Gly Lys Gly
 35 40 45
 gga tac ctc tcc acg atg gtg gcc aat gat gag cgc gag atc aat aaa 192
 Gly Tyr Leu Ser Thr Met Val Ala Asn Asp Glu Arg Glu Ile Asn Lys
 50 55 60
 cac tac gcc ctc tac tac gcg ctc tcc atg gag ggg ggt aag atg ttt 240
 His Tyr Ala Leu Tyr Tyr Ala Leu Ser Met Glu Gly Gly Lys Met Phe
 65 70 75 80
 gag ggg gat gag ctt gcc caa gag gag aag tgc ttc atc acg att aaa 288
 Glu Gly Asp Glu Leu Ala Gln Glu Glu Lys Cys Phe Ile Thr Ile Lys
 85 90 95
 gca ctc att cct gcc gat aat ccg acc tac ccc tct gtc acc cct ttg 336
 Ala Leu Ile Pro Ala Asp Asn Pro Thr Tyr Pro Ser Val Thr Pro Leu
 100 105 110
 gta cca gcg tgt gtc tgg tat gag aga gag gcg tat gat atg ttt gga 384
 Val Pro Ala Cys Val Trp Tyr Glu Arg Glu Ala Tyr Asp Met Phe Gly
 115 120 125
 ttg gtg gcg gag gga ttg cct gat aag cgg cgt cta gcc ctc agt gat 432
 Leu Val Ala Glu Gly Leu Pro Asp Lys Arg Arg Leu Ala Leu Ser Asp
 130 135 140
 gat tgg cct aat gat ctt ttc ccg ctt cgc aaa gat gcg atg gat tac 480
 Asp Trp Pro Asn Asp Leu Phe Pro Leu Arg Lys Asp Ala Met Asp Tyr
 145 150 155 160
 cgc tat cgt cct gat atg aga gag cac tat atg gag cca gag ttt gaa 528
 Arg Tyr Arg Pro Asp Met Arg Glu His Tyr Met Glu Pro Glu Phe Glu
 165 170 175
 ttc ttg cgc cct gag ggc tcg gga atc atc gat gtc ccc ttg ggg cct 576
 Phe Leu Arg Pro Glu Gly Ser Gly Ile Ile Asp Val Pro Leu Gly Pro

DESUanglais-seq1.txt															
180				185				190							
ctc	cat	atc	act	gca	gat	gaa	ccg	ggg	cat	ttc	agg	ctc	ttt	tgt	gat
Leu	His	Ile	Thr	Ala	Asp	Glu	Pro	Gly	His	Phe	Arg	Leu	Phe	Cys	Asp
		195					200					205			
gga	gat	acg	atc	att	gat	gcg	gat	tat	cga	ctc	ttt	tac	cag	cac	aga
Gly	Asp	Thr	Ile	Ile	Asp	Ala	Asp	Tyr	Arg	Leu	Phe	Tyr	Gln	His	Arg
	210					215					220				
ggg	atg	gag	aag	ctc	gcc	gag	aat	cgc	atg	aac	tac	gat	cag	atg	ggc
Gly	Met	Glu	Lys	Leu	Ala	Glu	Asn	Arg	Met	Asn	Tyr	Asp	Gln	Met	Gly
	225				230					235					240
tat	cta	gca	gag	agg	gtg	tgc	gga	atc	tgc	ggc	tac	gcg	cac	gcc	atc
Tyr	Leu	Ala	Glu	Arg	Val	Cys	Gly	Ile	Cys	Gly	Tyr	Ala	His	Ala	Ile
				245					250					255	
gcc	tgc	atc	gaa	gcg	gcg	gaa	aag	gcg	att	aat	ctc	cag	att	ccc	ttg
Ala	Cys	Ile	Glu	Ala	Ala	Glu	Lys	Ala	Ile	Asn	Leu	Gln	Ile	Pro	Leu
			260					265					270		
cgg	gct	cag	gcg	att	cgc	atc	gtc	tgt	ctg	gag	att	gag	agg	ctt	cac
Arg	Ala	Gln	Ala	Ile	Arg	Ile	Val	Cys	Leu	Glu	Ile	Glu	Arg	Leu	His
		275					280					285			
agc	cac	ctc	ctc	aat	ata	ggc	cta	gcg	tgc	gag	gtg	acg	ggc	aac	tac
Ser	His	Leu	Leu	Asn	Ile	Gly	Leu	Ala	Cys	Glu	Val	Thr	Gly	Asn	Tyr
	290					295					300				
aac	gcc	ttc	atg	cat	att	ttc	cga	atc	cgt	gaa	tac	tcc	atg	aag	cta
Asn	Ala	Phe	Met	His	Ile	Phe	Arg	Ile	Arg	Glu	Tyr	Ser	Met	Lys	Leu
	305				310					315					320
gcc	gag	ctg	gtc	acg	ggt	gga	cga	aag	acc	tat	gga	aat	gtc	gtg	atg
Ala	Glu	Leu	Val	Thr	Gly	Gly	Arg	Lys	Thr	Tyr	Gly	Asn	Val	Val	Met
			325						330					335	
ggt	gga	ctc	aga	cgc	gac	atg	acg	gga	act	gag	atc	aaa	gag	agc	cta
Gly	Gly	Leu	Arg	Arg	Asp	Met	Thr	Gly	Thr	Glu	Ile	Lys	Glu	Ser	Leu
			340					345					350		
aaa	att	ctt	cag	atc	atc	gag	acc	caa	gtg	gaa	gag	gtg	tgg	gat	gcg
Lys	Ile	Leu	Gln	Ile	Ile	Glu	Thr	Gln	Val	Glu	Glu	Val	Trp	Asp	Ala
		355					360					365			
gtg	atg	gac	gat	aag	cgc	cag	att	agc	cgc	tgg	aaa	ggc	gtg	ggg	att
Val	Met	Asp	Asp	Lys	Arg	Gln	Ile	Ser	Arg	Trp	Lys	Gly	Val	Gly	Ile
	370					375					380				
ttg	gat	aag	cag	gtg	gcg	aga	gac	ttc	tcc	cct	gtg	ggg	ccc	aat	atc
Leu	Asp	Lys	Gln	Val	Ala	Arg	Asp	Phe	Ser	Pro	Val	Gly	Pro	Asn	Ile
	385				390					395					400
cgc	gga	tgc	gga	atc	aag	cga	gac	act	cgc	tat	gac	cac	ccc	tat	gac
Arg	Gly	Cys	Gly	Ile	Lys	Arg	Asp	Thr	Arg	Tyr	Asp	His	Pro	Tyr	Asp
			405					410						415	
ttt	ttt	aat	cag	att	gag	ttt	gag	gtg	gcg	acc	gcc	cag	gga	ggc	gat
Phe	Phe	Asn	Gln	Ile	Glu	Phe	Glu	Val	Ala	Thr	Ala	Gln	Gly	Gly	Asp
			420					425					430		
gtc	ttt	gct	cgc	gag	atg	gtg	cgc	tat	atg	gag	ctt	aaa	agc	tct	gtc
Val	Phe	Ala	Arg	Glu	Met	Val	Arg	Tyr	Met	Glu	Leu	Lys	Ser	Ser	Val
		435				440						445			
tct	atc	att	cgc	cag	tgt	ttt	gag	ctg	atg	cct	cag	act	ccg	atc	atg
Ser	Ile	Ile	Arg	Gln	Cys	Phe	Glu	Leu	Met	Pro	Gln	Thr	Pro	Ile	Met
	450					455					460				
atc	gac	ccc	acc	ttc	cat	gtt	cag	cct	gag	aat	ttt	gct	ttg	gcc	tat
Ile	Asp	Pro	Thr	Phe	His	Val	Gln	Pro	Glu	Asn	Phe	Ala	Leu	Ala	Tyr
	465				470				475						480
gtt	gaa	gcg	cca	aga	gga	gat	aat	gtc	cat	tgg	atc	atg	caa	gga	agc
Val	Glu	Ala	Pro	Arg	Gly	Asp	Asn	Val	His	Trp	Ile	Met	Gln	Gly	Ser
			485					490					495		
gcc	caa	aag	gtc	tat	cgt	tgg	aga	tgt	cga	gcc	gcc	act	tat	aac	aac
Ala	Gln	Lys	Val	Tyr	Arg	Trp	Arg	Cys	Arg	Ala	Ala	Thr	Tyr	Asn	Asn
			500					505					510		
tgg	cca	agc	ttg	cga	ttc	cag	ttc	cgc	ggc	aac	aca	att	gcc	gat	gcg
Trp	Pro	Ser	Leu	Arg	Phe	Gln	Phe	Arg	Gly	Asn	Thr	Ile	Ala	Asp	Ala
		515				520						525			

DESUanglais-seq1.txt

gcg ctt atc gtc tgc agt ctt gat cca tgc tac tct tgt aca gag cgt 1632
 Ala Leu Ile Val Cys Ser Leu Asp Pro Cys Tyr Ser Cys Thr Glu Arg
 530 535 540

gtg acg gtg gtg gat gtg aga agt aaa aag agc aag att ttg acc cga 1680
 Val Thr Val Val Asp Val Arg Ser Lys Lys Ser Lys Ile Leu Thr Arg
 545 550 555 560

ttg gat ttg gaa gat ttc tcc aaa acc ctc aaa gga aat ccg tta aag 1728
 Leu Asp Leu Glu Asp Phe Ser Lys Thr Leu Lys Gly Asn Pro Leu Lys
 565 570 575

gat cta aaa tga 1740
 Asp Leu Lys

<210> 28
 <211> 579
 <212> PRT
 <213> Wolinella succinogenes

<400> 28
 Met Lys Cys Asp Ser Leu Ile Glu Ala Leu Ser Gln Arg Val Lys Val
 1 5 10 15
 Leu Glu Val Thr Arg Gln Tyr Glu Asp Gln Val Thr Ala Leu Val Glu
 20 25 30
 Leu Asn Asp Leu Pro Glu Ala Val Ser Phe Leu Tyr Tyr Gly Lys Gly
 35 40 45
 Gly Tyr Leu Ser Thr Met Val Ala Asn Asp Glu Arg Glu Ile Asn Lys
 50 55 60
 His Tyr Ala Leu Tyr Tyr Ala Leu Ser Met Glu Gly Gly Lys Met Phe
 65 70 75 80
 Glu Gly Asp Glu Leu Ala Gln Glu Glu Lys Cys Phe Ile Thr Ile Lys
 85 90 95
 Ala Leu Ile Pro Ala Asp Asn Pro Thr Tyr Pro Ser Val Thr Pro Leu
 100 105 110
 Val Pro Ala Cys Val Trp Tyr Glu Arg Glu Ala Tyr Asp Met Phe Gly
 115 120 125
 Leu Val Ala Glu Gly Leu Pro Asp Lys Arg Arg Leu Ala Leu Ser Asp
 130 135 140
 Asp Trp Pro Asn Asp Leu Phe Pro Leu Arg Lys Asp Ala Met Asp Tyr
 145 150 155 160
 Arg Tyr Arg Pro Asp Met Arg Glu His Tyr Met Glu Pro Glu Phe Glu
 165 170 175
 Phe Leu Arg Pro Glu Gly Ser Gly Ile Ile Asp Val Pro Leu Gly Pro
 180 185 190
 Leu His Ile Thr Ala Asp Glu Pro Gly His Phe Arg Leu Phe Cys Asp
 195 200 205
 Gly Asp Thr Ile Ile Asp Ala Asp Tyr Arg Leu Phe Tyr Gln His Arg
 210 215 220
 Gly Met Glu Lys Leu Ala Glu Asn Arg Met Asn Tyr Asp Gln Met Gly
 225 230 235 240
 Tyr Leu Ala Glu Arg Val Cys Gly Ile Cys Gly Tyr Ala His Ala Ile
 245 250 255
 Ala Cys Ile Glu Ala Ala Glu Lys Ala Ile Asn Leu Gln Ile Pro Leu
 260 265 270
 Arg Ala Gln Ala Ile Arg Ile Val Cys Leu Glu Ile Glu Arg Leu His
 275 280 285
 Ser His Leu Leu Asn Ile Gly Leu Ala Cys Glu Val Thr Gly Asn Tyr
 290 295 300
 Asn Ala Phe Met His Ile Phe Arg Ile Arg Glu Tyr Ser Met Lys Leu
 305 310 315 320

DESUanglais-seq1.txt

Ala Glu Leu Val Thr Gly Gly Arg Lys Thr Tyr Gly Asn Val Val Met
325 330 335

Gly Gly Leu Arg Arg Asp Met Thr Gly Thr Glu Ile Lys Glu Ser Leu
340 345 350

Lys Ile Leu Gln Ile Ile Glu Thr Gln Val Glu Glu Val Trp Asp Ala
355 360 365

Val Met Asp Asp Lys Arg Gln Ile Ser Arg Trp Lys Gly Val Gly Ile
370 375 380

Leu Asp Lys Gln Val Ala Arg Asp Phe Ser Pro Val Gly Pro Asn Ile
385 390 395 400

Arg Gly Cys Gly Ile Lys Arg Asp Thr Arg Tyr Asp His Pro Tyr Asp
405 410 415

Phe Phe Asn Gln Ile Glu Phe Glu Val Ala Thr Ala Gln Gly Gly Asp
420 425 430

Val Phe Ala Arg Glu Met Val Arg Tyr Met Glu Leu Lys Ser Ser Val
435 440 445

Ser Ile Ile Arg Gln Cys Phe Glu Leu Met Pro Gln Thr Pro Ile Met
450 455 460

Ile Asp Pro Thr Phe His Val Gln Pro Glu Asn Phe Ala Leu Ala Tyr
465 470 475 480

Val Glu Ala Pro Arg Gly Asp Asn Val His Trp Ile Met Gln Gly Ser
485 490 495

Ala Gln Lys Val Tyr Arg Trp Arg Cys Arg Ala Ala Thr Tyr Asn Asn
500 505 510

Trp Pro Ser Leu Arg Phe Gln Phe Arg Gly Asn Thr Ile Ala Asp Ala
515 520 525

Ala Leu Ile Val Cys Ser Leu Asp Pro Cys Tyr Ser Cys Thr Glu Arg
530 535 540

Val Thr Val Val Asp Val Arg Ser Lys Lys Ser Lys Ile Leu Thr Arg
545 550 555 560

Leu Asp Leu Glu Asp Phe Ser Lys Thr Leu Lys Gly Asn Pro Leu Lys
565 570 575

Asp Leu Lys

<210> 29
 <211> 1077
 <212> DNA
 <213> Methanosarcina mazei

<220>
 <221> CDS
 <222> (1)..(1077)
 <223>

<400> 29
 atg aca act gta ata cct ttt ggt cct cag cac ccc gtt tta ccc gaa 48
 Met Thr Thr Val Ile Pro Phe Gly Pro Gln His Pro Val Leu Pro Glu
 1 5 10 15

ccg gta gcg ttg aaa ctt gag ctt gac gac gat att gtt gtt gga gca 96
 Pro Val Ala Leu Lys Leu Glu Leu Asp Asp Ile Val Val Gly Ala
 20 25 30

ctt cct tca ata ggc tat gtg cac aga ggg ctt gag aag ttc ata gac 144
 Leu Pro Ser Ile Gly Tyr Val His Arg Gly Leu Glu Lys Phe Ile Asp
 35 40 45

aca aag gac tat gtt caa aca aca tac att tgt gaa aga atc tgt gga 192
 Thr Lys Asp Tyr Val Gln Thr Thr Tyr Ile Cys Glu Arg Ile Cys Gly
 50 55 60

ata tgc agt gcc ctc cat ggt ata act tat aca cgg gca gtt gag aaa 240
 Ile Cys Ser Ala Leu His Gly Ile Thr Tyr Thr Arg Ala Val Glu Lys
 65 70 75 80

tta ttc gat tta gaa ccc cct gaa aga gct cag tat atc agg gta ata 288
 Leu Phe Asp Leu Glu Pro Pro Glu Arg Ala Gln Tyr Ile Arg Val Ile

DESUanglais-seql.txt

85	90	95	
gtt ggt gaa ctc aat aga ctc cac agt cac ctt ctc tgg ctt ggt ctg Val Gly Glu Leu 100 Asn Arg Leu His Ser 105 His Leu Leu Trp Leu Gly Leu			336
ttt gct gat ggt ttt gga ttt gaa agc ctt ttt tat gaa tgc tgg aag Phe Ala Asp Gly Phe Gly Phe Glu Ser Leu Phe Tyr Glu Cys Trp Lys			384
tac aga gaa gga gta cag gat gca gcg gaa aga atc tgt gga aac agg Tyr Arg Glu Gly Val Gln Asp Ala Ala Glu Arg Ile Cys Gly Asn Arg			432
gtt ata cac tca ata tca aag gtc gga gga gtt acc aga gat ttg acc Val Ile His Ser Ile Ser Lys Val Gly Gly Val Thr Arg Asp Leu Thr			480
aaa gaa cat act gat atg ctt ctg aaa ctg tgc gat aca ctg gaa gac Lys Glu His Thr Asp Met Leu Leu Lys Leu Cys Asp Thr Leu Glu Asp			528
caa gtt aaa aac att gaa aag gtg ttc gta aat aat tac acc gtt aag Gln Val Lys Asn 180 Ile Glu Lys Val Phe Val Asn Asn Tyr Thr Val Lys			576
aaa aga act aag gga tta ggt gta atg tca aag cag gta gca tat gag Lys Arg Thr 195 Lys Gly Leu Gly Val Met Ser Lys Gln Val Ala Tyr Glu			624
ttg gga act gcc ggt cct aca ttg aga gga agc gat aac gcc att gac Leu Gly Thr 210 Ala Gly Pro Thr 215 Leu Arg Gly Ser 220 Asn Ala Ile Asp			672
gta aga gat ata gat gac tgg gca att tat aag gat ctc ggt ttt aag Val Arg Asp Ile Asp Asp Trp Ala Ile Tyr Lys Asp Leu Gly Phe Lys			720
aca gct gtg gag aaa gac gga gat tgt tac tca aga act aaa gta agg Thr Ala Val Glu Lys 245 Asp Gly Asp Cys Tyr 250 Ser Arg Thr Lys Val Arg			768
atc aac gaa gta ctt aat tct att gaa ata ata aga aat gca atc tcc Ile Asn Glu Val Leu Asn Ser Ile Glu Ile Ile Arg Asn Ala Ile Ser			816
agg ctg cct aat ggc gac att tca gta cct gta aag ggc ttc cct acc Arg Leu Pro 275 Asn Gly Asp Ile Ser 280 Val Pro Val Lys Gly 285 Phe Pro Thr			864
ggt gaa gca att atg aga aca gag cag ccc aga ggt gaa gtt gta tat Gly Glu Ala Ile Met Arg Thr 295 Glu Gln Pro Arg Gly 300 Glu Val Val Tyr			912
tac gtg aaa ggt aac ggt act aaa aac ctg gaa agg ctt aaa att agg Tyr Val Lys Gly Asn Gly Thr Lys Asn Leu Glu Arg Leu Lys Ile Arg			960
act cct acc ttt gca aac ata cct tca ctg cta gta atg ctc cca ggc Thr Pro Thr Phe Ala Asn Ile Pro Ser 330 Leu Val Met Leu Pro Gly			1008
gta aaa ctc gct gat gtt cct ata att gta ctc act ata gac ccc tgc Val Lys Leu Ala Asp Val Pro Ile Ile Val Leu Thr Ile Asp Pro Cys			1056
att agc tgc act gaa aga tga Ile Ser Cys Thr Glu Arg			1077
 <210> 30 <211> 358 <212> PRT <213> Methanosarcina mazei			
 <400> 30 Met Thr Thr Val Ile Pro Phe Gly Pro Gln His Pro Val Leu Pro Glu 1 5 10 15			
Pro Val Ala Leu Lys Leu Glu Leu Asp Asp Asp Ile Val Val Gly Ala 20 25 30			
Leu Pro Ser Ile Gly Tyr Val His Arg Gly Leu Glu Lys Phe Ile Asp 35 40 45			

DESUanglais-seql.txt

Thr Lys Asp Tyr Val Gln Thr Thr Tyr Ile Cys Glu Arg Ile Cys Gly
50 55 60

Ile Cys Ser Ala Leu His Gly Ile Thr Tyr Thr Arg Ala Val Glu Lys
65 70 75 80

Leu Phe Asp Leu Glu Pro Pro Glu Arg Ala Gln Tyr Ile Arg Val Ile
85 90 95

Val Gly Glu Leu Asn Arg Leu His Ser His Leu Leu Trp Leu Gly Leu
100 105 110

Phe Ala Asp Gly Phe Gly Phe Glu Ser Leu Phe Tyr Glu Cys Trp Lys
115 120 125

Tyr Arg Glu Gly Val Gln Asp Ala Ala Glu Arg Ile Cys Gly Asn Arg
130 135 140

Val Ile His Ser Ile Ser Lys Val Gly Gly Val Thr Arg Asp Leu Thr
145 150 155 160

Lys Glu His Thr Asp Met Leu Leu Lys Leu Cys Asp Thr Leu Glu Asp
165 170 175

Gln Val Lys Asn Ile Glu Lys Val Phe Val Asn Asn Tyr Thr Val Lys
180 185 190

Lys Arg Thr Lys Gly Leu Gly Val Met Ser Lys Gln Val Ala Tyr Glu
195 200 205

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

Val Arg Asp Ile Asp Asp Trp Ala Ile Tyr Lys Asp Leu Gly Phe Lys
225 230 235 240

Thr Ala Val Glu Lys Asp Gly Asp Cys Tyr Ser Arg Thr Lys Val Arg
245 250 255

Ile Asn Glu Val Leu Asn Ser Ile Glu Ile Ile Arg Asn Ala Ile Ser
260 265 270

Arg Leu Pro Asn Gly Asp Ile Ser Val Pro Val Lys Gly Phe Pro Thr
275 280 285

Gly Glu Ala Ile Met Arg Thr Glu Gln Pro Arg Gly Glu Val Val Tyr
290 295 300

Tyr Val Lys Gly Asn Gly Thr Lys Asn Leu Glu Arg Leu Lys Ile Arg
305 310 315 320

Thr Pro Thr Phe Ala Asn Ile Pro Ser Leu Leu Val Met Leu Pro Gly
325 330 335

Val Lys Leu Ala Asp Val Pro Ile Ile Val Leu Thr Ile Asp Pro Cys
340 345 350

Ile Ser Cys Thr Glu Arg
355

<210> 31
<211> 1077
<212> DNA
<213> Methanosarcina barkeri

<220>
<221> CDS
<222> (1)..(1077)
<223>

<400> 31
atg aca act gta ata cct ttt ggt cct caa cac ccc gtt tta ccc gaa 48
Met Thr Thr Val Ile Pro Phe Gly Pro Gln His Pro Val Leu Pro Glu
1 5 10 15

cca gta tcg tta aaa ctt gaa att gac gac aat gtt gtt gtt gga gta 96
Pro Val Ser Leu Lys Leu Glu Ile Asp Asp Asn Val Val Val Gly Val
20 25 30

ctt ccc tca ttg ggc tat gtt cac aga ggg ctt gag aca ttt ata aac 144
Leu Pro Ser Leu Gly Tyr Val His Arg Gly Leu Glu Thr Phe Ile Asn
35 40 45

aca aag gac ttt aat caa aca act tat gtt tgt gag aga ata tgc gga 192
Thr Lys Asp Phe Asn Gln Thr Thr Tyr Val Cys Glu Arg Ile Cys Gly

DESUanglais-seql.txt
60

50	ata tgc agc gct ctc cat ggt ata act tat aca cgg aca gta gaa aaa Ile Cys Ser Ala Leu His 70 Gly Ile Thr Tyr 75 Arg Thr Val Glu Lys 80	240
55	ttg ttt gac act gaa atc cct gaa aga gca caa tat ata aga gta ata Leu Phe Asp Thr Glu 85 Ile Pro Glu Arg Ala Gln Tyr Ile Arg Val Ile 95	288
	gtt ggt gaa ctt aat aga ctt cac agt cac ctc ctc tgg ctt ggc ctg Val Gly Glu 100 Leu Asn Arg Leu His 105 Ser His Leu Leu Trp 110 Glu Gly Leu	336
	ttt gcc gat ggt ttt ggg ttt gaa agc ctt ttt tac gaa tgc tgg aag Phe Ala Asp Gly Phe Gly Phe 120 Glu Ser Leu Phe Tyr 125 Glu Cys Trp Lys	384
	tac aga gaa gaa gta ctg gat gta gcg gaa aga att tgc gga aac aga Tyr Arg 130 Glu Glu Val Leu Asp 135 Val Ala Glu Arg Ile 140 Cys Gly Asn Arg	432
	gtc ata cat tca ata tcc aaa gtt gga gga gtt act aga gat ctg act Val Ile His Ser Ile 150 Lys Val Gly Gly Val 155 Thr Arg Asp Leu Thr 160	480
	aag gaa cat att gat atg ctt ttg aaa atg tgt gat tca ctg gaa act Lys Glu His Ile 165 Asp Met Leu Leu Lys 170 Met Cys Asp Ser Leu Glu Thr 175	528
	gaa att aaa aat att gaa aaa gtt ttc gta aac aat tac acg gtt aag Glu Ile Lys Asn Ile Glu Lys Val Phe 185 Val Asn Asn Tyr 190 Thr Val Lys	576
	caa aga ctt gtg gga tta gct aca ttg tca aag caa gtt gca tac gaa Gln Arg Leu Val 195 Gly Leu Ala Thr 200 Leu Ser Lys Gln Val 205 Ala Tyr Glu	624
	gtt gga acc gct ggt cct aca ctt aga gga agt ggg aac gct att gac Val Gly Thr Ala Gly Pro Thr 215 Leu Arg Gly Ser 220 Gly Asn Ala Ile Asp	672
	gtg cgg gaa aca cca gat tgg gat atc tat aag gat ctc ggt ttt aag Val Arg Glu Thr Pro 230 Trp Asp Ile Tyr 235 Asp Leu Gly Phe Lys 240	720
	acg gct gtt gaa aag gat gga gat tgt tac gcc aga act aaa gta aga Thr Ala Val Glu Lys 245 Asp Gly Asp Cys Tyr 250 Ala Arg Thr Lys Val 255 Arg	768
	att act gag cta tta aat tct ctt act att ata aga aat gca atc tcc Ile Thr Glu Leu 260 Leu Asn Ser Leu Thr 265 Ile Ile Arg Asn Ala Ile Ser	816
	aag atg cct gag ggt gag att gaa gta cgt gta aag ggc ttc cct acg Lys Met Pro Glu Gly Glu Ile 280 Glu Val Arg Val Lys 285 Gly Phe Pro Thr	864
	ggc gaa gcg att atg aga aca gag cag ccc aga ggt gaa gtc ata tac Gly Glu Ala Ile Met Arg Thr 295 Glu Gln Pro Arg 300 Glu Glu Val Ile Tyr	912
	tac gtg aaa ggt aat ggc acc aaa aaa ctg gaa aga ctt aaa gta agg Tyr Val Lys Gly Asn 310 Thr Lys Lys Leu Glu Arg Leu Lys Val Arg 320	960
	acg cct acc ttt gca aac ata cct tca ctg tta ctt atg tta ccg ggc Thr Pro Thr Phe Ala Asn Ile Pro Ser Leu 330 Leu Leu Met Leu Pro Gly 335	1008
	gtc aaa ctc gct gac gta cct ata gtt gta ctt act ata gat ccc tgc Val Lys Leu 340 Ala Asp Val Pro Ile 345 Val Leu Thr Ile 350 Asp Pro Cys	1056
	gtt agc tgc act gaa aga taa Val Ser Cys Thr Glu Arg 355	1077

<210> 32
 <211> 358
 <212> PRT
 <213> Methanosarcina barkeri

DESUanglais-seql.txt

<400> 32
Met Thr Thr Val Ile Pro Phe Gly Pro Gln His Pro Val Leu Pro Glu
1 5 10 15
Pro Val Ser Leu Lys Leu Glu Ile Asp Asp Asn Val Val Val Gly Val
20 25 30
Leu Pro Ser Leu Gly Tyr Val His Arg Gly Leu Glu Thr Phe Ile Asn
35 40 45
Thr Lys Asp Phe Asn Gln Thr Thr Tyr Val Cys Glu Arg Ile Cys Gly
50 55 60
Ile Cys Ser Ala Leu His Gly Ile Thr Tyr Thr Arg Thr Val Glu Lys
65 70 75 80
Leu Phe Asp Thr Glu Ile Pro Glu Arg Ala Gln Tyr Ile Arg Val Ile
85 90 95
Val Gly Glu Leu Asn Arg Leu His Ser His Leu Leu Trp Leu Gly Leu
100 105 110
Phe Ala Asp Gly Phe Gly Phe Glu Ser Leu Phe Tyr Glu Cys Trp Lys
115 120 125
Tyr Arg Glu Glu Val Leu Asp Val Ala Glu Arg Ile Cys Gly Asn Arg
130 135 140
Val Ile His Ser Ile Ser Lys Val Gly Gly Val Thr Arg Asp Leu Thr
145 150 155 160
Lys Glu His Ile Asp Met Leu Leu Lys Met Cys Asp Ser Leu Glu Thr
165 170 175
Glu Ile Lys Asn Ile Glu Lys Val Phe Val Asn Asn Tyr Thr Val Lys
180 185 190
Gln Arg Leu Val Gly Leu Ala Thr Leu Ser Lys Gln Val Ala Tyr Glu
195 200 205
Val Gly Thr Ala Gly Pro Thr Leu Arg Gly Ser Gly Asn Ala Ile Asp
210 215 220
Val Arg Glu Thr Pro Asp Trp Asp Ile Tyr Lys Asp Leu Gly Phe Lys
225 230 235 240
Thr Ala Val Glu Lys Asp Gly Asp Cys Tyr Ala Arg Thr Lys Val Arg
245 250 255
Ile Thr Glu Leu Leu Asn Ser Leu Thr Ile Ile Arg Asn Ala Ile Ser
260 265 270
Lys Met Pro Glu Gly Glu Ile Glu Val Arg Val Lys Gly Phe Pro Thr
275 280 285
Gly Glu Ala Ile Met Arg Thr Glu Gln Pro Arg Gly Glu Val Ile Tyr
290 295 300
Tyr Val Lys Gly Asn Gly Thr Lys Lys Leu Glu Arg Leu Lys Val Arg
305 310 315 320
Thr Pro Thr Phe Ala Asn Ile Pro Ser Leu Leu Leu Met Leu Pro Gly
325 330 335
Val Lys Leu Ala Asp Val Pro Ile Val Val Leu Thr Ile Asp Pro Cys
340 345 350
Val Ser Cys Thr Glu Arg
355

<210> 33
<211> 1281
<212> DNA
<213> Pyrococcus abyssi

<220>
<221> CDS
<222> (1)..(1281)
<223>

<400> 33
atg agc aag gtt gag tat tgg gtt aaa gtt cct ttt gga cca att cat
Met Ser Lys Val Glu Tyr Trp Val Lys Val Pro Phe Gly Pro Ile His
1 5 10 15

48

DESUanglais-seql.txt

cca gga ttg gag gaa cct gag aag ttc att cta aca ctg gat gga gag	96
Pro Gly Leu Glu Glu Pro Glu Lys Phe Ile Leu Thr Leu Asp Gly Glu	
20 25 30	
agg ata gtt aac gtt gat gtt aag ctg ggt tac aac ctc agg gga atc	144
Arg Ile Val Asn Val Asp Val Lys Leu Gly Tyr Asn Leu Arg Gly Ile	
35 40 45	
cag tgg ata gcg ttc agg agg aac tac gtt cag tta atg tac gtt gcg	192
Gln Trp Ile Ala Phe Arg Arg Asn Tyr Val Gln Leu Met Tyr Val Ala	
50 55 60	
gag agg att tgt gga atc tgt tcc ttt tct cat aac cat acg tac gtt	240
Glu Arg Ile Cys Gly Ile Cys Ser Phe Ser His Asn His Thr Tyr Val	
65 70 75 80	
agg gcc gtt gag gag atg gca ggg ata gag gtt cct gag aga gcc gag	288
Arg Ala Val Glu Glu Met Ala Gly Ile Glu Val Pro Glu Arg Ala Glu	
85 90 95	
tac att agg gtg ata ata gga gaa ctc gag agg att cac tcc cac cta	336
Tyr Ile Arg Val Ile Ile Gly Glu Leu Arg Ile His Ser His Leu	
100 105 110	
ctg aac ctt gga gtt cta ggg cat gac att ggg tac gat act gtt tta	384
Leu Asn Leu Gly Val Leu Gly His Asp Ile Gly Tyr Asp Thr Val Leu	
115 120 125	
cac cta acg tgg ttg gcc agg gag aag gtt atg gac gtc ctc gag gcg	432
His Leu Thr Trp Leu Ala Arg Glu Lys Val Met Asp Val Leu Glu Ala	
130 135 140	
ata acc gga aac agg gta aac tac agc atg atg acg atc gga ggg gtt	480
Ile Thr Gly Asn Arg Val Asn Tyr Ser Met Met Thr Ile Gly Gly Val	
145 150 155 160	
agg agg gac ata gag gaa aaa cac aga agg tta ctg ctc gat atg ata	528
Arg Arg Asp Ile Glu Glu Lys His Arg Arg Leu Leu Leu Asp Met Ile	
165 170 175	
aag tac tac agg gag ata atg ccc caa ata gag gat gta ttc cta cac	576
Lys Tyr Tyr Arg Glu Ile Met Pro Gln Ile Glu Asp Val Phe Leu His	
180 185 190	
gac tcg acg att gag gct aga ctt agg aac tgc gcg ata att ccc aag	624
Asp Ser Thr Ile Glu Ala Arg Leu Arg Asn Cys Ala Ile Ile Pro Lys	
195 200 205	
aaa cta gcc ata gag atg ggc gca gtt gga ccg acg gga agg ggt tct	672
Lys Leu Ala Ile Glu Met Gly Ala Val Gly Pro Thr Gly Arg Gly Ser	
210 215 220	
ggt gtc agg gat gat gca agg tgg agt gag aag cta gga gtt tac cca	720
Gly Val Arg Asp Asp Ala Arg Trp Ser Glu Lys Leu Gly Val Tyr Pro	
225 230 235 240	
gac ctc ggg att aaa cca atc atg cca gaa gac gtc aca gga gag aaa	768
Asp Leu Gly Ile Lys Pro Ile Met Pro Glu Asp Val Thr Gly Glu Lys	
245 250 255	
gct aga ggc gat gtc tac gat agg gcc gcc gtt agg ata gga gag ata	816
Ala Arg Gly Asp Val Tyr Asp Arg Ala Ala Val Arg Ile Gly Glu Ile	
260 265 270	
tgg cag agt ctc gag tta ata gag cat gct cta gat cag ata ccc aag	864
Trp Gln Ser Leu Glu Leu Ile Glu His Ala Leu Asp Gln Ile Pro Lys	
275 280 285	
gga aag ata aag aca ttc ccc aag gat aac gtt cta gtc gca aag ctc	912
Gly Lys Ile Lys Thr Phe Pro Lys Asp Asn Val Leu Val Ala Lys Leu	
290 295 300	
aaa ctg tta ggg gat ggt gaa gga ata gga aga tac gag gct cca agg	960
Lys Leu Leu Gly Asp Gly Glu Gly Ile Gly Arg Tyr Glu Ala Pro Arg	
305 310 315 320	
gga gag ctg gtt cac tac gtg aag ggg aag aaa gga agg gat gga cca	1008
Gly Glu Leu Val His Tyr Val Lys Gly Lys Lys Gly Arg Asp Gly Pro	
325 330 335	
gtt agg tgg aag atg agg gaa cca acg ttt ccg aac ctc ttc gca ata	1056
Val Arg Trp Lys Met Arg Glu Pro Thr Phe Pro Asn Leu Phe Ala Ile	
340 345 350	

DESUanglais-seq1.txt

gcg aag ggc ctt gaa gga aat cag tta gcg gac gtt gtt gtt gct ata 1104
Ala Lys Gly Leu Glu Gly Asn Gln Leu Ala Asp Val Val Val Ala Ile
355 360 365

gca tca ata gat cca tgc tta agc tgt aca gac agg gtg gcc gta att 1152
Ala Ser Ile Asp Pro Cys Leu Ser Cys Thr Asp Arg Val Ala Val Ile
370 375 380

acc gga gat aag aag gtt atc tta aca gag aaa gac ctt ctg aag ctt 1200
Thr Gly Asp Lys Lys Val Ile Leu Thr Glu Lys Asp Leu Leu Lys Leu
385 390 395 400

tca att caa aaa act agg gag ata aat cct gag ata agg gga gat cca 1248
Ser Ile Gln Lys Thr Arg Glu Ile Asn Pro Glu Ile Arg Gly Asp Pro
405 410 415

acc cca gca gga gtt gga tgt gtg agg ggg tga 1281
Thr Pro Ala Gly Val Gly Cys Val Arg Gly
420 425

<210> 34
<211> 426
<212> PRT
<213> Pyrococcus abyssi

<400> 34
Met Ser Lys Val Glu Tyr Trp Val Lys Val Pro Phe Gly Pro Ile His
1 5 10 15

Pro Gly Leu Glu Glu Pro Glu Lys Phe Ile Leu Thr Leu Asp Gly Glu
20 25 30

Arg Ile Val Asn Val Asp Val Lys Leu Gly Tyr Asn Leu Arg Gly Ile
35 40 45

Gln Trp Ile Ala Phe Arg Arg Asn Tyr Val Gln Leu Met Tyr Val Ala
50 55 60

Glu Arg Ile Cys Gly Ile Cys Ser Phe Ser His Asn His Thr Tyr Val
65 70 75 80

Arg Ala Val Glu Glu Met Ala Gly Ile Glu Val Pro Glu Arg Ala Glu
85 90 95

Tyr Ile Arg Val Ile Ile Gly Glu Leu Glu Arg Ile His Ser His Leu
100 105 110

Leu Asn Leu Gly Val Leu Gly His Asp Ile Gly Tyr Asp Thr Val Leu
115 120 125

His Leu Thr Trp Leu Ala Arg Glu Lys Val Met Asp Val Leu Glu Ala
130 135 140

Ile Thr Gly Asn Arg Val Asn Tyr Ser Met Met Thr Ile Gly Gly Val
145 150 155 160

Arg Arg Asp Ile Glu Glu Lys His Arg Arg Leu Leu Leu Asp Met Ile
165 170 175

Lys Tyr Tyr Arg Glu Ile Met Pro Gln Ile Glu Asp Val Phe Leu His
180 185 190

Asp Ser Thr Ile Glu Ala Arg Leu Arg Asn Cys Ala Ile Ile Pro Lys
195 200 205

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

Gly Val Arg Asp Asp Ala Arg Trp Ser Glu Lys Leu Gly Val Tyr Pro
225 230 235 240

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

Ala Arg Gly Asp Val Tyr Asp Arg Ala Ala Val Arg Ile Gly Glu Ile
260 265 270

Trp Gln Ser Leu Glu Leu Ile Glu His Ala Leu Asp Gln Ile Pro Lys
275 280 285

Gly Lys Ile Lys Thr Phe Pro Lys Asp Asn Val Leu Val Ala Lys Leu
290 295 300

DESUanglais-seq1.txt

Lys Leu Leu Gly Asp Gly Glu Gly Ile Gly Arg Tyr Glu Ala Pro Arg
 305 310 315 320
 Gly Glu Leu Val His Tyr Val Lys Gly Lys Gly Arg Asp Gly Pro
 325 330 335
 Val Arg Trp Lys Met Arg Glu Pro Thr Phe Pro Asn Leu Phe Ala Ile
 340 345 350
 Ala Lys Gly Leu Glu Gly Asn Gln Leu Ala Asp Val Val Ala Ile
 355 360 365
 Ala Ser Ile Asp Pro Cys Leu Ser Cys Thr Asp Arg Val Ala Val Ile
 370 375 380
 Thr Gly Asp Lys Lys Val Ile Leu Thr Glu Lys Asp Leu Leu Lys Leu
 385 390 395 400
 Ser Ile Gln Lys Thr Arg Glu Ile Asn Pro Glu Ile Arg Gly Asp Pro
 405 410 415
 Thr Pro Ala Gly Val Gly Cys Val Arg Gly
 420 425

<210> 35
 <211> 1767
 <212> DNA
 <213> Pyrococcus abyssi

<220>
 <221> CDS
 <222> (1)..(1767)
 <223>

<400> 35
 atg gag tgt aaa gcg tgt gaa aag ggg aag tgt agg aac gct aac ctt 48
 Met Glu Cys Lys Ala Cys Glu Lys Gly Lys Cys Arg Asn Ala Asn Leu
 1 5 10 15
 gag gaa gtg ctc tcc gag agg gag gga ttg cta gaa ttt tac gag gaa 96
 Glu Glu Val Leu Ser Glu Arg Glu Gly Leu Leu Glu Phe Tyr Glu Glu
 20 25 30
 ttc aag gag cac atc cac gag tgc aag agg atg agt tat ggc cag tac 144
 Phe Lys Glu His Ile His Glu Cys Lys Arg Met Ser Tyr Gly Gln Tyr
 35 40 45
 atg ttc gta atc gac aag gaa gtc ctc ccc aag gcc gtt cta tgg tgg 192
 Met Phe Val Ile Asp Lys Glu Val Leu Pro Lys Ala Val Leu Trp Trp
 50 55 60
 cac aac cat cct aag ttc aag gaa acc cac ctc tcc aca gct gtc gga 240
 His Asn His Pro Lys Phe Lys Glu Thr His Leu Ser Thr Ala Val Gly
 65 70 75 80
 acg gat gag acc ccg tta aat ggg aaa ttt gct tac atg ccc ttc ctc 288
 Thr Asp Glu Thr Pro Leu Asn Gly Lys Phe Ala Tyr Met Pro Phe Leu
 85 90 95
 agc gtt cag gtt gag cca ttt aac atg gat agg aat tac tgg gta ttc 336
 Ser Val Gln Val Glu Pro Phe Asn Met Asp Arg Asn Tyr Trp Val Phe
 100 105 110
 ctg aag gct tac ttg gat cca gag aac ccc gag ttt cca tcc gtc gcc 384
 Leu Lys Ala Tyr Leu Asp Pro Glu Asn Pro Glu Phe Pro Ser Val Ala
 115 120 125
 gct gaa cta cct gcg gcc ctt tgg ata gag agg gaa gtt caa gat ctc 432
 Ala Glu Leu Pro Ala Ala Leu Trp Ile Glu Arg Glu Val Gln Asp Leu
 130 135 140
 ctg gga ttt aaa gca ata aac cat cca gac ccc agg agg cta gtc ctc 480
 Leu Gly Phe Lys Ala Ile Asn His Pro Asp Pro Arg Arg Leu Val Leu
 145 150 155 160
 ccc gag gac tgg ccc gat gga gtt tat cca ctt agg aag tgc atg gac 528
 Pro Glu Asp Trp Pro Asp Gly Val Tyr Pro Leu Arg Lys Cys Met Asp
 165 170 175
 tac aga tac tcc cca atg gcc gag cca aag ata gag ctc aag aag cca 576
 Tyr Arg Tyr Ser Pro Met Ala Glu Pro Lys Ile Glu Leu Lys Lys Pro
 180 185 190

DESUanglais-seq1.txt																
cca Pro	gaa Glu	gga Gly 195	aca Thr	tcc Ser	acg Thr	gtc Val	cca Pro 200	atg Met	ggg Gly	ccg Pro	ctt Leu	cac His 205	atg Met	ggg Gly	ata Ile	624
gag Glu	gaa Glu 210	ccg Pro	gcc Ala	cac His	ttc Phe	aag Lys 215	ctc Leu	ttc Phe	gta Val	aag Lys	ggc Gly 220	gag Glu	gaa Glu	ata Ile	ggt Val	672
gac Asp 225	ggt Val	gac Asp	tat Tyr	cgc Arg	ggg Gly 230	ttc Phe	tac Tyr	tcc Ser	cat His	agg Arg 235	ggg Gly	ata Ile	gag Glu	aag Lys	ata Ile 240	720
ggg Gly	gag Glu	gga Gly	aga Arg	tta Leu 245	acc Thr	tat Tyr	aat Asn	caa Gln	gtc Val 250	ctc Leu	ttc Phe	ctc Leu	gcg Ala	gaa Glu 255	agg Arg	768
ata Ile	tgc Cys	gga Gly	atc Ile 260	tgc Cys	ggg Gly	tat Tyr	cag Gln	cac His 265	tcc Ser	ggt Val	tct Ser	tat Tyr	gcg Ala 270	atg Met	gcc Ala	816
att Ile	gag Glu	cgg Arg 275	ttg Leu	gcg Ala	gat Asp	gta Val	gaa Glu 280	ata Ile	cct Pro	gat Asp	agg Arg	gcc Ala 285	aga Arg	tac Tyr	ata Ile	864
aga Arg	acc Thr 290	ctg Leu	ctc Leu	ctc Leu	gag Glu	ctg Leu 295	gag Glu	agg Arg	ata Ile	cac His	aac Asn 300	cac His	ctc Leu	ctc Leu	tgg Trp	912
ggt Val 305	ggg Gly	ata Ile	gct Ala	gca Ala	cac His 310	ctt Leu	gta Val	ggg Gly	tac Tyr	gat Asp 315	acg Thr	ggc Gly	ttc Phe	atg Met	cat His 320	960
gcg Ala	tgg Trp	cgt Arg	atc Ile	agg Arg 325	gaa Glu	ccc Pro	gtc Val	atg Met	tgg Trp 330	ctc Leu	atg Met	gag Glu	cgc Arg	ttg Leu 335	acc Thr	1008
ggg Gly	aac Asn	agg Arg	aag Lys 340	cag Gln	tac Tyr	ggg Gly	atg Met	aac Asn 345	ata Ile	ggt Val	ggg Gly	ggc Gly	ggt Val 350	agg Arg	agg Arg	1056
gac Asp	ata Ile	ctc Leu 355	gac Asp	tac Tyr	agg Arg	aag Lys	gaa Glu 360	gag Glu	atc Ile	cta Leu	agg Arg	gtg Val 365	gta Val	agg Arg	gag Glu	1104
ata Ile	agg Arg 370	gag Glu	gaa Glu	ggt Val	aag Lys	aga Arg 375	ttc Phe	ctt Leu	gaa Glu	gta Val	ggt Val 380	ctc Leu	aac Asn	acg Thr	aac Asn	1152
acc Thr 385	ttc Phe	ata Ile	aag Lys	agg Arg	gcc Ala 390	gaa Glu	ggg Gly	ggt Val	gga Gly	att Ile 395	ctt Leu	ccc Pro	tat Tyr	aaa Lys	gta Val 400	1200
gct Ala	aag Lys	gaa Glu	ttc Phe	tgc Ser 405	ggt Val	ctt Leu	gga Gly	cct Pro	aca Thr 410	gct Ala	aga Arg	gct Ala	agc Ser	ggg Gly 415	agg Arg	1248
aag Lys	ata Ile	gac Asp	gca Ala 420	agg Arg	ctg Leu	gat Asp	caa Gln 425	gcc Ala	acc Thr	aag Lys	act Thr	gca Ala	acg Thr 430	gcc Ala	tac Tyr	1296
aac Asn	gag Glu	ctg Leu 435	gac Asp	tgg Trp	aag Lys	ggt Val	cca Pro 440	ggt Val	tac Tyr	aag Lys	gaa Glu	ggc Gly 445	gac Asp	ggt Val	cta Leu	1344
gct Ala	agg Arg 450	ggt Val	ctc Leu	ggt Val	agg Arg	atg Met 455	gac Asp	gag Glu	ctg Leu	ttc Phe	gag Glu 460	agt Ser	ata Ile	tgg Trp	ata Ile	1392
gtc Val 465	gag Glu	cag Gln	ggt Val	ata Ile	gac Asp 470	caa Gln	atg Met	ccg Pro	ggc Gly	ggg Gly 475	gac Asp	gta Val	atg Met	gtg Val	ccg Pro 480	1440
gtg Val	ggt Gly	aga Arg	ttg Leu	cca Pro 485	gag Glu	tac Tyr	gag Glu	gaa Glu	gcc Ala 490	cta Leu	ggc Gly	ttc Phe	act Thr	gag Glu 495	gcc Ala	1488
cac His	agg Arg	gga Gly	gag Glu 500	gtc Val	gtc Val	cac His	tac Tyr	gta Val 505	atg Met	acg Thr	gga Gly	gag Glu	aag Lys 510	aac Asn	aag Lys	1536
ggt Val	tac Tyr	cgc Arg 515	tgg Trp	aag Lys	ggt Val	agg Arg	gcc Ala 520	cca Pro	aca Thr	tac Tyr	aac Asn	aac Asn 525	ctc Leu	ccc Pro	gca Ala	1584
ggt	cct	gag	atg	ctc	aag	gga	tat	cac	ggt	gcg	gac	gct	ccg	ctg	ata	1632

DESUanglais-seql.txt
Val Pro Glu Met Leu Lys Gly Tyr His Val Ala Asp Ala Pro Leu Ile
530 535 540

atc gct agc ata gat cca tgt tat tcc tgc acc gag agg gtt cag ata 1680
Ile Ala Ser Ile Asp Pro Cys Tyr Ser Cys Thr Glu Arg Val Gln Ile
545 550 555 560

gtg gac gtg aga agt gga aag gta aag gtt cta acg gaa tcg gag ttc 1728
Val Asp Val Arg Ser Gly Lys Val Lys Val Leu Thr Glu Ser Glu Phe
565 570 575

aac gag ctc tca ata aag aga agc aag gag atg gtt tga 1767
Asn Glu Leu Ser Ile Lys Arg Ser Lys Glu Met Val
580 585

<210> 36
<211> 588
<212> PRT
<213> Pyrococcus abyssi

<400> 36
Met Glu Cys Lys Ala Cys Glu Lys Gly Lys Cys Arg Asn Ala Asn Leu
1 5 10 15

Glu Glu Val Leu Ser Glu Arg Glu Gly Leu Leu Glu Phe Tyr Glu Glu
20 25 30

Phe Lys Glu His Ile His Glu Cys Lys Arg Met Ser Tyr Gly Gln Tyr
35 40 45

Met Phe Val Ile Asp Lys Glu Val Leu Pro Lys Ala Val Leu Trp Trp
50 55 60

His Asn His Pro Lys Phe Lys Glu Thr His Leu Ser Thr Ala Val Gly
65 70 75 80

Thr Asp Glu Thr Pro Leu Asn Gly Lys Phe Ala Tyr Met Pro Phe Leu
85 90 95

Ser Val Gln Val Glu Pro Phe Asn Met Asp Arg Asn Tyr Trp Val Phe
100 105 110

Leu Lys Ala Tyr Leu Asp Pro Glu Asn Pro Glu Phe Pro Ser Val Ala
115 120 125

Ala Glu Leu Pro Ala Ala Leu Trp Ile Glu Arg Glu Val Gln Asp Leu
130 135 140

Leu Gly Phe Lys Ala Ile Asn His Pro Asp Pro Arg Arg Leu Val Leu
145 150 155 160

Pro Glu Asp Trp Pro Asp Gly Val Tyr Pro Leu Arg Lys Cys Met Asp
165 170 175

Tyr Arg Tyr Ser Pro Met Ala Glu Pro Lys Ile Glu Leu Lys Lys Pro
180 185 190

Pro Glu Gly Thr Ser Thr Val Pro Met Gly Pro Leu His Met Gly Ile
195 200 205

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

Asp Val Asp Tyr Arg Gly Phe Tyr Ser His Arg Gly Ile Glu Lys Ile
225 230 235 240

Gly Glu Gly Arg Leu Thr Tyr Asn Gln Val Leu Phe Leu Ala Glu Arg
245 250 255

Ile Cys Gly Ile Cys Gly Tyr Gln His Ser Val Ser Tyr Ala Met Ala
260 265 270

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

Arg Thr Leu Leu Leu Glu Leu Glu Arg Ile His Asn His Leu Leu Trp
290 295 300

Val Gly Ile Ala Ala His Leu Val Gly Tyr Asp Thr Gly Phe Met His
305 310 315 320

Ala Trp Arg Ile Arg Glu Pro Val Met Trp Leu Met Glu Arg Leu Thr
325 330 335

DESUanglais-seq1.txt

Gly Asn Arg Lys Gln Tyr Gly Met Asn Ile Val Gly Gly Val Arg Arg
 340 345 350

Asp Ile Leu Asp Tyr Arg Lys Glu Glu Ile Leu Arg Val Val Arg Glu
 355 360 365

Ile Arg Glu Glu Val Lys Arg Phe Leu Glu Val Val Leu Asn Thr Asn
 370 375 380

Thr Phe Ile Lys Arg Ala Glu Gly Val Gly Ile Leu Pro Tyr Lys Val
 385 390 395 400

Ala Lys Glu Phe Ser Val Leu Gly Pro Thr Ala Arg Ala Ser Gly Arg
 405 410 415

Lys Ile Asp Ala Arg Leu Asp Gln Ala Thr Lys Thr Ala Thr Ala Tyr
 420 425 430

Asn Glu Leu Asp Trp Lys Val Pro Val Tyr Lys Glu Gly Asp Val Leu
 435 440 445

Ala Arg Val Leu Val Arg Met Asp Glu Leu Phe Glu Ser Ile Trp Ile
 450 455 460

Val Glu Gln Val Ile Asp Gln Met Pro Gly Gly Asp Val Met Val Pro
 465 470 475 480

Val Gly Arg Leu Pro Glu Tyr Glu Glu Ala Leu Gly Phe Thr Glu Ala
 485 490 495

His Arg Gly Glu Val Val His Tyr Val Met Thr Gly Glu Lys Asn Lys
 500 505 510

Val Tyr Arg Trp Lys Val Arg Ala Pro Thr Tyr Asn Asn Leu Pro Ala
 515 520 525

Val Pro Glu Met Leu Lys Gly Tyr His Val Ala Asp Ala Pro Leu Ile
 530 535 540

Ile Ala Ser Ile Asp Pro Cys Tyr Ser Cys Thr Glu Arg Val Gln Ile
 545 550 555 560

Val Asp Val Arg Ser Gly Lys Val Lys Val Leu Thr Glu Ser Glu Phe
 565 570 575

Asn Glu Leu Ser Ile Lys Arg Ser Lys Glu Met Val
 580 585

<210> 37
 <211> 1283
 <212> DNA
 <213> Pyrococcus horikoshii

<220>
 <221> CDS
 <222> (1)..(1281)
 <223>

<400> 37
 atg agt aag aag gta gaa tat tgg gtt aag ata cct ttc ggc cca atc 48
 Met Ser Lys Lys Val Glu Tyr Trp Val Lys Ile Pro Phe Gly Pro Ile
 1 5 10 15

cat cct ggg tta gaa gag cct gaa aag ttc atc ctc acg cta gat gga 96
 His Pro Gly Leu Glu Glu Pro Glu Lys Phe Ile Leu Thr Leu Asp Gly
 20 25 30

gag agg ata gta aac gta gat att aag ctg ggg tat aac ctt agg gga 144
 Glu Arg Ile Val Asn Val Asp Ile Lys Leu Gly Tyr Asn Leu Arg Gly
 35 40 45

att caa tgg ata gct ttt agg agg aac tac gtt cag ctt atg tat ctc 192
 Ile Gln Trp Ile Ala Phe Arg Arg Asn Tyr Val Gln Leu Met Tyr Leu
 50 55 60

gcg gaa agg ata tgc gga ata tgt agc ttc tcc cac aat cat aca tat 240
 Ala Glu Arg Ile Cys Gly Ile Cys Ser Phe Ser His Asn His Thr Tyr
 65 70 75 80

gtt aga gca gtt gaa gag atg gct gga ata gaa gtt ccc gaa agg gcc 288
 Val Arg Ala Val Glu Glu Met Ala Gly Ile Glu Val Pro Glu Arg Ala
 85 90 95

gaa tac ata aga gcg ata att ggg gaa ctt gag aga ata cac tcc cat 336

DESUanglais-seql.txt																	
Glu Tyr Ile Arg Ala Ile Ile Gly Glu Leu Glu Arg Ile His Ser His	100	105	110														
ctc ctt aac ctc ggg gtc gta ggt cac gac ata ggg tac gac acc gtg	Leu Leu Asn Leu Gly Val Val Gly His Asp Ile Gly Tyr Asp Thr Val	384															
ctc cac tta aca tgg ctt gca agg gag aag gta atg gat gct cta gag	Leu His Leu Thr Trp Leu Ala Arg Glu Lys Val Met Asp Ala Leu Glu	432															
gcc ata acc ggc aac agg gta aac tac agt atg atg act att gga ggg	Ala Ile Thr Gly Asn Arg Val Asn Tyr Ser Met Met Thr Ile Gly Gly	480															
gtt agg agg gat ata gag gaa aag cac aag aga ttg ctc ctc gat atg	Val Arg Arg Asp Ile Glu Glu Lys His Lys Arg Leu Leu Leu Asp Met	528															
ata aag tac tat aga gaa ata atg ccc cag ata gaa gat gta ttc tta	Ile Lys Tyr Tyr Arg Glu Ile Met Pro Gln Ile Glu Asp Val Phe Leu	576															
cat gat tca act ata gaa gca aga ctt agg aac tgt gcg gta gtc cca	His Asp Ser Thr Ile Glu Ala Arg Leu Arg Asn Cys Ala Val Val Pro	624															
agg aaa cta gct ata gaa atg ggt gcg gtt ggg cca aca ggt agg gga	Arg Lys Leu Ala Ile Glu Met Gly Ala Val Gly Pro Thr Gly Arg Gly	672															
tcc ggg ata aag gat gat gca aga tgg agc gaa aaa ctt gga gtg tat	Ser Gly Ile Lys Asp Asp Ala Arg Trp Ser Glu Lys Leu Gly Val Tyr	720															
cca gat tta ggg atc aaa cca gta atg cca gaa gac gtc aca gga gag	Pro Asp Leu Gly Ile Lys Pro Val Met Pro Glu Asp Val Thr Gly Glu	768															
aag gct agg ggg gat gtc tat gat aga aca gca gtc aga atc ggt gaa	Lys Ala Arg Gly Asp Val Tyr Asp Thr Ala Val Arg Ile Gly Glu	816															
ata tat caa agc ctt gag ctg att gag cat gcg tta gat cag atg cca	Ile Tyr Gln Ser Leu Glu Leu Ile Glu His Ala Leu Asp Gln Met Pro	864															
gaa ggg aag ata aag gca ttt cct aaa gat aac att cta gtt gca aag	Glu Gly Lys Ile Lys Ala Phe Pro Lys Asp Asn Ile Leu Val Ala Lys	912															
ctc aag cta ctt gga gat gga gaa gga ata ggt agg tac gaa gct cca	Leu Lys Leu Leu Gly Asp Gly Glu Gly Ile Gly Arg Tyr Glu Ala Pro	960															
agg gga gaa ctc ata cat tat gta aaa ggg aag aag ggt agg gat ggt	Arg Gly Glu Leu Ile His Tyr Val Lys Gly Lys Lys Gly Arg Asp Gly	1008															
ccc gtc aga tgg aag atg agg gaa cca act ttt ccc aac ttg ttc aca	Pro Val Arg Trp Lys Met Arg Glu Pro Thr Phe Pro Asn Leu Phe Thr	1056															
ata gcg aag gga ttg gaa gga aat caa cta gcc gat gtc gtc gtt gca	Ile Ala Lys Gly Leu Glu Gly Asn Gln Leu Ala Asp Val Val Val Ala	1104															
ata gcc tct ata gat cca tgc cta agc tgt acc gat agg gta gcc gta	Ile Ala Ser Ile Asp Pro Cys Leu Ser Cys Thr Asp Arg Val Ala Val	1152															
gtg aaa gaa ggc aag aag att atc cta acc gaa aaa gat ctg cta aaa	Val Lys Glu Gly Lys Lys Ile Ile Leu Thr Glu Lys Asp Leu Leu Lys	1200															
ctt tca att cag aaa act cgg gaa ata aat cca gaa gta aaa ggg gat	Leu Ser Ile Gln Lys Thr Arg Glu Ile Asn Pro Glu Val Lys Gly Asp	1248															
ccc act ccc gcg gga gta gga tgc att agg ggg tg	Pro Thr Pro Ala Gly Val Gly Cys Ile Arg Gly	1283															

DESUanglais-seql.txt

<211> 427
 <212> PRT
 <213> Pyrococcus horikoshii
 <400> 38
 Met Ser Lys Lys Val Glu Tyr Trp Val Lys Ile Pro Phe Gly Pro Ile
 1 5 10 15
 His Pro Gly Leu Glu Glu Pro Glu Lys Phe Ile Leu Thr Leu Asp Gly
 20 25 30
 Glu Arg Ile Val Asn Val Asp Ile Lys Leu Gly Tyr Asn Leu Arg Gly
 35 40 45
 Ile Gln Trp Ile Ala Phe Arg Arg Asn Tyr Val Gln Leu Met Tyr Leu
 50 55 60
 Ala Glu Arg Ile Cys Gly Ile Cys Ser Phe Ser His Asn His Thr Tyr
 65 70 75 80
 Val Arg Ala Val Glu Glu Met Ala Gly Ile Glu Val Pro Glu Arg Ala
 85 90 95
 Glu Tyr Ile Arg Ala Ile Ile Gly Glu Leu Glu Arg Ile His Ser His
 100 105 110
 Leu Leu Asn Leu Gly Val Val Gly His Asp Ile Gly Tyr Asp Thr Val
 115 120 125
 Leu His Leu Thr Trp Leu Ala Arg Glu Lys Val Met Asp Ala Leu Glu
 130 135 140
 Ala Ile Thr Gly Asn Arg Val Asn Tyr Ser Met Met Thr Ile Gly Gly
 145 150 155 160
 Val Arg Arg Asp Ile Glu Glu Lys His Lys Arg Leu Leu Leu Asp Met
 165 170 175
 Ile Lys Tyr Tyr Arg Glu Ile Met Pro Gln Ile Glu Asp Val Phe Leu
 180 185 190
 His Asp Ser Thr Ile Glu Ala Arg Leu Arg Asn Cys Ala Val Val Pro
 195 200 205
 Arg Lys Leu Ala Ile Glu Met Gly Ala Val Gly Pro Thr Gly Arg Gly
 210 215 220
 Ser Gly Ile Lys Asp Asp Ala Arg Trp Ser Glu Lys Leu Gly Val Tyr
 225 230 235 240
 Pro Asp Leu Gly Ile Lys Pro Val Met Pro Glu Asp Val Thr Gly Glu
 245 250 255
 Lys Ala Arg Gly Asp Val Tyr Asp Arg Thr Ala Val Arg Ile Gly Glu
 260 265 270
 Ile Tyr Gln Ser Leu Glu Leu Ile Glu His Ala Leu Asp Gln Met Pro
 275 280 285
 Glu Gly Lys Ile Lys Ala Phe Pro Lys Asp Asn Ile Leu Val Ala Lys
 290 295 300
 Leu Lys Leu Leu Gly Asp Gly Glu Gly Ile Gly Arg Tyr Glu Ala Pro
 305 310 315 320
 Arg Gly Glu Leu Ile His Tyr Val Lys Gly Lys Lys Gly Arg Asp Gly
 325 330 335
 Pro Val Arg Trp Lys Met Arg Glu Pro Thr Phe Pro Asn Leu Phe Thr
 340 345 350
 Ile Ala Lys Gly Leu Glu Gly Asn Gln Leu Ala Asp Val Val Val Ala
 355 360 365
 Ile Ala Ser Ile Asp Pro Cys Leu Ser Cys Thr Asp Arg Val Ala Val
 370 375 380
 Val Lys Glu Gly Lys Lys Ile Ile Leu Thr Glu Lys Asp Leu Leu Lys
 385 390 395 400
 Leu Ser Ile Gln Lys Thr Arg Glu Ile Asn Pro Glu Val Lys Gly Asp
 405 410 415
 Pro Thr Pro Ala Gly Val Gly Cys Ile Arg Gly
 420 425

DESUanglais-seq1.txt

<210> 39
 <211> 1284
 <212> DNA
 <213> *Pyrococcus furiosus*

<220>
 <221> CDS
 <222> (1)..(1284)
 <223>

<400> 39
 atg aag aag gtc gaa tat tgg gtt aaa atc ccc ttt ggt ccc att cat 48
 Met Lys Lys Val Glu Tyr Trp Val Lys Ile Pro Phe Gly Pro Ile His
 1 5 10 15
 cca gga tta gaa gag cca gaa aag ttc atc ata acc cta gat gga gag 96
 Pro Gly Leu Glu Glu Pro Glu Lys Phe Ile Ile Thr Leu Asp Gly Glu
 20 25 30
 aga ata gta aac gtt gat gta aag ctt gga tat aac ctc aga ggt gtg 144
 Arg Ile Val Asn Val Asp Val Lys Leu Gly Tyr Asn Leu Arg Gly Val
 35 40 45
 caa tgg ata gga atg aga aga aac tac gtc cag atc atg tat ctg gca 192
 Gln Trp Ile Gly Met Arg Arg Asn Tyr Val Gln Ile Met Tyr Leu Ala
 50 55 60
 gag aga atg tgt gga att tgc tcc ttt tcc cat aac cac aca tac gta 240
 Glu Arg Met Cys Gly Ile Cys Ser Phe Ser His Asn His Thr Tyr Val
 65 70 75 80
 aga gct gtt gaa gag atg gcc gga ata gag gtt cca gag aga gca gaa 288
 Arg Ala Val Glu Glu Met Ala Gly Ile Glu Val Pro Glu Arg Ala Glu
 85 90 95
 tat atc aga gtt ata gtg ggg gag ctc gag aga att cac tcc cac ctc 336
 Tyr Ile Arg Val Ile Val Gly Glu Leu Glu Arg Ile His Ser His Leu
 100 105 110
 ttg aat ctc gga gta gtg ggg cac gac att gga tat gac aca gtc ctc 384
 Leu Asn Leu Gly Val Val Gly His Asp Ile Gly Tyr Asp Thr Val Leu
 115 120 125
 cat cta aca tgg ttg gct aga gaa aga gta atg gat gtc cta gaa gct 432
 His Leu Thr Trp Leu Ala Arg Glu Arg Val Met Asp Val Leu Glu Ala
 130 135 140
 gtt agt gga aac aga gtt aac tac tcc atg gta acc att gga gga gtc 480
 Val Ser Gly Asn Arg Glu Asn Tyr Ser Met Val Thr Ile Gly Gly Val
 145 150 155 160
 aga agg gat ata gga gag aaa caa aaa cga cta att ttg gat atg ata 528
 Arg Arg Asp Ile Gly Glu Lys Gln Lys Arg Leu Ile Leu Asp Met Ile
 165 170 175
 aaa tac tac aga gag gtt ctc cca caa ata gaa gac gtt ttt ctc cat 576
 Lys Tyr Tyr Arg Glu Val Leu Pro Gln Ile Glu Asp Val Phe Leu His
 180 185 190
 gac tca aca att gag gca aga tta agg gat gtt gca gtt gtt cca aaa 624
 Asp Ser Thr Ile Glu Ala Arg Leu Arg Asp Val Ala Val Val Pro Lys
 195 200 205
 aag ctt gca ata gag atg ggt gcc gtt ggc cca acg gcg aga gga agt 672
 Lys Leu Ala Ile Glu Met Gly Ala Val Gly Pro Thr Ala Arg Gly Ser
 210 215 220
 ggg att aaa gag gat tct aga tgg agt gag caa cta gga gtt tat ccc 720
 Gly Ile Lys Glu Asp Ser Arg Trp Ser Glu Gln Leu Gly Val Tyr Pro
 225 230 235 240
 gac ctg gga ata aaa cca gta acg ccc gaa gac gtt act gga gaa aag 768
 Asp Leu Gly Ile Lys Pro Val Thr Pro Glu Asp Val Thr Gly Glu Lys
 245 250 255
 gcc aga gga gat gtt tat gac aga atg gcc gta aga att ggg gag cta 816
 Ala Arg Gly Asp Val Tyr Asp Arg Met Ala Val Arg Ile Gly Glu Leu
 260 265 270
 tgg atg agt tta gat ttg ctg gaa cat gca ctc gat cag atg ccg gaa 864
 Trp Met Ser Leu Asp Leu Leu Glu His Ala Leu Asp Gln Met Pro Glu
 275 280 285

DESUanglais-seql.txt

gga aag ata aaa aca ttc ccc aaa gac aat atc tta gtc gct aag ctg 912
 Gly Lys Ile Lys Thr Phe Pro Lys Asp Asn Ile Leu Val Ala Lys Leu
 290 295 300

aag ctc ctt gga gat gga gaa gga ata gga agg tac gaa gct cct aga 960
 Lys Leu Leu Gly Asp Gly Glu Gly Ile Gly Arg Tyr Glu Ala Pro Arg
 305 310 315 320

gga gag cta gtc cac tac gtg aga gga caa aag gga aga gat ggg cct 1008
 Gly Glu Leu Val His Tyr Val Arg Gly Gln Lys Gly Arg Asp Gly Pro
 325 330 335

gta agg tgg aaa cca aga gag cca acc ttc ccg aat cta ttc aca atc 1056
 Val Arg Trp Lys Pro Arg Glu Pro Thr Phe Pro Asn Leu Phe Thr Ile
 340 345 350

gca aag gct cta gaa gga aat gag ctt gcg gac tta gtt gtt gcc ata 1104
 Ala Lys Ala Leu Glu Gly Asn Glu Leu Ala Asp Leu Val Val Ala Ile
 355 360 365

gct tca ata gat cca tgt cta agc tgt aca gac aga gta gcc ata gta 1152
 Ala Ser Ile Asp Pro Cys Leu Ser Cys Thr Asp Arg Val Ala Ile Val
 370 375 380

aaa gaa gga aag aag gta gtt cta act gaa aag gat cta tta aag ctt 1200
 Lys Glu Gly Lys Lys Val Val Leu Thr Glu Lys Asp Leu Leu Lys Leu
 385 390 395 400

tct att gaa aag aca aag gag atc aac cca aac gta aag gga gat cct 1248
 Ser Ile Glu Lys Thr Lys Glu Ile Asn Pro Asn Val Lys Gly Asp Pro
 405 410 415

aca cct act gga att gga tgt tct agg ggg gtg tga 1284
 Thr Pro Thr Gly Ile Gly Cys Ser Arg Gly Val
 420 425

<210> 40
 <211> 427
 <212> PRT
 <213> Pyrococcus furiosus

<400> 40
 Met Lys Lys Val Glu Tyr Trp Val Lys Ile Pro Phe Gly Pro Ile His
 1 5 10 15

Pro Gly Leu Glu Glu Pro Glu Lys Phe Ile Ile Thr Leu Asp Gly Glu
 20 25 30

Arg Ile Val Asn Val Asp Val Lys Leu Gly Tyr Asn Leu Arg Gly Val
 35 40 45

Gln Trp Ile Gly Met Arg Arg Asn Tyr Val Gln Ile Met Tyr Leu Ala
 50 55 60

Glu Arg Met Cys Gly Ile Cys Ser Phe Ser His Asn His Thr Tyr Val
 65 70 75 80

Arg Ala Val Glu Glu Met Ala Gly Ile Glu Val Pro Glu Arg Ala Glu
 85 90 95

Tyr Ile Arg Val Ile Val Gly Glu Leu Glu Arg Ile His Ser His Leu
 100 105 110

Leu Asn Leu Gly Val Val Gly His Asp Ile Gly Tyr Asp Thr Val Leu
 115 120 125

His Leu Thr Trp Leu Ala Arg Glu Arg Val Met Asp Val Leu Glu Ala
 130 135 140

Val Ser Gly Asn Arg Val Asn Tyr Ser Met Val Thr Ile Gly Gly Val
 145 150 155 160

Arg Arg Asp Ile Gly Glu Lys Gln Lys Arg Leu Ile Leu Asp Met Ile
 165 170 175

Lys Tyr Tyr Arg Glu Val Leu Pro Gln Ile Glu Asp Val Phe Leu His
 180 185 190

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

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

DESUanglais-seq1.txt
 Gly Ile Lys Glu Asp Ser Arg Trp Ser Glu Gln Leu Gly Val Tyr Pro
 225 230 235 240
 Asp Leu Gly Ile Lys Pro Val Thr Pro Glu Asp Val Thr Gly Glu Lys
 245 250 255
 Ala Arg Gly Asp Val Tyr Asp Arg Met Ala Val Arg Ile Gly Glu Leu
 260 265 270
 Trp Met Ser Leu Asp Leu Leu Glu His Ala Leu Asp Gln Met Pro Glu
 275 280 285
 Gly Lys Ile Lys Thr Phe Pro Lys Asp Asn Ile Leu Val Ala Lys Leu
 290 295 300
 Lys Leu Leu Gly Asp Gly Glu Gly Ile Gly Arg Tyr Glu Ala Pro Arg
 305 310 315 320
 Gly Glu Leu Val His Tyr Val Arg Gly Gln Lys Gly Arg Asp Gly Pro
 325 330 335
 Val Arg Trp Lys Pro Arg Glu Pro Thr Phe Pro Asn Leu Phe Thr Ile
 340 345 350
 Ala Lys Ala Leu Glu Gly Asn Glu Leu Ala Asp Leu Val Val Ala Ile
 355 360 365
 Ala Ser Ile Asp Pro Cys Leu Ser Cys Thr Asp Arg Val Ala Ile Val
 370 375 380
 Lys Glu Gly Lys Lys Val Val Leu Thr Glu Lys Asp Leu Leu Lys Leu
 385 390 395 400
 Ser Ile Glu Lys Thr Lys Glu Ile Asn Pro Asn Val Lys Gly Asp Pro
 405 410 415
 Thr Pro Thr Gly Ile Gly Cys Ser Arg Gly Val
 420 425

<210> 41
 <211> 1143
 <212> DNA
 <213> Methanococcus jannaschii

<220>
 <221> CDS
 <222> (1)..(1143)
 <223>

<400> 41
 atg agt gaa aat atg gca aca att cct ata gga cca att cat cca gta 48
 Met Ser Glu Asn Met Ala Thr Ile Pro Ile Gly Pro Ile His Pro Val
 1 5 10 15
 ttg aaa gag ccg tta agg att aaa ctt gtt tta gat gga gag aaa cct 96
 Leu Lys Glu Pro Leu Arg Ile Lys Leu Val Leu Asp Gly Glu Lys Pro
 20 25 30
 gtt gat gct gaa att gaa atg ggt tat gtt cat aga gga ata gaa aaa 144
 Val Asp Ala Glu Ile Glu Met Gly Tyr Val His Arg Gly Ile Glu Lys
 35 40 45
 att atg gaa gga aaa cat tgc cat aaa gga att cac tta gca gaa aga 192
 Ile Met Glu Gly Lys His Cys His Lys Gly Ile His Leu Ala Glu Arg
 50 55 60
 gtt tgt ggt atc tgt tcc tat gtg cat acg atg acg ttt gct gaa tgc 240
 Val Cys Gly Ile Cys Ser Tyr Val His Thr Met Thr Phe Ala Glu Cys
 65 70 75 80
 att gag cat ata tca aag ata gag att cca gac aag gca aaa tat ctt 288
 Ile Glu His Ile Ser Lys Ile Glu Ile Pro Asp Lys Ala Lys Tyr Leu
 85 90 95
 agg gta gtt act tgt gaa tta gag aga ata cac agc cat tta att gct 336
 Arg Val Val Thr Cys Glu Leu Glu Arg Ile His Ser His Leu Ile Ala
 100 105 110
 tca gca gtg tat aat tta tct att gaa cat gaa aca ctt gct atg tgg 384
 Ser Ala Val Tyr Asn Leu Ser Ile Glu His Glu Thr Leu Ala Met Trp
 115 120 125
 ctt ttg aat gtt agg gaa ata att atg gat tta atg gag atg att act 432
 Leu Leu Asn Val Arg Glu Ile Ile Met Asp Leu Met Glu Met Ile Thr

DESUanglais-seql.txt
140

130	135	140	480
gga aat agg gtt aat atg ggt tat aat gta att ggg gga gtt aga aga Gly Asn Arg Val Asn Met Gly Tyr Asn Val Ile Gly Gly Val Arg Arg 145 150 155 160			
gac ata aat aga gag atg atg gat gag ata tat aaa aaa ctc gat atc Asp Ile Asn Arg Glu Met Met Asp Glu Ile Tyr Lys Lys Leu Asp Ile 165 170 175			528
ttt gaa gat gaa cta aaa aat att att gag gtt ttt gaa aca ggg cct Phe Glu Asp Glu Leu Lys Asn Ile Ile Glu Val Phe Glu Thr Gly Pro 180 185 190			576
tta ata gct tta aga agt aaa gaa att ggt att ttg cca tat cat gaa Leu Ile Ala Leu Arg Ser Lys Glu Ile Gly Ile Leu Pro Tyr His Glu 195 200 205			624
gtt atg agg acg agg gct gtt ggg cca att tgt aga ggt tct gga ttg Val Met Arg Thr Arg Ala Val Gly Pro Ile Cys Arg Gly Ser Gly Leu 210 215 220			672
cca gaa agt gat tgg agg tta aga cat tca aca tat caa gag ttg aaa Pro Glu Ser Asp Trp Arg Leu Arg His Ser Thr Tyr Gln Glu Leu Lys 225 230 235 240			720
ttt aag cca gtg tgg agg gag gaa gga gat aac ttt gca agg atg atg Phe Lys Pro Val Trp Arg Glu Glu Gly Asp Asn Phe Ala Arg Met Met 245 250 255			768
gtt agg cat gaa gag att att gag agc gtt aga tta att aga gag gct Val Arg His Glu Glu Ile Ile Glu Ser Val Arg Leu Ile Arg Glu Ala 260 265 270			816
tta gag cat tat gaa gag tgt tct gga gat ata agg gtt aag gca gag Leu Glu His Tyr Glu Glu Cys Ser Gly Asp Ile Arg Val Lys Ala Glu 275 280 285			864
att aaa gga gga aaa gga gag tgg agg aat gaa gct cca aga gga gag Ile Lys Gly Gly Lys Gly Glu Trp Arg Asn Glu Ala Pro Arg Gly Glu 290 295 300			912
gta act tat agg atg gaa ata act gat gga ggg ata ata aag agg ata Val Thr Tyr Arg Met Glu Ile Thr Asp Gly Gly Ile Ile Lys Arg Ile 305 310 315 320			960
atg att aga act cct aca gtt atg aac ttg gag gcg tat aaa tat atg Met Ile Arg Thr Pro Thr Val Met Asn Leu Glu Ala Tyr Lys Tyr Met 325 330 335			1008
cta aag act tgt cca act gta gct gat gct gta tct gct tat aca agt Leu Lys Thr Cys Pro Thr Val Ala Asp Ala Val Ser Ala Tyr Thr Ser 340 345 350			1056
atc gac cct tgc gtt tca tgc aca gag aga tgc ata gtt gca gta aag Ile Asp Pro Cys Val Ser Cys Thr Glu Arg Cys Ile Val Ala Val Lys 355 360 365			1104
gat ggc aag gag att cca att agt att aaa ttt agg tga Asp Gly Lys Glu Ile Pro Ile Ser Ile Lys Phe Arg 370 375 380			1143

<210> 42
 <211> 380
 <212> PRT
 <213> Methanococcus jannaschii

<400> 42
 Met Ser Glu Asn Met Ala Thr Ile Pro Ile Gly Pro Ile His Pro Val
 1 5 10 15
 Leu Lys Glu Pro Leu Arg Ile Lys Leu Val Leu Asp Gly Glu Lys Pro
 20 25 30
 Val Asp Ala Glu Ile Glu Met Gly Tyr Val His Arg Gly Ile Glu Lys
 35 40 45
 Ile Met Glu Gly Lys His Cys His Lys Gly Ile His Leu Ala Glu Arg
 50 55 60
 Val Cys Gly Ile Cys Ser Tyr Val His Thr Met Thr Phe Ala Glu Cys
 65 70 75 80

DESUanglais-seq1.txt

Ile Glu His Ile Ser Lys Ile Glu Ile Pro Asp Lys Ala Lys Tyr Leu
85 90 95

Arg Val Val Thr Cys Glu Leu Glu Arg Ile His Ser His Leu Ile Ala
100 105 110

Ser Ala Val Tyr Asn Leu Ser Ile Glu His Glu Thr Leu Ala Met Trp
115 120 125

Leu Leu Asn Val Arg Glu Ile Ile Met Asp Leu Met Glu Met Ile Thr
130 135 140

Gly Asn Arg Val Asn Met Gly Tyr Asn Val Ile Gly Gly Val Arg Arg
145 150 155 160

Asp Ile Asn Arg Glu Met Met Asp Glu Ile Tyr Lys Lys Leu Asp Ile
165 170 175

Phe Glu Asp Glu Leu Lys Asn Ile Ile Glu Val Phe Glu Thr Gly Pro
180 185 190

Leu Ile Ala Leu Arg Ser Lys Glu Ile Gly Ile Leu Pro Tyr His Glu
195 200 205

Val Met Arg Thr Arg Ala Val Gly Pro Ile Cys Arg Gly Ser Gly Leu
210 215 220

Pro Glu Ser Asp Trp Arg Leu Arg His Ser Thr Tyr Gln Glu Leu Lys
225 230 235 240

Phe Lys Pro Val Trp Arg Glu Glu Gly Asp Asn Phe Ala Arg Met Met
245 250 255

Val Arg His Glu Glu Ile Ile Glu Ser Val Arg Leu Ile Arg Glu Ala
260 265 270

Leu Glu His Tyr Glu Glu Cys Ser Gly Asp Ile Arg Val Lys Ala Glu
275 280 285

Ile Lys Gly Gly Lys Gly Glu Trp Arg Asn Glu Ala Pro Arg Gly Glu
290 295 300

Val Thr Tyr Arg Met Glu Ile Thr Asp Gly Gly Ile Ile Lys Arg Ile
305 310 315 320

Met Ile Arg Thr Pro Thr Val Met Asn Leu Glu Ala Tyr Lys Tyr Met
325 330 335

Leu Lys Thr Cys Pro Thr Val Ala Asp Ala Val Ser Ala Tyr Thr Ser
340 345 350

Ile Asp Pro Cys Val Ser Cys Thr Glu Arg Cys Ile Val Ala Val Lys
355 360 365

Asp Gly Lys Glu Ile Pro Ile Ser Ile Lys Phe Arg
370 375 380

<210> 43
 <211> 1128
 <212> DNA
 <213> *Methanococcus maripaludis*

<220>
 <221> CDS
 <222> (1)..(1128)
 <223>

<400> 43
 atg tac gaa gga gaa att gca atc ggg cca gtg cac tct aca atg ctt 48
 Met Tyr Glu Gly Glu Ile Ala Ile Gly Pro Val His Ser Thr Met Leu
 1 5 10 15

gaa cct cac agg ctg aga tta ttt att gaa gat gag ata gta aaa gat 96
 Glu Pro His Arg Leu Arg Leu Phe Ile Glu Asp Glu Ile Val Lys Asp
 20 25 30

gca gaa ctt aca att ggt gta aat cac agg ggc gtt gaa cga tta atg 144
 Ala Glu Leu Thr Ile Gly Val Asn His Arg Gly Val Glu Arg Leu Met
 35 40 45

gaa ggc ctt cct gtt gaa aaa gca tgt att tta tgc gaa aaa atc tgc 192
 Glu Gly Leu Pro Val Glu Lys Ala Cys Ile Leu Cys Glu Lys Ile Cys
 50 55 60

gga atc tgt tca cac att cac ctt tgg agt gcg gca agg ctt gtt gaa 240
 Page 55

Gly Ile Cys Ser His Ile His Leu Trp Ser
 65 70 75 80
 atc ggg tgc aac atc gaa att cca gaa cgt gca aac cac ata aga att 288
 Ile Gly Cys Asn Ile Glu Ile Pro Glu Arg Ala Asn His Ile Arg Ile
 85 90 95
 atc gtg gaa gaa tta gag cga ctt cat tct cat aca tta ctt ttt gga 336
 Ile Val Glu Glu Leu Glu Arg Leu His Ser His Thr Leu Leu Phe Gly
 100 105 110
 cac gct ttt gag ata ttg ggc cat gaa aca atg tca atg aga tgt ttt 384
 His Ala Phe Glu Ile Leu Gly His Glu Thr Met Ser Met Arg Cys Phe
 115 120 125
 atg tta aga gaa cca ata atg cag gta ttt ttt gaa ata tct gga agc 432
 Met Leu Arg Glu Pro Ile Met Gln Val Phe Phe Glu Ile Ser Gly Ser
 130 135 140
 agg gtt cac tac tca tgc cca atc att ggc gga att cgg cca aga tgc 480
 Arg Val His Tyr Ser Cys Pro Ile Ile Gly Ile Arg Pro Arg Cys
 145 150 155 160
 aat att tct gaa act caa atc ccg cat ata ttg gat aaa att tca aaa 528
 Asn Ile Ser Glu Thr Gln Ile Pro His Ile Leu Asp Lys Ile Ser Lys
 165 170 175
 tac gaa gaa gga ctg aat aaa ttt ctt gaa aga atg tta aat gac ccg 576
 Tyr Glu Glu Gly Leu Asn Lys Phe Leu Glu Arg Met Leu Asn Asp Pro
 180 185 190
 atg att att tca aga gta aaa gat gtt ggg gta atg gat aga aaa acc 624
 Met Ile Ile Ser Arg Val Lys Asp Val Gly Val Met Asp Arg Lys Thr
 195 200 205
 gct gct aaa ttc cac gca gta ggg cct act gca agg ggt agc aac gtg 672
 Ala Ala Lys Phe His Ala Val Gly Pro Thr Ala Arg Gly Ser Asn Val
 210 215 220
 aaa tcc gac atg aga aag tgg ggc tgg gtt cca gaa tat gac cca tac 720
 Lys Ser Asp Met Arg Lys Trp Gly Trp Val Pro Glu Tyr Asp Pro Tyr
 225 230 235 240
 gac ttt gac gaa ata tta ttt gac agc gga gat gtt ttt gca agg ctt 768
 Asp Phe Asp Glu Ile Leu Phe Asp Ser Gly Asp Val Phe Ala Arg Leu
 245 250 255
 gct gtt agg ttt tac gag tgc ctt gaa agt gtt aaa att ata aga cag 816
 Ala Val Arg Phe Tyr Glu Cys Leu Glu Ser Val Lys Ile Ile Arg Gln
 260 265 270
 gca ctt gat gct tta aaa gat acc tct gac aaa agg ata tac aat cca 864
 Ala Leu Asp Ala Leu Lys Asp Thr Ser Asp Lys Arg Ile Tyr Asn Pro
 275 280 285
 aat tat gaa tta cac gaa ttt aag ccg ata aac tgc tac acc gaa gct 912
 Asn Tyr Glu Leu His Glu Phe Lys Pro Ile Asn Cys Tyr Thr Glu Ala
 290 295 300
 caa agg gga gag cag tac tat tca tac gga ttg gat gat gaa ggg ctt 960
 Gln Arg Gly Glu Gln Tyr Ser Tyr Gly Leu Asp Asp Glu Gly Leu
 305 310 315 320
 gta agg cag gca aaa atc agg act cct act gca aca aat ctt ggt gca 1008
 Val Arg Gln Ala Lys Ile Arg Thr Pro Thr Ala Thr Asn Leu Gly Ala
 325 330 335
 atg gaa gac att gta aaa gga tac cat gta agt gac gca gaa tta ata 1056
 Met Glu Asp Ile Val Lys Gly Tyr His Val Ser Asp Ala Glu Leu Ile
 340 345 350
 att gca agc tgt gat ccg tgt ttt aca tgt act gat agg tta atg gtt 1104
 Ile Ala Ser Cys Asp Pro Cys Phe Thr Cys Thr Asp Arg Leu Met Val
 355 360 365
 tta aaa gaa ccc ttt aaa aaa taa 1128
 Leu Lys Glu Pro Phe Lys Lys
 370 375

<210> 44
 <211> 375
 <212> PRT
 <213> Methanococcus maripaludis
 <400> 44

DESUanglais-seql.txt

Met Tyr Glu Gly Glu Ile Ala Ile Gly Pro Val His Ser Thr Met Leu
 1 5 10 15
 Glu Pro His Arg Leu Arg Leu Phe Ile Glu Asp Glu Ile Val Lys Asp
 20 25 30
 Ala Glu Leu Thr Ile Gly Val Asn His Arg Gly Val Glu Arg Leu Met
 35 40 45
 Glu Gly Leu Pro Val Glu Lys Ala Cys Ile Leu Cys Glu Lys Ile Cys
 50 55 60
 Gly Ile Cys Ser His Ile His Leu Trp Ser Ala Ala Arg Leu Val Glu
 65 70 75 80
 Ile Gly Cys Asn Ile Glu Ile Pro Glu Arg Ala Asn His Ile Arg Ile
 85 90 95
 Ile Val Glu Glu Leu Glu Arg Leu His Ser His Thr Leu Leu Phe Gly
 100 105 110
 His Ala Phe Glu Ile Leu Gly His Glu Thr Met Ser Met Arg Cys Phe
 115 120 125
 Met Leu Arg Glu Pro Ile Met Gln Val Phe Phe Glu Ile Ser Gly Ser
 130 135 140
 Arg Val His Tyr Ser Cys Pro Ile Ile Gly Gly Ile Arg Pro Arg Cys
 145 150 155 160
 Asn Ile Ser Glu Thr Gln Ile Pro His Ile Leu Asp Lys Ile Ser Lys
 165 170 175
 Tyr Glu Glu Gly Leu Asn Lys Phe Leu Glu Arg Met Leu Asn Asp Pro
 180 185 190
 Met Ile Ile Ser Arg Val Lys Asp Val Gly Val Met Asp Arg Lys Thr
 195 200 205
 Ala Ala Lys Phe His Ala Val Gly Pro Thr Ala Arg Gly Ser Asn Val
 210 215 220
 Lys Ser Asp Met Arg Lys Trp Gly Trp Val Pro Glu Tyr Asp Pro Tyr
 225 230 235 240
 Asp Phe Asp Glu Ile Leu Phe Asp Ser Gly Asp Val Phe Ala Arg Leu
 245 250 255
 Ala Val Arg Phe Tyr Glu Cys Leu Glu Ser Val Lys Ile Ile Arg Gln
 260 265 270
 Ala Leu Asp Ala Leu Lys Asp Thr Ser Asp Lys Arg Ile Tyr Asn Pro
 275 280 285
 Asn Tyr Glu Leu His Glu Phe Lys Pro Ile Asn Cys Tyr Thr Glu Ala
 290 295 300
 Gln Arg Gly Glu Gln Tyr Tyr Ser Tyr Gly Leu Asp Asp Glu Gly Leu
 305 310 315 320
 Val Arg Gln Ala Lys Ile Arg Thr Pro Thr Ala Thr Asn Leu Gly Ala
 325 330 335
 Met Glu Asp Ile Val Lys Gly Tyr His Val Ser Asp Ala Glu Leu Ile
 340 345 350
 Ile Ala Ser Cys Asp Pro Cys Phe Thr Cys Thr Asp Arg Leu Met Val
 355 360 365
 Leu Lys Glu Pro Phe Lys Lys
 370 375

<210> 45
 <211> 1230
 <212> DNA
 <213> Methanopyrus kandleri

<220>
 <221> CDS
 <222> (1)..(1230)
 <223>

<400> 45
 gtg aag cgc agg agg cgt gag atc caa tcc aac gtc caa gtc gtg gac

DESUanglais-seql.txt																	
Val 1	Lys	Arg	Arg	Arg 5	Arg	Glu	Ile	Gln	Ser 10	Asn	Val	Gln	Val	Val 15	Asp		
gtc Val	gag Glu	acg Thr	ggt Gly 20	gag Glu	atc Ile	gag Glu	ccg Pro 25	ata Ile	tca Ser	cac His	cgt Arg	gtc Val	ccc Pro 30	gtg Val	ggt Gly	96	
cct Pro	aat Asn	cat His 35	ccg Pro	atc Ile	ctc Leu	aaa Lys	gag Glu 40	ccc Pro	ctc Leu	cgg Arg	atc Ile	aag Lys 45	ctg Leu	gcg Ala	gtc Val	144	
cga Arg	gga Gly 50	gaa Glu	gag Glu	gtt Val	gtg Val	gac Asp 55	tgc Cys	aag Lys	gtg Val	gag Glu	atg Met 60	gga Gly	tac Tyr	tgc Cys	cac His	192	
cgt Arg 65	ggt Gly	atc Ile	gag Glu	aag Lys	atc Ile 70	atg Met	gag Glu	gga Gly	atg Met	ccc Pro 75	tgg Trp	cag Gln	aag Lys	gcc Ala 80	gcc Ala	240	
ttc Phe	ctc Leu	gct Ala	gaa Glu	cga Arg 85	gtc Val	tgc Cys	gga Gly	atc Ile	tgc Cys 90	tcc Ser	cac His	gcg Ala	cac His	aac Asn 95	atg Met	288	
tgc Cys	ttc Phe	atc Ile	gga Gly 100	ggt Gly	gtc Val	gag Glu	aaa Lys 105	ctc Leu	gcc Ala	gaa Glu	gga Gly	gat Asp	ccc Pro 110	gct Ala	ccg Pro	336	
cgt Arg	gga Gly 115	ttg Leu	ttc Phe	ctc Leu	cgc Arg	gtc Val	ctc Leu 120	gtg Val	caa Gln	gag Glu	cta Leu	gat Asp 125	agg Arg	att Ile	caa Gln	384	
tcc Ser 130	cac His	ctc Leu	atc Ile	gcc Ala	aac Asn	gcc Ala 135	gcc Ala	tac Tyr	ttc Phe	tac Tyr	tcg Ser 140	ata Ile	gag Glu	cat His	gag Glu	432	
act Thr 145	atg Met	ttc Phe	gtg Val	tgg Trp	aac Asn 150	atg Met	aac Asn	act Thr	cgt Arg	gag Glu 155	cgc Arg	gtc Val	ctg Leu	gac Asp	tgc Cys 160	480	
atc Ile	gaa Glu	gag Glu	ata Ile	acc Thr 165	ggt Gly	aac Asn	cgg Arg	atc Ile	ctg Leu 170	acg Thr	ggt Gly	tgg Trp	aac Asn	gtc Val 175	gtc Val	528	
ggt Gly	ggt Gly	gtt Val	cga Arg 180	atg Met	gac Asp	gtc Val	acc Thr	gag Glu 185	gac Asp	caa Gln	ctg Leu	aac Asn	aac Asn 190	gtc Val	ctc Leu	576	
gaa Glu	acc Thr	ctg Leu 195	gac Asp	gca Ala	atc Ile	cgt Arg	gac Asp 200	gac Asp	gtg Val	ata Ile	acg Thr	tac Tyr 205	cga Arg	cga Arg	atc Ile	624	
gcc Ala 210	aag Lys	aac Asn	gat Asp	ccc Pro	ttc Phe	atc Ile 215	aag Lys	ctc Leu	cga Arg	tcg Ser	cgt Arg 220	ggt Gly	gtc Val	ggg Gly	gtg Val	672	
atc Ile 225	act Thr	aag Lys	gac Asp	cat His	atc Ile 230	agg Arg	aag Lys	tac Tyr	cga Arg	gtc Val 235	gtt Val	ggg Gly	ccg Pro	cag Gln	gct Ala 240	720	
agg Arg	gct Ala	tcc Ser	gga Gly	gtc Val 245	ccc Pro	gag Glu	tct Ser	gac Asp	atg Met 250	cgt Arg	ctc Leu	caa Gln	gag Glu	ccc Pro 255	gtt Val	768	
tat Tyr	ccg Pro	gag Glu 260	ctg Leu	ggc Gly	ttc Phe	aag Lys	ccc Pro	gtt Val 265	tac Tyr	agg Arg	aag Lys	gag Glu	ggg Gly 270	gac Asp	aac Asn	816	
ctc Leu	gcc Ala	agg Arg 275	atc Ile	ttg Leu	gtc Val	cga Arg	tac Tyr 280	gac Asp	gag Glu	tgt Cys	ttg Leu	cag Gln 285	tcc Ser	ata Ile	gag Glu	864	
ctc Leu 290	atc Ile	gag Glu	cgg Arg	atc Ile	gtc Val	gat Asp 295	gag Glu	ttg Leu	ccc Pro	gaa Glu	ggg Gly 300	agg Arg	cat His	cga Arg	cgg Arg	912	
gag Glu 305	ctg Leu	gag Glu	gtg Val	aac Asn 310	gcg Ala	gga Gly	cac His	gtc Val	gat Asp 315	cgc Arg	gtc Val	gag Glu	gcc Ala	cca Pro 320		960	
cga Arg	ggg Gly	gaa Glu	ctc Leu 325	gtg Val	tac Tyr	gat Asp	atg Met	gaa Glu 330	cta Leu 330	gct Ala	cct Pro	gga Gly	gga Gly	gtc Val 335	gtg Val	1008	
aag	cgc	gtt	acg	atc	cgc	aca	cct	tcc	gtc	ccg	aat	atc	cga	gtc	ctg	1056	

<210> 46
<211> 409
<212> PRT
<213> Methanopyrus kandleri

<400> 46
Val Lys Arg Arg Arg Glu Ile Gln Ser Asn Val Gln Val Val Asp
1 5 10 15
Val Glu Thr Gly Glu Ile Glu Pro Ile Ser His Arg Val Pro Val Gly
20 25 30
Pro Asn His Pro Ile Leu Lys Glu Pro Leu Arg Ile Lys Leu Ala Val
35 40 45
Arg Gly Glu Glu Val Val Asp Cys Lys Val Glu Met Gly Tyr Cys His
50 55 60
Arg Gly Ile Glu Lys Ile Met Glu Gly Met Pro Trp Gln Lys Ala Ala
65 70 75
Phe Leu Ala Glu Arg Val Cys Gly Ile Cys Ser His Ala His Asn Met
85 90 95
Cys Phe Ile Gly Gly Val Glu Lys Leu Ala Glu Gly Asp Pro Ala Pro
100 105 110
Arg Gly Leu Phe Leu Arg Val Leu Val Gln Glu Leu Asp Arg Ile Gln
115 120 125
Ser His Leu Ile Ala Asn Ala Tyr Phe Tyr Ser Ile Glu His Glu
130 135 140
Thr Met Phe Val Trp Asn Met Asn Thr Arg Glu Arg Val Leu Asp Cys
145 150 155 160
Ile Glu Glu Ile Thr Gly Asn Arg Ile Leu Thr Gly Trp Asn Val Val
165 170 175
Gly Gly Val Arg Met Asp Val Thr Glu Asp Gln Leu Asn Asn Val Leu
180 185 190
Glu Thr Leu Asp Ala Ile Arg Asp Asp Val Ile Thr Tyr Arg Arg Ile
195 200 205
Ala Lys Asn Asp Pro Phe Ile Lys Leu Arg Ser Arg Gly Val Gly Val
210 215 220
Ile Thr Lys Asp His Ile Arg Lys Tyr Arg Val Val Gly Pro Gln Ala
225 230 235 240
Arg Ala Ser Gly Val Pro Glu Ser Asp Met Arg Leu Gln Glu Pro Val
245 250 255
Tyr Pro Glu Leu Gly Phe Lys Pro Val Tyr Arg Lys Glu Gly Asp Asn
260 265 270
Leu Ala Arg Ile Leu Val Arg Tyr Asp Glu Cys Leu Gln Ser Ile Glu
275 280 285
Leu Ile Glu Arg Ile Val Asp Glu Leu Pro Glu Gly Arg His Arg Arg
290 295 300
Glu Leu Glu Val Asn Ala Gly His Val Asp Asn Arg Val Glu Ala Pro
305 310 315 320

DESUanglais-seql.txt

Arg Gly Glu Leu Val Tyr Asp Met Glu Leu Ala Pro Gly Gly Val Val
 325 330 335
 Lys Arg Val Thr Ile Arg Thr Pro Ser Val Pro Asn Ile Arg Val Leu
 340 345 350
 Glu Ala Ile Ala Pro Gly Ser Pro Ser Ile Ala Asp Ala Val Ala Thr
 355 360 365
 Tyr Ala Ser Leu Asp Pro Cys Val Ala Cys Asn Glu Arg Phe Val Val
 370 375 380
 Ile Asp Glu Arg Glu Gly Lys Val Leu Leu Glu Gly Lys Ala Arg Glu
 385 390 395 400
 Val Ile Arg Ala Cys Ser Arg Thr Ser
 405

<210> 47
 <211> 1113
 <212> DNA
 <213> Methanobacterium thermoautotrophicum

<220>
 <221> CDS
 <222> (1)..(1113)
 <223>

<400> 47
 atg ata ctg cca ctt gga ccc atg cac ccg gga tac aag gag ccc ata 48
 Met Ile Leu Pro Leu Gly Pro Met His Pro Gly Tyr Lys Glu Pro Ile
 1 5 10 15
 agg ctc aag gtg aag acc cgg ggt gaa aag gtt ctc aaa gcc gaa ata 96
 Arg Leu Lys Val Lys Thr Arg Gly Glu Lys Val Leu Lys Ala Glu Ile
 20 25 30
 gaa tac gga tac gtt cac agg gga ata gag agg gtt atg agg aac aag 144
 Glu Tyr Gly Tyr Val His Arg Gly Ile Glu Arg Val Met Arg Asn Lys
 35 40 45
 acc tgg cag aag gcc atc tac ctc tct gaa cgc gtc tgc ggg ata tgt 192
 Thr Trp Gln Lys Ala Ile Tyr Tyr Leu Ser Glu Arg Val Cys Gly Ile Cys
 50 55 60
 tca tac ata cac aca cag acc ttt gca gag gcc ttt gag gcc ata tca 240
 Ser Tyr Ile His Thr Gln Thr Phe Ala Glu Ala Phe Glu Ala Ile Ser
 65 70 75 80
 gag gtc gag gca ccc ccc agg gca cag ttc ctc cgt gca tta aca aac 288
 Glu Val Glu Ala Pro Pro Arg Ala Gln Phe Leu Arg Ala Leu Thr Asn
 85 90 95
 gag ctt gac agg ata cag agt cac ctc atc gca aat tca acc tac ttc 336
 Glu Leu Asp Arg Ile Gln Ser His Leu Ile Ala Asn Ser Thr Tyr Phe
 100 105 110
 aag gcc ctg gac cat gag acc atg ttc atg tac atg ctg gcc ctc agg 384
 Lys Ala Leu Asp His Glu Thr Met Phe Met Tyr Met Leu Ala Leu Arg
 115 120 125
 gag cct gta atg gac gcc atc gag ctc ctg aca ggt aac cgg gtc aac 432
 Glu Pro Val Met Asp Ala Ile Glu Leu Leu Thr Gly Asn Arg Val Asn
 130 135 140
 atg ggc tgg aac gtg gtg ggt ggc gtg agg atg gac gcc tca gag agc 480
 Met Gly Trp Asn Val Val Gly Gly Val Arg Met Asp Ala Ser Glu Ser
 145 150 155 160
 cac ctg tca atg ata agg gag atc ata gtt gac ctt gaa aga gag ttc 528
 His Leu Ser Met Ile Arg Glu Ile Ile Val Asp Leu Glu Arg Glu Phe
 165 170 175
 gac cgt tac gtt gag atg ttc gag cac ggc cca ctc ata ggc ctc agg 576
 Asp Arg Tyr Val Glu Met Phe Glu His Gly Pro Leu Ile Gly Leu Arg
 180 185 190
 tca agg gag gtc ggt tac atg agc cag gag gag gca gag aag gcc agg 624
 Ser Arg Glu Val Gly Tyr Met Ser Gln Glu Glu Ala Glu Lys Ala Arg
 195 200 205
 gcc gtt gga cct ata ggg agg gcc tgc ggt ata agg tat gac ttc agg 672
 Ala Val Gly Pro Ile Gly Arg Ala Ser Gly Ile Arg Tyr Asp Phe Arg

DESUanglais-seql.txt
220

210	215		720
gag gac cac ccc acc tac agg gac cac ctg gac ttc agg acc atc tgg			
Glu Asp His Pro Thr Tyr Arg Asp His Leu Asp Phe Arg Thr Ile Trp			
225	230		240
agg gat gat ggc gac aac ttt gca cgg gtc atg aac cgt ttc gat gag			768
Arg Asp Asp Gly Asp Asn Phe Ala Arg Val Met Asn Arg Phe Asp Glu			
	245		255
atc agg gtc tca att gac ctc ata aag cag gtc ata gat gac atg cca			816
Ile Arg Val Ser Ile Asp Leu Ile Lys Gln Val Ile Asp Asp Met Pro			
	260		270
ggg gga ccc gtc agg acg aag gtt gac gtg aag gcg ggt tac ggt gag			864
Gly Gly Pro Val Arg Thr Lys Val Asp Val Lys Ala Gly Tyr Gly Glu			
	275		285
tgg aga aac gag gcc ccc cgg gga gag gtg gcc tac atg att gaa acc			912
Trp Arg Asn Glu Ala Pro Arg Gly Glu Val Ala Tyr Met Ile Glu Thr			
	290		300
aac ggc aac ctc ata aag aac ata tcc ata agg acc ccg agc ata atg			960
Asn Gly Asn Leu Ile Lys Asn Ile Ser Ile Arg Thr Pro Ser Ile Met			
	305		310
aac att gac gcc tgc gca aag tac atg ctg agg gac gtg gca aca gtt			1008
Asn Ile Asp Ala Cys Ala Lys Tyr Met Leu Arg Asp Val Ala Thr Val			
	315		325
gca gac gcc gtt gca aca tat gca agc gct gat cca tgc ata gca tgc			1056
Ala Asp Ala Val Thr Tyr Ala Ser Ala Asp Pro Cys Ile Ala Cys			
	330		345
gca gag agg gtc atg gtt gtt gat gaa gag agt ggg gag agg gag ata			1104
Ala Glu Arg Val Met Val Val Asp Glu Glu Ser Gly Glu Arg Glu Ile			
	350		365
ctc ctc taa			1113
Leu Leu			
	370		

<210> 48
 <211> 370
 <212> PRT
 <213> Methanobacterium thermoautotrophicum

<400> 48
 Met Ile Leu Pro Leu Gly Pro Met His Pro Gly Tyr Lys Glu Pro Ile
 1 5 10 15
 Arg Leu Lys Val Lys Thr Arg Gly Glu Lys Val Leu Lys Ala Glu Ile
 20 25 30
 Glu Tyr Gly Tyr Val His Arg Gly Ile Glu Arg Val Met Arg Asn Lys
 35 40 45
 Thr Trp Gln Lys Ala Ile Tyr Leu Ser Glu Arg Val Cys Gly Ile Cys
 50 55 60
 Ser Tyr Ile His Thr Gln Thr Phe Ala Glu Ala Phe Glu Ala Ile Ser
 65 70 75 80
 Glu Val Glu Ala Pro Pro Arg Ala Gln Phe Leu Arg Ala Leu Thr Asn
 85 90 95
 Glu Leu Asp Arg Ile Gln Ser His Leu Ile Ala Asn Ser Thr Tyr Phe
 100 105 110
 Lys Ala Leu Asp His Glu Thr Met Phe Met Tyr Met Leu Ala Leu Arg
 115 120 125
 Glu Pro Val Met Asp Ala Ile Glu Leu Leu Thr Gly Asn Arg Val Asn
 130 135 140
 Met Gly Trp Asn Val Val Gly Gly Val Arg Met Asp Ala Ser Glu Ser
 145 150 155 160
 His Leu Ser Met Ile Arg Glu Ile Ile Val Asp Leu Glu Arg Glu Phe
 165 170 175
 Asp Arg Tyr Val Glu Met Phe Glu His Gly Pro Leu Ile Gly Leu Arg
 180 185 190

DESUanglais-seql.txt

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

<210> 49
 <211> 1113
 <212> DNA
 <213> Methanobacterium thermoformicum

<220>
 <221> CDS
 <222> (1)..(1113)
 <223>

<400> 49
 atg ata ctg cca ctt gga ccc atg cac ccc ggc tac aag gag ccc ata 48
 Met Ile Leu Pro Leu Gly Pro Met His Pro Gly Tyr Lys Glu Pro Ile
 1 5 10 15
 agg ctc aag gtt aag aca agg ggt gag aag gtt ctc aag gcc gag ata 96
 Arg Leu Lys Val Lys Thr Arg Gly Glu Lys Val Leu Lys Ala Glu Ile
 20 25 30
 gag tat gga tac gtt cac agg gga ata gag agg gtg atg agg aac aag 144
 Glu Tyr Gly Tyr Val His Arg Glu Ile Glu Arg Val Met Arg Asn Lys
 35 40 45
 acc tgg cag aag gcc ata tac ctc tct gag cgg gtc tgc ggg ata tgc 192
 Thr Trp Gln Lys Ala Ile Tyr Leu Ser Glu Arg Val Cys Gly Ile Cys
 50 55 60
 tca tat ata cac aca cag acc ttt gca gag gca ttt gag gcc ata tct 240
 Ser Tyr Ile His Thr Gln Thr Phe Ala Glu Ala Phe Glu Ala Ile Ser
 65 70 75 80
 gag gtg gag gcc cca ccg agg gcc cag ttc ctc cgt gca ctg acc aac 288
 Glu Val Glu Ala Pro Pro Arg Ala Gln Phe Leu Arg Ala Leu Thr Asn
 85 90 95
 gaa ctt gac agg ata cag agt cac ctc att gca aat tca acc tac ttc 336
 Glu Leu Asp Arg Ile Gln Ser His Leu Ile Ala Asn Ser Thr Tyr Phe
 100 105 110
 aag gcc ctt gac cat gag aca atg ttc atg tac atg ctg gcc ctg agg 384
 Lys Ala Leu Asp His Glu Thr Met Phe Met Tyr Met Leu Ala Leu Arg
 115 120 125
 gag cct gtc atg gat gcc atc gag tta ctc aca ggt aac cgt gtc aac 432
 Glu Pro Val Met Asp Ala Ile Glu Leu Leu Thr Gly Asn Arg Val Asn
 130 135 140
 atg ggc tgg aac gtt gtg ggg ggt gtg agg atg gac gcc tca gag gat 480
 Met Gly Trp Asn Val Val Gly Gly Val Arg Met Asp Ala Ser Glu Asp

DESUanglais-seql.txt

145	150	155	160	
cac ctc tca agg ata agg gag atc ata gtg gac ctt gaa agg gaa ttc				528
His Leu Ser Arg Ile Arg Glu Ile Ile Val Asp Leu Glu Arg Glu Phe	165	170	175	
gac cgt tac gtt gaa atg ttc gag cac ggg cca ctc ata gga ctc agg				576
Asp Arg Tyr Val Glu Met Phe Glu His Gly Pro Leu Ile Gly Leu Arg	180	185	190	
tca agg gac gtg ggt tac atg agc cgt gag gag gca gag aag gcc cgg				624
Ser Arg Asp Val Gly Tyr Met Ser Arg Glu Glu Ala Glu Lys Ala Arg	195	200	205	
gca gtg gga ccc atc gga agg gcc tcg ggt ata cgg tat gac ttc agg				672
Ala Val Gly Pro Ile Gly Arg Ala Ser Gly Ile Arg Tyr Asp Phe Arg	210	215	220	
gag gat cac ccc acc tac cgg gat cac ctg gat ttc agg acg atc tgg				720
Glu Asp His Pro Thr Tyr Arg Asp His Leu Asp Phe Arg Thr Ile Trp	225	230	235	240
agg gat gag ggg gac aac ttt gca agg gtc atg aac cgc ttc gat gag				768
Arg Asp Glu Gly Asp Asn Phe Ala Arg Val Met Asn Arg Phe Asp Glu	245	250	255	
ata agg gtc tca att gac ctc ata aag cag gtg ata gac agt atc ccc				816
Ile Arg Val Ser Ile Asp Leu Ile Lys Gln Val Ile Asp Ser Ile Pro	260	265	270	
tcc ggc cct gtg agg agg aag gtg gat gtg aag gca ggc tac ggg gag				864
Ser Gly Pro Val Arg Arg Lys Val Asp Val Lys Ala Gly Tyr Gly Glu	275	280	285	
tgg aga aac gag gca ccc cgc ggc gag gtg gcc tac atg att gag acc				912
Trp Arg Asn Glu Ala Pro Arg Gly Glu Val Ala Tyr Met Ile Glu Thr	290	295	300	
aac gga aac ctc ata aag aac atc tcc ata agg acc ccc agc atc atg				960
Asn Gly Asn Leu Ile Lys Asn Ile Ser Ile Arg Thr Pro Ser Ile Met	305	310	315	320
aac atc gat gcc tgt gca aag tac atg ctg cgt gac gtt gca acc gtt				1008
Asn Ile Asp Ala Cys Ala Lys Tyr Met Leu Arg Asp Val Ala Thr Val	325	330	335	
gca gat gcc gtt gca acc tat gcc agt gca gac cca tgc ata gca tgt				1056
Ala Asp Ala Val Ala Thr Tyr Ala Ser Ala Asp Pro Cys Ile Ala Cys	340	345	350	
gca gag agg gtc gtg gtc ctg gac gag aat gag gga aag agg gag ata				1104
Ala Glu Arg Val Val Val Leu Asp Glu Asn Glu Gly Lys Arg Glu Ile	355	360	365	
ctc ctt taa				1113
Leu Leu				
370				

<210> 50

<211> 370

<212> PRT

<213> Methanobacterium thermoformicum

<400> 50

Met Ile Leu Pro Leu Gly Pro Met His Pro Gly Tyr Lys Glu Pro Ile

1

Arg Leu Lys Val Lys Thr Arg Gly Glu Lys Val Leu Lys Ala Glu Ile

20

Glu Tyr Gly Tyr Val His Arg Gly Ile Glu Arg Val Met Arg Asn Lys

35

Thr Trp Gln Lys Ala Ile Tyr Leu Ser Glu Arg Val Cys Gly Ile Cys

50

Ser Tyr Ile His Thr Gln Thr Phe Ala Glu Ala Phe Glu Ala Ile Ser

65

Glu Val Glu Ala Pro Pro Arg Ala Gln Phe Leu Arg Ala Leu Thr Asn

85

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

100

105

110

DESUanglais-seq1.txt

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

<210> 51
 <211> 1131
 <212> DNA
 <213> Methanobacterium thermoformicum

<220>
 <221> CDS
 <222> (1)..(1131)
 <223>

<400> 51
 atg gat ggg aaa agg gag ata att gag aca gaa ata aca atg ggt acc 48
 Met Asp Gly Lys Arg Glu Ile Ile Glu Thr Glu Ile Thr Met Gly Thr
 1 5 10 15
 gtg cac tcg gca gcc ata gaa ccc tac cgt gtg agg ctg ttc gtt gag 96
 Val His Ser Ala Ala Ile Glu Pro Tyr Arg Val Arg Leu Phe Val Glu
 20 25 30
 gat gaa ata gtc aga gac gcc gag ata acc gtc ggg gtc aac cac agg 144
 Asp Glu Ile Val Arg Asp Ala Glu Ile Thr Val Gly Val Asn His Arg
 35 40 45
 ggt att gaa agg ata atg gag ggc ctc ccc gtg gag aag gcc aac agc 192
 Gly Ile Glu Arg Ile Met Glu Gly Leu Pro Val Glu Lys Ala Asn Ser
 50 55 60
 ctg aca gag aag gta tgc gga atc tgt tca ggt gtc cac ctc tgg aat 240
 Leu Thr Glu Lys Val Cys Gly Ile Cys Ser Gly Val His Leu Trp Asn
 65 70 75 80
 tca atc ctg gtg gct gaa aag ggc ctt ggc gtg gag ata ccc gaa agg 288
 Ser Ile Leu Val Ala Glu Lys Gly Leu Gly Val Glu Ile Pro Glu Arg
 85 90 95

DESUanglais-seql.txt

gca tcc tac ata agg ata ata gtt ggg gaa ctt gaa aga atc cac agc 336
Ala Ser Tyr Ile Arg Ile Ile Val Gly Glu Leu Glu Arg Ile His Ser
100 105 110

cac ctt ctc tat ctg gcc cat gga aat gag gtc ctt ggc cat gaa aca 384
His Leu Leu Tyr Leu Ala His Gly Asn Glu Val Leu Gly His Glu Thr
115 120 125

ttc tcc atg agg cta ttc tac ata agg gag aca gtc atg gag ctt ttg 432
Phe Ser Met Arg Leu Phe Tyr Ile Arg Glu Thr Val Met Glu Leu Leu
130 135 140

agg ctc ata ggg ggt aac agg gta cag tac ggt gta ccc atc att ggt 480
Arg Leu Ile Gly Gly Asn Arg Val Gln Tyr Gly Val Pro Ile Ile Gly
145 150 160

ggt ata aga ccg agg gca gac ctt gat gag atg aag acc cag agg ata 528
Gly Ile Arg Pro Arg Ala Asp Leu Asp Glu Met Lys Thr Gln Arg Ile
165 170 175

agt gag gga atg gac ttc ata gag gag aag gtt gag gcc ttt gca gag 576
Ser Glu Gly Met Asp Phe Ile Glu Glu Lys Val Glu Ala Phe Ala Glu
180 185 190

agg ttc acc tcc gat cca atg gtg atg tcc cgt ata aca ggg gtc tgc 624
Arg Phe Thr Ser Asp Pro Met Val Met Ser Arg Ile Thr Gly Val Cys
195 200 205

ccc ata agc agg aag gat gcc ctc aga tta cat gta aca ggc cca aca 672
Pro Ile Ser Arg Lys Asp Ala Leu Arg Leu His Val Thr Gly Pro Thr
210 215 220

ctc agg gca act ggt gtt gaa ttt gac tta agg act gaa atg cca tgc 720
Leu Arg Ala Thr Gly Glu Phe Asp Leu Arg Thr Glu Met Pro Cys
225 230 235 240

tat gac cca ttt gaa ttt gat gtc ata acc cag gat ggt gga gat gtc 768
Tyr Asp Pro Phe Glu Phe Asp Val Ile Thr Gln Asp Gly Gly Asp Val
245 250 255

agg gca aac ctc ctc atg agg gtc ctc gag ata ttt gaa tcc ata aat 816
Arg Ala Asn Leu Leu Met Arg Val Leu Glu Ile Phe Glu Ser Ile Asn
260 265 270

ata ata aga cag gcc ctg agg gac ctc ccg gat gga agg gtt gtt gac 864
Ile Ile Arg Gln Ala Leu Arg Asp Leu Pro Asp Gly Arg Val Val Asp
275 280 285

agg aac tgg gag atg cag gat aca ggg ata gtg aag agc tac gtt gag 912
Arg Asn Trp Glu Met Gln Asp Thr Gly Ile Val Lys Ser Tyr Val Glu
290 295 300

gcc cca agg ggg aga ctc tac cac tcc tat gca ata gag gat gga agg 960
Ala Pro Arg Gly Arg Leu Tyr His Ser Tyr Ala Ile Glu Asp Gly Arg
305 310 315 320

gtg agg ggt tca ata ata agg aca ccc tca atg tca aac att ggt gcc 1008
Val Arg Gly Ser Ile Ile Arg Thr Pro Ser Met Ser Asn Ile Gly Ala
325 330 335

atg cag tat gcc tgc ata ggc cac cac atc acc gat gca cag ctc ggt 1056
Met Gln Tyr Ala Cys Ile Gly His His Ile Thr Asp Ala Gln Leu Gly
340 345 350

ata gtg cag tgc gat ccc tgc ttc aca tgc aca gac agg gca att gaa 1104
Ile Val Gln Cys Asp Pro Cys Phe Thr Cys Thr Asp Arg Ala Ile Glu
355 360 365

ata ata gac ctc aat gct gaa agg tga 1131
Ile Ile Asp Leu Asn Ala Glu Arg
370 375

<210> 52
<211> 376
<212> PRT
<213> Methanobacterium thermoformicum

<400> 52
Met Asp Gly Lys Arg Glu Ile Ile Glu Thr Glu Ile Thr Met Gly Thr
1 5 10 15
Val His Ser Ala Ala Ile Glu Pro Tyr Arg Val Arg Leu Phe Val Glu
20 25 30

DESUanglais-seql.txt

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

Gly Ile Glu Arg Ile Met Glu Gly Leu Pro Val Glu Lys Ala Asn Ser
 50 55 60

Leu Thr Glu Lys Val Cys Gly Ile Cys Ser Gly Val His Leu Trp Asn
 65 70 75 80

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

Ala Ser Tyr Ile Arg Ile Ile Val Gly Glu Leu Glu Arg Ile His Ser
 100 105 110

His Leu Leu Tyr Leu Ala His Gly Asn Glu Val Leu Gly His Glu Thr
 115 120 125

Phe Ser Met Arg Leu Phe Tyr Ile Arg Glu Thr Val Met Glu Leu Leu
 130 135 140

Arg Leu Ile Gly Gly Asn Arg Val Gln Tyr Gly Val Pro Ile Ile Gly
 145 150 155 160

Gly Ile Arg Pro Arg Ala Asp Leu Asp Glu Met Lys Thr Gln Arg Ile
 165 170 175

Ser Glu Gly Met Asp Phe Ile Glu Glu Lys Val Glu Ala Phe Ala Glu
 180 185 190

Arg Phe Thr Ser Asp Pro Met Val Met Ser Arg Ile Thr Gly Val Cys
 195 200 205

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

Leu Arg Ala Thr Gly Val Glu Phe Asp Leu Arg Thr Glu Met Pro Cys
 225 230 235 240

Tyr Asp Pro Phe Glu Phe Asp Val Ile Thr Gln Asp Gly Gly Asp Val
 245 250 255

Arg Ala Asn Leu Leu Met Arg Val Leu Glu Ile Phe Glu Ser Ile Asn
 260 265 270

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

Arg Asn Trp Glu Met Gln Asp Thr Gly Ile Val Lys Ser Tyr Val Glu
 290 295 300

Ala Pro Arg Gly Arg Leu Tyr His Ser Tyr Ala Ile Glu Asp Gly Arg
 305 310 315 320

Val Arg Gly Ser Ile Ile Arg Thr Pro Ser Met Ser Asn Ile Gly Ala
 325 330 335

Met Gln Tyr Ala Cys Ile Gly His His Ile Thr Asp Ala Gln Leu Gly
 340 345 350

Ile Val Gln Cys Asp Pro Cys Phe Thr Cys Thr Asp Arg Ala Ile Glu
 355 360 365

Ile Ile Asp Leu Asn Ala Glu Arg
 370 375

<210> 53
 <211> 3550
 <212> DNA
 <213> Desulfovibrio fructosovorans

<220>
 <221> CDS
 <222> (192)..(1133)
 <223>

<220>
 <221> CDS
 <222> (1208)..(2899)
 <223>

<220>
 <221> CDS
 <222> (2970)..(3467)

DESUanglais-seq1.txt

<223>

<400> 53

caaactcgtg	attaactgca	aaagggaaat	cgaaccgcgc	gacgcaggaa	cgacgcgctc	60
cgtcacatag	aggcgccggc	ggccgggttcg	cctgcgacgc	ccgcgtgccg	aacgggtcaa	120
cggatgctac	gtggcctggg	gatcatggga	cgccccggac	catgcctctc	gtaaaacaaa	180
ggaggacgtt	t atg aac ttt tcc gtg ggt ctt ggc agg gat gat gcg gaa	230				
	Met Asn Phe Ser Val Gly Leu Gly Arg Asp Asp Ala Glu					
	1 5 10					
aaa cgg ctt gtg caa aac ggc gtc tcc cgc cgc gaa ttc atg aaa ttt	278					
Lys Arg Leu Val Gln Asn Gly Val Ser Arg Arg Glu Phe Met Lys Phe						
	15 20 25					
tgc gcc acc gtg gcc gcg gcc atg ggc atg ggc ccc gcg ttc gcg ccc	326					
Cys Ala Thr Val Ala Ala Ala Met Gly Met Gly Pro Ala Phe Ala Pro						
	30 35 40 45					
aag gtc gcc gaa gca ttg acg gcc aaa cac cgt ccg tcc gtg gtc tgg	374					
Lys Val Ala Glu Ala Leu Thr Ala Lys His Arg Pro Ser Val Val Trp						
	50 55 60					
ctg cac aac gcc gag tgc acc ggc tgc acc gaa gcg gcg atc cgg acg	422					
Leu His Asn Ala Glu Cys Thr Gly Cys Thr Glu Ala Ala Ile Arg Thr						
	65 70 75					
atc aaa cct tat ata gac gcg ctc att ctc gac acc atc tcc ctg gat	470					
Ile Lys Pro Tyr Ile Asp Ala Leu Ile Leu Asp Thr Ile Ser Leu Asp						
	80 85 90					
tac cag gag acc atc atg gcc gcg gcc ggc gag acg tcc gag gcg gcc	518					
Tyr Gln Glu Thr Ile Met Ala Ala Ala Gly Glu Thr Ser Glu Ala Ala						
	95 100 105					
ctg cac cag gcc ctc gaa ggc aag gac ggc tac tac ctc gtg gtc gag	566					
Leu His Gln Ala Leu Glu Gly Lys Asp Gly Tyr Tyr Leu Val Val Glu						
	110 115 120 125					
ggc ggc ctg ccc acc atc gac ggc ggc cag tgg ggc atg gtt gcc ggc	614					
Gly Gly Leu Pro Thr Ile Asp Gly Gly Trp Gly Met Val Ala Gly						
	130 135 140					
cat ccc atg atc gag acc acc aag aag gcc gcg gcc aag gcc aag ggc	662					
His Pro Met Ile Glu Thr Thr Lys Lys Ala Ala Ala Lys Ala Lys Gly						
	145 150 155					
atc atc tgc atc ggc acc tgc tcc gcc tac ggc ggc gtc cag aag gcc	710					
Ile Ile Cys Ile Glu Thr Cys Ser Ala Tyr Gly Gly Val Gln Lys Ala						
	160 165 170					
aaa ccc aat ccc agc cag gcc aag ggc gtg tcc gaa gcc ctc ggc gtc	758					
Lys Pro Asn Pro Ser Gln Ala Lys Gly Val Ser Glu Ala Leu Gly Val						
	175 180 185					
aag acc atc aac atc ccc ggc tgc ccg ccc aac ccc atc aac ttc gtg	806					
Lys Thr Ile Asn Ile Pro Gly Cys Pro Pro Asn Pro Ile Asn Phe Val						
	190 195 200 205					
ggc gcc gtg gtc cat gtc ctg acc aag ggc atc ccg gat ctc gac gag	854					
Gly Ala Val Val His Val Leu Thr Lys Gly Ile Pro Asp Leu Asp Glu						
	210 215 220					
aac ggc cgt ccg aag ctc ttc tac ggc gag ctg gtc cac gac aac tgt	902					
Asn Gly Arg Pro Lys Leu Phe Tyr Gly Glu Leu Val His Asp Asn Cys						
	225 230 235					
ccg cgc ctg ccc cac ttc gag gcc tcc gaa ttc gcg ccc tcc ttc gat	950					
Pro Arg Leu Pro His Phe Glu Ala Ser Glu Phe Ala Pro Ser Phe Asp						
	240 245 250					
tcc gaa gag gcc aag aaa ggc ttc tgc ctc tac gaa ctc ggc tgc aag	998					
Ser Glu Glu Ala Lys Lys Gly Phe Cys Leu Tyr Glu Leu Gly Cys Lys						
	255 260 265					
ggc ccc gtt acc tac aac aac tgc ccc aag gtg ctg ttc aac cag gtc	1046					
Gly Pro Val Thr Tyr Asn Asn Cys Pro Lys Val Leu Phe Asn Gln Val						
	270 275 280 285					
aac tgg ccc gtc cag gcc ggc cac ccc tgc ctc ggc tgc agc gag ccg	1094					
Asn Trp Pro Val Gln Ala Gly His Pro Cys Leu Gly Cys Ser Glu Pro						
	290 295 300					
gac ttc tgg gac acc atg acg ccg ttc tac gag cag gcc taacccctc	1143					
Asp Phe Trp Asp Thr Met Thr Pro Phe Tyr Glu Gln Gly						

DESUanglais-seql.txt

305 310

ctttgtagcg gccagtaccc ggacaccttc aacagcaccg aacgtctcgt gacggaggaa 1203

gcat atg gct gag agc aaa ccc acg cca caa tcc acc ttc acc ggc ccc 1252
 Met Ala Glu Ser Lys Pro Thr Pro Gln Ser Thr Phe Thr Gly Pro
 315 320 325

atc gtg gtc gac ccc att acc cgg atc gaa ggt cac ttg cgg atc atg 1300
 Ile Val Val Asp Pro Ile Thr Arg Ile Glu Gly His Leu Arg Ile Met
 330 335 340 345

gtc gag gtg gaa aac ggt aag gtc aag gac gcc tgg agc tcc tcg cag 1348
 Val Glu Val Glu Asn Gly Lys Val Lys Asp Ala Trp Ser Ser Ser Gln
 350 355 360

ctc ttc cgc ggc ctg gaa atc atc ctc aaa ggc cgc gat ccc cgc gac 1396
 Leu Phe Arg Gly Leu Glu Ile Ile Leu Lys Gly Arg Asp Pro Arg Asp
 365 370 375

gcc cag cac ttc acc cag cgc gcc tgc ggc gtg tgc acg tac gtc cac 1444
 Ala Gln His Phe Thr Gln Arg Ala Cys Gly Val Cys Thr Tyr Val His
 380 385 390

gcc ctg gcc tcc agc cgc tgc gtc gat gac gcc gtc aag gtc agc atc 1492
 Ala Leu Ala Ser Ser Arg Cys Val Asp Asp Ala Val Lys Val Ser Ile
 395 400 405

ccg gcc aac gcc cgc atg atg cgc aac ctg gtc atg gcc tcc cag tat 1540
 Pro Ala Asn Ala Arg Met Met Arg Asn Leu Val Met Ala Ser Gln Tyr
 410 415 420 425

ctc cat gac cac ctc gtc cac ttc tat cac ctg cac gcc ctc gac tgg 1588
 Leu His Asp His Leu Val His Phe Tyr His Leu His Ala Leu Asp Trp
 430 435 440

gtc gac gtg acc gcc gcc ctc aag gcc gat ccc aac aag gcc gcc aaa 1636
 Val Asp Val Thr Ala Ala Leu Lys Ala Asp Pro Asn Lys Ala Ala Lys
 445 450 455

ctg gca gcc tcc atc gcc ccg gct cgg ccc ggc aac tcg gcc aag gcc 1684
 Leu Ala Ala Ser Ile Ala Pro Ala Arg Pro Gly Asn Ser Ala Lys Ala
 460 465 470

ctc aag gcc gtc cag gac aag ctg aaa gcc ttc gtc gag tcc gga cag 1732
 Leu Lys Ala Val Gln Asp Lys Leu Lys Ala Phe Val Glu Ser Gly Gln
 475 480 485

ctc ggc atc ttc acc aac gcc tac ttc ctc ggc ggc cac aaa gcc tac 1780
 Leu Gly Ile Phe Thr Asn Ala Tyr Phe Leu Gly Gly His Lys Ala Tyr
 490 495 500 505

tac ctg ccg ccc gag gtc aac ctc atc gcc acc gcc cac tac ctg gaa 1828
 Tyr Leu Pro Pro Glu Val Asn Leu Ile Ala Thr Ala His Tyr Leu Glu
 510 515 520

gcc ctg cac atg cag gtc aag gcg gcc agc gcc atg gcc atc ctc ggc 1876
 Ala Leu His Met Gln Val Lys Ala Ser Ala Met Ala Ile Leu Gly
 525 530 535

ggc aag aac ccc cac acc cag ttc acc gtc gtg ggc ggc tgc tcc aac 1924
 Gly Lys Asn Pro His Thr Gln Phe Thr Val Val Gly Gly Cys Ser Asn
 540 545 550

tac cag ggc ctg acc aag gac ccg ctg gcc aac tac ctg gcc ctg agc 1972
 Tyr Gln Gly Leu Thr Lys Asp Pro Leu Ala Asn Tyr Leu Ala Leu Ser
 555 560 565

aag gaa gtc tgc cag ttc gtc aac gag tgc tac atc cct gac ctg ctg 2020
 Lys Glu Val Cys Gln Phe Val Asn Glu Cys Tyr Ile Pro Asp Leu Leu
 570 575 580 585

gcc gtg gcc ggc ttc tac aag gac tgg ggc ggc atc ggc ggc acc agc 2068
 Ala Val Ala Gly Phe Tyr Lys Asp Trp Gly Gly Ile Gly Gly Thr Ser
 590 595 600

aac tac ctg gcc ttc ggc gag ttc gcc acc gac gac agc tcc ccc gag 2116
 Asn Tyr Leu Ala Phe Gly Glu Phe Ala Thr Asp Asp Ser Pro Glu
 605 610 615

aaa cac ctg gcc acc tcg cag ttt ccg tcc ggc gtc atc acc ggc cgc 2164
 Lys His Leu Ala Thr Ser Gln Phe Pro Ser Gly Val Ile Thr Gly Arg
 620 625 630

gac ctc ggc aag gtg gat aac gtg gac ctc ggc gcc atc tac gaa gac 2212
 Asp Leu Gly Lys Val Asp Asn Val Asp Leu Gly Ala Ile Tyr Glu Asp

DESUanglais-seql.txt																	
635					640					645							
gtc Val 650	aag Lys	tac Tyr	tcc Ser	tgg Trp	tac Tyr 655	gcc Ala	ccc Pro	ggc Gly	ggc Gly	gac Asp 660	ggc Gly	aag Lys	cac His	ccc Pro	tac Tyr 665	2260	
gac Asp	ggc Gly	gtc Val	acc Thr	gat Asp 670	ccc Pro	aag Lys	tac Tyr	acc Thr	aag Lys 675	ctc Leu	gac Asp	gac Asp	aag Lys	gac Asp 680	cac His	2308	
tac Tyr	tcc Ser	tgg Trp	atg Met 685	aag Lys	gcc Ala	ccc Pro	cgc Arg	tac Tyr 690	aag Lys	ggc Gly	aag Lys	gcc Ala	atg Met 695	gaa Glu	gtc Val	2356	
ggt Gly	ccc Pro	ctg Leu 700	ggc Ala	cgc Arg	acc Thr	ttc Phe	atc Ile 705	ggc Ala	tac Tyr	ggc Ala	aag Lys	ggg Gly 710	cag Gln	ccc Pro	gac Asp	2404	
ttc Phe 715	aaa Lys	aag Lys	gtc Val	gtg Val	gac Asp	atg Met 720	gtc Val	ctc Leu	ggc Gly	aaa Lys	ctc Leu 725	tcc Ser	gtc Val	ccg Pro	gcc Ala	2452	
acg Thr 730	gcc Ala	ctg Leu	cat His	tcg Ser	acc Thr 735	ctc Leu	gga Gly	cgc Arg	acc Thr	ggc Ala 740	ggc Ala	cgc Arg	ggc Gly	atc Ile	gag Glu 745	2500	
acc Thr	gcc Ala	atc Ile	gtc Val	tgc Cys 750	ggc Ala	aac Asn	atg Met	gag Glu	aag Lys 755	tgg Trp	atc Ile	aag Lys	gaa Glu	atg Met 760	ggc Ala	2548	
gac Asp	agc Ser	ggc Gly 765	ggc Ala	aag Lys	gac Asp	aac Asn	acc Thr	ctg Leu 770	tgc Cys	ggc Ala	aag Lys	tgg Trp	gag Glu 775	atg Met	ccc Pro	2596	
gag Glu	gag Glu	tcc Ser 780	aag Lys	ggc Gly	gtc Val	ggc Gly	ctg Leu 785	ggc Ala	gat Asp	gct Ala	ccc Pro	cgc Arg 790	ggc Gly	ggc Ala	ctg Leu	2644	
tcc Ser 795	cac His	tgg Trp	atc Ile	cgc Arg	atc Ile	aag Lys 800	ggc Gly	aag Lys	aag Lys	atc Ile	gac Asp 805	aac Asn	ttc Phe	cag Gln	ctg Leu	2692	
gtt Val 810	gtc Val	ccc Pro	tcg Ser	acc Thr	tgg Trp 815	aac Asn	ctc Leu	ggt Gly	ccc Pro	cgg Arg 820	ggc Gly	ggc Ala	cag Gln	ggc Gly	gac Asp 825	2740	
aag Lys	agc Ser	ccg Pro	gtg Val	gaa Glu 830	gag Glu	gcc Ala	ctt Leu	atc Ile	ggc Gly 835	acg Thr	ccc Pro	atc Ile	ggc Ala	gat Asp 840	ccc Pro	2788	
aaa Lys	cgc Arg	ccg Pro	gtc Val 845	gaa Glu	atc Ile	ctg Leu	cgc Arg	acg Thr 850	gtc Val	cac His	ggc Ala	ttc Phe	gac Asp 855	ccc Pro	tgc Cys	2836	
atc Ile	gcc Ala	tgc Cys 860	ggc Gly	gtg Val	cac His	gtc Val	atc Ile 865	gag Glu	ccc Pro	gag Glu	acc Thr	aac Asn 870	gag Glu	atc Ile	ctc Leu	2884	
aag Lys 875	ttc Phe	aag Lys	gtt Val	tgc Cys	taagagcggc aacgcccgtt atacgaagga cccggcttcg											2939	
gcccgggttct tcgtttctca aggaggtcgc									atg Met 880	tcc Ser 880	gat Asp	acc Thr	ccg Pro	cgc Arg	aaa Lys 885	atc Ile	2993
ctc Leu	atc Ile	ctc Leu	ggc Gly 890	gtc Val	ggc Gly	aac Asn	atc Ile	ctc Leu 895	tac Tyr	acc Thr	gac Asp	gag Glu	ggc Gly 900	gtc Val	ggc Gly	3041	
gtg Val	cgg Arg	ggc Ala 905	gtg Val	gag Glu	cgc Arg	ctt Leu	ctc Leu 910	gaa Glu	acc Thr	cac His	gat Asp	ttt Phe 915	tcc Ser	gac Asp	aac Asn	3089	
gtc Val	acc Thr 920	ctc Leu	atg Met	gac Asp	ggc Gly	ggc Gly 925	aac Asn	ctg Leu	ggc Gly	atg Met	aag Lys 930	ctc Leu	atg Met	ggc Ala	ccg Pro	3137	
ctc Leu 935	atg Met	gaa Glu	tgc Cys	gac Asp	tac Tyr 940	tgc Cys	atc Ile	gtg Val	ctc Leu	gac Asp 945	ggc Ala	gtg Val	ctc Leu	ggc Gly	ggc Gly 950	3185	
gac Asp	ggc Ala	ccc Pro	ggc Gly	acc Thr 955	atc Ile	tac Tyr	cgt Arg	ctc Leu	acc Thr 960	ggc Gly	gag Glu	gac Asp	ctg Leu	cgc Arg 965	aaa Lys	3233	

DESUanglais-seql.txt

tcc ctg gcc ttc aag gac tcc atg cac cag tcc gac ctc gtc gac acg 3281
 Ser Leu Ala Phe Lys Asp Ser Met His Gln Ser Asp Leu Val Asp Thr
 970 975 980

ctg atc tat tgc gaa ctg gcc gga cac cgc ccg gac acc gtg gtc atc 3329
 Leu Ile Tyr Cys Glu Leu Ala Gly His Arg Pro Asp Thr Val Val Ile
 985 990 995

ggc atg gag ccc ctc gat ttt cag aac atg agc atc gaa ctc tcg 3374
 Gly Met Glu Pro Leu Asp Phe Gln Asn Met Ser Ile Glu Leu Ser
 1000 1005 1010

ccc gcc atc gcc gaa cgc gtt ccg gcc atg atc gac atc gcc ctg 3419
 Pro Ala Ile Ala Glu Arg Val Pro Ala Met Ile Asp Ile Ala Leu
 1015 1020 1025

gcc gaa ctc gcc gcc gcc ggc ggc gtc gcc acg ccc aaa gga caa 3464
 Ala Glu Leu Ala Ala Ala Gly Gly Val Ala Thr Pro Lys Gly Gln
 1030 1035 1040

agt taggaagaaa ggaggtgcga gaggggaac cctttaaaaa ggggttctccc 3517
 Ser

ctctcgcgcc tctccccttc ctaaatttta taa 3550

<210> 54
 <211> 1044
 <212> PRT
 <213> Desulfovibrio fructosovorans

<400> 54
 Met Asn Phe Ser Val Gly Leu Gly Arg Asp Asp Ala Glu Lys Arg Leu
 1 5 10 15

Val Gln Asn Gly Val Ser Arg Arg Glu Phe Met Lys Phe Cys Ala Thr
 20 25 30

Val Ala Ala Ala Met Gly Met Gly Pro Ala Phe Ala Pro Lys Val Ala
 35 40 45

Glu Ala Leu Thr Ala Lys His Arg Pro Ser Val Val Trp Leu His Asn
 50 55 60

Ala Glu Cys Thr Gly Cys Thr Glu Ala Ala Ile Arg Thr Ile Lys Pro
 65 70 75 80

Tyr Ile Asp Ala Leu Ile Leu Asp Thr Ile Ser Leu Asp Tyr Gln Glu
 85 90 95

Thr Ile Met Ala Ala Ala Gly Glu Thr Ser Glu Ala Ala Leu His Gln
 100 105 110

Ala Leu Glu Gly Lys Asp Gly Tyr Tyr Leu Val Val Glu Gly Gly Leu
 115 120 125

Pro Thr Ile Asp Gly Gly Gln Trp Gly Met Val Ala Gly His Pro Met
 130 135 140

Ile Glu Thr Thr Lys Lys Ala Ala Ala Lys Ala Lys Gly Ile Ile Cys
 145 150 155 160

Ile Gly Thr Cys Ser Ala Tyr Gly Gly Val Gln Lys Ala Lys Pro Asn
 165 170 175

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

Asn Ile Pro Gly Cys Pro Pro Asn Pro Ile Asn Phe Val Gly Ala Val
 195 200 205

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

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

Pro His Phe Glu Ala Ser Glu Phe Ala Pro Ser Phe Asp Ser Glu Glu
 245 250 255

Ala Lys Lys Gly Phe Cys Leu Tyr Glu Leu Gly Cys Lys Gly Pro Val
 260 265 270

DESUanglais-seql.txt

Thr Tyr Asn Asn Cys Pro Lys Val Leu Phe Asn Gln Val Asn Trp Pro
 275 280 285

Val Gln Ala Gly His Pro Cys Leu Gly Cys Ser Glu Pro Asp Phe Trp
 290 295 300

Asp Thr Met Thr Pro Phe Tyr Glu Gln Gly Met Ala Glu Ser Lys Pro
 305 310 315 320

Thr Pro Gln Ser Thr Phe Thr Gly Pro Ile Val Val Asp Pro Ile Thr
 325 330 335

Arg Ile Glu Gly His Leu Arg Ile Met Val Glu Val Glu Asn Gly Lys
 340 345 350

Val Lys Asp Ala Trp Ser Ser Ser Gln Leu Phe Arg Gly Leu Glu Ile
 355 360 365

Ile Leu Lys Gly Arg Asp Pro Arg Asp Ala Gln His Phe Thr Gln Arg
 370 375 380

Ala Cys Gly Val Cys Thr Tyr Val His Ala Leu Ala Ser Ser Arg Cys
 385 390 395 400

Val Asp Asp Ala Val Lys Val Ser Ile Pro Ala Asn Ala Arg Met Met
 405 410 415

Arg Asn Leu Val Met Ala Ser Gln Tyr Leu His Asp His Leu Val His
 420 425 430

Phe Tyr His Leu His Ala Leu Asp Trp Val Asp Val Thr Ala Ala Leu
 435 440 445

Lys Ala Asp Pro Asn Lys Ala Lys Leu Ala Ala Ser Ile Ala Pro
 450 455 460

Ala Arg Pro Gly Asn Ser Ala Lys Ala Leu Lys Ala Val Gln Asp Lys
 465 470 475 480

Leu Lys Ala Phe Val Glu Ser Gly Gln Leu Gly Ile Phe Thr Asn Ala
 485 490 495

Tyr Phe Leu Gly Gly His Lys Ala Tyr Tyr Leu Pro Pro Glu Val Asn
 500 505 510

Leu Ile Ala Thr Ala His Tyr Leu Glu Ala Leu His Met Gln Val Lys
 515 520 525

Ala Ala Ser Ala Met Ala Ile Leu Gly Gly Lys Asn Pro His Thr Gln
 530 535 540

Phe Thr Val Val Gly Gly Cys Ser Asn Tyr Gln Gly Leu Thr Lys Asp
 545 550 555 560

Pro Leu Ala Asn Tyr Leu Ala Leu Ser Lys Glu Val Cys Gln Phe Val
 565 570 575

Asn Glu Cys Tyr Ile Pro Asp Leu Leu Ala Val Ala Gly Phe Tyr Lys
 580 585 590

Asp Trp Gly Gly Ile Gly Gly Thr Ser Asn Tyr Leu Ala Phe Gly Glu
 595 600 605

Phe Ala Thr Asp Asp Ser Ser Pro Glu Lys His Leu Ala Thr Ser Gln
 610 615 620

Phe Pro Ser Gly Val Ile Thr Gly Arg Asp Leu Gly Lys Val Asp Asn
 625 630 635 640

Val Asp Leu Gly Ala Ile Tyr Glu Asp Val Lys Tyr Ser Trp Tyr Ala
 645 650 655

Pro Gly Gly Asp Gly Lys His Pro Tyr Asp Gly Val Thr Asp Pro Lys
 660 665 670

Tyr Thr Lys Leu Asp Asp Lys Asp His Tyr Ser Trp Met Lys Ala Pro
 675 680 685

Arg Tyr Lys Gly Lys Ala Met Glu Val Gly Pro Leu Ala Arg Thr Phe
 690 695 700

Ile Ala Tyr Ala Lys Gly Gln Pro Asp Phe Lys Lys Val Val Asp Met
 705 710 715 720

DESUanglais-seql.txt

Val Leu Gly Lys Leu Ser Val Pro Ala Thr Ala Leu His Ser Thr Leu
725 730 735

Gly Arg Thr Ala Ala Arg Gly Ile Glu Thr Ala Ile Val Cys Ala Asn
740 745 750

Met Glu Lys Trp Ile Lys Glu Met Ala Asp Ser Gly Ala Lys Asp Asn
755 760 765

Thr Leu Cys Ala Lys Trp Glu Met Pro Glu Glu Ser Lys Gly Val Gly
770 775 780

Leu Ala Asp Ala Pro Arg Gly Ala Leu Ser His Trp Ile Arg Ile Lys
785 790 795 800

Gly Lys Lys Ile Asp Asn Phe Gln Leu Val Val Pro Ser Thr Trp Asn
805 810 815

Leu Gly Pro Arg Gly Ala Gln Gly Asp Lys Ser Pro Val Glu Glu Ala
820 825 830

Leu Ile Gly Thr Pro Ile Ala Asp Pro Lys Arg Pro Val Glu Ile Leu
835 840 845

Arg Thr Val His Ala Phe Asp Pro Cys Ile Ala Cys Gly Val His Val
850 855 860

Ile Glu Pro Glu Thr Asn Glu Ile Leu Lys Phe Lys Val Cys Met Ser
865 870 875 880

Asp Thr Pro Arg Lys Ile Leu Ile Leu Gly Val Gly Asn Ile Leu Tyr
885 890 895

Thr Asp Glu Gly Val Gly Val Arg Ala Val Glu Arg Leu Leu Glu Thr
900 905 910

His Asp Phe Ser Asp Asn Val Thr Leu Met Asp Gly Gly Asn Leu Gly
915 920 925

Met Lys Leu Met Ala Pro Leu Met Glu Cys Asp Tyr Cys Ile Val Leu
930 935 940

Asp Ala Val Leu Gly Gly Asp Ala Pro Gly Thr Ile Tyr Arg Leu Thr
945 950 955 960

Gly Glu Asp Leu Arg Lys Ser Leu Ala Phe Lys Asp Ser Met His Gln
965 970 975

Ser Asp Leu Val Asp Thr Leu Ile Tyr Cys Glu Leu Ala Gly His Arg
980 985 990

Pro Asp Thr Val Val Ile Gly Met Glu Pro Leu Asp Phe Gln Asn Met
995 1000 1005

Ser Ile Glu Leu Ser Pro Ala Ile Ala Glu Arg Val Pro Ala Met
1010 1015 1020

Ile Asp Ile Ala Leu Ala Glu Leu Ala Ala Ala Gly Gly Val Ala
1025 1030 1035

Thr Pro Lys Gly Gln Ser
1040

<210> 55
 <211> 2909
 <212> DNA
 <213> Desulfovibrio fructosovorans

<220>
 <221> CDS
 <222> (457)..(1719)
 <223>

<220>
 <221> CDS
 <222> (1825)..(2193)
 <223>

<400> 55
 gaccctctt caaaactttc caaggggcat ggtgaggatc ttttccctc ggcgtggcct 60
 tcaaggacaa cgaatccttt tatagcgcgt cgccagtcgc gaacacatgc ccccttcg 120
 cgggaaaaac ctttccaaa accgtgttcg cccctaacgc gtccctcttc atccctcgcg 180
 ctccctcc acgtgaaaaa atgcgcgggc aacccccact ttgccgcaag ggggcttgct 240
 ccatacggaa atttaaagta ttacgttttc gtgttacgaa attttatttc atactattta 300

DESUanglais-seq1.txt

aaacgaacta ttttcgtatg aatatacacg agaacttttt ccgctcgcct cccgccagct	360
ccaggggggt ccacaaaccg gtcgaaacgc accgcgcccc cgctcccgtg aaaaaccgcc	420
cgcaagggta acccatctaa ccgttgaggg ttgcgt atg agc cgc atc gag atg	474
	Met Ser Arg Ile Glu Met
	1 5
gca aag atc ttc tac gaa cag acc gtg ccg cct ccg ggc acg aac ctg	522
Ala Lys Ile Phe Tyr Glu Gln Thr Val Pro Pro Pro Gly Thr Asn Leu	
	10 15 20
gac cag gcc tat atc gtc cag gtc gac gag acc aaa tgc atc ggc tgc	570
Asp Gln Ala Tyr Ile Val Gln Asp Glu Thr Lys Cys Ile Gly Cys	
	25 30 35
gat acc tgc atg ggc tac tgc ccc acc gcg gcc atc acc ggc gaa tcc	618
Asp Thr Cys Met Gly Tyr Cys Pro Thr Ala Ala Ile Thr Gly Glu Ser	
	40 45 50
ggc gag ccc cac aag gtg gtc gat ccg gcc gcc tgc atc aac tgc ggc	666
Gly Glu Pro His Lys Val Val Asp Pro Ala Ala Cys Ile Asn Cys Gly	
	55 60 65 70
cag tgc ctc acc cac tgc ccg gtt gcg gcc atc tac gag acc gtg tcc	714
Gln Cys Leu Thr His Cys Pro Val Ala Ala Ile Tyr Glu Thr Val Ser	
	75 80 85
ttc gtc ccg gag gtc gaa gcc aag ctc aag gac aag aac gtc aag tgc	762
Phe Val Pro Glu Val Glu Ala Lys Leu Lys Asp Lys Asn Val Lys Cys	
	90 95 100
atc gcc atg ccg gcc ccg gcc gtg gcg tac gcc ctg ggc gat ccc ttc	810
Ile Ala Met Pro Ala Pro Ala Val Arg Tyr Ala Leu Gly Asp Pro Phe	
	105 110 115
ggc atg ccg ctc ggc gac gtc acc acg cga gca tat ctc acg ggc ctc	858
Gly Met Pro Leu Gly Asp Val Thr Thr Arg Ala Tyr Leu Thr Gly Leu	
	120 125 130
aag cag ctt ggc ttc gac aac gtc tgg gac aac gag ttc acg gcc gac	906
Lys Gln Leu Gly Phe Asp Asn Val Trp Asp Asn Glu Phe Thr Ala Asp	
	135 140 145 150
gtc acc atc tgg gaa gag ggc tcc gag ctt ctg gcc cgc atc acc aaa	954
Val Thr Ile Trp Glu Glu Gly Ser Glu Leu Leu Ala Arg Ile Thr Lys	
	155 160 165
aag ctc gac aag ccc ctg ccc cag ttc acc tcc tgc tgt ccc ggc tgg	1002
Lys Leu Asp Lys Pro Leu Pro Gln Phe Thr Ser Cys Cys Pro Gly Trp	
	170 175 180
cag aag tac gcc gag acc ttc tac ccc gag ctg ctg ccg cac ttc tcc	1050
Gln Lys Tyr Ala Glu Thr Phe Tyr Pro Glu Leu Leu Pro His Phe Ser	
	185 190 195
tcg tgc aag tgc ccc atc ggc atg atg ggt ccc ctg gcc aag acc tac	1098
Ser Cys Lys Ser Pro Ile Gly Met Met Gly Pro Leu Ala Lys Thr Tyr	
	200 205 210
ggg gcc aag gag ctc ggc tac gag ccc aag cag atc tac acc gtg tcc	1146
Gly Ala Lys Glu Leu Gly Tyr Glu Pro Lys Gln Ile Tyr Thr Val Ser	
	215 220 225 230
atc atg ccc tgc acg gcc aaa aaa ttc gaa ggc atg cgc ccg gag atg	1194
Ile Met Pro Cys Thr Ala Lys Lys Phe Glu Gly Met Arg Pro Glu Met	
	235 240 245
gac gcc ggc ggc ttc cgc gac atc gac gcc acc atc aac acc cgc gag	1242
Asp Ala Gly Gly Phe Arg Asp Ile Asp Ala Thr Ile Asn Thr Arg Glu	
	250 255 260
ctg gcc tac atg atg aaa aag gcc ggc atc gac ctg ccg aag atc gcc	1290
Leu Ala Tyr Met Met Lys Lys Ala Gly Ile Asp Leu Pro Lys Ile Ala	
	265 270 275
gat ggc aag cgc gac gcg gtc atg ggc gaa tcc acg ggc ggc gcg acc	1338
Asp Gly Lys Arg Asp Ala Val Met Gly Glu Ser Thr Gly Gly Ala Thr	
	280 285 290
atc ttc ggc gtt tcc ggc ggc gtc atg gaa gcg gcc ctg cgc ttt gcc	1386
Ile Phe Gly Val Ser Gly Gly Val Met Glu Ala Ala Leu Arg Phe Ala	
	295 300 305 310
tac cag gcc ctg acc aag aaa ccg ccc cag agc tgg gac ttc aag gcc	1434

DESUanglais-seq1.txt

Tyr Gln Ala Leu Thr Lys Lys Pro Pro Gln Ser Trp Asp Phe Lys Ala
315 320 325

gtg cgc ggc cta aac ggc atc aag gaa gcc acc atc aac atc ggc ggc 1482
Val Arg Gly Leu Asn Gly Ile Lys Glu Ala Thr Ile Asn Ile Gly Gly
330 335 340

acc gac gtc aaa gtg gcc gtg tca acc ggc ggc aag aac ttc gcc aag 1530
Thr Asp Val Lys Val Ala Val Ser Thr Gly Gly Lys Asn Phe Ala Lys
345 350 355

gtc tgc gac gag gtg aag gcc ggc aaa tcg ccc tac cac ttc atc gag 1578
Val Cys Asp Glu Val Lys Ala Gly Lys Ser Pro Tyr His Phe Ile Glu
360 365 370

ttc atg gcc tgc cca ggc ggc tgc gtc atg ggc ggc ggc cag ccc atc 1626
Phe Met Ala Cys Pro Gly Gly Cys Val Met Gly Gly Gly Gln Pro Ile
375 380 385 390

atg ccg acc gtg ctc gaa tcc atg aac cgg acc acc acg aag ttc tac 1674
Met Pro Thr Val Leu Glu Ser Met Asn Arg Thr Thr Thr Lys Phe Tyr
395 400 405

gcg tcg ctc aaa aag cgt ctg gcc ctc tac gac gcg caa aag gcg 1719
Ala Ser Leu Lys Lys Arg Leu Ala Leu Tyr Asp Ala Gln Lys Ala
410 415 420

taacacataa aaatacgttg gtatctttgc agaaataacg acccaggcgt gtgccctcg 1779

aaaccgcac aagcggtttc gcggaacgc gcccaggag gatct atg tcg ata ctt 1836
Met Ser Ile Leu
425

gcc acc acc cgg cgc ggc ttt atg aag acc gcc tgc gtg ctg acc ggc 1884
Ala Thr Thr Arg Arg Gly Phe Met Lys Thr Ala Cys Val Leu Thr Gly
430 435 440

ggc gcc ctg atc ggc ctg cgc ctg acc agc aag gcc gtt gcc gcc gcc 1932
Gly Ala Leu Ile Gly Leu Arg Leu Thr Ser Lys Ala Val Ala Ala Ala
445 450 455

aaa cag ctc aaa gag cat atg atg gac cgc gta aac gcc gtc tat ggg 1980
Lys Gln Leu Lys Glu His Met Met Asp Arg Val Asn Ala Val Tyr Gly
460 465 470

gcg gac gcc aaa ttc aag gtc cgg gcc tcc cag gac aac gcc cag gtc 2028
Ala Asp Ala Lys Phe Lys Val Arg Ala Ser Gln Asp Asn Ala Gln Val
475 480 485

atc acg ctc tac aag aaa ttc ctg cat gag ccc ctg tcc cac gag tcc 2076
Ile Thr Leu Tyr Lys Lys Phe Leu His Glu Pro Leu Ser His Glu Ser
490 495 500 505

gag cat ctg ctc cac acc aaa tgg gtg gac cgc tcc aag gat ctg gcg 2124
Glu His Leu Leu His Thr Lys Trp Val Asp Arg Ser Lys Asp Leu Ala
510 515 520

gca ctg aag gcc aag ggc ctg tac cca aca ccg cgg gcc aag gaa ttc 2172
Ala Leu Lys Ala Lys Gly Leu Tyr Pro Thr Pro Arg Ala Lys Glu Phe
525 530 535

gaa aag ccg tat cca ttc cag taaccccgcc cttccgttcc ggacgaaccc 2223
Glu Lys Pro Tyr Pro Phe Gln
540

gcggcaaggg ttttgctga ccctagggtt gcgtccctct gcaacacctc tcccgtccaa 2283
cttgccggcc gtgcgacgat cgcgcgacgc ccgcttgctt cttctctcgc catgcggcgt 2343
tgcgcgcttt tctccggcgc ttacttggg ccggttttctt gactattcct ccccgccac 2403
tgtaaatggc gcgaaaatgg ttggaatatg aacgatacag acgggaaaac acctgtcgct 2463
tcgtcgtcac gtcccgcca aaaacgcatt gccccggcgc gacgcgtaac agccgtcata 2523
cgcatccctc cctgatgccg gccgtctccc gcagccggca aaccgactga aataagggcc 2583
catgaaggat gccctcctgt ggaacgcgc gtttcgcca cgcgccagg gtcgttcgcc 2643
gtgcccgcgc cagagtgtcg tcccatggaa agtgctcatc aaccgcgca acgaggaagg 2703
atttggtatg aaacgtttta ccgtgctggc cctgctggcg gcgcttctgg cggggacggc 2763
cggcctggcc atggccgcga cagacgtgcg gatcacacgc gattcccgtg tgtacagcgt 2823
ctttttcagc ggcacaaact tcaccggtcg gaaagacgcg gcctggatct ccaacgcgcc 2883
gacctgtacc gccgcggca caaaac 2909

<210> 56

<211> 544

<212> PRT

<213> Desulfovibrio fructosovorans

<400> 56

Met Ser Arg Ile Glu Met Ala Lys Ile Phe Tyr Glu Gln Thr Val Pro

DESUanglais-seq1.txt

1	5	10	15
Pro	Pro	Gly	Thr
	20	Asn	Leu
		Asp	Gln
		Ala	25
		Tyr	Ile
		Val	Gln
		Val	30
		Asp	Glu
Thr	Lys	Cys	Ile
	35	Gly	Cys
		Asp	Thr
		40	Cys
		Met	Gly
		Tyr	Cys
		45	Pro
		Thr	Ala
Ala	Ile	Thr	Gly
	50	Glu	Ser
		Gly	55
		Glu	Pro
		His	Lys
		Val	60
		Val	Asp
		Pro	Ala
Ala	Cys	Ile	Asn
	65	Cys	Gly
		Gln	Cys
		Leu	Thr
		His	75
		Cys	Pro
		Val	Ala
		Ala	80
Ile	Tyr	Glu	Thr
	85	Val	Ser
		Phe	Val
		Pro	Glu
		90	Val
		Glu	Ala
		Lys	Leu
		95	Lys
Asp	Lys	Asn	Val
	100	Lys	Cys
		Ile	Ala
		Met	105
		Pro	Ala
		Pro	Ala
		Val	110
		Arg	Tyr
Ala	Leu	Gly	Asp
	115	Pro	Phe
		Gly	Met
		120	Pro
		Leu	Gly
		Asp	Val
		125	Thr
		Thr	Arg
Ala	Tyr	Leu	Thr
	130	Gly	Leu
		Lys	Gln
		135	Leu
		Gly	Phe
		140	Asn
		Val	Trp
		Asp	Asp
Asn	Glu	Phe	Thr
	145	Ala	Asp
		Val	Thr
		Ile	Trp
		Glu	155
		Glu	Gly
		Ser	Glu
		Leu	160
Leu	Ala	Arg	Ile
	165	Thr	Lys
		Lys	Lys
		Leu	Asp
		Lys	170
		Pro	Leu
		Pro	Gln
		175	Phe
		Thr	
Ser	Cys	Cys	Pro
	180	Gly	Trp
		Gln	Lys
		Tyr	185
		Ala	Glu
		Thr	Phe
		190	Tyr
		Pro	Glu
Leu	Leu	Pro	His
	195	Phe	Ser
		Ser	Ser
		Cys	200
		Lys	Ser
		Pro	Ile
		Gly	205
		Met	Met
		Gly	
Pro	Leu	Ala	Lys
	210	Thr	Tyr
		Gly	215
		Ala	Lys
		Glu	Leu
		Gly	220
		Tyr	Glu
		Pro	Lys
Gln	Ile	Tyr	Thr
	225	Val	Ser
		Ile	Met
		Pro	Cys
		Thr	235
		Ala	Lys
		Lys	Phe
		Glu	240
Gly	Met	Arg	Pro
	245	Glu	Met
		Asp	Ala
		Gly	Gly
		250	Phe
		Arg	Asp
		Ile	Asp
		255	Ala
Thr	Ile	Asn	Thr
	260	Arg	Glu
		Leu	Ala
		Tyr	265
		Met	Met
		Lys	Lys
		Ala	270
		Gly	Ile
Asp	Leu	Pro	Lys
	275	Ile	Ala
		Asp	Gly
		280	Lys
		Arg	Asp
		Ala	Val
		285	Met
		Gly	Glu
Ser	Thr	Gly	Gly
	290	Ala	Thr
		Ile	Phe
		295	Gly
		Val	Ser
		Gly	300
		Gly	Val
		Met	Glu
Ala	Ala	Leu	Arg
	305	Phe	Ala
		Tyr	Gln
		Ala	Leu
		Thr	315
		Lys	Lys
		Pro	Pro
		Gln	320
Ser	Trp	Asp	Phe
	325	Lys	Ala
		Val	Arg
		Gly	Leu
		330	Asn
		Gly	Ile
		Lys	Glu
		335	Ala
Thr	Ile	Asn	Ile
	340	Gly	Gly
		Thr	Asp
		Val	345
		Lys	Val
		Ala	Val
		350	Ser
		Thr	Gly
Gly	Lys	Asn	Phe
	355	Ala	Lys
		Val	Cys
		360	Asp
		Glu	Val
		Lys	Ala
		365	Gly
		Lys	Ser
Pro	Tyr	His	Phe
	370	Ile	Glu
		Phe	Met
		375	Ala
		Cys	Pro
		Gly	380
		Gly	Cys
		Val	Met
Gly	Gly	Gly	Gln
	385	Pro	Ile
		Met	Pro
		Thr	Val
		Leu	395
		Glu	Ser
		Met	Asn
		Arg	400
Thr	Thr	Thr	Lys
	405	Phe	Tyr
		Ala	Ser
		Leu	Lys
		410	Lys
		Arg	Leu
		Ala	Leu
		415	Tyr
Asp	Ala	Gln	Lys
	420	Ala	Met
		Ser	Ile
		Leu	425
		Ala	Thr
		Thr	Arg
		Arg	430
		Gly	Phe
Met	Lys	Thr	Ala
	435	Cys	Val
		Leu	Thr
		440	Gly
		Gly	Ala
		Leu	Ile
		445	Gly
		Leu	Arg
Leu	Thr	Ser	Lys
	450	Ala	Val
		Ala	Ala
		Ala	Lys
		Gln	Leu
		460	Lys
		Glu	His
		Met	

DESUanglais-seq1.txt

Met Asp Arg Val Asn Ala Val Tyr Gly Ala Asp Ala Lys Phe Lys Val
465 470 475 480

Arg Ala Ser Gln Asp Asn Ala Gln Val Ile Thr Leu Tyr Lys Lys Phe
485 490 495

Leu His Glu Pro Leu Ser His Glu Ser Glu His Leu Leu His Thr Lys
500 505 510

Trp Val Asp Arg Ser Lys Asp Leu Ala Ala Leu Lys Ala Lys Gly Leu
515 520 525

Tyr Pro Thr Pro Arg Ala Lys Glu Phe Glu Lys Pro Tyr Pro Phe Gln
530 535 540

<210> 57
<211> 3550
<212> DNA
<213> Desulfovibrio fructosovorans

<220>
<221> CDS
<222> (192)..(1133)
<223>

<220>
<221> CDS
<222> (1208)..(2899)
<223>

<220>
<221> CDS
<222> (2970)..(3467)
<223>

<400> 57
caaactcgtg attaaactgca aaagggaaat cgaacccggc gacgcaggaa cgcacgcgtc 60
cgtcacatag aggcggcggc ggccgggttcg cctgcgacgg ccgcgtgccc aacgggtcaa 120
cggatgctac gtggcctggg gatcatggga cgccccggac catgcctctc gtaaaacaaa 180

ggaggacgtt t atg aac ttt tcc gtg ggt ctt ggc agg gat gat gcg gaa 230
Met Asn Phe Ser Val Gly Leu Gly Arg Asp Asp Ala Glu
1 5 10

aaa cgg ctt gtg caa aac ggc gtc tcc cgc cgc gac ttc atg aaa ttt 278
Lys Arg Leu Val Gln Asn Gly Val Ser Arg Arg Asp Phe Met Lys Phe
15 20 25

tgc gcc acc gtg gcc gcg gcc atg ggc atg ggc ccc gcg ttc gcg ccc 326
Cys Ala Thr Val Ala Ala Met Gly Met Gly Pro Ala Phe Ala Pro
30 35 40 45

aag gtc gcc gaa gca ttg acg gcc aaa cac cgt ccg tcg gtg gtc tgg 374
Lys Val Ala Glu Ala Leu Thr Ala Lys His Arg Pro Ser Val Val Trp
50 55 60

ctg cac aac gcc gag tgc acc ggc tgc acc gaa gcg gcg atc cgg acg 422
Leu His Asn Ala Glu Cys Thr Gly Cys Thr Glu Ala Ala Ile Arg Thr
65 70 75

atc aaa cct tat ata gac gcg ctc att ctc gac acc atc tcc ctg gat 470
Ile Lys Pro Tyr Ile Asp Ala Leu Ile Leu Asp Thr Ile Ser Leu Asp
80 85 90

tac cag gag acc atc atg gcc gcg gcc ggc gag acg tcc gag gcg gcc 518
Tyr Gln Glu Thr Ile Met Ala Ala Ala Gly Glu Thr Ser Glu Ala Ala
95 100 105

ctg cac cag gcc ctc gaa ggc aag gac ggc tac tac ctc gtg gtc gag 566
Leu His Gln Ala Leu Glu Gly Lys Asp Gly Tyr Tyr Leu Val Val Glu
110 115 120 125

ggc ggc ctg ccc acc atc gac ggc ggc cag tgg ggc atg gtt gcc gcc 614
Gly Gly Leu Pro Thr Ile Asp Gly Gly Trp Gly Met Val Val Ala Gly
130 135 140

cat ccc atg atc gag acc acc aag aag gcc gcg gcc aag gcc aag gcc 662
His Pro Met Ile Glu Thr Thr Lys Lys Ala Ala Ala Lys Ala Lys Gly
145 150 155

atc atc tgc atc ggc acc tgc tcc gcc tac ggc ggc gtc cag aag gcc 710
Ile Ile Cys Ile Gly Thr Cys Ser Ala Tyr Gly Gly Val Gln Lys Ala
160 165 170

DESUanglais-seql.txt

aaa ccc aat ccc agc cag gcc aag ggc gtg tcc gaa gcc ctc ggc gtc 758
 Lys Pro Asn Pro Ser Gln Ala Lys Gly Val Ser Glu Ala Leu Gly Val
 175 180 185

aag acc atc aac atc ccc ggc tgc ccg ccc aac ccc atc aac ttc gtg 806
 Lys Thr Ile Asn Ile Pro Gly Cys Pro Pro Asn Pro Ile Asn Phe Val
 190 195 200 205

ggc gcc gtg gtc cat gtc ctg acc aag ggc atc ccg gat ctc gac gag 854
 Gly Ala Val Val His Val Leu Thr Lys Gly Ile Pro Asp Leu Asp Glu
 210 215 220

aac gcc cgt ccg aag ctc ttc tac ggc gag ctg gtc cac gac aac tgt 902
 Asn Gly Arg Pro Lys Leu Phe Tyr Gly Glu Leu Val His Asp Asn Cys
 225 230 235

ccg cgc ctg ccc cac ttc gag gcc tcc gaa ttc ggc ccc tcc ttc gat 950
 Pro Arg Leu Pro His Phe Glu Ala Ser Glu Phe Ala Pro Ser Phe Asp
 240 245 250

tcc gaa gag gcc aag aaa ggc ttc tgc ctc tac gaa ctc ggc tgc aag 998
 Ser Glu Glu Ala Lys Lys Gly Phe Cys Leu Tyr Glu Leu Gly Cys Lys
 255 260 265

ggc ccc gtt acc tac aac aac tgc ccc aag gtg ctg ttc aac cag gtc 1046
 Gly Pro Val Thr Tyr Asn Asn Cys Pro Lys Val Leu Phe Asn Gln Val
 270 275 280 285

aac tgg ccc gtc cag gcc ggc cac ccc tgc ctc ggc tgc agc gag ccg 1094
 Asn Trp Pro Val Gln Ala Gly His Pro Cys Leu Gly Cys Ser Glu Pro
 290 295 300

gac ttc tgg gac acc atg acg ccg ttc tac gag cag gcc taacccctc 1143
 Asp Phe Trp Asp Thr Met Thr Pro Phe Tyr Glu Gln Gly
 305 310

ctttgtagcg gccagtacc ggacaccttc aacagcaccg aacgtctcgt gacggaggaa 1203

gcat atg gct gag agc aaa ccc acg cca caa tcc acc ttc acc ggc ccc 1252
 Met Ala Glu Ser Lys Pro Thr Pro Gln Ser Thr Phe Thr Gly Pro
 315 320 325

atc gtg gtc gac ccc att acc cgg atc gaa ggt cac ttg cgg atc atg 1300
 Ile Val Val Asp Pro Ile Thr Arg Ile Glu Gly His Leu Arg Ile Met
 330 335 340 345

gtc gag gtg gaa aac ggt aag gtc aag gac gcc tgg agc tcc tcg cag 1348
 Val Glu Val Glu Asn Gly Lys Val Lys Asp Ala Trp Ser Ser Ser Gln
 350 355 360

ctc ttc cgc ggc ctg gaa atc atc ctc aaa ggc cgc gat ccc cgc gac 1396
 Leu Phe Arg Gly Leu Glu Ile Ile Leu Lys Gly Arg Asp Pro Arg Asp
 365 370 375

gcc cag cac ttc acc cag cgc gcc tgc ggc gtg tgc acg tac gtc cac 1444
 Ala Gln His Phe Thr Gln Arg Ala Cys Gly Val Cys Thr Tyr Val His
 380 385 390

gcc ctg gcc tcc agc cgc tgc gtc gat gac gcc gtc aag gtc agc atc 1492
 Ala Leu Ala Ser Ser Arg Cys Val Asp Asp Ala Val Lys Val Ser Ile
 395 400 405

ccg gcc aac gcc cgc atg atg cgc aac ctg gtc atg gcc tcc cag tat 1540
 Pro Ala Asn Ala Arg Met Met Arg Asn Leu Val Met Ala Ser Gln Tyr
 410 415 420 425

ctc cat gac cac ctc gtc cac ttc tat cac ctg cac gcc ctc gac tgg 1588
 Leu His Asp His Leu Val His Phe Tyr His Leu His Ala Leu Asp Trp
 430 435 440

gtc gac gtg acc gcc gcc ctc aag gcc gat ccc aac aag gcc gcc aaa 1636
 Val Asp Val Thr Ala Ala Leu Lys Ala Asp Pro Asn Lys Ala Ala Lys
 445 450 455

ctg gca gcc tcc atc gcc ccg gct cgg ccc ggc aac tcg gcc aag gcc 1684
 Leu Ala Ala Ser Ile Ala Pro Ala Arg Pro Gly Asn Ser Ala Lys Ala
 460 465 470

ctc aag gcc gtc cag gac aag ctg aaa gcc ttc gtc gag tcc gga cag 1732
 Leu Lys Ala Val Gln Asp Lys Leu Lys Ala Phe Val Glu Ser Gly Gln
 475 480 485

ctc gcc atc ttc acc aac gcc tac ttc ctc ggc gcc cac aaa gcc tac 1780
 Leu Gly Ile Phe Thr Asn Ala Tyr Phe Leu Gly Gly His Lys Ala Tyr
 490 495 500 505

DESUanglais-seq1.txt

tac	ctg	ccg	ccc	gag	gtc	aac	ctc	atc	gcc	acc	gcc	cac	tac	ctg	gaa	1828
Tyr	Leu	Pro	Pro	Glu	Val	Asn	Leu	Ile	Ala	Thr	Ala	His	Tyr	Leu	Glu	
				510					515					520		
gcc	ctg	cac	atg	cag	gtc	aag	gcg	gcc	agc	gcc	atg	gcc	atc	ctc	ggc	1876
Ala	Leu	His	Met	Gln	Val	Lys	Ala	Ala	Ser	Ala	Met	Ala	Ile	Leu	Gly	
			525					530					535			
ggc	aag	aac	ccc	cac	acc	cag	ttc	acc	gtc	gtg	ggc	ggc	tgc	tcc	aac	1924
Gly	Lys	Asn	Pro	His	Thr	Gln	Phe	Thr	Val	Val	Gly	Gly	Cys	Ser	Asn	
		540					545				550					
tac	cag	ggc	ctg	acc	aag	gac	ccg	ctg	gcc	aac	tac	ctg	gcc	ctg	agc	1972
Tyr	Gln	Gly	Leu	Thr	Lys	Asp	Pro	Leu	Ala	Asn	Tyr	Leu	Ala	Leu	Ser	
	555					560					565					
aag	gaa	gtc	tgc	cag	ttc	gtc	aac	gag	tgc	tac	atc	cct	gac	ctg	ctg	2020
Lys	Glu	Val	Cys	Gln	Phe	Val	Asn	Glu	Cys	Tyr	Ile	Pro	Asp	Leu	Leu	
	570				575					580					585	
gcc	gtg	gcc	ggc	ttc	tac	aag	gac	tgg	ggc	ggc	atc	ggc	ggc	acc	agc	2068
Ala	Val	Ala	Gly	Phe	Tyr	Lys	Asp	Trp	Gly	Gly	Ile	Gly	Gly	Thr	Ser	
				590					595					600		
aac	tac	ctg	gcc	ttc	ggc	gag	ttc	gcc	acc	gac	gac	agc	tcc	ccc	gag	2116
Asn	Tyr	Leu	Ala	Phe	Gly	Glu	Phe	Ala	Thr	Asp	Asp	Ser	Ser	Pro	Glu	
			605					610					615			
aaa	cac	ctg	gcc	acc	tgc	cag	ttt	ccg	tcc	ggc	gtc	atc	acc	ggc	cgc	2164
Lys	His	Leu	Ala	Thr	Ser	Gln	Phe	Pro	Ser	Gly	Val	Ile	Thr	Gly	Arg	
		620				625						630				
gac	ctc	ggc	aag	gtg	gat	aac	gtg	gac	ctc	ggc	gcc	atc	tac	gaa	gac	2212
Asp	Leu	Gly	Lys	Val	Asp	Asn	Val	Asp	Leu	Gly	Ala	Ile	Tyr	Glu	Asp	
	635					640					645					
gtc	aag	tac	tcc	tgg	tac	gcc	ccc	ggc	ggc	gac	ggc	aag	cac	ccc	tac	2260
Val	Lys	Tyr	Ser	Trp	Tyr	Ala	Pro	Gly	Gly	Asp	Gly	Lys	His	Pro	Tyr	
	650				655				660						665	
gac	ggc	gtc	acc	gat	ccc	aag	tac	acc	aag	ctc	gac	gac	aag	gac	cac	2308
Asp	Gly	Val	Thr	Asp	Pro	Lys	Tyr	Thr	Lys	Leu	Asp	Asp	Lys	Asp	His	
				670					675					680		
tac	tcc	tgg	atg	aag	gcc	ccc	cgc	tac	aag	ggc	aag	gcc	atg	gaa	gtc	2356
Tyr	Ser	Trp	Met	Lys	Ala	Pro	Arg	Tyr	Lys	Gly	Lys	Ala	Met	Glu	Val	
			685					690					695			
ggt	ccc	ctg	gcc	cgc	acc	ttc	atc	gcc	tac	gcc	aag	ggg	cag	ccc	gac	2404
Gly	Pro	Leu	Ala	Arg	Thr	Phe	Ile	Ala	Tyr	Ala	Lys	Gly	Gln	Pro	Asp	
		700					705					710				
ttc	aaa	aag	gtc	gtg	gac	atg	gtc	ctc	ggc	aaa	ctc	tcc	gtc	ccg	gcc	2452
Phe	Lys	Lys	Val	Val	Asp	Met	Val	Leu	Gly	Lys	Leu	Ser	Val	Pro	Ala	
	715					720					725					
acg	gcc	ctg	cat	tgc	acc	ctc	gga	cgc	acc	gcc	gcc	cgc	ggc	atc	gag	2500
Thr	Ala	Leu	His	Ser	Thr	Leu	Gly	Arg	Thr	Ala	Ala	Arg	Gly	Ile	Glu	
					735					740					745	
acc	gcc	atc	gtc	tgc	gcc	aac	atg	gag	aag	tgg	atc	aag	gaa	atg	gcc	2548
Thr	Ala	Ile	Val	Cys	Ala	Asn	Met	Glu	Lys	Trp	Ile	Lys	Glu	Met	Ala	
				750					755					760		
gac	agc	ggc	gcc	aag	gac	aac	acc	ctg	tgc	gcc	aag	tgg	gag	atg	ccc	2596
Asp	Ser	Gly	Ala	Lys	Asp	Asn	Thr	Leu	Cys	Ala	Lys	Trp	Glu	Met	Pro	
			765					770					775			
gag	gag	tcc	aag	ggc	gtc	ggc	ctg	gcc	gat	gct	ccc	cgc	ggc	gcc	ctg	2644
Glu	Glu	Ser	Lys	Gly	Val	Gly	Leu	Ala	Asp	Ala	Pro	Arg	Gly	Ala	Leu	
		780					785					790				
tcc	cac	tgg	atc	cgc	atc	aag	ggc	aag	aag	atc	gac	aac	ttc	cag	ctg	2692
Ser	His	Trp	Ile	Arg	Ile	Lys	Gly	Lys	Lys	Ile	Asp	Asn	Phe	Gln	Leu	
		795				800					805					
gtt	gtc	ccc	tgc	acc	tgg	aac	ctc	ggt	ccc	cgg	ggc	gcc	cag	ggc	gac	2740
Val	Val	Pro	Ser	Thr	Trp	Asn	Leu	Gly	Pro	Arg	Gly	Ala	Gln	Gly	Asp	
					815					820					825	
aag	agc	ccg	gtg	gaa	gag	gcc	ctt	atc	ggc	acg	ccc	atc	gcc	gat	ccc	2788
Lys	Ser	Pro	Val	Glu	Glu	Ala	Leu	Ile	Gly	Thr	Pro	Ile	Ala	Asp	Pro	
				830					835					840		

DESUanglais-seq1.txt

aaa cgc ccg gtc gaa atc ctg cgc acg gtc cac gcc ttc gac ccc tgc 2836
Lys Arg Pro Val Glu Ile Leu Arg Thr Val His Ala Phe Asp Pro Cys
845 850 855

atc gcc tgc ggc gtg cac gtc atc gag ccc gag acc aac gag atc ctc 2884
Ile Ala Cys Gly Val His Val Ile Glu Pro Glu Thr Asn Glu Ile Leu
860 865 870

aag ttc aag gtt tgc taagagcggc aacgccgctt atacgaagga cccggcttcg 2939
Lys Phe Lys Val Cys
875

gccgggttct tcgtttctca aggaggtcgc atg tcc gat acc ccg cgc aaa atc 2993
Met Ser Asp Thr Pro Arg Lys Ile
880 885

ctc atc ctc ggc gtc ggc aac atc ctc tac acc gac gag ggc gtc ggc 3041
Leu Ile Leu Gly Val Gly Asn Ile Leu Tyr Thr Asp Glu Gly Val Gly
890 895 900

gtg cgg gcc gtg gag cgc ctt ctc gaa acc cac gat ttt tcc gac aac 3089
Val Arg Ala Val Glu Arg Leu Leu Glu Thr His Asp Phe Ser Asp Asn
905 910 915

gtc acc ctc atg gac ggc ggc aac ctg ggc atg aag ctc atg gcc ccg 3137
Val Thr Leu Met Asp Gly Gly Asn Leu Gly Met Lys Leu Met Ala Pro
920 925 930

ctc atg gaa tgc gac tac tgc atc gtg ctc gac gcc gtg ctc ggc ggc 3185
Leu Met Glu Cys Asp Tyr Cys Ile Val Leu Asp Ala Val Leu Gly Gly
935 940 945 950

gac gcc ccc ggc acc atc tac cgt ctc acc ggc gag gac ctg cgc aaa 3233
Asp Ala Pro Gly Thr Ile Tyr Arg Leu Thr Gly Glu Asp Leu Arg Lys
955 960 965

tcc ctg gcc ttc aag gac tcc atg cac cag tcc gac ctc gtc gac acg 3281
Ser Leu Ala Phe Lys Asp Ser Met His Gln Ser Asp Leu Val Asp Thr
970 975 980

ctg atc tat tgc gaa ctg gcc gga cac cgc ccg gac acc gtg gtc atc 3329
Leu Ile Tyr Cys Glu Leu Ala Gly His Arg Pro Asp Thr Val Val Ile
985 990 995

ggc atg gag ccc ctc gat ttt cag aac atg agc atc gaa ctc tcg 3374
Gly Met Glu Pro Leu Asp Phe Gln Asn Met Ser Ile Glu Leu Ser
1000 1005 1010

ccc gcc atc gcc gaa cgc gtt ccg gcc atg atc gac atc gcc ctg 3419
Pro Ala Ile Ala Glu Arg Val Pro Ala Met Ile Asp Ile Ala Leu
1015 1020 1025

gcc gaa ctc gcc gcc gcc ggc ggc gtc gcc acg ccc aaa gga caa 3464
Ala Glu Leu Ala Ala Ala Gly Gly Val Ala Thr Pro Lys Gly Gln
1030 1035 1040

agt taggaagaaa ggaggtgcga gaggggaaac cctttaaaaa gggttctccc 3517
Ser

ctctcgcgcc tctcccttc ctaaatttta taa 3550

<210> 58
<211> 1044
<212> PRT
<213> Desulfovibrio fructosovorans

<400> 58
Met Asn Phe Ser Val Gly Leu Gly Arg Asp Asp Ala Glu Lys Arg Leu
1 5 10 15
Val Gln Asn Gly Val Ser Arg Arg Asp Phe Met Lys Phe Cys Ala Thr
20 25 30
Val Ala Ala Ala Met Gly Met Gly Pro Ala Phe Ala Pro Lys Val Ala
35 40 45
Glu Ala Leu Thr Ala Lys His Arg Pro Ser Val Val Trp Leu His Asn
50 55 60
Ala Glu Cys Thr Gly Cys Thr Glu Ala Ala Ile Arg Thr Ile Lys Pro
65 70 75 80
Tyr Ile Asp Ala Leu Ile Leu Asp Thr Ile Ser Leu Asp Tyr Gln Glu

DESUanglais-seql.txt

85 90 95
 Thr Ile Met Ala Ala Ala Gly Glu Thr Ser Glu Ala Ala Leu His Gln
 100 105 110
 Ala Leu Glu Gly Lys Asp Gly Tyr Tyr Leu Val Val Glu Gly Gly Leu
 115 120 125
 Pro Thr Ile Asp Gly Gly Gln Trp Gly Met Val Ala Gly His Pro Met
 130 135 140
 Ile Glu Thr Thr Lys Lys Ala Ala Ala Lys Ala Lys Gly Ile Ile Cys
 145 150 155 160
 Ile Gly Thr Cys Ser Ala Tyr Gly Gly Val Gln Lys Ala Lys Pro Asn
 165 170 175
 Pro Ser Gln Ala Lys Gly Val Ser Glu Ala Leu Gly Val Lys Thr Ile
 180 185 190
 Asn Ile Pro Gly Cys Pro Pro Asn Pro Ile Asn Phe Val Gly Ala Val
 195 200 205
 Val His Val Leu Thr Lys Gly Ile Pro Asp Leu Asp Glu Asn Gly Arg
 210 215 220
 Pro Lys Leu Phe Tyr Gly Glu Leu Val His Asp Asn Cys Pro Arg Leu
 225 230 235 240
 Pro His Phe Glu Ala Ser Glu Phe Ala Pro Ser Phe Asp Ser Glu Glu
 245 250 255
 Ala Lys Lys Gly Phe Cys Leu Tyr Glu Leu Gly Cys Lys Gly Pro Val
 260 265 270
 Thr Tyr Asn Asn Cys Pro Lys Val Leu Phe Asn Gln Val Asn Trp Pro
 275 280 285
 Val Gln Ala Gly His Pro Cys Leu Gly Cys Ser Glu Pro Asp Phe Trp
 290 295 300
 Asp Thr Met Thr Pro Phe Tyr Glu Gln Gly Met Ala Glu Ser Lys Pro
 305 310 315 320
 Thr Pro Gln Ser Thr Phe Thr Gly Pro Ile Val Val Asp Pro Ile Thr
 325 330 335
 Arg Ile Glu Gly His Leu Arg Ile Met Val Glu Val Glu Asn Gly Lys
 340 345 350
 Val Lys Asp Ala Trp Ser Ser Ser Gln Leu Phe Arg Gly Leu Glu Ile
 355 360 365
 Ile Leu Lys Gly Arg Asp Pro Arg Asp Ala Gln His Phe Thr Gln Arg
 370 375 380
 Ala Cys Gly Val Cys Thr Tyr Val His Ala Leu Ala Ser Ser Arg Cys
 385 390 395 400
 Val Asp Asp Ala Val Lys Val Ser Ile Pro Ala Asn Ala Arg Met Met
 405 410 415
 Arg Asn Leu Val Met Ala Ser Gln Tyr Leu His Asp His Leu Val His
 420 425 430
 Phe Tyr His Leu His Ala Leu Asp Trp Val Asp Val Thr Ala Ala Leu
 435 440 445
 Lys Ala Asp Pro Asn Lys Ala Ala Lys Leu Ala Ala Ser Ile Ala Pro
 450 455 460
 Ala Arg Pro Gly Asn Ser Ala Lys Ala Leu Lys Ala Val Gln Asp Lys
 465 470 475 480
 Leu Lys Ala Phe Val Glu Ser Gly Gln Leu Gly Ile Phe Thr Asn Ala
 485 490 495
 Tyr Phe Leu Gly Gly His Lys Ala Tyr Tyr Leu Pro Pro Glu Val Asn
 500 505 510
 Leu Ile Ala Thr Ala His Tyr Leu Glu Ala Leu His Met Gln Val Lys
 515 520 525
 Ala Ala Ser Ala Met Ala Ile Leu Gly Gly Lys Asn Pro His Thr Gln
 530 535 540

Phe Thr Val Val Gly Gly Cys Ser Asn Tyr Gln Gly Leu Thr Lys Asp
 545 550 555 560
 Pro Leu Ala Asn Tyr Leu Ala Leu Ser Lys Glu Val Cys Gln Phe Val
 565 570 575
 Asn Glu Cys Tyr Ile Pro Asp Leu Leu Ala Val Ala Gly Phe Tyr Lys
 580 585 590
 Asp Trp Gly Gly Ile Gly Gly Thr Ser Asn Tyr Leu Ala Phe Gly Glu
 595 600 605
 Phe Ala Thr Asp Asp Ser Ser Pro Glu Lys His Leu Ala Thr Ser Gln
 610 615 620
 Phe Pro Ser Gly Val Ile Thr Gly Arg Asp Leu Gly Lys Val Asp Asn
 625 630 635 640
 Val Asp Leu Gly Ala Ile Tyr Glu Asp Val Lys Tyr Ser Trp Tyr Ala
 645 650 655
 Pro Gly Gly Asp Gly Lys His Pro Tyr Asp Gly Val Thr Asp Pro Lys
 660 665 670
 Tyr Thr Lys Leu Asp Asp Lys Asp His Tyr Ser Trp Met Lys Ala Pro
 675 680 685
 Arg Tyr Lys Gly Lys Ala Met Glu Val Gly Pro Leu Ala Arg Thr Phe
 690 695 700
 Ile Ala Tyr Ala Lys Gly Gln Pro Asp Phe Lys Lys Val Val Asp Met
 705 710 715 720
 Val Leu Gly Lys Leu Ser Val Pro Ala Thr Ala Leu His Ser Thr Leu
 725 730 735
 Gly Arg Thr Ala Ala Arg Gly Ile Glu Thr Ala Ile Val Cys Ala Asn
 740 745 750
 Met Glu Lys Trp Ile Lys Glu Met Ala Asp Ser Gly Ala Lys Asp Asn
 755 760 765
 Thr Leu Cys Ala Lys Trp Glu Met Pro Glu Glu Ser Lys Gly Val Gly
 770 775 780
 Leu Ala Asp Ala Pro Arg Gly Ala Leu Ser His Trp Ile Arg Ile Lys
 785 790 795 800
 Gly Lys Lys Ile Asp Asn Phe Gln Leu Val Val Pro Ser Thr Trp Asn
 805 810 815
 Leu Gly Pro Arg Gly Ala Gln Gly Asp Lys Ser Pro Val Glu Glu Ala
 820 825 830
 Leu Ile Gly Thr Pro Ile Ala Asp Pro Lys Arg Pro Val Glu Ile Leu
 835 840 845
 Arg Thr Val His Ala Phe Asp Pro Cys Ile Ala Cys Gly Val His Val
 850 855 860
 Ile Glu Pro Glu Thr Asn Glu Ile Leu Lys Phe Lys Val Cys Met Ser
 865 870 875 880
 Asp Thr Pro Arg Lys Ile Leu Ile Leu Gly Val Gly Asn Ile Leu Tyr
 885 890 895
 Thr Asp Glu Gly Val Gly Val Arg Ala Val Glu Arg Leu Leu Glu Thr
 900 905 910
 His Asp Phe Ser Asp Asn Val Thr Leu Met Asp Gly Gly Asn Leu Gly
 915 920 925
 Met Lys Leu Met Ala Pro Leu Met Glu Cys Asp Tyr Cys Ile Val Leu
 930 935 940
 Asp Ala Val Leu Gly Gly Asp Ala Pro Gly Thr Ile Tyr Arg Leu Thr
 945 950 955 960
 Gly Glu Asp Leu Arg Lys Ser Leu Ala Phe Lys Asp Ser Met His Gln
 965 970 975
 Ser Asp Leu Val Asp Thr Leu Ile Tyr Cys Glu Leu Ala Gly His Arg
 980 985 990

DESUanglais-seq1.txt

Pro Asp Thr Val Val Ile Gly Met Glu Pro Leu Asp Phe Gln Asn Met
 995 1000 1005

Ser Ile Glu Leu Ser Pro Ala Ile Ala Glu Arg Val Pro Ala Met
 1010 1015 1020

Ile Asp Ile Ala Leu Ala Glu Leu Ala Ala Ala Gly Gly Val Ala
 1025 1030 1035

Thr Pro Lys Gly Gln Ser
 1040

<210> 59
 <211> 3550
 <212> DNA
 <213> Desulfovibrio fructosovorans

<220>
 <221> CDS
 <222> (192)..(1133)
 <223>

<220>
 <221> CDS
 <222> (1208)..(2899)
 <223>

<220>
 <221> CDS
 <222> (2970)..(3467)
 <223>

<400> 59
 caaactcgtg attaactgca aaagggaaat cgaacccggc gacgcaggaa cgcacgcgtc 60
 cgtcacatag aggcggcggc ggccgggttcg cctgcgacgg ccgcgtgccg aacgggtcaa 120
 cggatgctac gtggcctggg gatcatggga cgccccggac catgctcttc gtaaaacaaa 180

ggaggacgtt t atg aac ttt tcc gtg ggt ctt ggc agg gat gat gcg gaa 230
 Met Asn Phe Ser Val Gly Leu Gly Arg Asp Asp Ala Glu
 1 5 10

aaa cgg ctt gtg caa aac ggc gtc tcc cgc cgc cag ttc atg aaa ttt 278
 Lys Arg Leu Val Gln Asn Gly Val Ser Arg Arg Gln Phe Met Lys Phe
 15 20 25

tgc gcc acc gtg gcc gcc atg ggc atg ggc ccc gcg ttc gcg ccc 326
 Cys Ala Thr Val Ala Ala Met Gly Met Gly Pro Ala Phe Ala Pro
 30 35 40 45

aag gtc gcc gaa gca ttg acg gcc aaa cac cgt ccg tcg gtg gtc tgg 374
 Lys Val Ala Glu Ala Leu Thr Ala Lys His Arg Pro Ser Val Val Trp
 50 55 60

ctg cac aac gcc gag tgc acc ggc tgc acc gaa gcg gcg atc cgg acg 422
 Leu His Asn Ala Glu Cys Thr Gly Cys Thr Glu Ala Ala Ile Arg Thr
 65 70 75

atc aaa cct tat ata gac gcg ctc att ctc gac acc atc tcc ctg gat 470
 Ile Lys Pro Tyr Ile Asp Ala Leu Ile Leu Asp Thr Ile Ser Leu Asp
 80 85 90

tac cag gag acc atc atg gcc gcg gcc ggc gag acg tcc gag gcg gcc 518
 Tyr Gln Glu Thr Ile Met Ala Ala Ala Gly Glu Thr Ser Glu Ala Ala
 95 100 105

ctg cac cag gcc ctc gaa ggc aag gac ggc tac tac ctc gtg gtc gag 566
 Leu His Gln Ala Leu Glu Gly Lys Asp Gly Tyr Tyr Leu Val Val Glu
 110 115 120 125

ggc gcc ctg ccc acc atc gac ggc gcc cag tgg ggc atg gtt gcc gcc 614
 Gly Gly Leu Pro Thr Ile Asp Gly Gly Gln Trp Gly Met Val Ala Gly
 130 135 140

cat ccc atg atc gag acc acc aag aag gcc gcg gcc aag gcc aag gcc 662
 His Pro Met Ile Glu Thr Thr Lys Lys Ala Ala Ala Lys Ala Lys Gly
 145 150 155

atc atc tgc atc ggc acc tgc tcc gcc tac ggc gcc gtc cag aag gcc 710
 Ile Ile Cys Ile Gly Thr Cys Ser Ala Tyr Gly Gly Val Gln Lys Ala
 160 165 170

aaa ccc aat ccc agc cag gcc aag ggc gtg tcc gaa gcc ctc gcc gtc 758
 Lys Pro Asn Pro Ser Gln Ala Lys Gly Val Ser Glu Ala Leu Gly Val

DESUanglais-seql.txt

175	180	185	
aag acc atc aac atc ccc ggc tgc ccg ccc aac ccc atc aac ttc gtg Lys Thr Ile Asn Ile Pro Gly Cys Pro Pro Asn Pro Ile Asn Phe Val 190 195 200 205			806
ggc gcc gtg gtc cat gtc ctg acc aag ggc atc ccg gat ctc gac gag Gly Ala Val Val His Val Leu Thr Lys Gly Ile Pro Asp Leu Asp Glu 210 215 220			854
aac gcc cgt ccg aag ctc ttc tac ggc gag ctg gtc cac gac aac tgt Asn Gly Arg Pro Lys Leu Phe Tyr Gly Glu Leu Val His Asp Asn Cys 225 230 235			902
ccg cgc ctg ccc cac ttc gag gcc tcc gaa ttc gcg ccc tcc ttc gat Pro Arg Leu Pro His Phe Glu Ala Ser Glu Phe Ala Pro Ser Phe Asp 240 245 250			950
tcc gaa gag gcc aag aaa ggc ttc tgc ctc tac gaa ctc ggc tgc aag Ser Glu Glu Ala Lys Lys Gly Phe Cys Leu Tyr Glu Leu Gly Cys Lys 255 260 265			998
ggc ccc gtt acc tac aac aac tgc ccc aag gtg ctg ttc aac cag gtc Gly Pro Val Thr Tyr Asn Asn Cys Pro Lys Val Leu Phe Asn Gln Val 270 275 280 285			1046
aac tgg ccc gtc cag gcc ggc cac ccc tgc ctc ggc tgc agc gag ccg Asn Trp Pro Val Gln Ala Gly His Pro Cys Leu Gly Cys Ser Glu Pro 290 295 300			1094
gac ttc tgg gac acc atg acg ccg ttc tac gag cag ggc taacccccctc Asp Phe Trp Asp Thr Met Thr Pro Phe Tyr Glu Gln Gly			1143
305	310		
ctttgtagcg gccagtagcc ggacaccttc aacagcaccg aacgtctcgt gacggaggaa			1203
gcat atg gct gag agc aaa ccc acg cca caa tcc acc ttc acc ggc ccc Met Ala Glu Ser Lys Pro Thr Pro Gln Ser Thr Phe Thr Gly Pro 315 320 325			1252
atc gtg gtc gac ccc att acc cgg atc gaa ggt cac ttg ccg atc atg Ile Val Val Asp Pro Ile Thr Arg Ile Glu Gly His Leu Arg Ile Met 330 335 340 345			1300
gtc gag gtg gaa aac ggt aag gtc aag gac gcc tgg agc tcc tcg cag Val Glu Val Glu Asn Gly Lys Val Lys Asp Ala Trp Ser Ser Ser Gln 350 355 360			1348
ctc ttc cgc ggc ctg gaa atc atc ctc aaa ggc cgc gat ccc cgc gac Leu Phe Arg Gly Leu Glu Ile Ile Lys Gly Arg Asp Pro Arg Asp 365 370 375			1396
gcc cag cac ttc acc cag cgc gcc tgc ggc gtg tgc acg tac gtc cac Ala Gln His Phe Thr Gln Arg Ala Cys Gly Val Cys Thr Tyr Val His 380 385 390			1444
gcc ctg gcc tcc agc cgc tgc gtc gat gac gcc gtc aag gtc agc atc Ala Leu Ala Ser Ser Arg Cys Val Asp Asp Ala Lys Val Ser Ile 395 400 405			1492
ccg gcc aac gcc cgc atg atg cgc aac ctg gtc atg gcc tcc cag tat Pro Ala Asn Ala Arg Met Met Arg Asn Leu Val Met Ala Ser Gln Tyr 410 415 420 425			1540
ctc cat gac cac ctc gtc cac ttc tat cac ctg cac gcc ctc gac tgg Leu His Asp His Leu Val His Phe Tyr His Leu His Ala Leu Asp Trp 430 435 440			1588
gtc gac gtg acc gcc gcc ctc aag gcc gat ccc aac aag gcc gcc aaa Val Asp Val Thr Ala Ala Leu Lys Ala Asp Pro Asn Lys Ala Ala Lys 445 450 455			1636
ctg gca gcc tcc atc gcc ccg gct cgg ccc ggc aac tcg gcc aag gcc Leu Ala Ala Ser Ile Ala Pro Ala Arg Pro Gly Asn Ser Ala Lys Ala 460 465 470			1684
ctc aag gcc gtc cag gac aag ctg aaa gcc ttc gtc gag tcc gga cag Leu Lys Ala Val Gln Asp Lys Leu Lys Ala Phe Val Glu Ser Gly Gln 475 480 485			1732
ctc ggc atc ttc acc aac gcc tac ttc ctc ggc ggc cac aaa gcc tac Leu Gly Ile Phe Thr Asn Ala Tyr Phe Leu Gly Gly His Lys Ala Tyr 490 495 500 505			1780

DESUanglais-seq1.txt

tac	ctg	ccg	ccc	gag	gtc	aac	ctc	atc	gcc	acc	gcc	cac	tac	ctg	gaa	1828
Tyr	Leu	Pro	Pro	Glu	Val	Asn	Leu	Ile	Ala	Thr	Ala	His	Tyr	Leu	Glu	
				510					515					520		
gcc	ctg	cac	atg	cag	gtc	aag	gcg	gcc	agc	gcc	atg	gcc	atc	ctc	ggc	1876
Ala	Leu	His	Met	Gln	Val	Lys	Ala	Ala	Ser	Ala	Met	Ala	Ile	Leu	Gly	
			525					530					535			
ggc	aag	aac	ccc	cac	acc	cag	ttc	acc	gtc	gtg	ggc	ggc	tgc	tcc	aac	1924
Gly	Lys	Asn	Pro	His	Thr	Gln	Phe	Thr	Val	Val	Gly	Gly	Cys	Ser	Asn	
		540					545				550					
tac	cag	ggc	ctg	acc	aag	gac	ccg	ctg	gcc	aac	tac	ctg	gcc	ctg	agc	1972
Tyr	Gln	Gly	Leu	Thr	Lys	Asp	Pro	Leu	Ala	Asn	Tyr	Leu	Ala	Leu	Ser	
	555					560					565					
aag	gaa	gtc	tgc	cag	ttc	gtc	aac	gag	tgc	tac	atc	cct	gac	ctg	ctg	2020
Lys	Glu	Val	Cys	Gln	Phe	Val	Asn	Glu	Cys	Tyr	Ile	Pro	Asp	Leu	Leu	
	570				575					580					585	
gcc	gtg	gcc	ggc	ttc	tac	aag	gac	tgg	ggc	ggc	atc	ggc	ggc	acc	agc	2068
Ala	Val	Ala	Gly	Phe	Tyr	Lys	Asp	Trp	Gly	Gly	Ile	Gly	Gly	Thr	Ser	
				590					595					600		
aac	tac	ctg	gcc	ttc	ggc	gag	ttc	gcc	acc	gac	gac	agc	tcc	ccc	gag	2116
Asn	Tyr	Leu	Ala	Phe	Gly	Glu	Phe	Thr	Thr	Asp	Asp	Ser	Ser	Pro	Glu	
			605					610					615			
aaa	cac	ctg	gcc	acc	tgc	cag	ttt	ccg	tcc	ggc	gtc	atc	acc	ggc	cgc	2164
Lys	His	Leu	Ala	Thr	Ser	Gln	Phe	Pro	Ser	Gly	Val	Ile	Thr	Gly	Arg	
		620				625						630				
gac	ctc	ggc	aag	gtg	gat	aac	gtg	gac	ctc	ggc	gcc	atc	tac	gaa	gac	2212
Asp	Leu	Gly	Lys	Val	Asp	Val	Val	Asp	Leu	Gly	Ala	Ile	Tyr	Glu	Asp	
	635					640					645					
gtc	aag	tac	tcc	tgg	tac	gcc	ccc	ggc	ggc	gac	ggc	aag	cac	ccc	tac	2260
Val	Lys	Tyr	Ser	Trp	Tyr	Ala	Pro	Gly	Gly	Asp	Gly	Lys	His	Pro	Tyr	
	650				655					660					665	
gac	ggc	gtc	acc	gat	ccc	aag	tac	acc	aag	ctc	gac	gac	aag	gac	cac	2308
Asp	Gly	Val	Thr	Asp	Pro	Lys	Tyr	Thr	Lys	Leu	Asp	Asp	Lys	Asp	His	
				670					675					680		
tac	tcc	tgg	atg	aag	gcc	ccc	cgc	tac	aag	ggc	aag	gcc	atg	gaa	gtc	2356
Tyr	Ser	Trp	Met	Lys	Ala	Pro	Arg	Tyr	Lys	Gly	Lys	Ala	Met	Glu	Val	
			685					690					695			
ggt	ccc	ctg	gcc	cgc	acc	ttc	atc	gcc	tac	gcc	aag	ggc	cag	ccc	gac	2404
Gly	Pro	Leu	Ala	Arg	Thr	Phe	Ile	Ala	Tyr	Ala	Lys	Gly	Gln	Pro	Asp	
		700				705						710				
ttc	aaa	aag	gtc	gtg	gac	atg	gtc	ctc	ggc	aaa	ctc	tcc	gtc	ccg	gcc	2452
Phe	Lys	Lys	Val	Val	Asp	Met	Val	Leu	Gly	Lys	Leu	Ser	Val	Pro	Ala	
	715					720					725					
acg	gcc	ctg	cat	tgc	acc	ctc	gga	cgc	acc	gcc	gcc	cgc	ggc	atc	gag	2500
Thr	Ala	Leu	His	Ser	Thr	Leu	Gly	Arg	Thr	Ala	Ala	Arg	Gly	Ile	Glu	
	730				735					740					745	
acc	gcc	atc	gtc	tgc	gcc	aac	atg	gag	aag	tgg	atc	aag	gaa	atg	gcc	2548
Thr	Ala	Ile	Val	Cys	Ala	Asn	Met	Glu	Lys	Trp	Ile	Lys	Glu	Met	Ala	
				750					755					760		
gac	agc	ggc	gcc	aag	gac	aac	acc	ctg	tgc	gcc	aag	tgg	gag	atg	ccc	2596
Asp	Ser	Gly	Ala	Lys	Asp	Asn	Thr	Leu	Cys	Ala	Lys	Trp	Glu	Met	Pro	
			765					770					775			
gag	gag	tcc	aag	ggc	gtc	ggc	ctg	gcc	gat	gct	ccc	cgc	ggc	gcc	ctg	2644
Glu	Glu	Ser	Lys	Gly	Val	Gly	Leu	Ala	Asp	Ala	Pro	Arg	Gly	Ala	Leu	
		780					785					790				
tcc	cac	tgg	atc	cgc	atc	aag	ggc	aag	aag	atc	gac	aac	ttc	cag	ctg	2692
Ser	His	Trp	Ile	Arg	Ile	Lys	Gly	Lys	Lys	Ile	Asp	Asn	Phe	Gln	Leu	
	795					800					805					
gtt	gtc	ccc	tgc	acc	tgg	aac	ctc	ggt	ccc	cgc	ggc	gcc	cag	ggc	gac	2740
Val	Val	Pro	Ser	Thr	Trp	Asn	Leu	Gly	Pro	Arg	Gly	Ala	Gln	Gly	Asp	
	810				815					820					825	
aag	agc	ccg	gtg	gaa	gag	gcc	ctt	atc	ggc	acg	ccc	atc	gcc	gat	ccc	2788
Lys	Ser	Pro	Val	Glu	Glu	Ala	Leu	Ile	Gly	Thr	Pro	Ile	Ala	Asp	Pro	
				830					835					840		

DESUanglais-seql.txt

```

aaa cgc ccg gtc gaa atc ctg cgc acg gtc cac gcc ttc gac ccc tgc 2836
Lys Arg Pro Val Glu Ile Leu Arg Thr Val His Ala Phe Asp Pro Cys
845 850 855

atc gcc tgc ggc gtg cac gtc atc gag ccc gag acc aac gag atc ctc 2884
Ile Ala Cys Gly Val His Val Ile Glu Pro Glu Thr Asn Glu Ile Leu
860 865 870

aag ttc aag gtt tgc taagagcggc aacgccgctt atacgaagga cccggcttcg 2939
Lys Phe Lys Val Cys
875

gccgggttct tcgtttctca aggaggtcgc atg tcc gat acc ccg cgc aaa atc 2993
Met Ser Asp Thr Pro Arg Lys Ile
880 885

ctc atc ctc ggc gtc ggc aac atc ctc tac acc gac gag ggc gtc ggc 3041
Leu Ile Leu Gly Val Gly Asn Ile Leu Tyr Thr Asp Glu Gly Val Gly
890 895

gtg cgg gcc gtg gag cgc ctt ctc gaa acc cac gat ttt tcc gac aac 3089
Val Arg Ala Val Glu Arg Leu Leu Glu Thr His Asp Phe Ser Asp Asn
905 910 915

gtc acc ctc atg gac ggc ggc aac ctg ggc atg aag ctc atg gcc ccg 3137
Val Thr Leu Met Asp Gly Gly Asn Leu Gly Met Lys Leu Met Ala Pro
920 925 930

ctc atg gaa tgc gac tac tgc atc gtg ctc gac gcc gtg ctc ggc ggc 3185
Leu Met Glu Cys Asp Tyr Cys Ile Val Leu Asp Ala Val Leu Gly Gly
935 940 945 950

gac gcc ccc ggc acc atc tac cgt ctc acc ggc gag gac ctg cgc aaa 3233
Asp Ala Pro Gly Thr Ile Tyr Arg Leu Thr Gly Glu Asp Leu Arg Lys
955 960 965

tcc ctg gcc ttc aag gac tcc atg cac cag tcc gac ctc gtc gac acg 3281
Ser Leu Ala Phe Lys Asp Ser Met His Gln Ser Asp Leu Val Asp Thr
970 975 980

ctg atc tat tgc gaa ctg gcc gga cac cgc ccg gac acc gtg gtc atc 3329
Leu Ile Tyr Cys Glu Leu Ala Gly His Arg Pro Asp Thr Val Val Ile
985 990 995

ggc atg gag ccc ctc gat ttt cag aac atg agc atc gaa ctc tcg 3374
Gly Met Glu Pro Leu Asp Phe Gln Asn Met Ser Ile Glu Leu Ser
1000 1005 1010

ccc gcc atc gcc gaa cgc gtt ccg gcc atg atc gac atc gcc ctg 3419
Pro Ala Ile Ala Glu Arg Val Pro Ala Met Ile Asp Ile Ala Leu
1015 1020 1025

gcc gaa ctc gcc gcc gcc ggc ggc gtc gcc acg ccc aaa gga caa 3464
Ala Glu Leu Ala Ala Ala Gly Gly Val Ala Thr Pro Lys Gly Gln
1030 1035 1040

agt taggaagaaa ggaggtgcga gaggggaaac cctttaaaaa gggttctccc 3517
Ser

ctctcgcgcc tctccccttc ctaaatttta taa 3550

```

<210> 60
 <211> 1044
 <212> PRT
 <213> Desulfovibrio fructosovorans

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

DESUanglais-seql.txt

85	90	95
Thr Ile Met Ala Ala Ala Gly Glu Thr Ser Glu Ala Ala Leu His Gln		
100	105	110
Ala Leu Glu Gly Lys Asp Gly Tyr Tyr Leu Val Val Glu Gly Gly Leu		
115	120	125
Pro Thr Ile Asp Gly Gly Gln Trp Gly Met Val Ala Gly His Pro Met		
130	135	140
Ile Glu Thr Thr Lys Lys Ala Ala Ala Lys Ala Lys Gly Ile Ile Cys		
145	150	155
Ile Gly Thr Cys Ser Ala Tyr Gly Gly Val Gln Lys Ala Lys Pro Asn		
165	170	175
Pro Ser Gln Ala Lys Gly Val Ser Glu Ala Leu Gly Val Lys Thr Ile		
180	185	190
Asn Ile Pro Gly Cys Pro Pro Asn Pro Ile Asn Phe Val Gly Ala Val		
195	200	205
Val His Val Leu Thr Lys Gly Ile Pro Asp Leu Asp Glu Asn Gly Arg		
210	215	220
Pro Lys Leu Phe Tyr Gly Glu Leu Val His Asp Asn Cys Pro Arg Leu		
225	230	235
Pro His Phe Glu Ala Ser Glu Phe Ala Pro Ser Phe Asp Ser Glu Glu		
245	250	255
Ala Lys Lys Gly Phe Cys Leu Tyr Glu Leu Gly Cys Lys Gly Pro Val		
260	265	270
Thr Tyr Asn Asn Cys Pro Lys Val Leu Phe Asn Gln Val Asn Trp Pro		
275	280	285
Val Gln Ala Gly His Pro Cys Leu Gly Cys Ser Glu Pro Asp Phe Trp		
290	295	300
Asp Thr Met Thr Pro Phe Tyr Glu Gln Gly Met Ala Glu Ser Lys Pro		
305	310	315
Thr Pro Gln Ser Thr Phe Thr Gly Pro Ile Val Val Asp Pro Ile Thr		
325	330	335
Arg Ile Glu Gly His Leu Arg Ile Met Val Glu Val Glu Asn Gly Lys		
340	345	350
Val Lys Asp Ala Trp Ser Ser Ser Gln Leu Phe Arg Gly Leu Glu Ile		
355	360	365
Ile Leu Lys Gly Arg Asp Pro Arg Asp Ala Gln His Phe Thr Gln Arg		
370	375	380
Ala Cys Gly Val Cys Thr Tyr Val His Ala Leu Ala Ser Ser Arg Cys		
385	390	395
Val Asp Asp Ala Val Lys Val Ser Ile Pro Ala Asn Ala Arg Met Met		
405	410	415
Arg Asn Leu Val Met Ala Ser Gln Tyr Leu His Asp His Leu Val His		
420	425	430
Phe Tyr His Leu His Ala Leu Asp Trp Val Asp Val Thr Ala Ala Leu		
435	440	445
Lys Ala Asp Pro Asn Lys Ala Ala Lys Leu Ala Ala Ser Ile Ala Pro		
450	455	460
Ala Arg Pro Gly Asn Ser Ala Lys Ala Leu Lys Ala Val Gln Asp Lys		
465	470	475
Leu Lys Ala Phe Val Glu Ser Gly Gln Leu Gly Ile Phe Thr Asn Ala		
485	490	495
Tyr Phe Leu Gly Gly His Lys Ala Tyr Tyr Leu Pro Pro Glu Val Asn		
500	505	510
Leu Ile Ala Thr Ala His Tyr Leu Glu Ala Leu His Met Gln Val Lys		
515	520	525
Ala Ala Ser Ala Met Ala Ile Leu Gly Gly Lys Asn Pro His Thr Gln		
530	535	540

DESUanglais-seq1.txt

Phe Thr Val Val Gly Gly Cys Ser Asn Tyr Gln Gly Leu Thr Lys Asp
 545 550 555 560
 Pro Leu Ala Asn Tyr Leu Ala Leu Ser Lys Glu Val Cys Gln Phe Val
 565 570 575
 Asn Glu Cys Tyr Ile Pro Asp Leu Leu Ala Val Ala Gly Phe Tyr Lys
 580 585 590
 Asp Trp Gly Gly Ile Gly Gly Thr Ser Asn Tyr Leu Ala Phe Gly Glu
 595 600 605
 Phe Ala Thr Asp Asp Ser Ser Pro Glu Lys His Leu Ala Thr Ser Gln
 610 615 620
 Phe Pro Ser Gly Val Ile Thr Gly Arg Asp Leu Gly Lys Val Asp Asn
 625 630 635 640
 Val Asp Leu Gly Ala Ile Tyr Glu Asp Val Lys Tyr Ser Trp Tyr Ala
 645 650 655
 Pro Gly Gly Asp Gly Lys His Pro Tyr Asp Gly Val Thr Asp Pro Lys
 660 665 670
 Tyr Thr Lys Leu Asp Asp Lys Asp His Tyr Ser Trp Met Lys Ala Pro
 675 680 685
 Arg Tyr Lys Gly Lys Ala Met Glu Val Gly Pro Leu Ala Arg Thr Phe
 690 695 700
 Ile Ala Tyr Ala Lys Gly Gln Pro Asp Phe Lys Lys Val Val Asp Met
 705 710 715 720
 Val Leu Gly Lys Leu Ser Val Pro Ala Thr Ala Leu His Ser Thr Leu
 725 730 735
 Gly Arg Thr Ala Ala Arg Gly Ile Glu Thr Ala Ile Val Cys Ala Asn
 740 745 750
 Met Glu Lys Trp Ile Lys Glu Met Ala Asp Ser Gly Ala Lys Asp Asn
 755 760 765
 Thr Leu Cys Ala Lys Trp Glu Met Pro Glu Glu Ser Lys Gly Val Gly
 770 775 780
 Leu Ala Asp Ala Pro Arg Gly Ala Leu Ser His Trp Ile Arg Ile Lys
 785 790 795 800
 Gly Lys Lys Ile Asp Asn Phe Gln Leu Val Val Pro Ser Thr Trp Asn
 805 810 815
 Leu Gly Pro Arg Gly Ala Gln Gly Asp Lys Ser Pro Val Glu Glu Ala
 820 825 830
 Leu Ile Gly Thr Pro Ile Ala Asp Pro Lys Arg Pro Val Glu Ile Leu
 835 840 845
 Arg Thr Val His Ala Phe Asp Pro Cys Ile Ala Cys Gly Val His Val
 850 855 860
 Ile Glu Pro Glu Thr Asn Glu Ile Leu Lys Phe Lys Val Cys Met Ser
 865 870 875 880
 Asp Thr Pro Arg Lys Ile Leu Ile Leu Gly Val Gly Asn Ile Leu Tyr
 885 890 895
 Thr Asp Glu Gly Val Gly Val Arg Ala Val Glu Arg Leu Leu Glu Thr
 900 905 910
 His Asp Phe Ser Asp Asn Val Thr Leu Met Asp Gly Gly Asn Leu Gly
 915 920 925
 Met Lys Leu Met Ala Pro Leu Met Glu Cys Asp Tyr Cys Ile Val Leu
 930 935 940
 Asp Ala Val Leu Gly Gly Asp Ala Pro Gly Thr Ile Tyr Arg Leu Thr
 945 950 955 960
 Gly Glu Asp Leu Arg Lys Ser Leu Ala Phe Lys Asp Ser Met His Gln
 965 970 975
 Ser Asp Leu Val Asp Thr Leu Ile Tyr Cys Glu Leu Ala Gly His Arg
 980 985 990
 Pro Asp Thr Val Val Ile Gly Met Glu Pro Leu Asp Phe Gln Asn Met

DESUanglais-seq1.txt

995 1000 1005

Ser Ile Glu Leu Ser Pro Ala Ile Ala Glu Arg Val Pro Ala Met
1010 1015 1020

Ile Asp Ile Ala Leu Ala Glu Leu Ala Ala Ala Gly Gly Val Ala
1025 1030 1035

Thr Pro Lys Gly Gln Ser
1040

<210> 61
<211> 3550
<212> DNA
<213> *Desulfovibrio fructosovorans*

<220>
<221> CDS
<222> (192)..(1133)
<223>

<220>
<221> CDS
<222> (1208)..(2899)
<223>

<220>
<221> CDS
<222> (2970)..(3467)
<223>

<400> 61
caaaactcgtg attaaactgca aaagggaaat cgaaccgggc gacgcaggaa cgcacgcgtc 60
cgtcacatag aggcggcggc ggccgggttcg cctgcgacgg ccgcgtgccc aacgggtcaa 120
cggatgctac gtggcctggg gatcatggga cgccccggac catgcctctc gtaaaacaaa 180

ggaggacggtt t atg aac ttt tcc gtg ggt ctt ggc agg gat gat gcg gaa 230
Met Asn Phe Ser Val Gly Leu Gly Arg Asp Asp Ala Glu
1 5 10

aaa cgg ctt gtg caa aac ggc gtc tcc cgc cgc gtc ttc atg aaa ttt 278
Lys Arg Leu Val Gln Asn Gly Val Ser Arg Arg Val Phe Met Lys Phe
15 20 25

tgc gcc acc gtg gcc gcg gcc atg ggc atg ggc ccc gcg ttc gcg ccc 326
Cys Ala Thr Val Ala Ala Met Gly Met Gly Pro Ala Phe Ala Pro
30 35 40 45

aag gtc gcc gaa gca ttg acg gcc aaa cac cgt ccg tcg gtg gtc tgg 374
Lys Val Ala Glu Ala Leu Thr Ala Lys His Arg Pro Ser Val Val Trp
50 55 60

ctg cac aac gcc gag tgc acc ggc tgc acc gaa gcg gcg atc cgg acg 422
Leu His Asn Ala Glu Cys Thr Gly Cys Thr Glu Ala Ala Ile Arg Thr
65 70 75

atc aaa cct tat ata gac gcg ctc att ctc gac acc atc tcc ctg gat 470
Ile Lys Pro Tyr Ile Asp Ala Leu Ile Leu Asp Thr Ile Ser Leu Asp
80 85 90

tac cag gag acc atc atg gcc gcg gcc ggc gag acg tcc gag gcg gcc 518
Tyr Gln Glu Thr Ile Met Ala Ala Ala Gly Glu Thr Ser Glu Ala Ala
95 100 105

ctg cac cag gcc ctc gaa ggc aag gac ggc tac tac ctc gtg gtc gag 566
Leu His Gln Ala Leu Glu Gly Lys Asp Gly Tyr Tyr Leu Val Val Glu
110 115 120 125

ggc gcc ctg ccc acc atc gac ggc ggc cag tgg ggc atg gtt gcc gcc 614
Gly Gly Leu Pro Thr Ile Asp Gly Gly Gln Trp Gly Met Val Ala Gly
130 135 140

cat ccc atg atc gag acc acc aag aag gcc gcg gcc aag gcc aag gcc 662
His Pro Met Ile Glu Thr Thr Lys Lys Ala Ala Lys Lys Lys Gly
145 150 155

atc atc tgc atc ggc acc tgc tcc gcc tac ggc ggc gtc cag aag gcc 710
Ile Ile Cys Ile Gly Thr Cys Ser Ala Tyr Gly Gly Val Gln Lys Ala
160 165 170

aaa ccc aat ccc agc cag gcc aag ggc gtg tcc gaa gcc ctc ggc gtc 758
Lys Pro Asn Pro Ser Gln Ala Lys Gly Val Ser Glu Ala Leu Gly Val
175 180 185

aag acc atc aac atc ccc ggc tgc ccg ccc aac ccc atc aac ttc gtg 806

DESUanglais-seq1.txt															
Lys 190	Thr	Ile	Asn	Ile	Pro 195	Gly	Cys	Pro	Pro	Asn 200	Pro	Ile	Asn	Phe	Val 205
ggc Gly	gcc Ala	gtg Val	gtc Val	cat His 210	gtc Val	ctg Leu	acc Thr	aag Lys	ggc Gly 215	atc Ile	ccg Pro	gat Asp	ctc Leu	gac Asp 220	gag Glu
aac Asn	ggc Gly	cgt Arg	ccg Pro 225	aag Lys	ctc Leu	ttc Phe	tac Tyr	ggc Gly 230	gag Glu	ctg Leu	gtc Val	cac His	gac Asp 235	aac Asn	tgt Cys
ccg Pro	cgc Arg	ctg Leu 240	ccc Pro	cac His	ttc Phe	gag Glu	gcc Ala 245	tcc Ser	gaa Glu	ttc Phe	gcg Ala	ccc Pro 250	tcc Ser	ttc Phe	gat Asp
tcc Ser	gaa Glu 255	gag Glu	gcc Ala	aag Lys	aaa Lys	ggc Gly 260	ttc Phe	tgc Cys	ctc Leu	tac Tyr	gaa Glu 265	ctc Leu	ggc Gly	tgc Cys	aag Lys
ggc Gly 270	ccc Pro	gtt Val	acc Thr	tac Tyr	aac Asn 275	aac Asn	tgc Cys	ccc Pro	aag Lys	gtg Val 280	ctg Leu	ttc Phe	aac Asn	cag Gln	gtc Val 285
aac Asn	tgg Trp	ccc Pro	gtc Val	cag Gln 290	gcc Ala	ggc Gly	cac His	ccc Pro	tgc Cys 295	ctc Leu	ggc Gly	tgc Cys	agc Ser	gag Glu 300	ccg Pro
gac Asp	ttc Phe	tgg Trp	gac Asp 305	acc Thr	atg Met	acg Thr	ccg Pro	ttc Phe 310	tac Tyr	gag Glu	cag Gln	ggc Gly	taacccccctc		
ctttgtagcg gccagtagcc ggacaccttc aacagcaccg aacgtctcgt gacggaggaa															
gcat Met 315	atg Met	gct Ala	gag Glu	agc Ser	aaa Lys	ccc Pro 320	acg Thr	cca Pro	caa Gln	tcc Ser	acc Thr 325	ttc Phe	acc Thr	ggc Gly	ccc Pro
atc Ile 330	gtg Val	gtc Val	gac Asp	ccc Pro	att Ile 335	acc Thr	cgg Arg	atc Ile	gaa Glu	ggt Gly 340	cac His	ttg Leu	cgg Arg	atc Ile	atg Met 345
gtc Val	gag Glu	gtg Val	gaa Glu	aac Asn 350	ggt Gly	aag Lys	gtc Val	aag Lys	gac Asp 355	gcc Ala	tgg Trp	agc Ser	tcc Ser	tgc Ser 360	cag Gln
ctc Leu	ttc Phe	cgc Arg	ggc Gly 365	ctg Leu	gaa Glu	atc Ile	atc Ile	ctc Leu 370	aaa Lys	ggc Gly	cgc Arg	gat Asp	ccc Pro 375	cgc Arg	gac Asp
gcc Ala	cag Gln 380	cac His	ttc Phe	acc Thr	cag Gln	cgc Arg	gcc Ala 385	tgc Cys	ggc Gly	gtg Val	tgc Cys	acg Thr 390	tac Tyr	gtc Val	cac His
gcc Ala	ctg Leu 395	gcc Ala	tcc Ser	agc Ser	cgc Arg	tgc Cys 400	gtc Val	gat Asp	gac Asp	gcc Ala	gtc Val 405	aag Lys	gtc Val	agc Ser	atc Ile
ccg Pro 410	gcc Ala	aac Asn	gcc Ala	cgc Arg	atg Met 415	atg Met	cgc Arg	aac Asn	ctg Leu	gtc Val 420	atg Met	gcc Ala	tcc Ser	cag Gln	tat Tyr 425
ctc Leu	cat His	gac Asp	cac His	ctc Leu 430	gtc Val	cac His	ttc Phe	tat Tyr	cac His 435	ctg Leu	cac His	gcc Ala	ctc Leu	gac Asp 440	tgg Trp
gtc Val	gac Asp	gtg Val	acc Thr 445	gcc Glu	gcc Ala	ctc Leu	aag Lys	gcc Ala 450	gat Asp	ccc Pro	aac Asn	aag Lys	gcc Ala 455	gcc Ala	aaa Lys
ctg Leu	gca Ala 460	gcc Ala	tcc Ser	atc Ile	gcc Ala	ccg Pro	gct Ala 465	cgg Arg	ccc Pro	ggc Gly	aac Asn	tgc Ser 470	gcc Ala	aag Lys	gcc Ala
ctc Leu	aag Lys 475	gcc Ala	gtc Val	cag Gln	gac Asp	aag Lys 480	ctg Leu	aaa Lys	gcc Ala	ttc Phe	gtc Val 485	gag Glu	tcc Ser	gga Gly	cag Gln
ctc Leu 490	ggc Gly	atc Ile	ttc Phe	acc Thr	aac Asn 495	gcc Ala	tac Tyr	ttc Phe	ctc Leu	ggc Gly 500	ggc Gly	cac His	aaa Lys	gcc Ala	tac Tyr 505
tac Tyr	ctg Leu	ccg Pro	ccc Pro	gag Glu 510	gtc Val	aac Asn	ctc Leu	atc Ile	gcc Ala 515	acc Thr	gcc Ala	cac His	tac Tyr	ctg Leu 520	gaa Glu

DESUanglais-seq1.txt

gcc	ctg	cac	atg	cag	gtc	aag	gcg	gcc	agc	gcc	atg	gcc	atc	ctc	ggc	1876
Ala	Leu	His	Met	Gln	Val	Lys	Ala	Ala	Ser	Ala	Met	Ala	Ile	Leu	Gly	
			525						530							
ggc	aag	aac	ccc	cac	acc	cag	ttc	acc	gtc	gtg	ggc	ggc	tgc	tcc	aac	1924
Gly	Lys	Asn	Pro	His	Thr	Gln	Phe	Thr	Val	Val	Gly	Gly	Cys	Ser	Asn	
		540					545					550				
tac	cag	ggc	ctg	acc	aag	gac	ccg	ctg	gcc	aac	tac	ctg	gcc	ctg	agc	1972
Tyr	Gln	Gly	Leu	Thr	Lys	Asp	Pro	Leu	Ala	Asn	Tyr	Leu	Ala	Leu	Ser	
		555				560					565					
aag	gaa	gtc	tgc	cag	ttc	gtc	aac	gag	tgc	tac	atc	cct	gac	ctg	ctg	2020
Lys	Glu	Val	Cys	Gln	Phe	Val	Asn	Glu	Cys	Tyr	Ile	Pro	Asp	Leu	Leu	
		570			575					580					585	
gcc	gtg	gcc	ggc	ttc	tac	aag	gac	tgg	ggc	ggc	atc	ggc	ggc	acc	agc	2068
Ala	Val	Ala	Gly	Phe	Tyr	Lys	Asp	Trp	Gly	Gly	Ile	Gly	Gly	Thr	Ser	
				590					595					600		
aac	tac	ctg	gcc	ttc	ggc	gag	ttc	gcc	acc	gac	gac	agc	tcc	ccc	gag	2116
Asn	Tyr	Leu	Ala	Phe	Gly	Glu	Phe	Ala	Thr	Asp	Asp	Ser	Ser	Pro	Glu	
			605					610					615			
aaa	cac	ctg	gcc	acc	tgc	cag	ttt	ccg	tcc	ggc	gtc	atc	acc	ggc	cgc	2164
Lys	His	Leu	Ala	Thr	Ser	Gln	Phe	Pro	Ser	Gly	Val	Ile	Thr	Gly	Arg	
			620				625					630				
gac	ctc	ggc	aag	gtg	gat	aac	gtg	gac	ctc	ggc	gcc	atc	tac	gaa	gac	2212
Asp	Leu	Gly	Lys	Val	Asp	Asn	Val	Asp	Leu	Gly	Ala	Ile	Tyr	Glu	Asp	
		635				640					645					
gtc	aag	tac	tcc	tgg	tac	gcc	ccc	ggc	ggc	gac	ggc	aag	cac	ccc	tac	2260
Val	Lys	Tyr	Ser	Trp	Tyr	Ala	Pro	Gly	Gly	Asp	Gly	Lys	His	Pro	Tyr	
					655					660					665	
gac	ggc	gtc	acc	gat	ccc	aag	tac	acc	aag	ctc	gac	gac	aag	gac	cac	2308
Asp	Gly	Val	Thr	Asp	Pro	Lys	Tyr	Thr	Lys	Leu	Asp	Asp	Lys	Asp	His	
				670				675						680		
tac	tcc	tgg	atg	aag	gcc	ccc	cgc	tac	aag	ggc	aag	gcc	atg	gaa	gtc	2356
Tyr	Ser	Trp	Met	Lys	Ala	Pro	Arg	Tyr	Lys	Gly	Lys	Ala	Met	Glu	Val	
			685					690					695			
ggt	ccc	ctg	gcc	cgc	acc	ttc	atc	gcc	tac	gcc	aag	ggg	cag	ccc	gac	2404
Gly	Pro	Leu	Ala	Arg	Thr	Phe	Ile	Ala	Tyr	Ala	Lys	Gly	Gln	Pro	Asp	
		700					705					710				
ttc	aaa	aag	gtc	gtg	gac	atg	gtc	ctc	ggc	aaa	ctc	tcc	gtc	ccg	gcc	2452
Phe	Lys	Lys	Val	Val	Asp	Met	Val	Leu	Gly	Lys	Leu	Ser	Val	Pro	Ala	
		715				720					725					
acg	gcc	ctg	cat	tgc	acc	ctc	gga	cgc	acc	gcc	gcc	cgc	ggc	atc	gag	2500
Thr	Ala	Leu	His	Ser	Thr	Leu	Gly	Arg	Thr	Ala	Ala	Arg	Gly	Ile	Glu	
					735					740					745	
acc	gcc	atc	gtc	tgc	gcc	aac	atg	gag	aag	tgg	atc	aag	gaa	atg	gcc	2548
Thr	Ala	Ile	Val	Cys	Ala	Asn	Met	Glu	Lys	Trp	Ile	Lys	Glu	Met	Ala	
				750				755						760		
gac	agc	ggc	gcc	aag	gac	aac	acc	ctg	tgc	gcc	aag	tgg	gag	atg	ccc	2596
Asp	Ser	Gly	Ala	Lys	Asp	Asn	Thr	Leu	Cys	Ala	Lys	Trp	Glu	Met	Pro	
			765					770					775			
gag	gag	tcc	aag	ggc	gtc	ggc	ctg	gcc	gat	gct	ccc	cgc	ggc	gcc	ctg	2644
Glu	Glu	Ser	Lys	Gly	Val	Gly	Leu	Ala	Asp	Ala	Pro	Arg	Gly	Ala	Leu	
		780				785						790				
tcc	cac	tgg	atc	cgc	atc	aag	ggc	aag	aag	atc	gac	aac	ttc	cag	ctg	2692
Ser	His	Trp	Ile	Arg	Ile	Lys	Gly	Lys	Lys	Ile	Asp	Asn	Phe	Gln	Leu	
		795				800					805					
gtt	gtc	ccc	tgc	acc	tgg	aac	ctc	ggt	ccc	cgg	ggc	gcc	cag	ggc	gac	2740
Val	Val	Pro	Ser	Thr	Trp	Asn	Leu	Gly	Pro	Arg	Gly	Ala	Gln	Gly	Asp	
					815					820					825	
aag	agc	ccg	gtg	gaa	gag	gcc	ctt	atc	ggc	acg	ccc	atc	gcc	gat	ccc	2788
Lys	Ser	Pro	Val	Glu	Glu	Ala	Leu	Ile	Gly	Thr	Pro	Ile	Ala	Asp	Pro	
				830					835					840		
aaa	cgc	ccg	gtc	gaa	atc	ctg	cgc	acg	gtc	cac	gcc	ttc	gac	ccc	tgc	2836
Lys	Arg	Pro	Val	Glu	Ile	Leu	Arg	Thr	Val	His	Ala	Phe	Asp	Pro	Cys	
			845					850					855			

DESUanglais-seql.txt

atc gcc tgc ggc gtg cac gtc atc gag ccc gag acc aac gag atc ctc 2884
 Ile Ala Cys Gly Val His Val Ile Glu Pro Glu Thr Asn Glu Ile Leu
 860 865 870
 aag ttc aag gtt tgc taagagcggc aacgccgctt atacgaagga cccggcttcg 2939
 Lys Phe Lys Val Cys 875
 gccgggttct tcgtttctca aggaggtcgc atg tcc gat acc ccg cgc aaa atc 2993
 Met Ser Asp Thr Pro Arg Lys Ile 880 885
 ctc atc ctc ggc gtc ggc aac atc ctc tac acc gac gag ggc gtc ggc 3041
 Leu Ile Leu Gly Val Gly Asn Ile Leu Tyr Thr Asp Glu Gly Val Gly 890 895 900
 gtg cgg gcc gtg gag cgc ctt ctc gaa acc cac gat ttt tcc gac aac 3089
 Val Arg Ala Val Glu Arg Leu Leu Glu Thr His Asp Phe Ser Asp Asn 905 910 915
 gtc acc ctc atg gac ggc ggc aac ctg ggc atg aag ctc atg gcc ccg 3137
 Val Thr Leu Met Asp Gly Gly Asn Leu Gly Met Lys Leu Met Ala Pro 920 925 930
 ctc atg gaa tgc gac tac tgc atc gtg ctc gac gcc gtg ctc ggc ggc 3185
 Leu Met Glu Cys Asp Tyr Cys Ile Val Leu Asp Ala Val Leu Gly Gly 935 940 945 950
 gac gcc ccc ggc acc atc tac cgt ctc acc ggc gag gac ctg cgc aaa 3233
 Asp Ala Pro Gly Thr Ile Tyr Arg Leu Thr Gly Glu Asp Leu Arg Lys 955 960 965
 tcc ctg gcc ttc aag gac tcc atg cac cag tcc gac ctc gtc gac acg 3281
 Ser Leu Ala Phe Lys Asp Ser Met His Gln Ser Asp Leu Val Asp Thr 970 975 980
 ctg atc tat tgc gaa ctg gcc gga cac cgc ccg gac acc gtg gtc atc 3329
 Leu Ile Tyr Cys Glu Leu Ala Gly His Arg Pro Asp Thr Val Val Ile 985 990 995
 ggc atg gag ccc ctc gat ttt cag aac atg agc atc gaa ctc tcg 3374
 Gly Met Glu Pro Leu Asp Phe Gln Asn Met Ser Ile Glu Leu Ser 1000 1005 1010
 ccc gcc atc gcc gaa cgc gtt ccg gcc atg atc gac atc gcc ctg 3419
 Pro Ala Ile Ala Glu Arg Val Pro Ala Met Ile Asp Ile Ala Leu 1015 1020 1025
 gcc gaa ctc gcc gcc gcc ggc ggc gtc gcc acg ccc aaa gga caa 3464
 Ala Glu Leu Ala Ala Ala Gly Gly Val Ala Thr Pro Lys Gly Gln 1030 1035 1040
 agt taggaagaaa ggaggtgcga gaggggaaac cctttaaaaa gggttctccc 3517
 Ser
 ctctcgcgcc tctccccttc ctaaatttta taa 3550
 <210> 62
 <211> 1044
 <212> PRT
 <213> Desulfovibrio fructosovorans
 <400> 62
 Met Asn Phe Ser Val Gly Leu Gly Arg Asp Asp Ala Glu Lys Arg Leu
 1 5 10 15
 Val Gln Asn Gly Val Ser Arg Arg Val Phe Met Lys Phe Cys Ala Thr
 20 25 30
 Val Ala Ala Ala Met Gly Met Gly Pro Ala Phe Ala Pro Lys Val Ala
 35 40 45
 Glu Ala Leu Thr Ala Lys His Arg Pro Ser Val Val Trp Leu His Asn
 50 55 60
 Ala Glu Cys Thr Gly Cys Thr Glu Ala Ala Ile Arg Thr Ile Lys Pro
 65 70 75 80
 Tyr Ile Asp Ala Leu Ile Leu Asp Thr Ile Ser Leu Asp Tyr Gln Glu
 85 90 95
 Thr Ile Met Ala Ala Ala Gly Glu Thr Ser Glu Ala Ala Leu His Gln
 100 105 110

DESUanglais-seq1.txt

Ala Leu Glu Gly Lys Asp Gly Tyr Tyr Leu Val Val Glu Gly Gly Leu
 115 120 125
 Pro Thr Ile Asp Gly Gly Gln Trp Gly Met Val Ala Gly His Pro Met
 130 135 140
 Ile Glu Thr Thr Lys Lys Ala Ala Ala Lys Ala Lys Gly Ile Ile Cys
 145 150 155 160
 Ile Gly Thr Cys Ser Ala Tyr Gly Gly Val Gln Lys Ala Lys Pro Asn
 165 170 175
 Pro Ser Gln Ala Lys Gly Val Ser Glu Ala Leu Gly Val Lys Thr Ile
 180 185 190
 Asn Ile Pro Gly Cys Pro Pro Asn Pro Ile Asn Phe Val Gly Ala Val
 195 200 205
 Val His Val Leu Thr Lys Gly Ile Pro Asp Leu Asp Glu Asn Gly Arg
 210 215 220
 Pro Lys Leu Phe Tyr Gly Glu Leu Val His Asp Asn Cys Pro Arg Leu
 225 230 235 240
 Pro His Phe Glu Ala Ser Glu Phe Ala Pro Ser Phe Asp Ser Glu Glu
 245 250 255
 Ala Lys Lys Gly Phe Cys Leu Tyr Glu Leu Gly Cys Lys Gly Pro Val
 260 265 270
 Thr Tyr Asn Asn Cys Pro Lys Val Leu Phe Asn Gln Val Asn Trp Pro
 275 280 285
 Val Gln Ala Gly His Pro Cys Leu Gly Cys Ser Glu Pro Asp Phe Trp
 290 295 300
 Asp Thr Met Thr Pro Phe Tyr Glu Gln Gly Met Ala Glu Ser Lys Pro
 305 310 315 320
 Thr Pro Gln Ser Thr Phe Thr Gly Pro Ile Val Val Asp Pro Ile Thr
 325 330 335
 Arg Ile Glu Gly His Leu Arg Ile Met Val Glu Val Glu Asn Gly Lys
 340 345 350
 Val Lys Asp Ala Trp Ser Ser Ser Gln Leu Phe Arg Gly Leu Glu Ile
 355 360 365
 Ile Leu Lys Gly Arg Asp Pro Arg Asp Ala Gln His Phe Thr Gln Arg
 370 375 380
 Ala Cys Gly Val Cys Thr Tyr Val His Ala Leu Ala Ser Ser Arg Cys
 385 390 395 400
 Val Asp Asp Ala Val Lys Val Ser Ile Pro Ala Asn Ala Arg Met Met
 405 410 415
 Arg Asn Leu Val Met Ala Ser Gln Tyr Leu His Asp His Leu Val His
 420 425 430
 Phe Tyr His Leu His Ala Leu Asp Trp Val Asp Val Thr Ala Ala Leu
 435 440 445
 Lys Ala Asp Pro Asn Lys Ala Ala Lys Leu Ala Ala Ser Ile Ala Pro
 450 455 460
 Ala Arg Pro Gly Asn Ser Ala Lys Ala Leu Lys Ala Val Gln Asp Lys
 465 470 475 480
 Leu Lys Ala Phe Val Glu Ser Gly Gln Leu Gly Ile Phe Thr Asn Ala
 485 490 495
 Tyr Phe Leu Gly Gly His Lys Ala Tyr Tyr Leu Pro Pro Glu Val Asn
 500 505 510
 Leu Ile Ala Thr Ala His Tyr Leu Glu Ala Leu His Met Gln Val Lys
 515 520 525
 Ala Ala Ser Ala Met Ala Ile Leu Gly Gly Lys Asn Pro His Thr Gln
 530 535 540
 Phe Thr Val Val Gly Gly Cys Ser Asn Tyr Gln Gly Leu Thr Lys Asp
 545 550 555 560
 Pro Leu Ala Asn Tyr Leu Ala Leu Ser Lys Glu Val Cys Gln Phe Val

Page 93

1010
1015
1020
1025
1030
1035
1040

DESUanglais-seq1.txt

Ile Asp Ile Ala Leu Ala Glu Leu Ala Ala Ala Gly Gly Val Ala
Thr Pro Lys Gly Gln Ser

INTERNATIONAL SEARCH REPORT

International application No

PCT/EP2006/050942

A. CLASSIFICATION OF SUBJECT MATTER

INV. C12P3/00 C12N9/02 C12N15/01 C22B3/18 C02F3/34

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

C12P C12N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, PAJ, WPI Data, BIOSIS

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	WO 02/16660 A (THE UNIVERSITY OF BIRMINGHAM; HARRIS, IVOR, REX; MACASKIE, LYNNE, ELAI) 28 February 2002 (2002-02-28) abstract page 1, paragraphs 3,4 page 2, paragraph 1 - page 5, paragraph 2 page 6, paragraph 2 - page 15, last paragraph; examples 1-7 ----- -/--	1-10,16, 17,19-25



Further documents are listed in the continuation of Box C.



See patent family annex.

* Special categories of cited documents :

A document defining the general state of the art which is not considered to be of particular relevance

E earlier document but published on or after the international filing date

L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

O document referring to an oral disclosure, use, exhibition or other means

P document published prior to the international filing date but later than the priority date claimed

T later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

X document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

Y document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

Z document member of the same patent family

Date of the actual completion of the international search

10 May 2006

Date of mailing of the international search report

22/05/2006

Name and mailing address of the ISA/

European Patent Office, P.B. 5818 Patentlaan 2
NL - 2280 HV Rijswijk
Tel. (+31-70) 340-2040, Tx. 31 651 epo nl,
Fax: (+31-70) 340-3016

Authorized officer

Mateo Rose11, A.M.

INTERNATIONAL SEARCH REPORT

International application No

PCT/EP2006/050942

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	VARGAS DE I ET AL: "BIOSORPTION OF PALLADIUM AND PLATINUM BY SULFATE-REDUCING BACTERIA" JOURNAL OF CHEMICAL TECHNOLOGY AND BIOTECHNOLOGY. (INTERNATIONAL JOURNAL OF BIOTECHNICAL AND CHEMICAL PROCESSES), ELSEVIER APPLIED SCIENCE PUBLISHERS. BARKING, GB, vol. 79, no. 1, January 2004 (2004-01), pages 49-56, XP001209093 ISSN: 0268-2575 cited in the application abstract page 49, right-hand column, paragraph 1 page 50, left-hand column, paragraph 1 page 52, left-hand column, paragraph 2 page 52, right-hand column, paragraph 3 page 53, right-hand column, last paragraph - page 54, right-hand column, paragraph 1 page 55, right-hand column, paragraph 2 -----	1-10,16, 17,19-25
Y	MALKI SOURIA ET AL: "Characterization of an Operon Encoding an NADP-Reducing Hydrogenase in Desulfovibrio fructosovorans" JOURNAL OF BACTERIOLOGY, vol. 177, no. 10, 1995, pages 2628-2636, XP002347800 ISSN: 0021-9193 abstract page 2632, right-hand column, paragraph 2 page 2634, left-hand column, paragraph 2 - page 2635, right-hand column, last paragraph; figure 8 -----	1-10,16, 17,19-25
Y	MALKI SOURIA ET AL: "Physiological characteristics and growth behavior of single and double hydrogenase mutants of Desulfovibrio fructosovorans" ARCHIVES OF MICROBIOLOGY, vol. 167, no. 1, 1997, pages 38-45, XP002347801 ISSN: 0302-8933 cited in the application abstract page 40, right-hand column, last paragraph - page 41, left-hand column, paragraph 1; figures 2A,B page 42, left-hand column, paragraphs 2,3 page 43, left-hand column, paragraph 2; figure 4 ----- -/--	1-10,16, 17,19-25

INTERNATIONAL SEARCH REPORT

International application No

PCT/EP2006/050942

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	CASALOT LAURENCE ET AL: "Evidence for a fourth hydrogenase in <i>Desulfovibrio fructosovorans</i>" JOURNAL OF BACTERIOLOGY, vol. 184, no. 3, February 2002 (2002-02), pages 853-856, XP002347804 ISSN: 0021-9193 cited in the application abstract page 853, left-hand column, paragraph 2 - page 854, left-hand column, paragraph 1 -----	1-10, 16, 17, 19-25
Y	DEMENTIN SEBASTIEN ET AL: "A glutamate is the essential proton transfer gate during the catalytic cycle of the (NiFe) hydrogenase." JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 279, no. 11, 12 March 2004 (2004-03-12), pages 10508-10513, XP002347802 ISSN: 0021-9258 abstract page 10509, left-hand column, paragraph 1 page 10512, left-hand column, paragraph 2 - right-hand column, paragraph 1 page 10512, right-hand column, last paragraph - page 10513, last paragraph -----	19
A	DE LUCA GILLES ET AL: "Reduction of technetium(VII) by <i>Desulfovibrio fructosovorans</i> is mediated by the nickel-iron hydrogenase" APPLIED AND ENVIRONMENTAL MICROBIOLOGY, vol. 67, no. 10, October 2001 (2001-10), pages 4583-4587, XP002347803 ISSN: 0099-2240 cited in the application the whole document -----	
A	YONG P ET AL: "A novel electrobiotechnology for the recovery of precious metals from spent automotive catalysts." ENVIRONMENTAL TECHNOLOGY, vol. 24, no. 3, March 2003 (2003-03), pages 289-297, XP008053502 ISSN: 0959-3330 cited in the application the whole document -----	

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No

PCT/EP2006/050942

Patent document cited in search report		Publication date		Patent family member(s)	Publication date
WO 0216660	A	28-02-2002	AU	8229301 A	04-03-2002