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(54) **Title:** YIELD INCREASE IN PLANTS OVEREXPRESSING THE ACCDP GENES

(57) **Abstract:** A transgenic crop plant transformed by a l-AminoCyclopropane-l-Carboxylate Deaminase- like Polypeptide (ACCDP) coding nucleic acid, wherein expression of the nucleic acid sequence in the crop plant results in the plant's increased root growth, and/or increased yield, and/or increased tolerance to environmental stress as compared to a wild type variety of the plant. Also provided are agricultural products, including seeds, produced by the transgenic crop plants. Also provided are isolated novel ACCDPs, and isolated novel nucleic acids encoding ACCDPs, and vectors and transgenic plant containing the same.

YIELD INCREASE IN PLANTS OVEREXPRESSING THE ACCDP GENES

CROSS REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the priority benefit of U.S. Provisional Application Serial No. 60/700,096 filed July 18, 2005, the entire content of which is hereby incorporated by reference.

BACKGROUND OF THE INVENTION

Field of the Invention

[0002] This invention relates generally to nucleic acid sequences encoding polypeptides that are associated with root development, which contribute to plant growth and, ultimately affect plant production (i.e. yield) under abiotic stress or non-stress conditions. In particular, this invention relates to isolated nucleic acid sequences encoding polypeptides that confer upon the plant increased root growth, increased yield, and/or increased drought, cold, and/or salt tolerance, and the use of such isolated nucleic acids.

Background Art

[0003] The yield of crop plants is central to the well being of humans and is directly affected by the growth of plants under physical environment. Abiotic environmental stresses, such as drought stress, salinity stress, heat stress, and cold stress, are major limiting factors of plant growth and productivity. Crop losses and crop yield losses of major crops such as soybean, rice, maize (corn), cotton, and wheat caused by these stresses represent a significant economic and political factor and contribute to food shortages in many underdeveloped countries.

[0004] Plant biomass is the total yield for forage crops like alfalfa, silage corn and hay. Many proxies for yield have been used in grain crops. Chief amongst these are estimates of plant size. Plant size can be measured in many ways depending on species and developmental stage, but include total plant dry weight, above-ground dry weight, above-ground fresh weight, leaf area, stem volume, plant height, rosette diameter, leaf length, root length, root mass, tiller number and leaf number. Many species maintain a conservative ratio between the size of different parts of the plant at a given developmental stage. These allometric relationships are used to extrapolate from one of these measures of size to another. Plant size at an early developmental stage will typically correlate with plant size later in development. A larger plant with a greater leaf area can typically absorb more light and carbon dioxide than a smaller plant and therefore will likely gain a greater weight during the same period. This is in addition to the potential continuation of the micro-environmental or genetic advantage that the plant had to achieve the larger size initially. There is a strong genetic component to plant size and growth rate, and so for a range of diverse genotypes plant size under one environmental condition is likely to correlate with size under another. In this way a standard environment is used as a proxy for the diverse and dynamic environments encountered at different locations and times by crops in the field.

[0005] Harvest index, the ratio of seed yield to above-ground dry weight, is relatively stable under many environmental conditions and so a robust correlation between plant size and grain yield can often be obtained. These processes are intrinsically linked because the majority of grain biomass is dependent on current or stored photosynthetic productivity by the leaves and stem of the plant. Therefore, selecting for plant size, even at early stages of development, has been used as an indicator for future potential. When testing for the impact of genetic differences on stress tolerance, the ability to standardize soil properties, temperature, water and nutrient availability and light intensity is an intrinsic advantage of greenhouse or plant growth chamber environments compared to the field. However, artificial limitations on yield due to poor pollination due to the absence of wind or insects, or insufficient space for mature root or canopy growth, can restrict the use of these controlled environments for testing yield differences. Therefore, measurements of plant size in early development, under standardized conditions in a growth chamber or greenhouse, are standard practices to provide indication of potential genetic yield advantages.

[0006] During the life cycle, plants are typically exposed to conditions of reduced environmental water content. Most plants have evolved strategies to protect themselves against these conditions of desiccation. However, if the severity and duration of the drought conditions are too great, the effects on development, growth, plant size, and yield of most crop plants are profound. Continuous exposure to drought conditions causes major alterations in the plant metabolism which ultimately lead to cell death and consequently yield losses.

[0007] Developing stress-tolerant plants is therefore a strategy that has the potential to solve or mediate at least some of these problems. However, traditional plant breeding strategies to develop new lines of plants that exhibit resistance and/or tolerance to these types of stresses are relatively slow and require specific resistant lines for crossing with the desired line. Limited germplasm resources for stress tolerance and incompatibility in crosses between distantly related plant species represent significant problems encountered in conventional breeding. Additionally, the cellular processes leading to drought, cold, and salt tolerance in model drought-, cold- and/or salt-tolerant plants are complex in nature and involve multiple mechanisms of cellular adaptation and numerous metabolic pathways. This multi-component nature of stress tolerance has not only made breeding for tolerance largely unsuccessful, but has also limited the ability to genetically engineer stress tolerant plants using biotechnological methods.

[0008] Therefore, what is needed is the identification of the genes and proteins involved in these multi-component processes leading to increased growth and/or increased stress tolerance. Elucidating the function of genes expressed in stress tolerant plants will not only advance our understanding of plant adaptation and tolerance to environmental stresses, but also may provide important information for designing new strategies for crop improvement.

[0009] Roots are an important organ of higher plants. Plant root systems are fundamental to the proper growth and development of all terrestrial plant species. In addition to uptake of water and

nutrients and providing physical support, roots mediate a complex but poorly understood exchange of communication between soil microbes and other plants. In agronomic systems, production is impacted by the availability of water and nutrients in the soil: root growth has a direct or indirect influence on growth and yield of aerial organs, particularly under conditions of nutrient limitation. Roots are also relevant for the production of secondary plant products, such as defense compounds and plant hormones. Establishment of proper root architecture is an important factor for the plant to effectively use the water and nutrients available in the environment and to maximize plant growth and production. In addition, under conditions of drought, roots can adapt to continue growth while at the same time producing and sending early warning signals to shoots which inhibit plant growth above ground.

[0010] Moreover, improved root growth of crop plants will also enhance competitiveness with weedy plants and will improve growth in arid areas, by increasing water accessibility and uptake. Improved root growth is also relevant for ecological purposes, such as bioremediation and prevention/arrest of soil erosion. Longer roots can alleviate not only the effects of water depletion from soil but also improve plant anchorage and standability thus reducing lodging. Also, longer roots have the ability to cover a larger volume of soil and improve nutrient uptake. Therefore, altering root biomass, and in particular increasing root length, will improve plant growth as well as increase crop yield.

[0011] Roots are also storage organs in a number of important staple crops, for example, in sugar beets, potato, manioc (cassava), yams and sweet potato (batate). Roots are also the relevant organ for consumption in a number of vegetables (e.g. carrots, radish), herbs (e.g. ginger, kukuma) and medicinal plants (e.g. ginseng). In addition, some of the secondary plant products found in roots are of economic importance for the chemical and pharmaceutical industry, for instance, the basic molecules for the synthesis of steroid hormones is found in yams, and the roots of *Lithospermum erythrorhizon* produce shikonin, which is widely used because of its anti-inflammatory, anti-tumor and wound-healing properties.

[0012] Root architecture is an area that has remained largely unexplored through classical breeding because of difficulties with assessing this trait in the field. Thus, biotechnology could have significant impact on the improvement of this trait.

[0013] The structure of root systems results from a combination of genetic predisposition and physical environment. Additionally, soil microbes can also have a beneficial effect on plant growth either by reducing the deleterious effects of other pathogenic microbes, by producing compounds promoting plant growth, or by increasing the uptake efficiency of nutrients from the environment. A microbe may use one or all of these mechanisms at different stages of the plant life cycle.

[0014] The plant hormone ethylene has been implicated in a wide spectrum of plant growth and development processes. In plants, 1-aminocyclopropane-1-carboxylate (ACC) is an essential

biosynthetic precursor of ethylene. Studies in the late 70's revealed that soil bacteria expressing an ACC deaminase can reduce the levels of ethylene in the plants thus leading to root elongation (Brown, 1974, Ann. Rev. Phytopathol. 12:181-197; Honma and Shimomura, 1978, Agric. Biol. Chem. 42:1825-1831). These results were supported by experiments where genes encoding ACC deaminase were mobilized into non-growth promoting bacteria which in turn, conferred a growth promoting effect (Shah et al., 1998, Can. J. Microbiol. 44:833-843). More recently, microbial genes encoding ACC deaminase were expressed directly in transgenic plants and shown to promote root elongation (Klee et al., 1991, Plant Cell 3(11):1187-93; Reed et al., 1996, J. Ag. Food Chem. 44(1):388-394).

[0015] Although some genes that are involved in stress responses in plants have been characterized, the characterization and cloning of plant genes that confer stress tolerance remains largely incomplete and fragmented. For example, certain studies have indicated that drought and salt stress in some plants may be due to additive gene effects, in contrast to other research that indicates specific genes are transcriptionally activated in vegetative tissue of plants under osmotic stress conditions. Although it is generally assumed that stress-induced proteins have a role in tolerance, direct evidence is still lacking, and the functions of many stress-responsive genes are unknown.

[0016] There is a need, therefore, to identify additional genes expressed in stress tolerant plants that have the capacity to confer increased root growth, and/or increased yield, and/or stress tolerance to its host plant and to other plant species. Newly generated stress tolerant plants will have many advantages, such as an increased range in which the crop plants can be cultivated by, for example, decreasing the water requirements of a plant species.

SUMMARY OF THE INVENTION

[0017] This invention relates to isolated nucleic acids which encode polypeptides capable of modulating root growth, and/or plant growth, and/or yield, and/or stress tolerance under normal or stress conditions as compared to a wild type variety of the plant. In particular, the invention concerns the use of the isolated nucleic acids encode 1-AminoCyclopropane-1-Carboxylate Deaminase-like Polypeptides (ACCDPs) that are important for modulating a plant's root growth, yield, and/or response to an environmental stress. More particularly, overexpression of these ACCDP coding nucleic acids in a crop plant results in increased root growth, and/or increased yield under normal or stress conditions, and/or increased tolerance to an environmental stress.

[0018] Therefore, in a first embodiment, the invention concerns a transgenic crop plant transformed with an isolated nucleic acid, wherein the nucleic acid comprises a polynucleotide selected from the group consisting of:

a) a polynucleotide having a sequence as set forth in any of SEQ ID NOS as provided in Column No. 3 of Table 1 and Table 2;

b) a polynucleotide encoding a polypeptide having a sequence as set forth in any of SEQ ID NOS as provided in Column No. 4 of Table 1 and Table 2;

c) a polynucleotide having at least 70% sequence identity to a polynucleotide having a sequence as set forth in any of SEQ ID NOS as provided in Column No. 3 of Table 1 and Table 2;

d) a polynucleotide encoding a polypeptide having at least 70% sequence identity to a polypeptide having a sequence as set forth in any of SEQ ID NOS as provided in Column No. 4 of Table 1 and Table 2; and

e) a polynucleotide that hybridizes under stringent conditions to the complement of any of the polynucleotides of a) through d) above.

[0019] Preferably, the transgenic crop plant expresses such isolated nucleic acid, so as preferably to alter the phenotype of the plants in relation to non-transformed, wild-type plants. In particular, the transgenic crop plants will exhibit modulated root growth (preferably, increased root growth), and/or plant growth, and/or yield, and/or stress tolerance under normal or stress conditions as compared to a wild type variety of the plant. Preferably, the ACCDP is from *Arabidopsis thaliana*, canola, soybean, rice, wheat, linseed, barley, sunflower or maize.

[0020] In another embodiment, the invention concerns transgenic crop plants which overexpress the ACCDP coding nucleic acid and demonstrate an increase in root growth, and more preferably, demonstrate an increase in root length under normal or stress condition as compared to a wild type variety of the plant. In one embodiment, the overexpression of the ACCDP coding nucleic acid in the plant demonstrates an increased tolerance to an environmental stress as compared to a wild-type variety of the plant. In yet another embodiment, the overexpression of the ACCDP coding nucleic acid in the plant demonstrates increased yield as compared to a wild-type variety of the plant. It is provided that the environmental stress can be salinity, drought, temperature, metal, chemical, pathogenic and oxidative stresses, or combinations thereof. Preferably, the environmental stress is drought stress.

[0021] In yet another embodiment, the invention concerns a seed produced by a transgenic crop plant transformed by an ACCDP coding nucleic acid, wherein the plant is true breeding for increased root growth, and/or increased yield, and/or increased tolerance to environmental stress as compared to a wild type variety of the plant.

[0022] In a further embodiment, the invention concerns a method of growing crop plants in an agricultural locus, wherein the method comprises obtaining the aforesaid transgenic crop plant and growing the plant in an agricultural locus.

[0023] In a still further aspect, the invention concerns product produced by or from the transgenic plants, their plant parts, or their seeds, such as a foodstuff, feedstuff, food supplement, feed supplement, cosmetic or pharmaceutical.

[0024] In another embodiment, the invention concerns a method of increasing root growth and/or yield, and/or increasing stress tolerance to an environmental stress of a crop plant under normal or stress condition as compared to a wild type variety of the plant, wherein the method comprises obtaining the aforesaid transgenic crop plant and growing the plant under a condition that the isolated nucleic acid is expressed.

[0025] In yet another embodiment, the invention concerns a method of producing the aforesaid transgenic crop plant, wherein the method comprises (a) transforming a plant cell with an expression vector comprising an ACCDP coding nucleic acid, and (b) generating from the plant cell the transgenic crop plant that expresses the encoded polypeptide. Preferably, the polynucleotide is operably linked to one or more regulatory sequences, and the expression of the polynucleotide in the plant results in increased root growth, and/or increased yield, and/or increased tolerance to environmental stress under normal or stress conditions as compared to a wild type variety of the plant. Preferably, the one or more regulatory sequences include a promoter. More preferably, the promoter is a tissue specific or developmental regulated promoter.

[0026] In a further embodiment, the invention concerns an isolated, novel ACCDP coding nucleic acid, wherein the nucleic acid comprising a polynucleotide selected from the group consisting of:

a) a polynucleotide having a sequence as set forth in any of SEQ ID NOS as provided in Column No. 3 of Table 2;

b) a polynucleotide encoding a polypeptide having a sequence as set forth in any of SEQ ID NOS as provided in Column No. 4 of Table 2;

c) a polynucleotide having at least 80% sequence identity to a polynucleotide having a sequence as set forth in any of SEQ ID NOS as provided in Column No. 3 of Table 2;

d) a polynucleotide encoding a polypeptide having at least 80% sequence identity to a polypeptide having a sequence as set forth in any of SEQ ID NOS as provided in Column No. 4 of Table 2;

e) a polynucleotide that hybridizes under stringent conditions to the complement of any of the polynucleotides of a) through d) above; and

f) a polynucleotide complementary to any of the polynucleotides of a) through d) above.

[0027] In another embodiment, the invention concerns a transgenic plant transformed with such isolated nucleic acids, and a seed produced by such transgenic plant. Preferably, the transgenic plant expresses such isolated nucleic acids, so as preferably to alter the phenotype of the plants in relation to non-transformed, wild-type plants. In particular, the transgenic plant will exhibit modified (preferably, increased) root growth, and/or plant growth, and/or yield, and/or stress tolerance under normal or stress conditions as compared to a wild type variety of the plant.

[0028] In still another embodiment, the invention concerns a recombinant expression vector comprising an isolated ACCDP coding nucleic acid, wherein the nucleic acid comprises a polynucleotide selected from the group consisting of:

a) a polynucleotide having a sequence as set forth in any of SEQ ID NOS as provided in Column No. 3 of Table 1 and Table 2;

b) a polynucleotide encoding a polypeptide having a sequence as set forth in any of SEQ ID NOS as provided in Column No. 4 of Table 1 and Table 2;

c) a polynucleotide having at least 80% sequence identity to a polynucleotide having a sequence as set forth in any of SEQ ID NOS as provided in Column No. 3 of Table 1 and Table 2;

d) a polynucleotide encoding a polypeptide having at least 80% sequence identity to a polypeptide having a sequence as set forth in any of SEQ ID NOS as provided in Column No. 4 of Table 1 and Table 2;

e) a polynucleotide that hybridizes under stringent conditions to the complement of any of the polynucleotides of a) through d) above; and

f) a polynucleotide complementary to any of the polynucleotides of a) through d) above.

[0029] Preferably, the polynucleotide is operably linked to one or more regulatory sequences. More preferably, the one or more regulatory sequences include a promoter. Further preferably, the promoter is a tissue specific or developmental regulated promoter.

[0030] In a further embodiment, the invention concerns a transgenic plant comprising such recombinant vector. Preferably, the expression of the ACCDP coding nucleic acid in the plant results in increased root growth, and/or increased yield, and/or increased tolerance to environmental stress as compared to a wild type variety of the plant.

[0031] In yet another embodiment, the invention concerns a method of identifying a novel ACCDP, comprising (a) raising a specific antibody response to an ACCDP, or fragment thereof, as described below; (b) screening putative ACCDP material with the antibody, wherein specific binding of the antibody to the material indicates the presence of a potentially novel ACCDP; and (c) identifying from the bound material a novel ACCDP in comparison to known ACCDP. Alternatively, hybridization with nucleic acid probes as described below can be used to identify novel ACCDP nucleic acids.

[0032] In a further embodiment, the invention also concerns methods of modifying the root growth, and/or yield, and/or stress tolerance of a plant comprising, modifying the expression of an ACCDP coding nucleic acid in the plant. Preferably, such modification results in increased or decreased root growth, and/or yield, and/or stress tolerance as compared to a wild type variety of the plant. Preferably, the root growth, and/or yield, and/or stress tolerance is increased in a plant via increasing expression of an ACCDP coding nucleic acid.

BRIEF DESCRIPTION OF THE DRAWINGS

[0033] Figure 1 shows the nucleotide sequence of the AtACCD gene (SEQ ID NO:1; At1g48420) used for Arabidopsis transformation, which is 1246 bp in length. The coding region of the gene is 1203 bp in length with the start codon (i.e. ATG) and the stop codon (i.e. TAG) underlined.

[0034] Figure 2 shows the predicted 401 amino acid sequence of the AtACCD (SEQ ID NO:2) gene used for *Arabidopsis* transformation.

[0035] Figure 3 shows a schematic of the binary vector T-DNA used to transform the AtACCD gene (SEQ ID NO:1). LB, left border; pAHAS, *Arabidopsis* AHAS promoter; 3'AHAS, AHAS termination signal; SP, Superpromoter; AtACCD, cDNA of AtACCD; 3'NOS, termination signal; RB, Right Border.

[0036] Figures 4A and 4B show a plate analysis of the *Arabidopsis* AtACCD (SEQ ID NO:1) transgenic plants. 4A demonstrates that all lines showed an increased root length phenotype. Lines 2, 3, 5, 6, and 9 showed a more significant root length increase compared to the wild type controls. 4B shows the gene level analysis of the AtACCD transgenic plants, confirming that AtACCD plants exhibited an increased root length phenotype. Based on this analysis, AtACCD transgenic plants exhibited a 13.8% increase in root length. In both 4A and 4B, the attached tables show the actual mean values used to generate the bar charts.

[0037] Figure 5 shows the in soil analysis of roots of the AtACCD (SEQ ID NO:1) plants, where the root length of AtACCD *Arabidopsis* lines was measured.

[0038] Figure 6 shows the gene level ANOVA analysis of the AtACCD (SEQ ID NO:1) transgenic plants. The analysis data of all transgenic lines was combined to determine the overall gene performance.

[0039] Figure 7 shows the gene level ANOVA analysis of rosette dry weights in the AtACCD (SEQ ID NO:1) transgenic plants.

[0040] Figure 8 shows the tblastn analysis results of AtACCD (SEQ ID NO:2) against the proprietary crop sequence database. The table shows the sequence identity percentage between the amino acid sequences of AtACCD (SEQ ID NO:2) and GmACCD-1 (SEQ ID NO:355), OsACCD (SEQ ID NO:353), ZmACCD-1 (SEQ ID NO:351), or TaACCD (SEQ ID NO:357).

[0041] Figure 9 shows the Blast alignment between the amino acid sequences of AtACCD (SEQ ID NO:2, "Query") and GmACCD (SEQ ID NO:355, "Sbjct").

[0042] Figure 10 shows the Blast alignment between the amino acid sequences of AtACCD (SEQ ID NO:2, "Query") and OsACCD (SEQ ID NO:353, "Sbjct").

[0043] Figure 11 shows the Blast alignment between the amino acid sequences of AtACCD (SEQ ID NO:2, "Query") and and ZmACCD (SEQ ID NO:351, "Sbjct").

[0044] Figure 12 shows the Blast alignment between the amino acid sequences of AtACCD (SEQ ID NO:2, "Query") and TaACCD (SEQ ID NO:357, "Sbjct").

DETAILED DESCRIPTION OF THE INVENTION

[0045] The present invention may be understood more readily by reference to the following detailed description of the preferred embodiments of the invention and the Examples included herein. However, before the present compounds, compositions, and methods are disclosed and described, it is to be understood that this invention is not limited to specific nucleic acids, specific polypeptides, specific cell types, specific host cells, specific conditions, or specific methods, etc., as such may, of course, vary, and the numerous modifications and variations therein will be apparent to those skilled in the art. It is also to be understood that the terminology used herein is for the purpose of describing specific embodiments only and is not intended to be limiting. In particular, the designation of the amino acid sequences as polypeptide "1-AminoCyclopropane-1-Carboxylate Deaminase-like Polypeptides" (ACCDPs), in no way limits the functionality of those sequences.

[0046] The present invention relates to ACCDPs and ACCDP coding nucleic acids that are important in increasing plant root growth, and/or yiled, and/or for modulating a plant's response to an environmental stress. More particularly, overexpression of these ACCDP coding nucleic acids in a crop plant results in modulation (increase or decrease, preferably increase) in root growth, and/or increased yield, and/or increased tolerance to an environmental stress. Representative members of the ACCDP genus are AtACCD, ZmACCD, OsACCD, GmACCD, and TaACCD. In a preferred embodiment, all members of the genus are biologically active enzymes that can convert ACC to α–ketobutyrate and ammonia.

[0047] Accordingly, the present invention encompasses a transgenic crop plant comprising ACCDP polynucleotide and polypeptide sequences and a method of producing such transgenic crop plant, wherein the expression of the ACCDP polypeptide in the plant results in increased root growth, and/or yield, and/or tolerance to an environmental stress. In one embodiment, the ACCDP sequences are from a plant, preferably an *Arabidopsis* plant, a canola plant, a soybean plant, a rice plant, a barley plant, a sunflower plant, a linseed plant, a wheat plant, or a maize plant. In another embodiment, the ACCDP sequences are the genes as summarized in Table 1 and Table 2. Preferably, the disclosed ACCDP sequences have significant percent identity to known ACCDP enzymes.

Table 1. ACCDP genes, their origin, nucleotide sequence and corresponding amino acid sequence, and their percentage of identity shared with AtACCD (SEQ ID NO:2) at the amino acid level (Needleman-Wunsch algorithm for global sequence alignment, J. Mol. Biol. 48(3):443-53; Matrix: Blosum 62; Gap opening penalty: 10.0; Gap extension penalty: 2.0).

Column No. 1	Column No. 2	Column No. 3	Column No. 4	Column No. 5
Gene Name	Organism	Nucleotide SEQ ID NO:	Amino acide SEQ ID NO:	Identity to AtACCD (%)
AtACCD	Arabidopsis thaliana	1	2	100
BPS_WIPO_PROT|SL00 0001.11101	Arabidopsis thaliana		3	70
BPS_WIPO_PROT|US20 040123343A1.159474	Oryza sativa	4	5	31
BPS_WIPO_PROT|US20 040214272A1.227458	Zea mays	6	7	35
BPS_WIPO_PROT|US20 040214272A1.227458	Zea mays	8	9	69
AP_002534	Escherichia coli	10	11	29
NP_142071	Pyrococcus horikoshii	12	13	30
NP_281783	Campylobacter jejuni	14	15	20
NP_288380	Escherichia coli	16	17	31
NP_420839	Caulobacter crescentus	18	19	30
NP_456516	Salmonella enterica	20	21	29
NP_460906	Salmonella typhimurium	22	23	30
NP_488487	Nostoc sp.	24	25	22
NP_577739	Pyrococcus furiosus	26	27	30
NP_669768	Yersinia pestis	28	29	28
NP_707806	Shigella flexneri 2a str.	30	31	30
NP_744159	Pseudomonas putida	32	33	20
NP_754225	Escherichia coli	34	35	29
NP_794910	Pseudomonas syringae	36	37	27
NP_822695	Streptomyces avermitilis	38	39	29
NP_824185	Streptomyces avermitilis	40	41	21
NP_832957	Bacillus cereus	42	43	30
NP_845541	Bacillus anthracis	44	45	30
NP_891079	Bordetella bronchiseptica	46	47	29
NP_917071	Oryza sativa	48	49	21
NP_979563	Bacillus cereus	50	51	29
XP_366736	Magnaporthe grisea	52	53	28
XP_382854	Gibberella zeae	54	55	24
XP_468034	Oryza sativa	56	57	68
XP_682168	Aspergillus nidulans	58	59	23
XP_748001	Aspergillus fumigatus	60	61	26
XP_749239	Aspergillus fumigatus	62	63	25
XP_782004	Strongylocentrotus purpuratus	64	65	37

Column No. 1	Column No. 2	Column No. 3	Column No. 4	Column No. 5
Gene Name	Organism	Nucleotide SEQ ID NO:	Amino acide SEQ ID NO:	Identity to AtACCD (%)
XP_783308	Strongylocentrotus purpuratus	66	67	38
XP_787534	Strongylocentrotus purpuratus	68	69	39
XP_797948	Strongylocentrotus purpuratus	70	71	38
XP_959200	Neurospora crassa	72	73	24
YP_011858	Desulfovibrio vulgaris	74	75	26
YP_037315	Bacillus thuringiensis	76	77	30
YP_045480	Acinetobacter sp.	78	79	23
YP_049633	Erwinia carotovora	80	81	31
YP_065241	Desulfotalea psychrophila	82	83	27
YP_065245	Desulfotalea psychrophila	84	85	28
YP_070243	Yersinia pseudotuberculosis	86	87	28
YP_084517	Bacillus cereus	88	89	30
YP_103707	Burkholderia mallei	90	91	27
YP_109214	Burkholderia pseudomallei	92	93	27
YP_150207	Salmonella enterica	94	95	30
YP_164989	Silicibacter pomeroyi	96	97	32
YP_167867	Silicibacter pomeroyi	98	99	33
YP_216944	Salmonella enterica	100	101	30
YP_233469	Pseudomonas syringae	102	103	27
YP_234762	Pseudomonas syringae	104	105	21
YP_234886	Pseudomonas syringae	106	107	24
YP_257395	Pseudomonas fluorescens	108	109	27
YP_264886	Psychrobacter arcticus	110	111	29
YP_271227	Colwellia psychrerythraea	112	113	23
YP_272646	Pseudomonas syringae	114	115	27
YP_273913	Pseudomonas syringae	116	117	22
YP_273996	Pseudomonas syringae	118	119	24
YP_297784	Ralstonia eutropha	120	121	26
YP_300428	Staphylococcus saprophyticus	122	123	32
YP_310154	Shigella sonnei	124	125	29
YP_321891	Anabaena variabilis	126	127	23
YP_335503	Burkholderia pseudomallei	128	129	24

Column No. 1	Column No. 2	Column No. 3	Column No. 4	Column No. 5
Gene Name	Organism	Nucleotide SEQ ID NO:	Amino acide SEQ ID NO:	Identity to AtACCD (%)
YP_341190	Pseudoalteromonas haloplanktis	130	131	24
YP_345978	Pseudomonas fluorescens	132	133	27
YP_366559	Burkholderia sp.	134	135	30
YP_373615	Burkholderia sp.	136	137	25
YP_389072	Desulfovibrio desulfuricans	138	139	28
YP_391222	Thiomicrospira crunogena	140	141	22
YP_402750	Shigella dysenteriae	142	143	30
YP_407560	Shigella boydii	144	145	31
YP_435720	Hahella chejuensis	146	147	22
YP_439298	Burkholderia thailandensis	148	149	24
YP_454591	Sodalis glossinidius	150	151	26
YP_464642	Anaeromyxobacter dehalogenans	152	153	32
YP_510818	Jannaschia sp.	154	155	26
YP_527135	Saccharophagus degradans	156	157	34
YP_527202	Saccharophagus degradans	158	159	23
YP_541124	Escherichia coli	160	161	29
YP_548994	Polaromonas sp.	162	163	26
YP_550624	Polaromonas sp.	164	165	25
YP_554094	Burkholderia xenovorans	166	167	24
YP_581089	Psychrobacter cryohalolentis	168	169	29
ZP_00105754	Nostoc punctiforme	170	171	22
ZP_00204949	Pseudomonas aeruginosa	172	173	21
ZP_00235416	Bacillus cereus	174	175	30
ZP_00241961	Rubrivivax gelatinosus	176	177	24
ZP_00308173	Cytophaga hutchinsonii	178	179	24
ZP_00378456	Brevibacterium linens	180	181	30
ZP_00378517	Brevibacterium linens	182	183	25
ZP_00422441	Burkholderia vietnamiensis	184	185	24
ZP_00452460	Burkholderia cenocepacia	186	187	24
ZP_00619434	Kineococcus radiotolerans	188	189	29
ZP_00655563	Nocardioides sp.	190	191	26
ZP_00655579	Nocardioides sp.	192	193	24
ZP_00666038	Syntrophobacter fumaroxidans	194	195	28

Column No. 1	Column No. 2	Column No. 3	Column No. 4	Column No. 5
Gene Name	Organism	Nucleotide SEQ ID NO:	Amino acide SEQ ID NO:	Identity to AtACCD (%)
ZP_00686013	Burkholderia ambifaria	196	197	24
ZP_00695539	Shigella boydii	198	199	29
ZP_00704208	Escherichia coli	200	201	30
ZP_00706049	Escherichia coli	202	203	29
ZP_00715158	Escherichia coli	204	205	29
ZP_00774185	Pseudoalteromonas atlantica	206	207	22
ZP_00774405	Pseudoalteromonas atlantica	208	209	32
ZP_00777501	Pseudoalteromonas atlantica	210	211	28
ZP_00791500	Yersinia pseudotuberculosis	212	213	28
ZP_00799744	Alkaliphilus metalliredigenes	214	215	35
ZP_00808738	Rhodopseudomonas palustris	216	217	30
ZP_00861350	Bradyrhizobium sp.	218	219	24
ZP_00923697	Escherichia coli	220	221	29
ZP_00944339	Ralstonia solanacearum	222	223	24
ZP_00959540	Roseovarius nubinhibens	224	225	25
ZP_00961132	Roseovarius nubinhibens	226	227	30
ZP_00968640	Pseudomonas aeruginosa	228	229	21
ZP_00974363	Pseudomonas aeruginosa	230	231	21
ZP_00976764	Burkholderia cenocepacia	232	233	22
ZP_00978652	Burkholderia cenocepacia	234	235	25
ZP_00983649	Burkholderia dolosa	236	237	25
ZP_01019104	Polaromonas naphthalenivorans	238	239	26
ZP_01027677	Burkholderia mallei	240	241	27
ZP_01035983	Roseovarius sp.	242	243	29
ZP_01037089	Roseovarius sp.	244	245	32
ZP_01050656	Cellulophaga sp.	246	247	24
ZP_01053873	Tenacibaculum sp	248	249	25
ZP_01060636	Flavobacterium sp.	250	251	24
ZP_01070075	Campylobacter jejuni	252	253	20
ZP_01074915	Marinomonas sp.	254	255	20
ZP_01102706	gamma proteobacterium	256	257	30
ZP_01104195	gamma proteobacterium	258	259	26
ZP_01107544	Flavobacteriales bacterium	260	261	25

Column No. 1	Column No. 2	Column No. 3	Column No. 4	Column No. 5
Gene Name	Organism	Nucleotide SEQ ID NO:	Amino acide SEQ ID NO:	Identity to AtACCD (%)
ZP_01110185	Alteromonas macleodii	262	263	21
ZP_01116950	Polaribacter irgensii	264	265	24
ZP_01120549	Robiginitalea biformata	266	267	23
ZP_01129787	marine actinobacterium	268	269	24
ZP_01150242	Desulfotomaculum reducens	270	271	28
ZP_01150249	Desulfotomaculum reducens	272	273	29
ZP_01168090	Oceanospirillum sp.	274	275	21
ZP_01184367	Bacillus weihenstephanensis	276	277	31
ZP_01196859	Xanthobacter autotrophicus	278	279	26
ZP_01200770	Xanthobacter autotrophicus	280	281	27
ZP_01201978	Flavobacteria bacterium	282	283	24
ZP_01223813	marine gamma	284	285	34
ZP_01246005	Flavobacterium johnsoniae	286	287	24
ZP_01252717	Psychroflexus torquis	288	289	24
ZP_01296455	Pseudomonas aeruginosa	290	291	21
Q1WLF4_RHIME	Rhizobium meliloti	292	293	24
Q2U8N3_ASPOR	Aspergillus oryzae	294	295	27
Q2UA44_ASPOR	Aspergillus oryzae	296	297	25
Q872C9_NEUCR	Neurospora crassa	298	299	26
Q8KJA8_RHILO	Rhizobium loti	300	301	24
Q8W4C7_ARATH	Arabidopsis thaliana	302	303	95
Q9P964_PENCI	Penicillium citrinum	304	305	25
Q9SX74_ARATH	Arabidopsis thaliana	306	307	96
1A1D_BRAJA	Bradyrhizobium japonicum	308	309	24
1A1D_BURMA	Burkholderia mallei	310	311	24
1A1D_CRYNE	Cryptococcus neoformans	312	313	25
1A1D_ENTCL	Enterobacter cloacae	314	315	23
1A1D_PSEFL	Pseudomonas fluorescens	316	317	25
1A1D_PSEPU	Pseudomonas putida	318	319	24
1A1D_PSES0	Pseudomonas sp Pseudomonas	320	321	24
1A1D_PSESM	Pseudomonas syringae	322	323	24
1A1D_PSEUD	Pseudomonas sp	324	325	24
1A1D_PYRAB	Pyrococcus abyssi	326	327	30
1A1D_RALSO	Ralstonia solanacearum	328	329	24

Column No. 1	Column No. 2	Column No. 3	Column No. 4	Column No. 5
Gene Name	Organism	Nucleotide SEQ ID NO:	Amino acide SEQ ID NO:	Identity to AtACCD (%)
1A1D_RHILO	Rhizobium loti	330	331	23
1A1D_RHILV	Rhizobium leguminosarum	332	333	24
1A1D_SCHPO	Schizosaccharomyces pombe	334	335	27
1A1D_THEMA	Thermotoga maritima	336	337	32
1A1D_VARPD	Variovorax paradoxus	338	339	23
DCYD_YERPE	Yersinia pestis	340	341	28

Table 2. Novel ACCDP genes, their origin, nucleotide sequence and corresponding amino acid sequence, and their percentage of identity shared with AtACCD (SEQ ID NO:2) at the amino acid level (Needleman-Wunsch algorithm for global sequence alignment, J. Mol. Biol. 48(3):443-53; Matrix: Blosum 62; Gap opening penalty: 10.0; Gap extension penalty: 2.0).

Column No. 1	Column No. 2	Column No. 3	Column No. 4	Column No. 5
Gene Name	Organism	Nucleotide SEQ ID NO:	Amino acide SEQ ID NO:	Identity to AtACCD (%)
GmACCD-2 (48982441__singleclone)	Glycine max	342	343	72
BnACCD (49287365__singleclone)	Brassica napus	344	345	86
ZmACCD-2 (62053108__singleclone)	Zea mays	346	347	68
ZmACCD-3 (62053108__singlecloneDLM)	Zea mays	348	349	57
ZmACCD-1	Zea mays	350	351	69
OsACCD	rice	352	353	69
GmACCD-1	Glycine max	354	355	74
TaACCD	wheat	356	357	67

[0048] The present invention further encompasses novel ACCDP polynucleotide and polypeptide sequences and their use for increasing a plant's root growth, and/or yield, and/or tolerance to an environmental stress. In this embodiment, the ACCDP sequences are from canola, soybean, rice, wheat or maize, or homologous thereto. Preferably in this embodiment, the ACCDP polynucleotide and polypeptide sequences are those from canola, soybean, rice, wheat or maize as set forth in any of SEQ ID NOS as provided in Column Nos. 3 and 4 of Table 2.

[0049] The present invention provides a transgenic plant transformed by an ACCDP coding nucleic acid, wherein expression of the nucleic acid sequence in the plant results in increased root growth, and/or increased yield, and/or increased tolerance to an environmental stress as compared to a wild type variety of the plant. In particular, the increased root growth is an increase in the length of the roots. The term "plant" as used herein can, depending on context, be understood to refer to whole plants, plant cells, and plant parts including seeds. The word "plant" also refers to any plant, particularly, to seed plant, and may include, but not limited to, crop plants. Plant parts include, but

are not limited to, stems, roots, ovules, stamens, leaves, embryos, meristematic regions, callus tissue, gametophytes, sporophytes, pollen, microspores, and the like. In one embodiment, the transgenic plant is male sterile. Also provided is a plant seed produced by a transgenic plant transformed by an ACCDP coding nucleic acid, wherein the seed contains the ACCDP coding nucleic acid, and wherein the plant is true breeding for increased root growth, and/or increased yield, and/or increased tolerance to environmental stress as compared to a wild type variety of the plant. The invention further provides a seed produced by a transgenic plant expressing an ACCDP, wherein the seed contains the ACCDP, and wherein the plant is true breeding for increased root growth, and/or increased yield, and/or increased tolerance to environmental stress as compared to a wild type variety of the plant. The invention also provides a product produced by or from the transgenic plants expressing the ACCDP coding nucleic acid, their plant parts, or their seeds. The product can be obtained using various methods well known in the art. As used herein, the word "product" includes, but not limited to, a foodstuff, feedstuff, a food supplement, feed supplement, cosmetic or pharmaceutical. Foodstuffs are regarded as compositions used for nutrition. These also include compositions for supplementing nutrition. Animal feedstuffs and animal feed supplements, in particular, are regarded as foodstuffs. The invention further provides an agricultural product produced by any of the transgenic plants, plant parts, and plant seeds. Agricultural products include, but are not limited to, plant extracts, proteins, amino acids, carbohydrates, fats, oils, polymers, vitamins, and the like.

[0050] As used herein, the term "variety" refers to a group of plants within a species that share constant characters that separate them from the typical form and from other possible varieties within that species. While possessing at least one distinctive trait, a variety is also characterized by some variation between individuals within the variety, based primarily on the Mendelian segregation of traits among the progeny of succeeding generations. A variety is considered "true breeding" for a particular trait if it is genetically homozygous for that trait to the extent that, when the true-breeding variety is self-pollinated, a significant amount of independent segregation of the trait among the progeny is not observed. In the present invention, the trait arises from the transgenic expression of one or more DNA sequences introduced into a plant variety.

[0051] The crop plants according to the invention will be understood to include dicotyledonous crop plants such as, for example, from the families of the Leguminosae such as pea, alfalfa and soybean; the family of the Umbelliferae, particularly the genus Daucus (very particularly the species carota (carrot)) and Apium (very particularly the species graveolens var. dulce (celery)) and many others; the family of the Solanaceae, particularly the genus Lycopersicon, very particularly the species esculentum (tomato) and the genus Solanum, very particularly the species tuberosum (potato) and melongena (aubergine), tobacco and many others; and the genus Capsicum, very particularly the species annum (pepper) and many others; the family of the Leguminosae, particularly the genus Glycine, very particularly the species max (soybean) and many others; and the family of the Cruciferae, particularly the genus Brassica, very particularly the species napus (oilseed rape),

campestris (beet), oleracea cv Tastie (cabbage), oleracea cv Snowball Y (cauliflower) and oleracea cv Emperor (broccoli); and the genus Arabidopsis, very particularly the species thaliana and many others; the family of the Compositae, particularly the genus Lactuca, very particularly the species sativa (lettuce) and many others; and the family of the Malvaceae, particularly the genus Gossypium, very particularly the species known as cotton; and the family of the Fabaceae, particularly the genus Arachis, very particularly the species hypogaea (peanut).

[0052] The crop plants according to the invention also include monocotyledonous crop plants, such as, for example, cereals such as wheat, barley, sorghum and millet, rye, triticale, maize, rice or oats, and sugarcane. Further preferred are trees such as apple, pear, quince, plum, cherry, peach, nectarine, apricot, papaya, mango, and other woody species including coniferous and deciduous trees such as poplar, pine, sequoia, cedar, oak, etc. Especially preferred are Arabidopsis thaliana, Nicotiana tabacum, oilseed rape, soybean, corn (maize), wheat, linseed, potato and tagetes.

[0053] The present invention describes for the first time that the ACCDP is useful for increasing a crop plant's root growth, and/or yield, and/or tolerance to environmental stress. As used herein, the term polypeptide refers to a chain of at least four amino acids joined by peptide bonds. The chain may be linear, branched, circular, or combinations thereof. Accordingly, the present invention provides for use in crop plants of isolated ACCDPs selected from any of the organisms as provided in Column No. 2 of Table 1 and Table 2, and homologs thereof. In preferred embodiments, the ACCDP is selected from: 1) any of ACCDP polypeptides as provided in Column No. 4 of Table 1 and Table 2; and 2) homologs and orthologs thereof. Homologs and orthologs of the amino acid sequences are defined below.

[0054] The ACCDPs of the present invention are preferably produced by recombinant DNA techniques. For example, a nucleic acid molecule encoding the polypeptide is cloned into an expression vector (as described below), the expression vector is introduced into a host cell (as described below) and the ACCDP is expressed in the host cell. The ACCDP can then be isolated from the cells by an appropriate purification scheme using standard polypeptide purification techniques. For the purposes of the invention, the term "recombinant polynucleotide" refers to a polynucleotide that has been altered, rearranged, or modified by genetic engineering. Examples include any cloned polynucleotide, and polynucleotides that are linked or joined to heterologous sequences. The term "recombinant" does not refer to alterations to polynucleotides that result from naturally occurring events, such as spontaneous mutations. Alternative to recombinant expression, an ACCDP, or peptide thereof, can be synthesized chemically using standard peptide synthesis techniques. Moreover, native ACCDP can be isolated from cells (e.g., *Arabidopsis thaliana* cells), for example using an anti-ACCDP antibody, which can be produced by standard techniques utilizing an ACCDP or fragment thereof.

[0055] As used herein, the term "environmental stress" refers to sub-optimal conditions associated with salinity, drought, temperature, metal, chemical, pathogenic and oxidative stresses, or

combinations thereof. In preferred embodiments, the environmental stress can be selected from one or more of the group consisting of salinity, drought, or temperature, or combinations thereof, and in particular, can be selected from one or more of the group consisting of high salinity, low water content (drought), or low temperature. In a more preferred embodiment, the environmental stress is drought stress. As also used herein, the term "water use efficiency" refers to the amount of organic matter produced by a plant divided by the amount of water used by the plant in producing it, i.e. the dry weight of a plant in relation to the plant's water use. As used herein, the term "dry weight" refers to everything in the plant other than water, and includes, for example, carbohydrates, proteins, oils, and mineral nutrients. It is also to be understood that as used in the specification and in the claims, "a" or "an" can mean one or more, depending upon the context in which it is used. Thus, for example, reference to "a cell" can mean that at least one cell can be utilized.

[0056] As also used herein, the term "nucleic acid" and "polynucleotide" refer to RNA or DNA that is linear or branched, single or double stranded, or a hybrid thereof. The term also encompasses RNA/DNA hybrids. These terms also encompass untranslated sequence located at both the 3' and 5' ends of the coding region of the gene: at least about 1000 nucleotides of sequence upstream from the 5' end of the coding region and at least about 200 nucleotides of sequence downstream from the 3' end of the coding region of the gene. Less common bases, such as inosine, 5-methylcytosine, 6-methyladenine, hypoxanthine, and others can also be used for antisense, dsRNA, and ribozyme pairing. For example, polynucleotides that contain C-5 propyne analogues of uridine and cytidine have been shown to bind RNA with high affinity and to be potent antisense inhibitors of gene expression. Other modifications, such as modification to the phosphodiester backbone, or the 2'-hydroxy in the ribose sugar group of the RNA can also be made. The antisense polynucleotides and ribozymes can consist entirely of ribonucleotides, or can contain mixed ribonucleotides and deoxyribonucleotides. The polynucleotides of the invention may be produced by any means, including genomic preparations, cDNA preparations, *in vitro* synthesis, RT-PCR, and *in vitro* or *in vivo* transcription.

[0057] An "isolated" nucleic acid molecule is one that is substantially separated from other nucleic acid molecules, which are present in the natural source of the nucleic acid (i.e., sequences encoding other polypeptides). Preferably, an "isolated" nucleic acid is free of some of the sequences, which naturally flank the nucleic acid (i.e. sequences located at the 5' and 3' ends of the nucleic acid) in its naturally occurring replicon. For example, a cloned nucleic acid is considered isolated. In various embodiments, the isolated ACCDP coding nucleic acid molecule can contain less than about 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb, or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived (e.g., an *Arabidopsis thaliana* cell). A nucleic acid is also considered isolated if it has been altered by human intervention, or placed in a locus or location that is not its natural site, or if it is introduced into a cell by agroinfection. Moreover, an "isolated" nucleic acid molecule, such as a cDNA molecule, can be

free from some of the other cellular material with which it is naturally associated, or culture medium when produced by recombinant techniques, or chemical precursors or other chemicals when chemically synthesized.

[0058] Specifically excluded from the definition of "isolated nucleic acids" are: naturally-occurring chromosomes (such as chromosome spreads), artificial chromosome libraries, genomic libraries, and cDNA libraries that exist either as an *in vitro* nucleic acid preparation or as a transfected/transformed host cell preparation, wherein the host cells are either an *in vitro* heterogeneous preparation or plated as a heterogeneous population of single colonies. Also specifically excluded are the above libraries wherein a specified nucleic acid makes up less than 5% of the number of nucleic acid inserts in the vector molecules. Further specifically excluded are whole cell genomic DNA or whole cell RNA preparations (including whole cell preparations that are mechanically sheared or enzymatically digested). Even further specifically excluded are the whole cell preparations found as either an *in vitro* preparation or as a heterogeneous mixture separated by electrophoresis wherein the nucleic acid of the invention has not further been separated from the heterologous nucleic acids in the electrophoresis medium (e.g., further separating by excising a single band from a heterogeneous band population in an agarose gel or nylon blot).

[0059] A nucleic acid molecule according to the present invention, e.g., a nucleic acid molecule having a nucleotide sequence as set forth in any of SEQ ID NOS as provided in Column No. 3 of Table 1 and Table 2, or a portion thereof, can be isolated using standard molecular biology techniques and the sequence information provided herein. For example, an ACCDP cDNA can be isolated from any crop library using all or a portion of any of SEQ ID NOS as provided in Column No. 3 of Table 1 and Table 2. Moreover, a nucleic acid molecule encompassing all or a portion of any of SEQ ID NOS as provided in Column No. 3 of Table 1 and Table 2 can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this sequence. For example, mRNA can be isolated from plant cells (e.g., by the guanidinium-thiocyanate extraction procedure of Chirgwin et al., 1979, Biochemistry 18:5294-5299), and cDNA can be prepared using reverse transcriptase (e.g., Moloney MLV reverse transcriptase, available from Gibco/BRL, Bethesda, MD; or AMV reverse transcriptase, available from Seikagaku America, Inc., St. Petersburg, FL). Synthetic oligonucleotide primers for polymerase chain reaction amplification can be designed based upon the nucleotide sequence as set forth in any of sequences shown in Column No. 3 of Table 1 and Table 2. A nucleic acid molecule of the invention can be amplified using cDNA or, alternatively, genomic DNA, as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid molecule so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to an ACCDP nucleotide sequence can be prepared by standard synthetic techniques, e.g., using an automated DNA synthesizer.

[0060] In a preferred embodiment, an isolated nucleic acid molecule according to the invention comprises the nucleotide sequences as set forth in any of sequences shown in Column No. 3 of Table 1 and Table 2. These cDNAs may comprise sequences encoding the ACCDPs, (i.e., the "coding region"), as well as 5' untranslated sequences and 3' untranslated sequences. Alternatively, the nucleic acid molecules according to the present invention can comprise only the coding region of any of the sequences as provided in Column No. 3 of Table 1 and Table 2, or can contain whole genomic fragments isolated from genomic DNA. The present invention also includes ACCDP coding nucleic acids that encode ACCDPs as described herein. Preferred is an ACCDP coding nucleic acid that encodes ACCDP as shown in any of SEQ ID NOS as provided in Column No. 4 of Table 1 and Table 2.

[0061] Moreover, the nucleic acid molecule according to the invention can comprise a portion of the coding region of any of the sequences as provided in Column No. 3 of Table 1 and Table 2, for example, a fragment that can be used as a probe or primer or a fragment encoding a biologically active portion of an ACCDP. The nucleotide sequences determined from the cloning of the ACCDP gene from any of the organisms as provided in Table 1 and Table 2 allows for the generation of probes and primers designed for use in identifying and/or cloning ACCDP homologs in other cell types and organisms, as well as ACCDP homologs from crop plants and related species. The portion of the coding region can also encode a biologically active fragment of an ACCDP.

[0062]. As used herein, the term "biologically active portion of" an ACCDP is intended to include a portion, e.g., a domain/motif, of an ACCDP that participates in modulation of root growth, and/or yield, and/or stress tolerance in a plant, and more preferably, drought tolerance. For the purposes of the present invention, modulation of root growth, and/or yield, and/or stress tolerance refers to at least a 10% increase or decrease in the growth of the roots, and/or yield, and/or stress tolerance of a transgenic plant comprising an ACCDP expression cassette (or expression vector) as compared to the root growth, and/or yield, and/or stress tolerance of a non-transgenic control plant. Methods for quantitating growth, and/or yield, and/or stress tolerance are provided at least in Examples 5, 6, and 17-19 below. In a preferred embodiment, the biologically active portion of an ACCDP increases a plant's root growth, preferably by increasing the root length.

[0063] Biologically active portions of an ACCDP include peptides comprising amino acid sequences derived from the amino acid sequence of an ACCDP, e.g., an amino acid sequence of any of SEQ ID NOS as provided in Column No. 4 of Table 1 and Table 2, or the amino acid sequence of a polypeptide identical to an ACCDP, which includes fewer amino acids than a full length ACCDP or the full length polypeptide which is identical to an ACCDP, and exhibits at least one activity of an ACCDP. Typically, biologically active portions (e.g., peptides which are, for example, 5, 10, 15, 20, 30, 35, 36, 37, 38, 39, 40, 50, 100, or more amino acids in length) comprise a domain or motif with at least one activity of an ACCDP. Moreover, other biologically active portions in which other regions of the polypeptide are deleted, can be prepared by recombinant techniques and evaluated for one or

more of the activities described herein. Preferably, the biologically active portion of an ACCDP includes one or more selected domains/motifs or portions thereof having function to convert ACC to α-ketobutyrate and ammonia.

[0064] The invention also provides ACCDP chimeric or fusion polypeptides. As used herein, an ACCDP "chimeric polypeptide" or "fusion polypeptide" comprises an ACCDP operatively linked to a non-ACCDP. An ACCDP refers to a polypeptide having an amino acid sequence corresponding to an ACCDP, whereas a non-ACCDP refers to a polypeptide having an amino acid sequence corresponding to a polypeptide which is not substantially identical to the ACCDP, e.g., a polypeptide that is different from the ACCDP and is derived from the same or a different organism. With respect to the fusion polypeptide, the term "operatively linked" is intended to indicate that the ACCDP and the non-ACCDP are fused to each other so that both sequences fulfill the proposed function attributed to the sequence used. The non-ACCDP can be fused to the N-terminus or C-terminus of the ACCDP. For example, in one embodiment, the fusion polypeptide is a GST-ACCDP fusion polypeptide in which the ACCDP sequences are fused to the C-terminus of the GST sequences. Such fusion polypeptides can facilitate the purification of recombinant ACCDPs. In another embodiment, the fusion polypeptide is an ACCDP containing a heterologous signal sequence at its N-terminus. In certain host cells (e.g., mammalian host cells), expression and/or secretion of an ACCDP can be increased through use of a heterologous signal sequence.

[0065] Preferably, an ACCDP chimeric or fusion polypeptide of the invention is produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, for example by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and re-amplified to generate a chimeric gene sequence (See, for example, Current Protocols in Molecular Biology, Eds. Ausubel et al. John Wiley & Sons: 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (e.g., a GST polypeptide). An ACCDP encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the ACCDP.

[0066] In addition to fragments and fusion polypeptides of the ACCDPs described herein, the present invention includes homologs and analogs of naturally occurring ACCDPs and ACCDP encoding nucleic acids in a plant. "Homologs" are defined herein as two nucleic acids or polypeptides that have similar, or "identical," nucleotide or amino acid sequences, respectively. Homologs include allelic variants, orthologs, paralogs, agonists, and antagonists of ACCDPs as

defined hereafter. The term "homolog" further encompasses nucleic acid molecules that differ from the nucleotide sequence as set forth in any of SEQ ID NOS as provided in Column No. 3 of Table 1 and Table 2 (and portions thereof) due to degeneracy of the genetic code and thus encode the same ACCDP as that encoded by the corresponding nucleotide sequence as set forth in such a SEQ ID NO as provided in Column No. 3 of Table 1 and Table 2. As used herein, a "naturally occurring" ACCDP refers to an ACCDP amino acid sequence that occurs in nature. Preferably, a naturally occurring ACCDP comprises an amino acid sequence of any of SEQ ID NOS as provided in Column No. 4 of Table 1 and Table 2.

[0067] An agonist of the ACCDP can retain substantially the same, or a subset, of the biological activities of the ACCDP. An antagonist of the ACCDP can inhibit one or more of the activities of the naturally occurring form of the ACCDP.

[0068] Nucleic acid molecules corresponding to natural allelic variants and analogs, orthologs, and paralogs of an ACCDP cDNA can be isolated based on their identity to the ACCDP nucleic acids described herein using ACCDP cDNAs, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions. In an alternative embodiment, homologs of the ACCDP can be identified by screening combinatorial libraries of mutants, e.g., truncation mutants, of the ACCDP for ACCDP agonist or antagonist activity. In one embodiment, a variegated library of ACCDP variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of ACCDP variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential ACCDP sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion polypeptides (e.g., for phage display) containing the set of ACCDP sequences therein. There are a variety of methods that can be used to produce libraries of potential ACCDP homologs from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene is then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential ACCDP sequences. Methods for synthesizing degenerate oligonucleotides are known in the art.

[0069] In addition, libraries of fragments of the ACCDP coding regions can be used to generate a variegated population of ACCDP fragments for screening and subsequent selection of homologs of an ACCDP. In one embodiment, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of an ACCDP coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA, which can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting fragment library into an

expression vector. By this method, an expression library can be derived which encodes N-terminal, C-terminal, and internal fragments of various sizes of the ACCDP.

[0070] Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of ACCDP homologs. The most widely used techniques, which are amenable to high throughput analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a technique that enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify ACCDP homologs (Arkin and Yourvan, 1992, PNAS 89:7811-7815; Delgrave et al., 1993, Polypeptide Engineering 6(3):327-331). In another embodiment, cell based assays can be exploited to analyze a variegated ACCDP library, using methods well known in the art. The present invention further provides a method of identifying a novel ACCDP, comprising (a) raising a specific antibody response to an ACCDP, or a fragment thereof, as described herein; (b) screening putative ACCDP material with the antibody, wherein specific binding of the antibody to the material indicates the presence of a potentially novel ACCDP; and (c) analyzing the bound material in comparison to known ACCDP, to determine its novelty.

[0071] As stated above, the present invention relates to ACCDPs and homologs thereof. To determine the percent sequence identity of two amino acid sequences (e.g., the sequence of any of SEQ ID NOS as provided in Column No. 4 of Table 1 and Table 2, and a mutant form thereof), the sequences are aligned for optimal comparison purposes (e.g., gaps can be introduced in the sequence of one polypeptide for optimal alignment with the other polypeptide or nucleic acid). The amino acid residues at corresponding amino acid positions are then compared. When a position in one sequence (e.g., the sequence of any of SEQ ID NOS as provided in Column No. 4 of Table 1 and Table 2) is occupied by the same amino acid residue as the corresponding position in the other sequence (e.g., the sequence of a mutant form of the corresponding SEQ ID NO as provided in Column No. 4 of Table 1 and Table 2), then the molecules are identical at that position. The same type of comparison can be made between two nucleic acid sequences.

[0072] The percent sequence identity between the two sequences is a function of the number of identical positions shared by the sequences (i.e., percent sequence identity = numbers of identical positions/total numbers of positions x 100). Preferably, the isolated amino acid homologs included in the present invention are at least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-75%, 75-80%, 80-85%, 85-90%, or 90-95%, and most preferably at least about 96%, 97%, 98%, 99%, or more identical to an entire amino acid sequence shown in any of SEQ

ID NOS as provided in Column No. 4 of Table 1 and Table 2. In yet another embodiment, the isolated amino acid homologs included in the present invention are at least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-75%, 75-80%, 80-85%, 85-90%, or 90-95%, and most preferably at least about 96%, 97%, 98%, 99%, or more identical to an entire amino acid sequence encoded by a nucleic acid sequence shown in any of SEQ ID NOS as provided in Column No. 3 of Table 1 and Table 2.

[0073] In another preferred embodiment, an isolated nucleic acid homolog of the invention comprises a nucleotide sequence which is at least about 40-60%, preferably at least about 60-70%, more preferably at least about 70-75%, 75-80%, 80-85%, 85-90%, or 90-95%, and even more preferably at least about 95%, 96%, 97%, 98%, 99%, or more identical to a nucleotide sequence shown in any of SEQ ID NOS as provided in Column No. 3 of Table 1 and Table 2, or to a portion comprising at least 60 consecutive nucleotides thereof. The preferable length of sequence comparison for nucleic acids is at least 75 nucleotides, more preferably at least 100 nucleotides, and most preferably the entire length of the coding region. It is even more preferable that the nucleic acid homologs encode proteins having homology with any of SEQ ID NOS as provided in Column No. 4 of Table 1 and Table 2.

[0074] It is further preferred that the isolated nucleic acid homolog of the invention encodes an ACCDP, or portion thereof, that is at least 80% identical to an amino acid sequence of any of SEQ ID NOS as provided in Column No. 4 of Table 1 and Table 2, and that functions as a modulator of root growth, and/or yield, and/or an environmental stress response in a plant. In a more preferred embodiment, overexpression of the nucleic acid homolog in a plant increases the plant's root growth, and/or yield, and/or the tolerance of the plant to an environmental stress. In a further preferred embodiment, the nucleic acid homolog encodes an ACCDP that can convert ACC to α–ketobutyrate and ammonia.

[0075] For the purposes of the invention, the percent sequence identity between two nucleic acid or polypeptide sequences is determined using the Vector NTI 9.0 (PC) software package (Invitrogen, 1600 Faraday Ave., Carlsbad, CA92008). A gap opening penalty of 15 and a gap extension penalty of 6.66 are used for determining the percent identity of two nucleic acids. A gap opening penalty of 10 and a gap extension penalty of 0.1 are used for determining the percent identity of two polypeptides. All other parameters are set at the default settings. For purposes of a multiple alignment (Clustal W algorithm), the gap opening penalty is 10, and the gap extension penalty is 0.05 with blosum62 matrix. It is to be understood that for the purposes of determining sequence identity when comparing a DNA sequence to an RNA sequence, a thymidine nucleotide is equivalent to a uracil nucleotide.

[0076] In another aspect, the invention relates to an isolated nucleic acid comprising a polynucleotide that hybridizes to the polynucleotide of any of SEQ ID NOS as provided in Column

No. 3 of Table 1 and Table 2 under stringent conditions. More particularly, an isolated nucleic acid molecule according to the invention is at least 15 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising a nucleotide sequence of any of SEQ ID NOS as provided in Column No. 3 of Table 1 and Table 2. In other embodiments, the nucleic acid is at least 30, 50, 100, 250, or more nucleotides in length. Preferably, an isolated nucleic acid homolog of the invention comprises a nucleotide sequence which hybridizes under highly stringent conditions to the nucleotide sequence shown in any of SEQ ID NOS as provided in Column No. 3 of Table 1 and Table 2 and functions as a modulator of root growth, and/or yield, and/or stress tolerance in a plant. In a further preferred embodiment, overexpression of the isolated nucleic acid homolog in a plant increases a plant's root growth, and/or yield, and/or tolerance to an environmental stress. In an even further preferred embodiment, the isolated nucleic acid homolog encodes an ACCDP that can convert ACC to α–ketobutyrate and ammonia.

[0077] As used herein with regard to hybridization for DNA to a DNA blot, the term "stringent conditions" may refer to hybridization overnight at 60°C in 10X Denhart's solution, 6X SSC, 0.5% SDS, and 100 μg/ml denatured salmon sperm DNA. Blots are washed sequentially at 62°C for 30 minutes each time in 3X SSC/0.1% SDS, followed by 1X SSC/0.1% SDS, and finally 0.1X SSC/0.1% SDS. In a preferred embodiment, the phrase "stringent conditions" refers to hybridization in a 6X SSC solution at 65°C. As also used herein, "highly stringent conditions" refers to hybridization overnight at 65°C in 10X Denharts solution, 6X SSC, 0.5% SDS, and 100 μg/ml denatured salmon sperm DNA. Blots are washed sequentially at 65°C for 30 minutes each time in 3X SSC/0.1% SDS, followed by 1X SSC/0.1% SDS, and finally 0.1X SSC/0.1% SDS. Methods for nucleic acid hybridizations are described in Meinkoth and Wahl, 1984, Anal. Biochem. 138:267-284; Current Protocols in Molecular Biology, Chapter 2, Ausubel et al. Eds., Greene Publishing and Wiley-Interscience, New York, 1995; and Tijssen, 1993, Laboratory Techniques in Biochemistry and Molecular Biology: Hybridization with Nucleic Acid Probes, Part I, Chapter 2, Elsevier, New York, 1993. Preferably, an isolated nucleic acid molecule of the invention that hybridizes under stringent or highly stringent conditions to a sequence of any of SEQ ID NOS as provided in Column No. 3 of Table 1 and Table 2 corresponds to a naturally occurring nucleic acid molecule. As used herein, a "naturally occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (e.g., encodes a natural polypeptide). In one embodiment, the nucleic acid encodes a naturally occurring ACCDP.

[0078] Using the above-described methods, and others known to those of skill in the art, one of ordinary skill in the art can isolate homologs of the ACCDPs comprising amino acid sequences shown in any of SEQ ID NOS as provided in Column No. 4 of Table 1 and Table 2. One subset of these homologs is allelic variants. As used herein, the term "allelic variant" refers to a nucleotide sequence containing polymorphisms that lead to changes in the amino acid sequences of an ACCDP

and that exist within a natural population (e.g., a plant species or variety). Such natural allelic variations can typically result in 1-5% variance in an ACCDP nucleic acid. Allelic variants can be identified by sequencing the nucleic acid sequence of interest in a number of different plants, which can be readily carried out by using hybridization probes to identify the same ACCDP genetic locus in those plants. Any and all such nucleic acid variations and resulting amino acid polymorphisms or variations in an ACCDP that are the result of natural allelic variation and that do not alter the functional activity of an ACCDP, are intended to be within the scope of the invention.

[0079] Moreover, nucleic acid molecules encoding ACCDPs from the same or other species such as ACCDP analogs, orthologs, and paralogs, are intended to be within the scope of the present invention. As used herein, the term "analogs" refers to two nucleic acids that have the same or similar function, but that have evolved separately in unrelated organisms. As used herein, the term "orthologs" refers to two nucleic acids from different species, but that have evolved from a common ancestral gene by speciation. Normally, orthologs encode polypeptides having the same or similar functions. As also used herein, the term "paralogs" refers to two nucleic acids that are related by duplication within a genome. Paralogs usually have different functions, but these functions may be related (Tatusov, R.L. et al., 1997, Science 278(5338):631-637). Analogs, orthologs, and paralogs of a naturally occurring ACCDP can differ from the naturally occurring ACCDP by post-translational modifications, by amino acid sequence differences, or by both. Post-translational modifications include *in vivo* and *in vitro* chemical derivatization of polypeptides, e.g., acetylation, carboxylation, phosphorylation, or glycosylation, and such modifications may occur during polypeptide synthesis or processing or following treatment with isolated modifying enzymes. In particular, orthologs of the invention will generally exhibit at least 80-85%, more preferably, 85-90% or 90-95%, and most preferably 95%, 96%, 97%, 98%, or even 99% identity, or 100% sequence identity, with all or part of a naturally occurring ACCDP amino acid sequence, and will exhibit a function similar to an ACCDP. Preferably, an ACCDP ortholog of the present invention functions as a modulator of growth and/or an environmental stress response in a plant and/or converts ACC to α–ketobutyrate and ammonia. More preferably, an ACCDP ortholog increases the growth and/or stress tolerance of a plant. In one embodiment, the ACCDP orthologs can convert ACC to α–ketobutyrate and ammonia.

[0080] In addition to naturally-occurring variants of an ACCDP sequence that may exist in the population, the skilled artisan will further appreciate that changes can be introduced by mutation into a nucleotide sequence of any of SEQ ID NOS as provided in Column No. 4 of Table 1 and Table 2, thereby leading to changes in the amino acid sequence of the encoded ACCDP, without altering the functional activity of the ACCDP. For example, nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues can be made in a sequence of any of SEQ ID NOS as provided in Column No. 3 of Table 1 and Table 2. A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of one of the ACCDPs without altering the

activity of said ACCDP, whereas an "essential" amino acid residue is required for ACCDP activity. Other amino acid residues, however, (e.g., those that are not conserved or only semi-conserved in the domain having ACCDP activity) may not be essential for activity and thus are likely to be amenable to alteration without altering ACCDP activity.

[0081] Accordingly, another aspect of the invention pertains to nucleic acid molecules encoding ACCDPs that contain changes in amino acid residues that are not essential for ACCDP activity. Such ACCDPs differ in amino acid sequence from a sequence contained in any of SEQ ID NOS as provided in Column No. 4 of Table 1 and Table 2, yet retain at least one of the ACCDP activities described herein. In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a polypeptide, wherein the polypeptide comprises an amino acid sequence at least about 50-60% identical to the sequence of any of SEQ ID NOS as provided in Column No. 4 of Table 1 and Table 2, more preferably at least about 60-70% identical to the sequence of any of SEQ ID NOS as provided in Column No. 4 of Table 1 and Table 2, even more preferably at least about 70-75%, 75-80%, 80-85%, 85-90%, or 90-95% identical to the sequence of any of SEQ ID NOS as provided in Column No. 4 of Table 1 and Table 2, and most preferably at least about 96%, 97%, 98%, or 99% identical to the sequence of any of SEQ ID NOS as provided in Column No. 4 of Table 1 and Table 2. The preferred ACCDP homologs of the present invention preferably participate in a plant's root growth, and/or yield, and/or a stress tolerance response in a plant, or more particularly, can convert ACC to α–ketobutyrate and ammonia.

[0082] An isolated nucleic acid molecule encoding an ACCDP having sequence identity with a polypeptide sequence of any of SEQ ID NOS as provided in Column No. 4 of Table 1 and Table 2 can be created by introducing one or more nucleotide substitutions, additions, or deletions into a nucleotide sequence of any of SEQ ID NOS as provided in Column No. 3 of Table 1 and Table 2, such that one or more amino acid substitutions, additions, or deletions are introduced into the encoded polypeptide. Mutations can be introduced into the sequence of any of SEQ ID NOS as provided in Column No. 3 of Table 1 and Table 2 by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain.

[0083] Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (e.g., lysine, arginine, histidine), acidic side chains (e.g., aspartic acid, glutamic acid), uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (e.g., alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (e.g., threonine, valine, isoleucine), and aromatic side chains (e.g., tyrosine, phenylalanine, tryptophan,

histidine). Thus, a predicted nonessential amino acid residue in an ACCDP is preferably replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of an ACCDP coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for an ACCDP activity described herein to identify mutants that retain ACCDP activity. Following mutagenesis of the sequence of any of SEQ ID NOS as provided in Column No. 3 of Table 1 and Table 2 the encoded polypeptide can be expressed recombinantly and the activity of the polypeptide can be determined by analyzing the root growth, and/or yield, and/or stress tolerance of a plant expressing the polypeptide as described at least in Examples 5, 6, and 17-19.

[0084] Additionally, optimized ACCDP nucleic acids can be created. Preferably, an optimized ACCDP nucleic acid encodes an ACCDP that modulates a plant's root growth, and/or yield, and/or tolerance to an environmental stress, and more preferably increases a plant's root growth, and/or yield, and/or tolerance to an environmental stress upon its overexpression in the plant. As used herein, "optimized" refers to a nucleic acid that is genetically engineered to increase its expression in a given plant or animal. To provide plant optimized ACCDP nucleic acids, the DNA sequence of the gene can be modified to 1) comprise codons preferred by highly expressed plant genes; 2) comprise an A+T content in nucleotide base composition to that substantially found in plants; 3) form a plant initiation sequence; or 4) to eliminate sequences that cause destabilization, inappropriate polyadenylation, degradation and termination of RNA, or that form secondary structure hairpins or RNA splice sites. Increased expression of ACCDP nucleic acids in plants can be achieved by utilizing the distribution frequency of codon usage in plants in general or in a particular plant. Methods for optimizing nucleic acid expression in plants can be found in EPA 0359472; EPA 0385962; PCT Application No. WO 91/16432; U.S. Patent No. 5,380,831; U.S. Patent No. 5,436,391; Perlack et al., 1991, Proc. Natl. Acad. Sci. USA 88:3324-3328; and Murray et al., 1989, Nucleic Acids Res. 17:477-498.

[0085] As used herein, "frequency of preferred codon usage" refers to the preference exhibited by a specific host cell in usage of nucleotide codons to specify a given amino acid. To determine the frequency of usage of a particular codon in a gene, the number of occurrences of that codon in the gene is divided by the total number of occurrences of all codons specifying the same amino acid in the gene. Similarly, the frequency of preferred codon usage exhibited by a host cell can be calculated by averaging frequency of preferred codon usage in a large number of genes expressed by the host cell. It is preferable that this analysis be limited to genes that are highly expressed by the host cell. The percent deviation of the frequency of preferred codon usage for a synthetic gene from that employed by a host cell is calculated first by determining the percent deviation of the frequency of usage of a single codon from that of the host cell followed by obtaining the average deviation over all codons. As defined herein, this calculation includes unique codons (i.e., ATG and TGG). In general terms, the overall average deviation of the codon usage of an

optimized gene from that of a host cell is calculated using the equation $1A = n = 1\ Z\ X_n - Y_n\ X_n$ times 100 Z where X_n = frequency of usage for codon n in the host cell; Y_n = frequency of usage for codon n in the synthetic gene; n represents an individual codon that specifies an amino acid; and the total number of codons is Z. The overall deviation of the frequency of codon usage, A, for all amino acids should preferably be less than about 25%, and more preferably less than about 10%.

[0086] Hence, an ACCDP nucleic acid can be optimized such that its distribution frequency of codon usage deviates, preferably, no more than 25% from that of highly expressed plant genes and, more preferably, no more than about 10%. In addition, consideration is given to the percentage G+C content of the degenerate third base (monocotyledons appear to favor G+C in this position, whereas dicotyledons do not). It is also recognized that the XCG (where X is A, T, C, or G) nucleotide is the least preferred codon in dicots whereas the XTA codon is avoided in both monocots and dicots. Optimized ACCDP nucleic acids of this invention also preferably have CG and TA doublet avoidance indices closely approximating those of the chosen host plant (e.g., *Arabidopsis thaliana, Oryza sativa,* etc.). More preferably these indices deviate from that of the host by no more than about 10-15%.

[0087] In addition to the nucleic acid molecules encoding the ACCDPs described above, another aspect of the invention pertains to isolated nucleic acid molecules that are antisense thereto. Antisense polynucleotides are thought to inhibit gene expression of a target polynucleotide by specifically binding the target polynucleotide and interfering with transcription, splicing, transport, translation, and/or stability of the target polynucleotide. Methods are described in the prior art for targeting the antisense polynucleotide to the chromosomal DNA, to a primary RNA transcript, or to a processed mRNA. Preferably, the target regions include splice sites, translation initiation codons, translation termination codons, and other sequences within the open reading frame.

[0088] The term "antisense," for the purposes of the invention, refers to a nucleic acid comprising a polynucleotide that is sufficiently complementary to all or a portion of a gene, primary transcript, or processed mRNA, so as to interfere with expression of the endogenous gene. "Complementary" polynucleotides are those that are capable of base pairing according to the standard Watson-Crick complementarity rules. Specifically, purines will base pair with pyrimidines to form a combination of guanine paired with cytosine (G:C) and adenine paired with either thymine (A:T) in the case of DNA, or adenine paired with uracil (A:U) in the case of RNA. It is understood that two polynucleotides may hybridize to each other even if they are not completely complementary to each other, provided that each has at least one region that is substantially complementary to the other. The term "antisense nucleic acid" includes single stranded RNA as well as double-stranded DNA expression cassettes that can be transcribed to produce an antisense RNA. "Active" antisense nucleic acids are antisense RNA molecules that are capable of selectively hybridizing with a primary transcript or mRNA encoding a polypeptide having at least 80% sequence identity with the polypeptide of any of SEQ ID NOS as provided in Column No. 4 of Table 1 and Table 2.

[0089] The antisense nucleic acid can be complementary to an entire ACCDP coding strand, or to only a portion thereof. In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding an ACCDP. The term "coding region" refers to the region of the nucleotide sequence comprising codons that are translated into amino acid residues. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding an ACCDP. The term "noncoding region" refers to 5' and 3' sequences that flank the coding region that are not translated into amino acids (i.e., also referred to as 5' and 3' untranslated regions). The antisense nucleic acid molecule can be complementary to the entire coding region of ACCDP mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of ACCDP mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of ACCDP mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45, or 50 nucleotides in length. Typically, the antisense molecules of the present invention comprise an RNA having 60-100% sequence identity with at least 14 consecutive nucleotides of any of SEQ ID NOS as provided in Column No. 3 of Table 1 and Table 2 or a polynucleotide encoding a polypeptide of any of SEQ ID NOS as provided in Column No. 4 of Table 1 and Table 2. Preferably, the sequence identity will be at least 70%, more preferably at least 75%, 80%, 85%, 90%, 95%, or 98%, and most preferably 99%.

[0090] An antisense nucleic acid of the invention can be constructed using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (e.g., an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, e.g., phosphorothioate derivatives and acridine substituted nucleotides can be used. Examples of modified nucleotides which can be used to generate the antisense nucleic acid include 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxylmethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5- oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense

orientation (i.e., RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

[0091] In yet another embodiment, the antisense nucleic acid molecule of the invention is an α-anomeric nucleic acid molecule. An α-anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β-units, the strands run parallel to each other (Gaultier et al., 1987, Nucleic Acids. Res. 15:6625-6641). The antisense nucleic acid molecule can also comprise a 2'-O-methylribonucleotide (Inoue et al., 1987, Nucleic Acids Res. 15:6131-6148) or a chimeric RNA-DNA analogue (Inoue et al., 1987, FEBS Lett. 215:327-330).

[0092] The antisense nucleic acid molecules of the invention are typically administered to a cell or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding an ACCDP to thereby inhibit expression of the polypeptide, e.g., by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule which binds to DNA duplexes, through specific interactions in the major groove of the double helix. The antisense molecule can be modified such that it specifically binds to a receptor or an antigen expressed on a selected cell surface, e.g., by linking the antisense nucleic acid molecule to a peptide or an antibody which binds to a cell surface receptor or antigen. The antisense nucleic acid molecule can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of the antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong prokaryotic, viral, or eukaryotic (including plant) promoter are preferred.

[0093] As an alternative to antisense polynucleotides, ribozymes, sense polynucleotides, or double stranded RNA (dsRNA) can be used to reduce expression of an ACCDP polypeptide. As used herein, the term "ribozyme" refers to a catalytic RNA-based enzyme with ribonuclease activity that is capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which it has a complementary region. Ribozymes (e.g., hammerhead ribozymes described in Haselhoff and Gerlach, 1988, Nature 334:585-591) can be used to catalytically cleave ACCDP mRNA transcripts to thereby inhibit translation of ACCDP mRNA. A ribozyme having specificity for an ACCDP-encoding nucleic acid can be designed based upon the nucleotide sequence of an ACCDP cDNA, as disclosed herein (i.e., any of SEQ ID NOS as provided in Column No. 3 of Table 1 and Table 2) or on the basis of a heterologous sequence to be isolated according to methods taught in this invention. For example, a derivative of a *Tetrahymena* L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an ACCDP-encoding mRNA. See, e.g., U.S. Patent Nos. 4,987,071 and 5,116,742 to Cech et al. Alternatively, ACCDP mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a

pool of RNA molecules. See, e.g., Bartel, D. and Szostak, J.W., 1993, Science 261:1411-1418. In preferred embodiments, the ribozyme will contain a portion having at least 7, 8, 9, 10, 12, 14, 16, 18, or 20 nucleotides, and more preferably 7 or 8 nucleotides, that have 100% complementarity to a portion of the target RNA. Methods for making ribozymes are known to those skilled in the art. See, e.g., U.S. Patent Nos. 6,025,167; 5,773,260; and 5,496,698.

[0094] The term "dsRNA," as used herein, refers to RNA hybrids comprising two strands of RNA. The dsRNAs can be linear or circular in structure. In a preferred embodiment, dsRNA is specific for a polynucleotide encoding either the polypeptide of any of SEQ ID NOS as provided in Column No. 4 of Table 1 and Table 2 or a polypeptide having at least 80% sequence identity with a polypeptide of any of SEQ ID NOS as provided in Column No. 4 of Table 1 and Table 2. The hybridizing RNAs may be substantially or completely complementary. By "substantially complementary," is meant that when the two hybridizing RNAs are optimally aligned using the BLAST program as described above, the hybridizing portions are at least 95% complementary. Preferably, the dsRNA will be at least 100 base pairs in length. Typically, the hybridizing RNAs will be of identical length with no over hanging 5' or 3' ends and no gaps. However, dsRNAs having 5' or 3' overhangs of up to 100 nucleotides may be used in the methods of the invention.

[0095] The dsRNA may comprise ribonucleotides, ribonucleotide analogs such as 2'-O-methyl ribosyl residues, or combinations thereof. See, e.g., U.S. Patent Nos. 4,130,641 and 4,024,222. A dsRNA polyriboinosinic acid:polyribocytidylic acid is described in U.S. patent 4,283,393. Methods for making and using dsRNA are known in the art. One method comprises the simultaneous transcription of two complementary DNA strands, either *in vivo*, or in a single *in vitro* reaction mixture. See, e.g., U.S. Patent No. 5,795,715. In one embodiment, dsRNA can be introduced into a plant or plant cell directly by standard transformation procedures. Alternatively, dsRNA can be expressed in a plant cell by transcribing two complementary RNAs.

[0096] Other methods for the inhibition of endogenous gene expression, such as triple helix formation (Moser et al., 1987, Science 238:645-650 and Cooney et al., 1988, Science 241:456-459) and co-suppression (Napoli et al., 1990, The Plant Cell 2:279-289) are known in the art. Partial and full-length cDNAs have been used for the cosuppression of endogenous plant genes. See, e.g., U.S. Patent Nos. 4,801,340, 5,034,323, 5,231,020, and 5,283,184; Van der Kroll et al., 1990, The Plant Cell 2:291-299; Smith et al., 1990, Mol. Gen. Genetics 224:477-481; and Napoli et al., 1990, The Plant Cell 2:279-289.

[0097] For sense suppression, it is believed that introduction of a sense polynucleotide blocks transcription of the corresponding target gene. The sense polynucleotide will have at least 65% sequence identity with the target plant gene or RNA. Preferably, the percent identity is at least 80%, 90%, 95%, or more. The introduced sense polynucleotide need not be full length relative to the target gene or transcript. Preferably, the sense polynucleotide will have at least 65% sequence identity with at least 100 consecutive nucleotides of any of SEQ ID NOS as provided in Column No.

3 of Table 1 and Table 2. The regions of identity can comprise introns and/or exons and untranslated regions. The introduced sense polynucleotide may be present in the plant cell transiently, or may be stably integrated into a plant chromosome or extrachromosomal replicon.

[0098] Alternatively, ACCDP gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of an ACCDP nucleotide sequence (e.g., an ACCDP promoter and/or enhancer) to form triple helical structures that prevent transcription of an ACCDP gene in target cells. See generally, Helene, C., 1991, Anticancer Drug Des. 6(6):569-84; Helene, C. et al., 1992, Ann. N.Y. Acad. Sci. 660:27-36; and Maher, L.J., 1992, Bioassays 14(12):807-15.

[0099] In addition to the ACCDP nucleic acids and polypeptides described above, the present invention encompasses these nucleic acids and polypeptides attached to a moiety. These moieties include, but are not limited to, detection moieties, hybridization moieties, purification moieties, delivery moieties, reaction moieties, binding moieties, and the like. A typical group of nucleic acids having moieties attached are probes and primers. Probes and primers typically comprise a substantially isolated oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, preferably about 25, more preferably about 40, 50, or 75 consecutive nucleotides of a sense strand of the sequence set forth in any of SEQ ID NOS as provided in Column No. 3 of Table 1 and Table 2; an anti-sense sequence of the sequence set forth in any of SEQ ID NOS as provided in Column No. 3 of Table 1 and Table 2; or naturally occurring mutants thereof. Primers based on a nucleotide sequence of any of SEQ ID NOS as provided in Column No. 3 of Table 1 and Table 2 can be used in PCR reactions to clone ACCDP homologs. Probes based on the ACCDP nucleotide sequences can be used to detect transcripts or genomic sequences encoding the same or substantially identical polypeptides. In preferred embodiments, the probe further comprises a label group attached thereto, e.g. the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as a part of a genomic marker test kit for identifying cells which express an ACCDP, such as by measuring a level of an ACCDP-encoding nucleic acid, in a sample of cells, e.g., detecting ACCDP mRNA levels or determining whether a genomic ACCDP gene has been mutated or deleted.

[00100] In particular, a useful method to ascertain the level of transcription of the gene (an indicator of the amount of mRNA available for translation to the gene product) is to perform a Northern blot (For reference, see, for example, Ausubel et al., 1988, Current Protocols in Molecular Biology, Wiley: New York). The information from a Northern blot at least partially demonstrates the degree of transcription of the transformed gene. Total cellular RNA can be prepared from cells, tissues, or organs by several methods, all well-known in the art, such as that described in Bormann, E.R. et al., 1992, Mol. Microbiol. 6:317-326. To assess the presence or relative quantity of polypeptide translated from this mRNA, standard techniques, such as a Western blot, may be

employed. These techniques are well known to one of ordinary skill in the art. (See, for example, Ausubel et al., 1988, Current Protocols in Molecular Biology, Wiley: New York).

[00101]The invention further provides an isolated recombinant expression vector comprising an ACCDP nucleic acid, wherein expression of the vector in a host cell results in increased root growth, and/or yield, and/or tolerance to environmental stress as compared to a wild type variety of the host cell. As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid," which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (e.g., bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (e.g., non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "expression vectors." In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (e.g., replication defective retroviruses, adenoviruses, and adeno-associated viruses), which serve equivalent functions.

[00102]The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is operatively linked to the nucleic acid sequence to be expressed. As used herein with respect to a recombinant expression vector, "operatively linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleotide sequence (e.g., in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, enhancers, and other expression control elements (e.g., polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel, Gene Expression Technology: Methods in Enzymology 185, Academic Press, San Diego, CA (1990) and Gruber and Crosby, in: Methods in Plant Molecular Biology and Biotechnology, eds. Glick and Thompson, Chapter 7, 89-108, CRC Press: Boca Raton, Florida, including the references therein. Regulatory sequences include those that direct constitutive expression of a nucleotide sequence in many types of host cells and those that direct expression of the nucleotide sequence only in certain host cells or under certain conditions. It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed,

the level of expression of polypeptide desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce polypeptides or peptides, including fusion polypeptides or peptides, encoded by nucleic acids as described herein (e.g., ACCDPs, mutant forms of ACCDPs, fusion polypeptides, etc.).

[00103]The recombinant expression vectors of the invention can be designed for expression of ACCDPs in prokaryotic or eukaryotic cells. For example, ACCDP genes can be expressed in bacterial cells such as *C. glutamicum*, insect cells (using baculovirus expression vectors), yeast and other fungal cells (See Romanos, M.A. et al., 1992, Foreign gene expression in yeast: a review, Yeast 8:423-488; van den Hondel, C.A.M.J.J. et al., 1991, Heterologous gene expression in filamentous fungi, in: More Gene Manipulations in Fungi, J.W. Bennet & L.L. Lasure, eds., p. 396-428: Academic Press: San Diego; and van den Hondel, C.A.M.J.J. & Punt, P.J., 1991, Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, Peberdy, J.F. et al., eds., p. 1-28, Cambridge University Press: Cambridge), algae (Falciatore et al., 1999, Marine Biotechnology 1(3):239-251), ciliates of the types: Holotrichia, Peritrichia, Spirotrichia, Suctoria, Tetrahymena, Paramecium, Colpidium, Glaucoma, Platyophrya, Potomacus, Pseudocohnilembus, Euplotes, Engelmaniella, and Stylonychia, especially of the genus Stylonychia lemnae with vectors following a transformation method as described in PCT Application No. WO 98/01572, and multicellular plant cells (See Schmidt, R. and Willmitzer, L., 1988, High efficiency *Agrobacterium tumefaciens*-mediated transformation of *Arabidopsis thaliana* leaf and cotyledon explants, Plant Cell Rep. 583-586; Plant Molecular Biology and Biotechnology, C Press, Boca Raton, Florida, chapter 6/7, S.71-119 (1993); F.F. White, B. Jenes et al., Techniques for Gene Transfer, in: Transgenic Plants, Vol. 1, Engineering and Utilization, eds. Kung und R. Wu, 128-43, Academic Press: 1993; Potrykus, 1991, Annu. Rev. Plant Physiol. Plant Molec. Biol. 42:205-225 and references cited therein), or mammalian cells. Suitable host cells are discussed further in Goeddel, Gene Expression Technology: Methods in Enzymology 185, Academic Press: San Diego, CA (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

[00104]Expression of polypeptides in prokaryotes is most often carried out with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion polypeptides. Fusion vectors add a number of amino acids to a polypeptide encoded therein, usually to the amino terminus of the recombinant polypeptide but also to the C-terminus or fused within suitable regions in the polypeptides. Such fusion vectors typically serve three purposes: 1) to increase expression of a recombinant polypeptide; 2) to increase the solubility of a recombinant polypeptide; and 3) to aid in the purification of a recombinant polypeptide by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant polypeptide to enable separation of the recombinant polypeptide from the fusion moiety subsequent to purification of the fusion polypeptide.

Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin, and enterokinase.

[00105] Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith, D.B. and Johnson, K.S., 1988, Gene 67:31-40), pMAL (New England Biolabs, Beverly, MA), and pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase (GST), maltose E binding polypeptide, or polypeptide A, respectively, to the target recombinant polypeptide. In one embodiment, the coding sequence of the ACCDP is cloned into a pGEX expression vector to create a vector encoding a fusion polypeptide comprising, from the N-terminus to the C-terminus, GST-thrombin cleavage site-X polypeptide. The fusion polypeptide can be purified by affinity chromatography using glutathione-agarose resin. Recombinant ACCDP unfused to GST can be recovered by cleavage of the fusion polypeptide with thrombin.

[00106] Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amann et al., 1988, Gene 69:301-315) and pET 11d (Studier et al., Gene Expression Technology: Methods in Enzymology 185, Academic Press, San Diego, California (1990) 60-89). Target gene expression from the pTrc vector relies on host RNA polymerase transcription from a hybrid trp-lac fusion promoter. Target gene expression from the pET 11d vector relies on transcription from a T7 gn10-lac fusion promoter mediated by a co-expressed viral RNA polymerase (T7 gn1). This viral polymerase is supplied by host strains BL21(DE3) or HMS174(DE3) from a resident prophage harboring a T7 gn1 gene under the transcriptional control of the lacUV 5 promoter.

[00107] One strategy to maximize recombinant polypeptide expression is to express the polypeptide in a host bacterium with an impaired capacity to proteolytically cleave the recombinant polypeptide (Gottesman, S., Gene Expression Technology: Methods in Enzymology 185, Academic Press, San Diego, California (1990) 119-128). Another strategy is to alter the sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in the bacterium chosen for expression, such as *C. glutamicum* (Wada et al., 1992, Nucleic Acids Res. 20:2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

[00108] In another embodiment, the ACCDP expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari, et al., 1987, EMBO J. 6:229-234), pMFa (Kurjan and Herskowitz, 1982, Cell 30:933-943), pJRY88 (Schultz et al., 1987, Gene 54:113-123), and pYES2 (Invitrogen Corporation, San Diego, CA). Vectors and methods for the construction of vectors appropriate for use in other fungi, such as the filamentous fungi, include those detailed in: van den Hondel, C.A.M.J.J. & Punt, P.J., 1991, "Gene transfer systems and vector development for filamentous fungi," in: Applied Molecular Genetics of Fungi, J.F. Peberdy, et al., eds., p. 1-28, Cambridge University Press: Cambridge.

[00109] In a preferred embodiment of the present invention, the ACCDPs are expressed in plants and plants cells such as unicellular plant cells (e.g. algae) (See Falciatore et al., 1999, Marine

Biotechnology 1(3):239-251 and references therein) and plant cells from higher plants (e.g., the spermatophytes, such as crop plants). AN ACCDP may be "introduced" into a plant cell by any means, including transfection, transformation or transduction, electroporation, particle bombardment, agroinfection, and the like. One transformation method known to those of skill in the art is the dipping of a flowering plant into an *Agrobacteria* solution, wherein the *Agrobacteria* contain the ACCDP nucleic acid, followed by breeding of the transformed gametes.

[00110] Other suitable methods for transforming or transfecting host cells including plant cells can be found in Sambrook, et al. (Molecular Cloning: A Laboratory Manual. latest ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989) and other laboratory manuals such as Methods in Molecular Biology, 1995, Vol. 44, *Agrobacterium* protocols, ed: Gartland and Davey, Humana Press, Totowa, New Jersey. As increased growth and increased biotic and abiotic stress tolerance are general traits wished to be inherited into a wide variety of plants like maize, wheat, rye, oat, triticale, rice, barley, sorghum, millet, sugarcane, soybean, peanut, cotton, rapeseed and canola, manihot, pepper, sunflower and tagetes, solanaceous plants like potato, tobacco, eggplant, and tomato, Vicia species, pea, alfalfa, bushy plants (coffee, cacao, tea), Salix species, trees (oil palm, coconut), perennial grasses, and forage crops, these crop plants are also preferred target plants for a genetic engineering as one further embodiment of the present invention. Forage crops include, but are not limited to, Wheatgrass, Canarygrass, Bromegrass, Wildrye Grass, Bluegrass, Orchardgrass, Alfalfa, Salfoin, Birdsfoot Trefoil, Alsike Clover, Red Clover, and Sweet Clover.

[00111] In one embodiment of the present invention, transfection of an ACCDP into a plant is achieved by *Agrobacterium* mediated gene transfer. *Agrobacterium* mediated plant transformation can be performed using for example the GV3101(pMP90) (Koncz and Schell, 1986, Mol. Gen. Genet. 204:383-396) or LBA4404 (Clontech) *Agrobacterium tumefaciens* strain. Transformation can be performed by standard transformation and regeneration techniques (Deblaere et al., 1994, Nucl. Acids. Res. 13:4777-4788; Gelvin, Stanton B. and Schilperoort, Robert A, Plant Molecular Biology Manual, 2nd Ed. - Dordrecht: Kluwer Academic Publ., 1995. - in Sect., Ringbuc Zentrale Signatur: BT11-P ISBN 0-7923-2731-4; Glick, Bernard R.; Thompson, John E., Methods in Plant Molecular Biology and Biotechnology, Boca Raton: CRC Press, 1993 360 S., ISBN 0-8493-5164-2). For example, rapeseed can be transformed via cotyledon or hypocotyl transformation (Moloney et al., 1989, Plant Cell Report 8:238-242; De Block et al., 1989, Plant Physiol. 91:694-701). Use of antibiotics for *Agrobacterium* and plant selection depends on the binary vector and the *Agrobacterium* strain used for transformation. Rapeseed selection is normally performed using kanamycin as the selectable plant marker. *Agrobacterium* mediated gene transfer to flax can be performed using, for example, a technique described by Mlynarova et al., 1994, Plant Cell Report 13:282-285. Additionally, transformation of soybean can be performed using for example a technique described in European Patent No. 0424 047, U.S. Patent No. 5,322,783, European Patent

No. 0397 687, U.S. Patent No. 5,376,543, or U.S. Patent No. 5,169,770. Transformation of maize can be achieved by particle bombardment, polyethylene glycol mediated DNA uptake, or via the silicon carbide fiber technique. (See, for example, Freeling and Walbot "The maize handbook" Springer Verlag: New York (1993) ISBN 3-540-97826-7). A specific example of maize transformation is found in U.S. Patent No. 5,990,387, and a specific example of wheat transformation can be found in PCT Application No. WO 93/07256.

[00112] According to the present invention, the introduced ACCDP may be maintained in the plant cell stably if it is incorporated into a non-chromosomal autonomous replicon or integrated into the plant chromosomes. Alternatively, the introduced ACCDP may be present on an extra-chromosomal non-replicating vector and may be transiently expressed or transiently active.

[00113] In one embodiment, a homologous recombinant microorganism can be created wherein the ACCDP is integrated into a chromosome, a vector is prepared which contains at least a portion of an ACCDP gene into which a deletion, addition, or substitution has been introduced to thereby alter, e.g., functionally disrupt, the ACCDP gene. Preferably, the ACCDP gene is any of ACCDP genes as provided in Table 1 and Table 2, but it can be a homolog from a related plant or yeast, or even from a mammalian or insect source. In one embodiment, the vector is designed such that, upon homologous recombination, the endogenous ACCDP gene is functionally disrupted (i.e., no longer encodes a functional polypeptide; also referred to as a knock-out vector). Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous ACCDP gene is mutated or otherwise altered but still encodes a functional polypeptide (e.g., the upstream regulatory region can be altered to thereby alter the expression of the endogenous ACCDP). To create a point mutation via homologous recombination, DNA-RNA hybrids can be used in a technique known as chimeraplasty (Cole-Strauss et al., 1999, Nucleic Acids Research 27(5):1323-1330 and Kmiec, 1999, Gene Therapy American Scientist 87(3):240-247). Homologous recombination procedures in *Arabiodopsis thaliana*, for example, are well known in the art and are contemplated for use herein.

[00114] Whereas in the homologous recombination vector, the altered portion of the ACCDP gene is flanked at its 5' and 3' ends by an additional nucleic acid molecule of the ACCDP gene to allow for homologous recombination to occur between the exogenous ACCDP gene carried by the vector and an endogenous ACCDP gene, in a microorganism or plant. The additional flanking ACCDP nucleic acid molecule is of sufficient length for successful homologous recombination with the endogenous gene. Typically, several hundreds of base pairs up to kilobases of flanking DNA (both at the 5' and 3' ends) are included in the vector (See e.g., Thomas, K.R., and Capecchi, M.R., 1987, Cell 51:503 for a description of homologous recombination vectors). The vector is introduced into a microorganism or plant cell (e.g., via polyethylene glycol mediated DNA), and cells in which the introduced ACCDP gene has homologously recombined with the endogenous ACCDP gene are selected using art-known techniques.

[00115] In another embodiment, recombinant microorganisms can be produced that contain selected systems that allow for regulated expression of the introduced gene. For example, inclusion of an ACCDP gene on a vector placing it under control of the lac operon permits expression of the ACCDP gene only in the presence of IPTG. Such regulatory systems are well known in the art.

[00116] Whether present in an extra-chromosomal non-replicating vector or a vector that is integrated into a chromosome, the ACCDP polynucleotide preferably resides in a plant expression cassette. A plant expression cassette preferably contains regulatory sequences capable of driving gene expression in plant cells that are operatively linked so that each sequence can fulfill its function, for example, termination of transcription by polyadenylation signals. Preferred polyadenylation signals are those originating from *Agrobacterium tumefaciens* t-DNA such as the gene 3 known as octopine synthase of the Ti-plasmid pTiACH5 (Gielen et al., 1984, EMBO J. 3:835) or functional equivalents thereof, but also all other terminators functionally active in plants are suitable. As plant gene expression is very often not limited on transcriptional levels, a plant expression cassette preferably contains other operatively linked sequences like translational enhancers such as the overdrive-sequence containing the 5′-untranslated leader sequence from tobacco mosaic virus enhancing the polypeptide per RNA ratio (Gallie et al., 1987, Nucl. Acids Research 15:8693-8711). Examples of plant expression vectors include those detailed in: Becker, D., Kemper, E., Schell, J. and Masterson, R., 1992, New plant binary vectors with selectable markers located proximal to the left border, Plant Mol. Biol. 20: 1195-1197; and Bevan, M.W., 1984, Binary *Agrobacterium* vectors for plant transformation, Nucl. Acid. Res. 12:8711-8721; Vectors for Gene Transfer in Higher Plants; in: Transgenic Plants, Vol. 1, Engineering and Utilization, eds.: Kung and R. Wu, Academic Press, 1993, S. 15-38.

[00117] Plant gene expression should be operatively linked to an appropriate promoter conferring gene expression in a timely, cell specific, or tissue specific manner. Promoters useful in the expression cassettes of the invention include any promoter that is capable of initiating transcription in a plant cell. Such promoters include, but are not limited to, those that can be obtained from plants, plant viruses, and bacteria that contain genes that are expressed in plants, such as *Agrobacterium* and *Rhizobium.*

[00118] The promoter may be constitutive, inducible, developmental stage-preferred, cell type-preferred, tissue-preferred, or organ-preferred. Constitutive promoters are active under most conditions. Examples of constitutive promoters include the CaMV 19S and 35S promoters (Odell et al., 1985, Nature 313:810-812), the sX CaMV 35S promoter (Kay et al., 1987, Science 236:1299-1302) the Sep1 promoter, the rice actin promoter (McElroy et al., 1990, Plant Cell 2:163-171), the *Arabidopsis* actin promoter, the ubiquitan promoter (Christensen et al., 1989, Plant Molec. Biol. 18:675-689), pEmu (Last et al., 1991, Theor. Appl. Genet. 81:581-588), the figwort mosaic virus 35S promoter, the Smas promoter (Velten et al., 1984, EMBO J 3:2723-2730), the super-promoter (US Patent No. 5,955,646), the GRP1-8 promoter, the cinnamyl alcohol dehydrogenase promoter (U.S. Patent No. 5,683,439), promoters from the T-DNA of *Agrobacterium*, such as mannopine synthase,

nopaline synthase, and octopine synthase, the small subunit of ribulose biphosphate carboxylase (ssuRUBISCO) promoter, and the like.

[0119] Inducible promoters are preferentially active under certain environmental conditions, such as the presence or absence of a nutrient or metabolite, heat or cold, light, pathogen attack, anaerobic conditions, and the like. For example, the hsp80 promoter from *Brassica* is induced by heat shock; the PPDK promoter is induced by light; the PR-1 promoter from tobacco, *Arabidopsis*, and maize are inducible by infection with a pathogen; and the Adh1 promoter is induced by hypoxia and cold stress. Plant gene expression can also be facilitated via an inducible promoter (For review, see Gatz, 1997, Annu. Rev. Plant Physiol. Plant Mol. Biol. 48:89-108). Chemically inducible promoters are especially suitable if gene expression is wanted to occur in a time specific manner. Examples of such promoters are a salicylic acid inducible promoter (PCT Application No. WO 95/19443), a tetracycline inducible promoter (Gatz et al., 1992, Plant J. 2:397-404), and an ethanol inducible promoter (PCT Application No. WO 93/21334).

[0120] In one preferred embodiment of the present invention, the inducible promoter is a stress-inducible promoter. For the purposes of the invention, stress inducible promoters are preferentially active under one or more of the following stresses: sub-optimal conditions associated with salinity, drought, temperature, metal, chemical, pathogenic, and oxidative stresses. Stress inducible promoters include, but are not limited to, Cor78 (Chak et al., 2000, Planta 210:875-883; Hovath et al., 1993, Plant Physiol. 103:1047-1053), Cor15a (Artus et al., 1996, PNAS 93(23):13404-09), Rci2A (Medina et al., 2001, Plant Physiol. 125:1655-66; Nylander et al., 2001, Plant Mol. Biol. 45:341-52; Navarre and Goffeau, 2000, EMBO J. 19:2515-24; Capel et al., 1997, Plant Physiol. 115:569-76), Rd22 (Xiong et al., 2001, Plant Cell 13:2063-83; Abe et al., 1997, Plant Cell 9:1859-68; Iwasaki et al., 1995, Mol. Gen. Genet. 247:391-8), cDet6 (Lang and Palve, 1992, Plant Mol. Biol. 20:951-62), ADH1 (Hoeren et al., 1998, Genetics 149:479-90), KAT1 (Nakamura et al., 1995, Plant Physiol. 109:371-4), KST1 (Müller-Röber et al., 1995, EMBO 14:2409-16), Rha1 (Terryn et al., 1993, Plant Cell 5:1761-9; Terryn et al., 1992, FEBS Lett. 299(3):287-90), ARSK1 (Atkinson et al., 1997, GenBank Accession # L22302, and PCT Application No. WO 97/20057), PtxA (Plesch et al., GenBank Accession # X67427), SbHRGP3 (Ahn et al., 1996, Plant Cell 8:1477-90), GH3 (Liu et al., 1994, Plant Cell 6:645-57), the pathogen inducible PRP1-gene promoter (Ward et al., 1993, Plant. Mol. Biol. 22:361-366), the heat inducible hsp80-promoter from tomato (U.S. Patent No. 5187267), cold inducible alpha-amylase promoter from potato (PCT Application No. WO 96/12814), or the wound-inducible pinII-promoter (European Patent No. 375091). For other examples of drought, cold, and salt-inducible promoters, such as the RD29A promoter, see Yamaguchi-Shinozalei et al., 1993, Mol. Gen. Genet. 236:331-340.

[0121] Developmental stage-preferred promoters are preferentially expressed at certain stages of development. Tissue and organ preferred promoters include those that are preferentially expressed in certain tissues or organs, such as leaves, roots, seeds, or xylem. Examples of tissue

preferred and organ preferred promoters include, but are not limited to fruit-preferred, ovule-preferred, male tissue-preferred, seed-preferred, integument-preferred, tuber-preferred, stalk-preferred, pericarp-preferred, and leaf-preferred, stigma-preferred, pollen-preferred, anther-preferred, a petal-preferred, sepal-preferred, pedicel-preferred, silique-preferred, stem-preferred, root-preferred promoters, and the like. Seed preferred promoters are preferentially expressed during seed development and/or germination. For example, seed preferred promoters can be embryo-preferred, endosperm preferred, and seed coat-preferred. See Thompson et al., 1989, BioEssays 10:108. Examples of seed preferred promoters include, but are not limited to, cellulose synthase (celA), Cim1, gamma-zein, globulin-1, maize 19 kD zein (cZ19B1), and the like.

[0122] Other suitable tissue-preferred or organ-preferred promoters include the napin-gene promoter from rapeseed (U.S. Patent No. 5,608,152), the USP-promoter from Vicia faba (Baeumlein et al., 1991, Mol. Gen. Genet. 225(3):459-67), the oleosin-promoter from *Arabidopsis* (PCT Application No. WO 98/45461), the phaseolin-promoter from *Phaseolus vulgaris* (U.S. Patent No. 5,504,200), the Bce4-promoter from *Brassica* (PCT Application No. WO 91/13980), or the legumin B4 promoter (LeB4; Baeumlein et al., 1992, Plant Journal, 2(2):233-9), as well as promoters conferring seed specific expression in monocot plants like maize, barley, wheat, rye, rice, etc. Suitable promoters to note are the lpt2 or lpt1-gene promoter from barley (PCT Application No. WO 95/15389 and PCT Application No. WO 95/23230) or those described in PCT Application No. WO 99/16890 (promoters from the barley hordein-gene, rice glutelin gene, rice oryzin gene, rice prolamin gene, wheat gliadin gene, wheat glutelin gene, oat glutelin gene, Sorghum kasirin-gene, and rye secalin gene).

[0123] Other promoters useful in the expression cassettes of the invention include, but are not limited to, the major chlorophyll a/b binding protein promoter, histone promoters, the Ap3 promoter, the β-conglycin promoter, the napin promoter, the soybean lectin promoter, the maize 15kD zein promoter, the 22kD zein promoter, the 27kD zein promoter, the g-zein promoter, the waxy, shrunken 1, shrunken 2, and bronze promoters, the Zm13 promoter (U.S. Patent No. 5,086,169), the maize polygalacturonase promoters (PG) (U.S. Patent Nos. 5,412,085 and 5,545,546), and the SGB6 promoter (U.S. Patent No. 5,470,359), as well as synthetic or other natural promoters.

[0124] Additional flexibility in controlling heterologous gene expression in plants may be obtained by using DNA binding domains and response elements from heterologous sources *(i.e.*, DNA binding domains from non-plant sources). An example of such a heterologous DNA binding domain is the LexA DNA binding domain (Brent and Ptashne, 1985, Cell 43:729-736).

[0125] The invention further provides a recombinant expression vector comprising an ACCDP DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively linked to a regulatory sequence in a manner that allows for expression (by transcription of the DNA molecule) of an RNA molecule that is antisense to an ACCDP mRNA. Regulatory sequences operatively linked to a nucleic acid molecule cloned in the

antisense orientation can be chosen which direct the continuous expression of the antisense RNA molecule in a variety of cell types. For instance, viral promoters and/or enhancers, or regulatory sequences can be chosen which direct constitutive, tissue specific, or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid, or attenuated virus wherein antisense nucleic acids are produced under the control of a high efficiency regulatory region. The activity of the regulatory region can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes, see Weintraub, H. et al., 1986, Antisense RNA as a molecular tool for genetic analysis, Reviews - Trends in Genetics, Vol. 1(1), and Mol et al., 1990, FEBS Letters 268:427-430.

[0126] Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but they also apply to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein. A host cell can be any prokaryotic or eukaryotic cell. For example, an ACCDP can be expressed in bacterial cells such as *C. glutamicum*, insect cells, fungal cells, or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells), algae, ciliates, plant cells, fungi, or other microorganisms like *C. glutamicum*. Other suitable host cells are known to those skilled in the art.

[0127] A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (i.e., express) an ACCDP. Accordingly, the invention further provides methods for producing ACCDPs using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding an ACCDP has been introduced, or into which genome has been introduced a gene encoding a wild-type or altered ACCDP) in a suitable medium until the ACCDP is produced. In another embodiment, the method further comprises isolating ACCDPs from the medium or the host cell.

[0128] Another aspect of the invention pertains to isolated ACCDPs, and biologically active portions thereof. An "isolated" or "purified" polypeptide or biologically active portion thereof is free of some of the cellular material when produced by recombinant DNA techniques, or chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of ACCDP in which the polypeptide is separated from some of the cellular components of the cells in which it is naturally or recombinantly produced. In one embodiment, the language "substantially free of cellular material" includes preparations of an ACCDP having less than about 30% (by dry weight) of non-ACCDP material (also referred to herein as a "contaminating polypeptide"), more preferably less than about 20% of non-ACCDP material,

still more preferably less than about 10% of non-ACCDP material, and most preferably less than about 5% non-ACCDP material.

[0129] The nucleic acid molecules, polypeptides, polypeptide homologs, fusion polypeptides, primers, vectors, and host cells described herein can be used in one or more of the following methods: identification of any of the organisms as provided in Column No. 2 of Table 1 and Table 2 and related organisms; mapping of genomes of organisms related to any of the organisms as provided in Column No. 2 of Table 1 and Table 2; identification and localization of the sequences of interest of any of the organisms as provided in Column No. 2 of Table 1 and Table 2; evolutionary studies; determination of ACCDP regions required for function; modulation of an ACCDP activity; modulation of the metabolism of one or more cell functions; modulation of the transmembrane transport of one or more compounds; modulation of stress resistance; and modulation of expression of ACCDP nucleic acids. In one embodiment of these methods, the ACCDP can convert ACC to α–ketobutyrate and ammonia.

[0130] The ACCDP nucleic acid molecules according to the invention have a variety of uses. Most importantly, the nucleic acid and amino acid sequences of the present invention can be used to transform plants, particularly crop plants, thereby inducing tolerance to stresses such as drought, high salinity, and cold. The present invention therefore provides a transgenic plant transformed by an ACCDP nucleic acid, wherein expression of the nucleic acid sequence in the plant results in increased root growth and/or tolerance to environmental stress as compared to a wild type variety of the plant. The transgenic plant can be a monocot or a dicot. The invention further provides that the transgenic plant can be selected from maize, wheat, rye, oat, triticale, rice, barley, sorghum, millet, sugarcane, soybean, peanut, cotton, rapeseed, canola, manihot, pepper, sunflower, tagetes, solanaceous plants, potato, tobacco, eggplant, tomato, Vicia species, pea, alfalfa, coffee, cacao, tea, Salix species, oil palm, coconut, perennial grass, and forage crops, for example.

[0131] In particular, the present invention describes using the expression of ACCDP coding nucleic acids to engineer plants with increased root growth, and/or increased yield, and/or that are drought-tolerant, salt-tolerant, and/or cold-tolerant. This strategy has herein been demonstrated using AtACCD (SEQ ID NO:1) in *Arabidopsis thaliana* and corn, but its application is not restricted to this gene or to these plants. Accordingly, the invention provides a transgenic crop plant containing an ACCDP as defined in any of SEQ ID NOS as provided in Column No. 4 of Table 1 and Table 2, wherein the plant has increased root growth, and/or increased yield, and/or increased tolerance to an environmental stress selected from one or more of the group consisting of drought, increased salt, or decreased or increased temperature. In preferred embodiments, the environmental stress is drought. In other preferred embodiments, the increased root growth is an increase in root length, preferably under water-limiting conditions.

[0132] The invention also provides a method of producing a transgenic crop plant containing an ACCDP coding nucleic acid, wherein expression of the nucleic acid(s) in the plant results in increased root growth, and/or increased yield, and/or increased tolerance to environmental stress as compared to a wild type variety of the plant comprising: (a) introducing into a plant cell an expression vector comprising an ACCDP nucleic acid, and (b) generating from the plant cell a transgenic plant with a increased root growth, and/or increased yield, and/or increased tolerance to environmental stress as compared to a wild type variety of the plant. The plant cell includes, but is not limited to, a protoplast, gamete producing cell, and a cell that regenerates into a whole plant. As used herein, the term "transgenic" refers to any plant, plant cell, callus, plant tissue, or plant part that contains all or part of at least one recombinant polynucleotide. In many cases, all or part of the recombinant polynucleotide is stably integrated into a chromosome or stable extra-chromosomal element, so that it is passed on to successive generations. In preferred embodiments, the ACCDP nucleic acid encodes a protein comprising the polypeptide of any of SEQ ID NOS as provided in Column No. 4 of Table 1 and Table 2.

[0133] The present invention also provides a method of modulating a plant's root growth, and/or yield, and/or tolerance to an environmental stress comprising, modifying the expression of an ACCDP coding nucleic acid in the plant. The plant's root growth, and/or yield, and/or tolerance to the environmental stress can be increased or decreased as achieved by increasing or decreasing the expression of an ACCDP, respectively. Preferably, the plant's root growth, and/or yield, and/or tolerance to the environmental stress is increased by increasing expression of an ACCDP. Expression of an ACCDP can be modified by any method known to those of skill in the art. The methods of increasing expression of ACCDPs can be used wherein the plant is either transgenic or not transgenic. In cases when the plant is transgenic, the plant can be transformed with a vector containing any of the above described ACCDP coding nucleic acids, or the plant can be transformed with a promoter that directs expression of native ACCDP in the plant, for example. The invention provides that such a promoter can be tissue preferred, developmentally regulated, stress inducible, or a combination thereof. Alternatively, non-transgenic plants can have native ACCDP expression modified by inducing a native promoter. The expression of ACCDP as defined in any of SEQ ID NOS as provided in Column No. 4 of Table 1 and Table 2 in target plants can be accomplished by, but is not limited to, one of the following examples: (a) constitutive promoter, (b) stress-inducible promoter, (c) chemical-induced promoter, and (d) engineered promoter overexpression with, for example, zinc-finger derived transcription factors (Greisman and Pabo, 1997, Science 275:657).

[0134] In a preferred embodiment, transcription of the ACCDP is modulated using zinc-finger derived transcription factors (ZFPs) as described in Greisman and Pabo, 1997, Science 275:657 and manufactured by Sangamo Biosciences, Inc. These ZFPs comprise both a DNA recognition domain and a functional domain that causes activation or repression of a target nucleic acid such as an ACCDP nucleic acid. Therefore, activating and repressing ZFPs can be created that

specifically recognize the ACCDP promoters described above and used to increase or decrease ACCDP expression in a plant, thereby modulating the yield and/or stress tolerance of the plant. The present invention also includes identification of the homologs of ACCDP coding nucleic acids as defined in any of SEQ ID NOS as provided in Column No. 3 of Table 1 and Table 2 in a target plant, as well as the homolog's promoter. The invention also provides a method of increasing expression of a gene of interest within a host cell as compared to a wild type variety of the host cell, wherein the gene of interest is transcribed in response to an ACCDP, comprising: (a) transforming the host cell with an expression vector comprising an ACCDP coding nucleic acid, and (b) expressing the ACCDP within the host cell, thereby increasing the expression of the gene transcribed in response to the ACCDP, as compared to a wild type variety of the host cell.

[0135] In addition to introducing the ACCDP nucleic acid sequences into transgenic plants, these sequences can also be used to identify an organism as being any of the organisms as provided in Column No. 2 of Table 1 and Table 2, or a close relative thereof. Also, they may be used to identify the presence of any of the organisms as provided in Column No. 2 of Table 1 and Table 2, or a relative thereof in a mixed population of organisms. The invention relates to the nucleic acid sequences of a number of genes from any of the organisms as provided in Column No. 2 of Table 1 and Table 2; by probing the extracted genomic DNA of a culture of a unique or mixed population of organisms under stringent conditions with a probe spanning a region of a particular gene that is unique to the corresponding organism according to Table 1 and Table 2, one can ascertain whether this organism is present.

[0136] Further, the nucleic acid and polypeptide molecules according to the invention may serve as markers for specific regions of the genome. This has utility not only in the mapping of the genome, but also in functional studies of the polypeptides encoded by such genome. For example, to identify the region of the genome to which a particular organism's DNA-binding polypeptide binds, the organism's genome could be digested, and the fragments incubated with the DNA-binding polypeptide. Those fragments that bind the polypeptide may be additionally probed with the nucleic acid molecules of the invention, preferably with readily detectable labels. Binding of such a nucleic acid molecule to the genome fragment enables the localization of the fragment to the genome map of such an organism and, when performed multiple times with different enzymes, facilitates a rapid determination of the nucleic acid sequence to which the polypeptide binds. Further, the nucleic acid molecules of the invention may be sufficiently identical to the sequences of related species such that these nucleic acid molecules may serve as markers for the construction of a genomic map in related plants.

[0137] The ACCDP nucleic acid molecules of the invention are also useful for evolutionary and polypeptide structural studies. The amino acid conversion processes in which the molecules of the invention participate are utilized by a wide variety of prokaryotic and eukaryotic cells; by comparing the sequences of the nucleic acid molecules of the present invention to those encoding

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

[0138] Manipulation of the ACCDP nucleic acid molecules of the invention may result in the production of ACCDPs having functional differences from the wild-type ACCDPs. These polypeptides may be improved in efficiency or activity, may be present in greater numbers in the cell than is usual, or may be decreased in efficiency or activity.

[0139] There are a number of mechanisms by which the alteration of an ACCDP of the invention may directly affect root growth, and/or yield, and/or stress response and/or stress tolerance. In the case of plants expressing ACCDP, the enzyme might act to stimulate root elongation by sequestering and hydrolyzing ACC from germinating seeds, thus lowering the level of ACC and consequently lowering the level of ethylene in the seeds. For many plants, ethylene stimulates germination. It has been noted that if ethylene concentration remains high after germination, root elongation is inhibited (Jackson (1991), p. 159-181. In A.K. Matoo and J.C. Suttle (ed.) The Plant Hormone Ethylene, CRC Press, Boca Raton, FL). Therefore, lowering ethylene concentrations in seeds after germination leads to an increase in root length, and improved plant water use efficiency.

[0140] The effect of the genetic modification in plants, *C. glutamicum*, fungi, algae, or ciliates on root growth and/or stress tolerance can be assessed by growing the modified microorganism or plant under less than suitable conditions and then analyzing the growth characteristics and/or metabolism of the plant. Such analysis techniques are well known to one skilled in the art, and include dry weight, wet weight, polypeptide synthesis, carbohydrate synthesis, lipid synthesis, evapotranspiration rates, general plant and/or crop yield, flowering, reproduction, seed setting, root growth, respiration rates, photosynthesis rates, etc. (Applications of HPLC in Biochemistry in: Laboratory Techniques in Biochemistry and Molecular Biology, vol. 17; Rehm et al., 1993 Biotechnology, vol. 3, Chapter III: Product recovery and purification, page 469-714, VCH: Weinheim; Belter, P.A. et al., 1988, Bioseparations: downstream processing for biotechnology, John Wiley and Sons; Kennedy, J.F. and Cabral, J.M.S., 1992, Recovery processes for biological materials, John Wiley and Sons; Shaeiwitz, J.A. and Henry, J.D., 1988, Biochemical separations, in: Ulmann's Encyclopedia of Industrial Chemistry, vol. B3, Chapter 11, page 1-27, VCH: Weinheim; and Dechow, F.J., 1989; Separation and purification techniques in biotechnology, Noyes Publications).

[0141] For example, yeast expression vectors comprising the nucleic acids disclosed herein, or fragments thereof, can be constructed and transformed into *Saccharomyces cerevisiae* using standard protocols. The resulting transgenic cells can then be assayed for fail or alteration of their

increased growth and/or tolerance to drought, salt, and temperature stresses. Similarly, plant expression vectors comprising the nucleic acids disclosed herein, or fragments thereof, can be constructed and transformed into an appropriate plant cell such as *Arabidopsis*, soy, rape, maize, wheat, *Medicago truncatula*, etc., using standard protocols. The resulting transgenic cells and/or plants derived there from can then be assayed for fail or alteration of their increased root growth and/or tolerance to drought, salt, and temperature stresses.

[0142] Additionally, the sequences disclosed herein, or fragments thereof, can be used to generate knockout mutations in the genomes of various organisms, such as bacteria, mammalian cells, yeast cells, and plant cells (Girke, T., 1998, The Plant Journal 15:39-48). The resultant knockout cells can then be evaluated for their ability or capacity to tolerate various stress conditions, their response to various stress conditions, and the effect on the phenotype and/or genotype of the mutation. For other methods of gene inactivation, see U.S. Patent No. 6,004,804 "Non-Chimeric Mutational Vectors" and Puttaraju et al., 1999, Spliceosome-mediated RNA *trans*-splicing as a tool for gene therapy, Nature Biotechnology 17:246-252.

[0143] The aforementioned mutagenesis strategies for ACCDPs resulting in increased root growth, and/or yield, and/or stress tolerance are not meant to be limiting; variations on these strategies will be readily apparent to one skilled in the art. Using such strategies, and incorporating the mechanisms disclosed herein, the nucleic acid and polypeptide molecules of the invention may be utilized to generate algae, ciliates, plants, fungi, or other microorganisms like *C. glutamicum* expressing mutated ACCDP nucleic acid and polypeptide molecules such that the root growth and/or stress tolerance is improved.

[0144] The present invention also provides antibodies that specifically bind to an ACCDP, or a portion thereof, as encoded by a nucleic acid described herein. Antibodies can be made by many well-known methods (See, e.g., Harlow and Lane, "Antibodies; A Laboratory Manual," Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, (1988)). Briefly, purified antigen can be injected into an animal in an amount and in intervals sufficient to elicit an immune response. Antibodies can either be purified directly, or spleen cells can be obtained from the animal. The cells can then fused with an immortal cell line and screened for antibody secretion. The antibodies can be used to screen nucleic acid clone libraries for cells secreting the antigen. Those positive clones can then be sequenced. (See, for example, Kelly et al., 1992, Bio/Technology 10:163-167; Bebbington et al., 1992, Bio/Technology 10:169-175).

[0145] The phrases "selectively binds" and "specifically binds" with the polypeptide refer to a binding reaction that is determinative of the presence of the polypeptide in a heterogeneous population of polypeptides and other biologics. Thus, under designated immunoassay conditions, the specified antibodies bound to a particular polypeptide do not bind in a significant amount to other polypeptides present in the sample. Selective binding of an antibody under such conditions may require an antibody that is selected for its specificity for a particular polypeptide. A variety of

immunoassay formats may be used to select antibodies that selectively bind with a particular polypeptide. For example, solid-phase ELISA immunoassays are routinely used to select antibodies selectively immunoreactive with a polypeptide. See Harlow and Lane, "Antibodies, A Laboratory Manual" Cold Spring Harbor Publications, New York, (1988), for a description of immunoassay formats and conditions that could be used to determine selective binding.

[0146] In some instances, it is desirable to prepare monoclonal antibodies from various hosts. A description of techniques for preparing such monoclonal antibodies may be found in Stites et al., eds., "Basic and Clinical Immunology," (Lange Medical Publications, Los Altos, Calif., Fourth Edition) and references cited therein, and in Harlow and Lane "Antibodies, A Laboratory Manual" Cold Spring Harbor Publications, New York, 1988.

[0147] Throughout this application, various publications are referenced. The disclosures of all of these publications and those references cited within those publications in their entireties are hereby incorporated by reference into this application in order to more fully describe the state of the art to which this invention pertains.

[0148] It should also be understood that the foregoing relates to preferred embodiments of the present invention and that numerous changes may be made therein without departing from the scope of the invention. The invention is further illustrated by the following examples, which are not to be construed in any way as imposing limitations upon the scope thereof. On the contrary, it is to be clearly understood that resort may be had to various other embodiments, modifications, and equivalents thereof, which, after reading the description herein, may suggest themselves to those skilled in the art without departing from the spirit of the present invention and/or the scope of the appended claims.

EXAMPLES

Example 1

Total DNA isolation from plant material

[0149] The details for the isolation of total DNA relate to the working up of one gram fresh weight of plant material. The materials used include the following buffers: CTAB buffer: 2% (w/v) N-cethyl-N,N,N-trimethylammonium bromide (CTAB); 100 mM Tris HCl pH 8.0; 1.4 M NaCl; 20 mM EDTA; N-Laurylsarcosine buffer: 10% (w/v) N-laurylsarcosine; 100 mM Tris HCl pH 8.0; and 20 mM EDTA.

[0150] The plant material was triturated under liquid nitrogen in a mortar to give a fine powder and transferred to 2 ml Eppendorf vessels. The frozen plant material was then covered with a layer of 1 ml of decomposition buffer (1 ml CTAB buffer, 100 µl of N-laurylsarcosine buffer, 20 µl of β-mercaptoethanol, and 10 µl of proteinase K solution, 10 mg/ml) and incubated at 60°C for one hour with continuous shaking. The homogenate obtained was distributed into two Eppendorf vessels (2 ml) and extracted twice by shaking with the same volume of chloroform/isoamyl alcohol (24:1). For phase separation, centrifugation was carried out at 8000 x g and room temperature for 15 minutes

in each case. The DNA was then precipitated at -70°C for 30 minutes using ice-cold isopropanol. The precipitated DNA was sedimented at 4°C and 10,000 g for 30 minutes and resuspended in 180 µl of TE buffer (Sambrook et al., 1989, Cold Spring Harbor Laboratory Press: ISBN 0-87969-309-6). For further purification, the DNA was treated with NaCl (1.2 M final concentration) and precipitated again at -70°C for 30 minutes using twice the volume of absolute ethanol. After a washing step with 70% ethanol, the DNA was dried and subsequently taken up in 50 µl of H_2O + RNAse (50 mg/ml final concentration). The DNA was dissolved overnight at 4°C, and the RNAse digestion was subsequently carried out at 37°C for 1 hour. Storage of the DNA took place at 4°C.

Example 2

Preparation of total RNA and cDNA from Arabidopsis plant material

[0151] AtACCD was isolated by preparing RNA from Arabidopsis leaves using the RNA mini-isolation kit (Qiagen kit) following the manufacturer's recommendations. Reverse transcription reactions and amplification of the cDNA were performed as described below.

1. Use 2 µl of RNA (0.5 – 2.0 µg) preparation in a 10 µl Dnase reaction, move the tube to 37°C for 15 minutes, add 1µl 25 mM EDTA, and then heat reaction to 65°C for 15 minutes.
   a. Buffer (10X: 200 mM Tris, 500 mM KCl, 20 mM $MgCl_2$) – 1µl
   b. RNA – 2µl
   c. Dnase (10 U/µl)– 1µl
   d. H_2O – 6µl
2. Use 1µl of the above reaction in a room temperature reaction, and heat to 65°C for 5 minutes.
   a. Dnased RNA (0.025-0.1 µg depending on the starting amount)– 1µl
   b. 10 mM dNTPs – 1µl
   c. Primer (10 µM)– 1µl
   d. H_2O – up to 10µl
3. Prepare a reaction mix with these reagents in a separate tube
   a. SuperScript II RT buffer (10X)– 2µl
   b. 25 mM $MgCl_2$ – 4µl
   c. DTT (0.1 M) – 2µl
   d. Rnase Out Rnase Inhibitor (40 U/µl)– 1µl
4. Add the 9 µl reaction mix to the denatured RNA solution, and hold at 42°C for 2 minutes.
5. Add 1 µl of SuperScriptII RT (50 U/µl), and incubate at 42°C for 50 minutes.
6. Terminate reaction at 70°C for 15 minutes.
7. Optional: add 1µl of RNAseH to reaction to remove RNA.
8. Perform PCR as you would using 1-2 µl of the new cDNA.

Tissue harvest, RNA isolation, and cDNA library construction

[0152] Crop plants were grown under a variety of conditions and treatments, and different tissues were harvested at various developmental stages. Plant growth and harvesting were done in a strategic manner such that the probability of harvesting all expressable genes in at least one or more of the resulting libraries is maximized. The mRNA was isolated as described above from each of the collected samples, and cDNA libraries were constructed. No amplification steps were used in the library production process in order to minimize redundancy of genes within the sample and to retain expression information. All libraries were 3' generated from mRNA purified on oligo dT columns. Colonies from the transformation of the cDNA library into *E. coli* were randomly picked and placed into microtiter plates.

PCR Amplification of cDNA Inserts and Spotting

[0153] The cDNA inserts from each clone from the microtiter plates were PCR amplified. Plasmid DNA was isolated from the *E. coli* colonies and then spotted on membranes. No purification step was necessary prior to spotting samples to nylon membranes.

Example 3

Cloning of AtACCD

[0154] The cDNA isolated as described in Example 2 was used to clone the AtACCD gene by RT-PCR. The following primers were used: The forward primer was 5'-5'GGGGTCGACGAAGCAATGAGAGGACGAAGCT -3' (SEQ ID NO:358). The reverse primer was 5'- GGGTTAATTAACAGATTTTGTTGTGCTAGAAC -3' (SEQ ID NO:359). PCR reactions for the amplification included: 1x PCR buffer, 0.2 mM dNTP, 100 ng *Arabidopsis thaliana* DNA, 25 pmol reverse primer, 2.5 u Pfu or Herculase DNA polymerase.

[0155] PCR was performed according to standard conditions and to manufacturer's protocols (Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, 2nd Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, Biometra T3 Thermocycler). The parameters for the reaction were: 1 cycle for 3 minutes at 94°C; followed by 25 cycles of 30 seconds at 94°C, 30 seconds at 55°C, and 1.5 minutes at 72°C.

[0156] The amplified fragments were then extracted from agarose gel with a QIAquick Gel Extraction Kit (Qiagen) and ligated into the TOPO pCR 2.1 vector (Invitrogen) following manufacture's instructions. Recombinant vectors were transformed into Top10 cells (Invitrogen) using standard conditions (Sambrook et al. 1989. Molecular Cloning, A Laboratory Manual, 2nd Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY). Transformed cells were selected for on LB agar containing 100 μg/ml carbenicillin, 0.8 mg X-gal (5-bromo-4-chloro-3-indolyl-β-D-galactoside) and 0.8 mg IPTG (isopropylthio-β-D-galactoside) grown overnight at 37°C. White colonies were selected and used to inoculate 3 ml of liquid LB containing 100 μg/ml ampicillin and grown overnight at 37°C. Plasmid DNA was extracted using the QIAprep Spin Miniprep Kit (Qiagen) following manufacture's instructions. Analyses of subsequent clones and

restriction mapping were performed according to standard molecular biology techniques (Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, 2nd Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY).

[0157] The clones were sequenced, which confirmed that the identity of the cloned gene was identical to the sequence deposited in the *Arabidopsis thaliana* database (SEQ ID NO:1). The deduced amino acid sequence of AtACCD is shown at SEQ ID NO:2.

[0158] The AtACCD gene was then cloned into a binary vector and expressed under the Superpromoter (Figure 3). The Superpromoter is constitutive, but root preferential (U.S. Patent Nos. 5,428,147 and 5,217,903).

Example 4

Arabidopsis Plant Transformation

[0159] Transgenic *Arabidopsis thaliana* (Col) plants were generated by the dipping infiltration method (Bechtold et al., 1993, "In planta Agrobacterium-mediated gene transfer by infiltration of adult Arabidopsis thaliana plants," C. R. Acad. Sci. Paris Life Sci. 316:1194-1199) . The binary vectors were transformed into Agrobacteria strain C58C1 or pMP90 using electroporation. Culture of the transformed Agrobacteria was grown, and the bacteria was resuspended in dipping infiltration media (1/2 MS, 5% sucrose, 0.5 mg/ml MES, pH 5.7 and with 200 ppm Silwet L-77 (Lehle Seeds) added.) Each culture was used to transform 3 pots of approximately 5 week-old Col0 Arabidopsis plants by dipping pots 5 minutes each in resuspended Agrobacterium cultures. The plants were then grown to seed under standard Arabidopsis conditions (23°C day/20°C night, 18 hour day and 65% humidity). T1 seeds were screened on MS plates using 100 nM Pursuit (BASF).

Screening of Transformed Plants

[0160] T1 seeds were sterilized according to standard protocols (Xiong et al., 1999, Plant Molecular Biology Reporter 17: 159-170). Seeds were selected on ½ Murashige and Skoog media (MS) (Sigma-Aldrich), 0.6% agar and supplemented with 1% sucrose, and 2 μg/ml benomyl (Sigma-Aldrich). Seeds on plates were vernalized for four days at 4°C. The seeds were germinated in a climatic chamber at an air temperature of 22°C and light intensity of 40 micromols$^{-1}m2$ (white light; Philips TL 65W/25 fluorescent tube) and 16 hours light and 8 hours dark day length cycle. Transformed seedlings were selected after 14 days and transferred to ½ MS media supplemented with 0.6% agar, 1% sucrose, and allowed to recover for five to seven days.

[0161] Seeds of T2 generation were used for plant root analysis in soil and *in vitro*.

Example 5

In vitro Root Analysis of Transformed Arabidopsis Plants

[0162] For *in vitro* root analysis of transformed plants, square plates measuring 12 cm x 12 cm were used. For each plate, 52 ml of MS media (0.5X MS salts, 0.5% sucrose, 0.5 g/L MES

buffer, 1% Phytagar) without selection was used. Plates were allowed to dry in the sterile hood for one hour to reduce future condensation.

[0163] Seed aliquots were sterilized in glass vials with ethanol for 5 minutes, the ethanol was removed, and the seeds were allowed to dry in the sterile hood for one hour. Seeds were spotted in the plates using the Vacuseed Device (Lehle). In the experimental design, every plate contained both wild type and AtACCD transgenic plants. Therefore, every line was always compared to the controls grown in the same plate(s) to account for microenvironment variation. After the seeds were spotted on the plates, the plates were wrapped with Ventwrap and placed vertically in racks in the dark at 4°C for four days to stratify the seeds. The plates were transferred to a C5 Percival Growth Chamber and placed vertically for fourteen days. The growth chamber conditions were 23°C day/21°C night and 16 hour days/8 hour nights.

[0164] For data collection a high resolution flat-bed scanner was used. Analysis of the roots was done using the WinRhizo software package.

[0165] The results of these experiments were also analyzed at the gene level. To do this, root length of all plants for all transgenic lines was averaged and compared against the average of the wild type plants. Presence of the transgene and copy number of the events were determined targeting the NOS terminator in real time PCR. The NOS Primers used for the analysis were: Forward primer 5'-TCCCCGATCGTTCAAACATT-3' (SEQ ID NO:360), Reverse primer 5'-CCATCTCATAAATAACGTCATGCAT-3' (SEQ ID NO:361). The reactions were run in a 96-well optical plate (Applied Biosystems, 4314320), and the endogenous control and gene of interest reactions were run on the same plate simultaneously. A master mix was made for both primer sets. The master mixes and the 96-well plate for assay should be kept on ice. Calculations are included for 52 reactions, which is suitable for half of the plate with use of a multichannel pipetter. The Eurogentec kit, (cat#RTSNRT032X-1) was used, and reactions were prepared using manufacturer's recommendations. A GeneAmp 5700 was used to run the reactions and collect data.

Results

[0166] The results show that transgenic AtACCD plants evaluated in plates have a longer root phenotype. Figure 4A shows the results of the plants grown in vertical plates on a per line basis. The majority of AtACCD transgenic lines screened exhibited a longer root phenotype in comparison to wild-type control plant roots. The phenotype was more clearly observed in lines 2, 3, 5, 6, and 9.

[0167] The gene level analysis of the AtACCD transgenic plants, as seen in Figure 4B, confirmed that the AtACCD plants exhibited an increased root length phenotype. Based on this analysis, ACCDP transgenic *Arabidopsis* plants exhibited a 13.8% increase in root length.

Example 6

Soil Root Analysis of Transformed Arabidopsis Plants

[0168] For soil root analysis, seeds were imbibed at 4°C for 2 days in water and were planted directly in soil with no selection. Deepots (Hummert D40) were used with a saturated peat pellet (Jiffy 727) at the base and filled with water saturated Metromix. After planting, pots were covered with plastic wrap to prevent drying. Plants were grown using only water present at media preparation, as the water in the soil in these large pots is sufficient for 3 weeks of growth, and encourages rapid root growth. The plastic wrapping of the pots was removed after 12 days and morphological data was documented. At day 17 the aerial parts of the plant were harvested, dried at 65°C for 2 days and the dry weight was measured. To examine the roots, the peat pellet was pushed towards the top of the pot to remove the soil and roots as a unit. The soil was then separated from the roots in a tray and the maximum root length was measured.

[0169] To determine the impact of the root phenotype in the above ground tissues of the transgenic plants, the dry weight of the rosette was measured and compared against the wild type plants.

Results

[0170] Roots of the AtACCD lines were also evaluated in soil as described above. The results indicated transgenic plants exhibited a longer root phenotype when plants are grown in soil (Figures 5 and 6). In general, all AtACCD lines analyzed exhibited increased growth in the soil-based assay. Lines 2, 4, 7, 10 and 11 showed the greatest increase in root length (Figure 5). Figure 6 shows the ANOVA of the overall performance of the AtACCD gene, demonstrating that the AtACCD transgenic plants performed significantly better than the wild type controls.

[0171] The dry weight of the rosette was measured, and the ANOVA analysis of the results is shown in Figure 7. No significant differences were observed between the transgenic plants and the wild type controls. Therefore the rosette biomass does not appear to be affected by the over-expression of the AtACCD gene.

Example 7

Identification of Homologs to AtACCD

[0172] The algorithms used in the present invention include: FASTA (Very sensitive sequence database searches with estimates of statistical significance; Pearson, 1990, Rapid and sensitive sequence comparison with FASTP and FASTA, Methods Enzymol. 183:63-98); BLAST (Very sensitive sequence database searches with estimates of statistical significance; Altschul et al., Basic local alignment search tool, Journal of Molecular Biology 215:403-10); PREDATOR (High-accuracy secondary structure prediction from single and multiple sequences; Frishman and Argos, 1997, 75% accuracy in protein secondary structure prediction. Proteins 27:329-335); CLUSTALW (Multiple sequence alignment; Thompson et al., 1994, CLUSTAL W (improving the sensitivity of progressive multiple sequence alignment through sequence weighting, positions-specific gap

penalties and weight matrix choice), Nucleic Acids Research 22:4673-4680); TMAP (Transmembrane region prediction from multiply aligned sequences; Persson and Argos, 1994, Prediction of transmembrane segments in proteins utilizing multiple sequence alignments, J. Mol. Biol. 237:182-192); ALOM2 (Transmembrane region prediction from single sequences; Klein et al., Prediction of protein function from sequence properties: A discriminate analysis of a database. Biochim. Biophys. Acta 787:221-226 (1984). Version 2 by Dr. K. Nakai); PROSEARCH (Detection of PROSITE protein sequence patterns; Kolakowski et al., 1992, ProSearch: fast searching of protein sequences with regular expression patterns related to protein structure and function. Biotechniques 13, 919-921); BLIMPS (Similarity searches against a database of ungapped blocks, Wallace and Henikoff, 1992); PATMAT (a searching and extraction program for sequence, pattern and block queries and databases, CABIOS 8:249-254. Written by Bill Alford).

[0173] Homologs of the AtACCD gene were found in the public and proprietary databases. These homologs were evaluated to determine the level of relationship to AtACCD. The tblastn program from the BLAST family of algorithms was used to compare the AtACCD protein sequence against the proprietary crop databases translated in all six reading frames. Sequences with significant homology were found in each crop library. The sequence identity percentage at amino acid level of each sequence as compared to AtACCD is shown in Column No. 5 of Table 1 and Table 2.

[0174] The BLAST alignments at amino acid level between AtACCD (SEQ ID NO:2) and ACCDP from crops such as soybean, rice, maize and wheat are shown in Figures 9-12. The ACCDP from soybean, rice, maize and wheat as shown in Figures 9-12 are considered to be full-length. Full length sequences for the remaining partial sequences may be obtained using primer sequences based on the disclosed partial cDNA sequences using standard molecular biology techniques (See Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, 2nd Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY).

Example 8

Engineering soybean plants by overexpressing the ACCDP gene

[0175] Seeds of soybean are surface sterilized with 70% ethanol for 4 minutes at room temperature with continuous shaking, followed by 20% (v/v) Clorox supplemented with 0.05% (v/v) Tween for 20 minutes with continuous shaking. Then, the seeds are rinsed 4 times with distilled water and placed on moistened sterile filter paper in a Petri dish at room temperature for 6 to 39 hours. The seed coats are peeled off, and cotyledons are detached from the embryo axis. The embryo axis is examined to make sure that the meristematic region is not damaged. The excised embryo axes are collected in a half-open sterile Petri dish and air-dried to a moisture content less than 20% (fresh weight) in a sealed Petri dish until further use.

[0176] *Agrobacterium tumefaciens* culture is prepared from a single colony in LB solid medium plus appropriate selection agents followed by growth of the single colony in liquid LB medium to an optical density at 600 nm of 0.8. Then, the bacteria culture is pelleted at 7000 rpm for

7 minutes at room temperature, and resuspended in MS medium supplemented with 100 μM acetosyringone. Bacteria cultures are incubated in this pre-induction medium for 2 hours at room temperature before use. The axis of soybean zygotic seed embryos at approximately 15% moisture content are imbibed for 2 hours at room temperature with the pre-induced *Agrobacterium* suspension culture. The embryos are removed from the imbibition culture and are transferred to Petri dishes containing solid MS medium supplemented with 2% sucrose and incubated for 2 days in the dark at room temperature. Alternatively, the embryos are placed on top of moistened (liquid MS medium) sterile filter paper in a Petri dish and incubated under the same conditions described above. After this period, the embryos are transferred to either solid or liquid MS medium supplemented with 500 mg/L carbenicillin or 300 mg/L cefotaxime to kill the *Agrobacteria.* The liquid medium is used to moisten the sterile filter paper. The embryos are incubated during 4 weeks at 25°C, under 150 μmol $m^{-2}sec^{-1}$ and 12 hours photoperiod. Once the seedlings produce roots, they are transferred to sterile metromix soil. The medium of the *in vitro* plants is washed off before transferring the plants to soil. The plants are kept under a plastic cover for 1 week to favor the acclimatization process. Then the plants are transferred to a growth room where they are incubated at 25°C, under 150 μmol $m^{-2}sec^{-1}$ light intensity and 12 hours photoperiod for about 80 days.

[0177] The transgenic plants are screened for their improved root growth and/or stress tolerance, demonstrating that transgene expression confers increased root growth, stress tolerance, and/or increased water use efficiency.

Example 9

Engineering Rapeseed/Canola Plants By Overexpressing the ACCDP Gene

[0178] The method of plant transformation described herein is applicable to *Brassica* and other crops. Seeds of canola are surface sterilized with 70% ethanol for 4 minutes at room temperature with continuous shaking, followed by 20% (v/v) Clorox supplemented with 0.05 % (v/v) Tween for 20 minutes, at room temperature with continuous shaking. Then, the seeds are rinsed 4 times with distilled water and placed on moistened sterile filter paper in a Petri dish at room temperature for 18 hours. Then the seed coats are removed, and the seeds are air dried overnight in a half-open sterile Petri dish. During this period, the seeds lose approximately 85% of their water content. The seeds are then stored at room temperature in a sealed Petri dish until further use. DNA constructs and embryo imbibition are as described in Example 10. Samples of the primary transgenic plants (T0) are analyzed by PCR to confirm the presence of T-DNA. These results are confirmed by Southern hybridization in which DNA is electrophoresed on a 1% agarose gel and transferred to a positively charged nylon membrane (Roche Diagnostics). The PCR DIG Probe Synthesis Kit (Roche Diagnostics) is used to prepare a digoxigenin-labelled probe by PCR, and used as recommended by the manufacturer.

[0179] The transgenic plants are screened for their improved root growth and/or stress tolerance, demonstrating that transgene expression confers increased root growth, stress tolerance, and/or increased water use efficiency.

Example 10

Engineering Corn Plants By Overexpressing the ACCDP gene

[0180] Transformation of maize (*Zea Mays L.*) with the gene of interest is performed with the method described by Ishida et al., 1996, Nature Biotech. 14745-50. Immature embryos are co-cultivated with *Agrobacterium tumefaciens* that carry "super binary" vectors, and transgenic plants are recovered through organogenesis. This procedure provides a transformation efficiency of between 2.5% and 20%. The transgenic plants are screened for their improved root growth and/or stress tolerance, demonstrating that transgene expression confers increased root growth, stress tolerance, and/or increased water use efficiency.

Example 11

Engineering Rice Plants By Overexpressing the ACCDP gene

[0181] Transformation of rice with the gene of interest can be undertaken by direct gene transfer techniques utilizing protoplasts or particle bombardment. Protoplast-mediated transformation has been described for Japonica-types and Indica-types (Zhang et al., 1988, Plant Cell Rep. 7:379-384; Shimamoto et al., 1989, Nature 338:274-277; Datta et al., 1990, Biotechnology 8:736-740). Both types are also routinely transformable using particle bombardment (Christou et al., 1991, Biotechnology 9:957-962). The transgenic plants are screened for their improved growth and/or stress tolerance, demonstrating that transgene expression confers increased root growth, stress tolerance, and/or increased water use efficiency.

Example 12

Identification of Homologous and Heterologous Genes

[0182] Gene sequences can be used to identify homologous or heterologous genes from cDNA or genomic libraries. Homologous genes (e. g. full-length cDNA clones) can be isolated via nucleic acid hybridization using for example cDNA libraries. Depending on the abundance of the gene of interest, 100,000 up to 1,000,000 recombinant bacteriophages are plated and transferred to nylon membranes. After denaturation with alkali, DNA is immobilized on the membrane by, e.g., UV cross linking. Hybridization is carried out at high stringency conditions. In aqueous solution, hybridization and washing is performed at an ionic strength of 1 M NaCl and a temperature of 68°C. Hybridization probes are generated by, e.g., radioactive (^{32}P) nick transcription labeling (High Prime, Roche, Mannheim, Germany). Signals are detected by autoradiography.

[0183] Partially homologous or heterologous genes that are related but not identical can be identified in a manner analogous to the above-described procedure using low stringency hybridization and washing conditions. For aqueous hybridization, the ionic strength is normally kept at 1 M NaCl while the temperature is progressively lowered from 68 to 42°C.

[0184] Isolation of gene sequences with homologies (or sequence identity/similarity) only in a distinct domain of (for example 10-20 amino acids) can be carried out by using synthetic radio labeled oligonucleotide probes. Radiolabeled oligonucleotides are prepared by phosphorylation of the 5-prime end of two complementary oligonucleotides with T4 polynucleotide kinase. The complementary oligonucleotides are annealed and ligated to form concatemers. The double stranded concatemers are then radiolabeled by, for example, nick transcription. Hybridization is normally performed at low stringency conditions using high oligonucleotide concentrations.

Oligonucleotide hybridization solution:

6 x SSC

0.01 M sodium phosphate

1 mM EDTA (pH 8)

0.5 % SDS

100 µg/ml denatured salmon sperm DNA

0.1 % nonfat dried milk

[0185] During hybridization, the temperature is lowered stepwise to 5-10°C below the estimated oligonucleotide T_m, or down to room temperature, followed by washing steps and autoradiography. Washing is performed with low stringency, such as 3 washing steps using 4 x SSC. Further details are described by Sambrook, J. et al., 1989, "Molecular Cloning: A Laboratory Manual", Cold Spring Harbor Laboratory Press or Ausubel, F.M. et al., 1994, "Current Protocols in Molecular Biology", John Wiley & Sons.

Example 13

Identification of Homologous Genes by Screening Expression Libraries with Antibodies

[0186] c-DNA clones can be used to produce recombinant protein for example in *E. coli* (e.g. Qiagen QIAexpress pQE system). Recombinant proteins are then normally affinity purified via Ni-NTA affinity chromatography (Qiagen). Recombinant proteins are then used to produce specific antibodies for example by using standard techniques for rabbit immunization. Antibodies are affinity purified using a Ni-NTA column saturated with the recombinant antigen as described by Gu et al., 1994, BioTechniques 17:257-262. The antibody can be used to screen expression cDNA libraries to identify homologous or heterologous genes via an immunological screening (Sambrook, J. et al., 1989, "Molecular Cloning: A Laboratory Manual", Cold Spring Harbor Laboratory Press or Ausubel, F.M. et al., 1994, "Current Protocols in Molecular Biology", John Wiley & Sons).

Example 14

In vivo Mutagenesis

[0187] *In vivo* mutagenesis of microorganisms can be performed by passage of plasmid (or other vector) DNA through *E. coli* or other microorganisms (e.g. *Bacillus spp.* or yeasts such as *Saccharomyces cerevisiae*) which are impaired in their capabilities to maintain the integrity of their genetic information. Typical mutator strains have mutations in the genes for the DNA repair system

(e.g., mutHLS, mutD, mutT, etc.; for reference, see Rupp, W.D., 1996, DNA repair mechanisms, in: *Escherichia coli* and *Salmonella*, p. 2277-2294, ASM: Washington.) Such strains are well known to those skilled in the art. The use of such strains is illustrated, for example, in Greener, A. and Callahan, M., 1994, Strategies 7:32-34. Transfer of mutated DNA molecules into plants is preferably done after selection and testing in microorganisms. Transgenic plants are generated according to various examples within the exemplification of this document.

Example 15

In vitro Analysis of the Function of Arabidopsis Genes in Transgenic Organisms

[0188] The determination of activities and kinetic parameters of enzymes is well established in the art. Experiments to determine the activity of any given altered enzyme must be tailored to the specific activity of the wild-type enzyme, which is well within the ability of one skilled in the art. Overviews about enzymes in general, as well as specific details concerning structure, kinetics, principles, methods, applications, and examples for the determination of many enzyme activities may be found, for example, in the following references: Dixon, M., and Webb, E.C., 1979, Enzymes. Longmans: London; Fersht, 1985, Enzyme Structure and Mechanism. Freeman: New York; Walsh, 1979, Enzymatic Reaction Mechanisms. Freeman: San Francisco; Price, N.C., Stevens, L., 1982, Fundamentals of Enzymology. Oxford Univ. Press: Oxford; Boyer, P.D., ed., 1983, The Enzymes, 3rd ed. Academic Press: New York; Bisswanger, H., 1994, Enzymkinetik, 2nd ed. VCH: Weinheim (ISBN 3527300325); Bergmeyer, H.U., Bergmeyer, J., Graßl, M., eds., 1983-1986, Methods of Enzymatic Analysis, 3rd ed., vol. I-XII, Verlag Chemie: Weinheim; and Ullmann's Encyclopedia of Industrial Chemistry, 1987, vol. A9, Enzymes. VCH: Weinheim, p. 352-363.

[0189] The activity of proteins which bind to DNA can be measured by several well-established methods, such as DNA band-shift assays (also called gel retardation assays). The effect of such proteins on the expression of other molecules can be measured using reporter gene assays (such as that described in Kolmar, H. et al., 1995, EMBO J. 14: 3895-3904 and references cited therein). Reporter gene test systems are well known and established for applications in both pro- and eukaryotic cells, using enzymes such as β-galactosidase, green fluorescent protein, and several others.

[0190] The determination of activity of membrane-transport proteins can be performed according to techniques such as those described in Gennis, R.B., 1989, Pores, Channels and Transporters, in Biomembranes, Molecular Structure and Function, pp. 85-137, 199-234 and 270-322, Springer: Heidelberg.

Example 16

Purification of the Desired Product from Transformed Organisms

[0191] Recovery of the desired product from plant material, fungi, algae, ciliates, *C. glutamicum* cells, or other bacterial cells transformed with the nucleic acid sequences described herein, or the supernatant of the above-described cultures can be performed by various methods well

known in the art. If the desired product is not secreted from the cells, the cells can be harvested from the culture by low-speed centrifugation, and the cells can be lysed by standard techniques, such as mechanical force or sonification. Organs of plants can be separated mechanically from other tissue or organs. Following homogenization, cellular debris is removed by centrifugation, and the supernatant fraction containing the soluble proteins is retained for further purification of the desired compound. If the product is secreted from desired cells, then the cells are removed from the culture by low-speed centrifugation, and the supernate fraction is retained for further purification.

[0192] The supernatant fraction from either purification method is subjected to chromatography with a suitable resin, in which the desired molecule is either retained on a chromatography resin while many of the impurities in the sample are not, or where the impurities are retained by the resin while the sample is not. Such chromatography steps may be repeated as necessary, using the same or different chromatography resins. One skilled in the art would be well-versed in the selection of appropriate chromatography resins and in their most efficacious application for a particular molecule to be purified. The purified product may be concentrated by filtration or ultrafiltration, and stored at a temperature at which the stability of the product is maximized.

[0193] There is a wide array of purification methods known to the art and the preceding method of purification is not meant to be limiting. Such purification techniques are described, for example, in Bailey, J.E. & Ollis, 1986, D.F. Biochemical Engineering Fundamentals, McGraw-Hill: New York. Additionally, the identity and purity of the isolated compounds may be assessed by techniques standard in the art. These include high-performance liquid chromatography (HPLC), spectroscopic methods, staining methods, thin layer chromatography, NIRS, enzymatic assay, or microbiologically. Such analysis methods are reviewed in: Patek et al., 1994, Appl. Environ. Microbiol. 60:133-140; Malakhova et al., 1996, Biotekhnologiya 11:27-32; and Schmidt et al., 1998, Bioprocess Engineer. 19:67-70; Ulmann's Encyclopedia of Industrial Chemistry, 1996, vol. A27, VCH: Weinheim, p. 89-90, p. 521-540, p. 540-547, p. 559-566, 575-581, and p. 581-587; Michal, G., 1999, Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, John Wiley and Sons; Fallon, A. et al., 1987, Applications of HPLC in Biochemistry in: Laboratory Techniques in Biochemistry and Molecular Biology, vol. 17.

Example 17

Salt Tolerance Screening

Salt test on MS plate

[0194] Seedlings are transferred to filter paper soaked in ½ MS and placed on ½ MS 0.6% agar supplemented with 2ug/ml benomyl the night before the stress screening. For the stress screening, the filter paper with the seedlings is moved to stacks of sterile filter paper, soaked in 50mM NaCl, in a petri dish. After two hours, the filter paper with the seedlings is moved to stacks of sterile filter paper, soaked with 200mM NaCl, in a petri dish. After two hours, the filter paper with the seedlings is moved to stacks of sterile filter paper, soaked in 600mM NaCl, in a petri dish. After

10 hours, the seedlings are moved to petri dishes containing ½ MS 0.6% agar supplemented with 2ug/ml benomyl. The seedlings are scored after 5 days, demonstrating that transgene expression confers salt tolerance

Soil test for salt tolerance

[0195] Seeds of plants to be tested are sterilized (100% bleach, 0.1% TritonX for five minutes two times and rinsed five times with ddH2O). Seeds are plated on non-selection media (1/2 MS, 0.6% phytagar, 0.5g/L MES, 1% sucrose, 2 µg/ml benamyl).

[0196] Seeds are allowed to germinate for approximately ten days. At the 4-5 leaf stage, transgenic plants are potted into 5.5 cm diameter pots filled with loosely packed soil (Metromix 360, Scotts) wetted with 1 g/L 20-20-20 fertilizer (Peters Professional, Scotts).

[0197] The plants are allowed to grow (22°C, continuous light) for approximately seven days, watering as needed. When the plants are just about to bolt, the water is removed from the tray and the assay is started. To begin the assay, three liters of 100 mM NaCl and 1/8 MS is added to the tray under the pots. To the tray containing the control plants, three liters of 1/8 MS is added. After 10 days, the NaCl treated and the control plants are given water. Ten days later, the plants are photographed.

Example 18

Drought Tolerance Screening

[0198] T1 and T2 seedlings are transferred to dry, sterile filter paper in a petri dish and allowed to desiccate for two hours at 80% RH (relative humidity) in a Sanyo Growth Cabinet MLR-350H, micromols^{-1}m2 (white light; Philips TL 65W/25 fluorescent tube). The RH is then decreased to 60% and the seedlings are desiccated further for eight hours. Seedlings are then removed and placed on ½ MS 0.6% agar plates supplemented with 2 µg/ml benomyl and scored after five days.

[0199] The transgenic plants are screened for their improved drought tolerance demonstrating that transgene expression confers drought tolerance.

Example 19

Freezing Tolerance Screening

[0200] Seedlings are moved to petri dishes containing ½ MS 0.6% agar supplemented with 2% sucrose and 2ug/ml benomyl. After four days, the seedlings are incubated at +4°C for 1 hour and then covered with shaved ice. The seedlings are then placed in an Environmental Specialist ES2000 Environmental Chamber and incubated for 3.5 hours beginning at –1.0°C decreasing –1°C hour. The seedlings are then incubated at –5.0°C for 24 hours and then allowed to thaw at +5°C for 12 hours. The water is poured off and the seedlings are scored after 5 days.

[0201] The transgenic plants are screened for their improved cold tolerance demonstrating that transgene expression confers cold tolerance.

CLAIMS

WE CLAIM:

1. A transgenic crop plant transformed with an isolated nucleic acid, wherein the nucleic acid comprises a polynucleotide selected from the group consisting of:

a) a polynucleotide having a sequence as set forth in any of SEQ ID NOS as provided in Column No. 3 of Table 1 and Table 2;

b) a polynucleotide encoding a polypeptide having a sequence as set forth in any of SEQ ID NOS as provided in Column No. 4 of Table 1 and Table 2;

c) a polynucleotide having at least 70% sequence identity to a polynucleotide having a sequence as set forth in any of SEQ ID NOS as provided in Column No. 3 of Table 1 and Table 2;

d) a polynucleotide encoding a polypeptide having at least 70% sequence identity to a polypeptide having a sequence as set forth in any of SEQ ID NOS as provided in Column No. 4 of Table 1 and Table 2; and

e) a polynucleotide that hybridizes under stringent conditions to the complement of any of the polynucleotides of a) through d) above.

2. The transgenic crop plant of claim 1, wherein the expression of the polynucleotide in the plant results in increased yield under normal or stress conditions as compared to a wild type variety of the plant.

3. The transgenic crop plant of claim 1, wherein the expression of the polynucleotide in the plant results in increased stress tolerance to an environmental stress as compared to a wild type variety of the plant.

4. The transgenic crop plant of claim 1, wherein the expression of the polynucleotide in the plant results in increased root growth under normal or stress conditions as compared to a wild type variety of the plant.

5. The transgenic crop plant of claim 1, wherein the plant is a monocot.

6. The transgenic crop plant of claim 1, wherein the plant is a dicot.

7. The transgenic crop plant of claim 1, wherein the plant is selected from the group consisting of maize, wheat, rye, oat, triticale, rice, barley, sorghum, millet, sugarcane, soybean, peanut, cotton, rapeseed, canola, manihot, pepper, sunflower, tagetes, solanaceous plants, potato, tobacco, eggplant, tomato, Vicia species, pea, alfalfa, coffee, cacao, tea, Salix species, oil palm, coconut, perennial grass and a forage crop plant.

8. The transgenic crop plant of claim 1, wherein the plant is a whole plant, a plant cell, a plant part, or a plant seed.

9. A crop plant seed produced by the transgenic crop plant of claim 1, wherein the seed comprises the isolated nucleic acid.

10. The seed of claim 9, wherein the seed is true breeding for increased yield under normal or stress conditions as compared to a wild type variety of the seed.

11. The seed of claim 9, wherein the seed is true breeding for increased stress tolerance to an environmental stress as compared to a wild type variety of the seed.

12. The seed of claim 9, wherein the seed is true breeding for an increased root growth under normal or stress conditions as compared to a wild type variety of the seed.

13. A method of producing a transgenic crop plant containing an isolated nucleic acid encoding a polypeptide, wherein the method comprises the steps of, transforming a plant cell with an expression vector comprising the nucleic acid, and generating from the plant cell the transgenic plant that expresses the polypeptide, wherein the nucleic acid comprises a polynucleotide selected from the group consisting of:

a) a polynucleotide having a sequence as set forth in any of SEQ ID NOS as provided in Column No. 3 of Table 1 and Table 2;

b) a polynucleotide encoding a polypeptide having a sequence as set forth in any of SEQ ID NOS as provided in Column No. 4 of Table 1 and Table 2;

c) a polynucleotide having at least 70% sequence identity to a polynucleotide having a sequence as set forth in any of SEQ ID NOS as provided in Column No. 3 of Table 1 and Table 2;

d) a polynucleotide encoding a polypeptide having at least 70% sequence identity to a polypeptide having a sequence as set forth in any of SEQ ID NOS as provided in Column No. 4 of Table 1 and Table 2; and

e) a polynucleotide that hybridizes under stringent conditions to the complement of any of the polynucleotides of a) through d) above.

14. The method of claim 13, wherein the expression of the polynucleotide in the plant results in increased yield under normal or stress conditions as compared to a wild type variety of the plant.

15. The method of claim 13, wherein the expression of the polynucleotide in the plant results in increased stress tolerance to an environmental stress as compared to a wild type variety of the plant.

16. The method of claim 13, wherein the expression of the polynucleotide in the plant results in increased root growth under normal or stress conditions as compared to a wild type variety of the plant.

17. The method of claim 13, wherein the crop plant is a monocot.

18. The method of claim 13, wherein the crop plant is a dicot.

19. The method of claim 13, wherein the crop plant is selected from the group consisting of maize, wheat, rye, oat, triticale, rice, barley, sorghum, millet, sugarcane, soybean, peanut, cotton, rapeseed, canola, manihot, pepper, sunflower, tagetes, solanaceous plants, potato, tobacco, eggplant, tomato, Vicia species, pea, alfalfa, coffee, cacao, tea, Salix species, oil palm, coconut, perennial grass and a forage crop plant.

20. The method of claim 13, wherein the nucleic acid comprises a polynucleotide having a sequence as set forth in any of SEQ ID NOS as provided in Column No. 3 of Table 1 and Table 2.

21. The method of claim 13, wherein the nucleic acid comprises a polynucleotide having at least 70% sequence identity to a polynucleotide having a sequence as set forth in any of SEQ ID NOS as provided in Column No. 4 of Table 1 and Table 2.

22. The method of claim 13, wherein the nucleic acid comprises a polynucleotide encoding a polypeptide having a sequence as set forth in any of SEQ ID NOS as provided in Column No. 3 of Table 1 and Table 2.

23. The method of claim 13, wherein the nucleic acid comprises a polynucleotide encoding a polypeptide having at least 70% sequence identity to a polypeptide having a sequence as set forth in any of SEQ ID NOS as provided in Column No. 4 of Table 1 and Table 2.

24. The method of claim 13, wherein the nucleic acid is operably linked to one or more regulatory sequences.

25. The method of claim 24, wherein the regulatory sequence is a promoter.

26 The method of claim 25, wherein the promoter is tissue specific.

27. The method of claim 25, wherein the promoter is developmentally regulated.

28. An isolated nucleic acid, wherein the nucleic acid comprises a polynucleotide selected from the group consisting of:

a) a polynucleotide having a sequence as set forth in any of SEQ ID NOS as provided in Column No. 3 of Table 2;

b) a polynucleotide encoding a polypeptide having a sequence as set forth in any of SEQ ID NOS as provided in Column No. 4 of Table 2;

c) a polynucleotide having at least 80% sequence identity to a polynucleotide having a sequence as set forth in any of SEQ ID NOS as provided in Column No. 3 of Table 2;

d) a polynucleotide encoding a polypeptide having at least 80% sequence identity to a polypeptide having a sequence as set forth in any of SEQ ID NOS as provided in Column No. 4 of Table 2;

e) a polynucleotide that hybridizes under stringent conditions to the complement of any of the polynucleotides of a) through d) above; and

f) a polynucleotide complementary to any of the polynucleotides of a) through d) above.

29. The isolated nucleic acid of claim 28, wherein the nucleic acid comprises a polynucleotide having a sequence as set forth in any of SEQ ID NOS as provided in Column No. 3 of Table 2.

30. The isolated nucleic acid of claim 28, wherein the nucleic acid comprises a polynucleotide having at least 80% sequence identity to a polynucleotide having a sequence as set forth in any of SEQ ID NOS as provided in Column No. 3 of Table 2.

31. The isolated nucleic acid of claim 28, wherein the nucleic acid comprises a polynucleotide encoding a polypeptide having a sequence as set forth in any of SEQ ID NOS as provided in Column No. 4 of Table 2.

32. The isolated nucleic acid of claim 28, wherein the nucleic acid comprises a polynucleotide encoding a polypeptide having at least 80% sequence identity to a polypeptide having a sequence as set forth in any of SEQ ID NOS as provided in Column No. 4 of Table 2.

33. A transgenic plant transformed with an isolated nucleic acid, wherein the nucleic acid comprises a polynucleotide selected from the group consisting of:

a) a polynucleotide having a sequence as set forth in any of SEQ ID NOS as provided in Column No. 3 of Table 2;

b) a polynucleotide encoding a polypeptide having a sequence as set forth in any of SEQ ID NOS as provided in Column No. 4 of Table 2;

c) a polynucleotide having at least 80% sequence identity to a polynucleotide having a sequence as set forth in any of SEQ ID NOS as provided in Column No. 3 of Table 2;

d) a polynucleotide encoding a polypeptide having at least 80% sequence identity to a polypeptide having a sequence as set forth in any of SEQ ID NOS as provided in Column No. 4 of Table 2; and

e) a polynucleotide that hybridizes under stringent conditions to the complement of any of the polynucleotides of a) through d) above.

34. The transgenic plant of claim 33, wherein expression of the polynucleotide in the plant results in increased yield under normal or stress conditions as compared to a wild type variety of the plant.

35. The transgenic plant of claim 33, wherein expression of the polynucleotide in the plant results in increased stress tolerance to an environmental stress as compared to a wild type variety of the plant.

36. The transgenic plant of claim 33, wherein expression of the polynucleotide in the plant results in increased root growth under normal or stress conditions as compared to a wild type variety of the plant.

37. The transgenic plant of claim 33, wherein the plant is a whole plant, a plant cell, a plant part, or a plant seed.

38. A plant seed produced by the transgenic plant of claim 33, wherein the seed comprises the isolated nucleic acid.

39. The seed of claim 38, wherein the seed is true breeding for increased yield under normal or stress conditions as compared to a wild type variety of the seed.

40. The seed of claim 38, wherein the seed is true breeding for increased stress tolerance to an environmental stress as compared to a wild type variety of the seed.

41. The seed of claim 38, wherein the seed is true breeding for an increased root growth under normal or stress conditions as compared to a wild type variety of the seed.

42. The transgenic plant of claim 33, wherein the plant is a monocot.

43. The transgenic plant of claim 33, wherein the plant is a dicot.

44. A recombinant expression vector comprising an isolated nucleic acid, wherein the nucleic acid comprises a polynucleotide selected from the group consisting of:

a) a polynucleotide having a sequence as set forth in any of SEQ ID NOS as provided in Column No. 3 of Table 1 and Table 2;

b) a polynucleotide encoding a polypeptide having a sequence as set forth in any of SEQ ID NOS as provided in Column No. 4 of Table 1 and Table 2;

c) a polynucleotide having at least 80% sequence identity to a polynucleotide having a sequence as set forth in any of SEQ ID NOS as provided in Column No. 3 of Table 1 and Table 2;

d) a polynucleotide encoding a polypeptide having at least 80% sequence identity to a polypeptide having a sequence as set forth in any of SEQ ID NOS as provided in Column No. 4 of Table 1 and Table 2;

e) a polynucleotide that hybridizes under stringent conditions to the complement of any of the polynucleotides of a) through d) above; and

f) a polynucleotide complementary to any of the polynucleotides of a) through d) above.

45. The recombinant expression vector of claim 44, wherein the vector further comprises one or more regulatory sequences.

46. The recombinant expression vector of claim 45, wherein the regulatory sequence is a promoter.

47. The recombinant expression vector of claim 46, wherein the promoter is tissue specific.

48. The recombinant expression vector of claim 46, wherein the promoter is developmentally regulated.

Figure 1

GGGGTCGACGAAGCAATGAGAGGACGAAGCTTGACACTCTCAAGAGTAAAGCTCGAGCTTGCGAGAAG
AAGCATGTCTGCAACATCCGTACCTTCAATGGCGGATTTTCTCACCAAAAAACCTTACTCTCCTCCTT
CTTGGGCTTCTCATCTTCGTCCGCTTCCTTCTCACACTTTCTCCCTCGCTCACCTTCCTACTCCGATC
CATCGATGGAATCTTCCTGGTCTTCCTAATGGCACAGAACTCTGGATCAAGCGAGATGATTTCACCGG
AATGGAATTGAGTGGAAACAAAGTACGAAAACTCGAATTCTTAATGGCGGAAGCTGTTGATCAACACG
CTGATACTGTAATCACTATCGGCGGTATTCAGAGCAATCATTGTCGTGCTACAGCCACTGCATCTAAC
TATCTTAATCTCAATTCTCATCTTATTCTCCGTACTTCCAAGCTTCTTGCTGATGAAGATCCTGGATT
GGTTGGGAATCTCCTTGTCGAGCGTCTCGTTGGAGCTAATGTTCATCTAATCTCTAAAGAAGAGTATT
CTTCCATTGGGAGTGAGGCTCTTACTAATGCTCTGAAAGAGAAACTGGAAAAAGAAGGAAAGAAACCC
TATGTTATTCCAGTCGGTGGATCGAACTCTTTGGGAACTTGGGGTTATATAGAAGCAGCAAGGGAAAT
TGAGGAGCAGCTGAATTATAGACCCGATGACCTGAAATTTGATGATATTGTGGTAGCATGTGGCAGTG
GTGGTACAATTGCTGGTATTTCATTGGGGTCTTGGTTGGGAGCTCTAAAAGCCAAGGTTCATGCTTTC
TCGGTTTGCGATGATCCTGATTACTTCTATGACTTTGTCCAAGGGCTTCTGGATGGACTTCACGCTGG
TGTTAACTCTCGTGATATCGTCAACATCCACAATGCCAAAGGAAAAGGATATGCCATGAACACGTCAG
AGGAGCTTGAGTTTGTAAAGAAAGTAGCAAGTTCAACTGGTGTTATTCTTGATCCGGTTTACAGTGGG
AAAGCTGCGTATGGTTTGATAAATGAGATCACCAAAGATCCCAAATGTTGGGAGGGAAGGAAGATATT
GTTCATACACACTGGTGGGCTTCTTGGGTTGTATGATAAGGTTGATCAAATGGCATCTCTGATGGGTA
ATTGGTCCCGGATGGATGTTTCAGAATCCGTTCCAAGAAAAGATGGTGTTGGGAAAATGTTCTAGCAC
AACAAAATCTGTTAATTAACCC

Figure 2

MRGRSLTLSRVKLELARRSMSATSVPSMADFLTKKPYSPPSWASHLRPLPSHTFSLAHLPTPIHRWNL
PGLPNGTELWIKRDDFTGMELSGNKVRKLEFLMAEAVDQHADTVITIGGIQSNHCRATATASNYLNLN
SHLILRTSKLLADEDPGLVGNLLVERLVGANVHLISKEEYSSIGSEALTNALKEKLEKEGKKPYVIPV
GGSNSLGTWGYIEAAREIEEQLNYRPDDLKFDDIVVACGSGGTIAGISLGSWLGALKAKVHAFSVCDD
PDYFYDFVQGLLDGLHAGVNSRDIVNIHNAKGKGYAMNTSEELEFVKKVASSTGVILDPVYSGKAAYG
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Figure 3

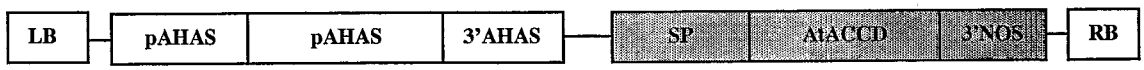


Figure 4

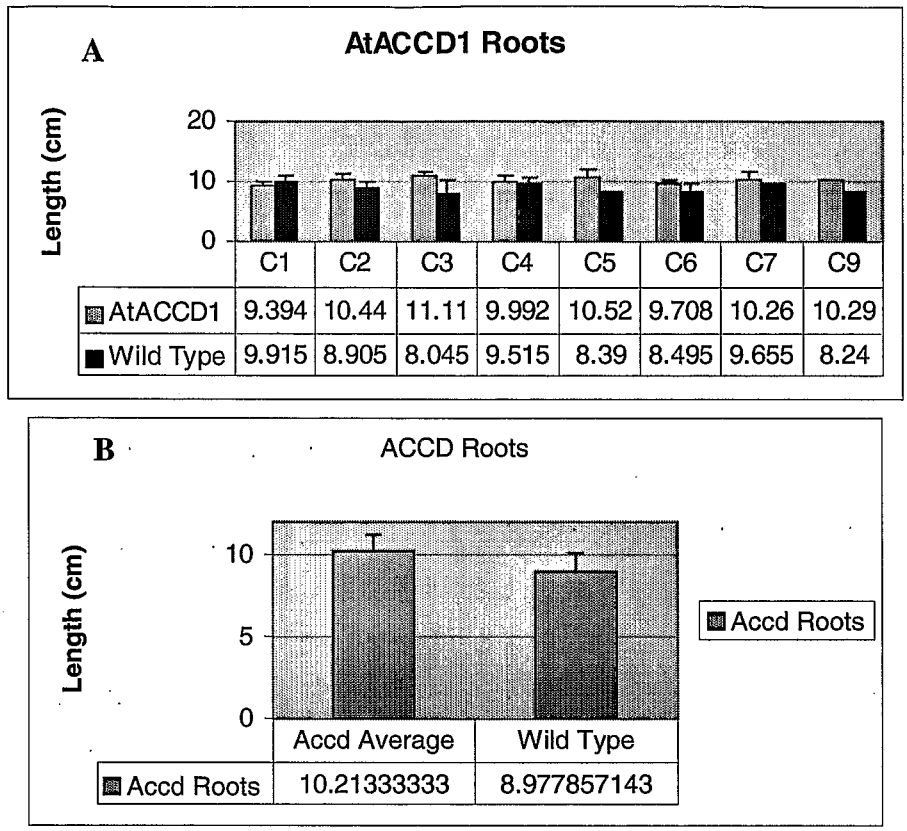


Figure 5

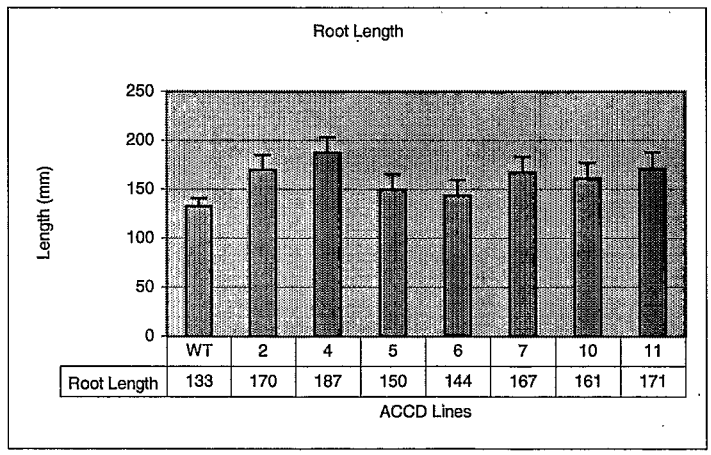


Figure 6

Gene	Root Length (mm)	Standard	Diff to Control
ID	**LSMEAN**	**Error**	**P**
WT	132.8	8.0	-
1.1 AtACCD	164.3	6.0	0.0055

Figure 7

Gene	Shoot Dry Weight (g)	Standard	Diff to Control
ID	**LSMEAN**	**Error**	**P**
WT	0.0123	0.0013	-
AtACCD	0.0135	0.0010	0.8197

Figure 8

Query gene	Tblasn hits (gene names and SEQ ID)	Identity percentage	Length (aa)
AtACCD(SEQ ID NO:2, 401 aa)	GmACCD-1 (SEQ ID NO:355)	74	388
	OsACCD (SEQ ID NO:353)	69	381
	ZmACCD-1 (SEQ ID NO:351)	69	380
	TaACCD (SEQ ID NO:357)	67	401

Figure 9

```
>Contig1481_48982441Dec03 1406bp 11m +
           48982441.f_115_1|Soybean|Lib:AC040|cluID:7088|varID:1077
           3|RTA56564033F.1.15.1
          Length = 1406

 Score =  591 bits (1523), Expect = e-168
 Identities = 288/388 (74%), Positives = 332/388 (85%).
 Frame = +2

Query: 14   ELARRSMSATSVPSMADFLTKKPYSPPSWASHLRPLPSHTFSLAHLPTPIHRWNLPGLPN 73
            EL R+SM+++       +FLTKKPYSPPSWASHL PLPSH FSLAHLPTPIHRWNLP LP
Sbjct: 50   ELVRKSMASSLG---FEFLTKKPYSPPSWASHLHPLPSHFFSLAHLPTPIHRWNLPNLPT 220

Query: 74   GTELWIKRDDFTGMELSGNKVRKLEFLMAEAVDQHADTVITIGGIQSNHCRATATASNYL 133
             TELWIKRDD +GM+LSGNKVRKLEFLMA+A+ Q AD++ITIGGIQSNHCRATA A+ YL
Sbjct: 221  NTELWIKRDDLSGMQLSGNKVRKLEFLMADAIAQGADSIITIGGIQSNHCRATAVAAKYL 400

Query: 134  NLNSHLILRTSKLLADEDPGLVGNLLVERLVGANVHLISKEEYSSIGSEALTNAXXXXXX 193
            NL+  LILRTS LL D+DPGL GNLLVER+VGA+VHLISK+EY+ IGS  LTN
Sbjct: 401  NLDCFLILRTSDLLVDQDPGLTGNLLVERMVGAHVHLISKQEYAKIGSVTLTNVLKEKLI 580

Query: 194  XXXXXPYVIPVGGSNSLGTWGYIEAAREIEEQLNYRPDDLKFDDIVVACGSGGTIAGISL 253
                  PYVIPVGGSNSLGTWGYIEA REIE+Q+     ++KFDDIVVACGSGGTIAG+SL
Sbjct: 581  KEGRRPYVIPVGGSNSLGTWGYIEAVREIEQQIQKGTGNVKFDDIVVACGSGGTIAGLSL 760

Query: 254  GSWLGALKAKVHAFSVCDDPDYFYDFVQGLLDGLHAGVNSRDIVNIHNAKGKGYAMNTSE 313
            GS L ALKA+VHAFSVCDDPDYF++F QGLLDGL AGV+SRDIV+I NAKG GYAMNTSE
Sbjct: 761  GSSLSALKARVHAFSVCDDPDYFHNFAQGLLDGLKAGVSSRDIVHIQNAKGLGYAMNTSE 940

Query: 314  ELEFVKKVASSTGVILDPVYSGKAAYGLINEITKDPKCWEGRKILFIHTGGLLGLYDKVD 373
            EL FVK+VA++TGV+LDPVYSGKAAY ++ +++++PK WE RKILFIHTGGLLGLYDKVD
Sbjct: 941  ELNFVKEVAATTGVVLDPVYSGKAAYAMLKDMSENPKKWERRKILFIHTGGLLGLYDKVD
1120

Query: 374  QMASLMGNWSRMDVSESVPRKDGVGKMF 401
            Q+AS +GNW RMDV+ESVPR+DG+GKMF
Sbjct: 1121 QLASFVGNWQRMDVNESVPRQDGIGKMF 1204
```

Figure 10

```
>Contig19555_30859453Dec03 1402bp 8m +
30859453.f_f17_1|Rice|Lib:AC003t|cluID:706|varID:779|RT
          A56560012F.f.17.1
         Length = 1402

 Score =  560 bits (1442), Expect = e-159
 Identities = 266/381 (69%), Positives = 318/381 (83%)
 Frame = +2

Query: 21  SATSVPSMADFLTKKPYSPPSWASHLRPLPSHTFSLAHLPTPIHRWNLPGLPNGTELWIK 80
           +A++   +  FL+K+PY+PPSWASHL P PS TFSL H PTPIH+WNLP LPNGTE+WIK
Sbjct: 53  AASAAGKIGSFLSKRPYAPPSWASHLSPAPSQTFSLGHFPTPIHKWNLPNLPNGTEVWIK 232

Query: 81  RDDFTGMELSGNKVRKLEFLMAEAVDQHADTVITIGGIQSNHCRATATASNYLNLNSHLI 140
           RDD +GM+LSGNKVRKLEFLMA+AV Q AD VIT+GGIQSNHCRATA A+ Y+NL+ +LI
Sbjct: 233 RDDISGMQLSGNKVRKLEFLMADAVAQGADCVITVGGIQSNHCRATAVAAKYINLDCYLI 412

Query: 141 LRTSKLLADEDPGLVGNLLVERLVGANVHLISKEEYSSIGSEALTNAXXXXXXXXXXXPY 200
           LRTSKLL D+DPGLVGNLLVERLVGA++ L+SKEEY  IGS AL +            PY
Sbjct: 413 LRTSKLLVDKDPGLVGNLLVERLVGAHIDLVSKEEYGKIGSVALADLLKKKLLEEGRKPY 592

Query: 201 VIPVGGSNSLGTWGYIEAAREIEEQLNYRPDDLKFDDIVVACGSGGTIAGISLGSWLGAL 260
           VIPVGGSNSLGTWGYIEA REIE Q+     D++FDDIVVACGSGGTIAG++LGS L +L
Sbjct: 593 VIPVGGSNSLGTWGYIEAIREIEHQIQI-SGDVQFDDIVVACGSGGTIAGLALGSKLSSL 769

Query: 261 KAKVHAFSVCDDPDYFYDFVQGLLDGLHAGVNSRDIVNIHNAKGKGYAMNTSEELEFVKK 320
           KAKVHAFSVCDDP YF+ +VQ L+DGLH+ + S D+VNI NAKG GYAMNT+EEL+FVK
Sbjct: 770 KAKVHAFSVCDDPGYFHSYVQDLIDGLHSDLRSHDLVNIENAKGLGYAMNTAEELKFVKD 949

Query: 321 VASSTGVILDPVYSGKAAYGLINEITKDPKCWEGRKILFIHTGGLLGLYDKVDQMASLMG 380
           +A++TG++LDPVYSGKAAYG++ ++  +P  WEGRKILF+HTGGLLGLYDKVD+++SL G
Sbjct: 950 IATATGIVLDPVYSGKAAYGMLKDMGANPAKWEGRKILFVHTGGLLGLYDKVDELSSLSG
1129

Query: 381 NWSRMDVSESVPRKDGVGKMF 401
           +W RMD+ ESVPRKDG GKMF
Sbjct: 1130SWRRMDLEESVPRKDGTGKMF 1192
```

Figure 11

```
>Contig14714_57817161Dec03 1383bp 4m +
57817161.f_h20_1|Maize|Lib:AC080|cluID:57802|varID:6856
          1|RTA56568132F.h.20.1
         Length = 1383

 Score =  560 bits (1442), Expect = e-159
 Identities = 265/380 (69%), Positives = 319/380 (83%)
 Frame = +3

Query: 22  ATSVPSMADFLTKKPYSPPSWASHLRPLPSHTFSLAHLPTPIHRWNLPGLPNGTELWIKR 81
           +++   +  FL+KKPY+PP WA+HL P+P HTFSL H PTPIH+WNLP LP GTE+WIKR
Sbjct: 90  SSATAQIGGFLSKKPYAPPLWATHLSPMPCHTFSLGHFPTPIHKWNLPNLPEGTEVWIKR 269

Query: 82  DDFTGMELSGNKVRKLEFLMAEAVDQHADTVITIGGIQSNHCRATATASNYLNLNSHLIL 141
           DD +GM+LSGNKVRKLEFLMA+AV Q AD VIT+GGIQSNHCRATA A+ YLNL+ +LIL
Sbjct: 270 DDLSGMQLSGNKVRKLEFLMADAVAQGADCVITVGGIQSNHCRATAVAAKYLNLDCYLIL 449

Query: 142 RTSKLLADEDPGLVGNLLVERLVGANVHLISKEEYSSIGSEALTNAXXXXXXXXXXXPYV 201
           RTSKLL D+DPGLVGNLLVERLVGA+V L+SKEEY  IGS AL +            PYV
Sbjct: 450 RTSKLLVDKDPGLVGNLLVERLVGAHVDLVSKEEYGKIGSVALADLLKKRLLEEGRKPYV 629

Query: 202 IPVGGSNSLGTWGYIEAAREIEEQLNYRPDDLKFDDIVVACGSGGTIAGISLGSWLGALK 261
           IPVGGSNSLGTWGYIEA REIE+Q+  +  D++FDDIVVACGSGGTIAG++LGS L +L
Sbjct: 630 IPVGGSNSLGTWGYIEAIREIEQQIQ-QSADVQFDDIVVACGSGGTIAGLALGSRLSSLN 806

Query: 262 AKVHAFSVCDDPDYFYDFVQGLLDGLHAGVNSRDIVNIHNAKGKGYAMNTSEELEFVKKV 321
            KVHAFSVCDDP+YFYD+VQGL+DGL++G++S DIV+I NAKG GYAMNT+EEL+FVK +
Sbjct: 807 TKVHAFSVCDDPEYFYDYVQGLIDGLNSGLDSHDIVSIENAKGLGYAMNTAEELKFVKDI 986

Query: 322 ASSTGVILDPVYSGKAAYGLINEITKDPKCWEGRKILFIHTGGLLGLYDKVDQMASLMGN 381
           A+STG++LDPVYSGKA YGL+ ++  +P  W+GRK+LFIHTGGLLGLYDK DQ++SL G+
Sbjct: 987 AASTGIVLDPVYSGKAVYGLLKDMAGNPAKWKGRKVLFIHTGGLLGLYDKADQLSSLAGS
1166

Query: 382 WSRMDVSESVPRKDGVGKMF 401
           W RMD+ +SVPRKDG GKMF
Sbjct: 1167WRRMDLEDSVPRKDGTGKMF 1226
```

Figure 12

```
>Contig15977_54201209Dec03 1463bp 5m +
54201209.f_k01_1|Wheat|Lib:AC062|cluID:9364|varID:69571
          |RTA56566095F.k.01.1
         Length = 1463

 Score =  558 bits (1439), Expect = e-159
 Identities = 269/401 (67%), Positives = 324/401 (80%), Gaps = 5/401 (1%)
 Frame = +3

Query: 6    LTLSRVKLELARRSMSATSVPSMA-----DFLTKKPYSPPSWASHLRPLPSHTFSLAHLP 60
             L   R +  +A   M+  S  S A      FL+KKPY+PPSWASHL   PSHTFSL H P
Sbjct: 81   LAAVRRRCSIAATGMAGVSAASPAAAQIGSFLSKKPYAPPSWASHLALAPSHTFSLGHFP 260

Query: 61   TPIHRWNLPGLPNGTELWIKRDDFTGMELSGNKVRKLEFLMAEAVDQHADTVITIGGIQS 120
             TPIH+WNLP LP GTE+WIKRDD +GM+LSGNKVRKLEFL+++AV Q AD VIT+GGIQS
Sbjct: 261  TPIHKWNLPNLPEGTEVWIKRDDLSGMQLSGNKVRKLEFLLSDAVAQGADCVITVGGIQS 440

Query: 121  NHCRATATASNYLNLNSHLILRTSKLLADEDPGLVGNLLVERLVGANVHLISKEEYSSIG 180
             NHCRATA A+ YLNL+ +LILRTSKLL D+DPGLVGNLLVERL+GA++ L+SKEEY  IG
Sbjct: 441  NHCRATAVAAKYLNLDCYLILRTSKLLVDQDPGLVGNLLVERLLGAHIDLVSKEEYGKIG 620

Query: 181  SEALTNAXXXXXXXXXXXPYVIPVGGSNSLGTWGYIEAAREIEEQLNYRPDDLKFDDIVV 240
             S AL +             PYVIPVGGSNSLGTWGYIEA RE+E+Q+     D++FDDIVV
Sbjct: 621  SVALADLLKKRLLEEGRKPYVIPVGGSNSLGTWGYIEAVRELEQQIQL-SGDVQFDDIVV 797

Query: 241  ACGSGGTIAGISLGSWLGALKAKVHAFSVCDDPDYFYDFVQGLLDGLHAGVNSRDIVNIH 300
             ACGSGGTIAG++LGS L +L AKVHAFSVCDDP+YFYD+VQGL+DGL +G++S DIV+I
Sbjct: 798  ACGSGGTIAGLALGSKLSSLTAKVHAFSVCDDPEYFYDYVQGLIDGLQSGLDSHDIVSIQ 977

Query: 301  NAKGKGYAMNTSEELEFVKKVASSTGVILDPVYSGKAAYGLINEITKDPKCWEGRKILFI 360
             NAKG GYAMNT+EEL+FVK +A++TG++LDPVYSGK AY ++ ++  +P  W+GRK+LF+
Sbjct: 978  NAKGLGYAMNTAEELKFVKDIATATGIVLDPVYSGKGAYAMLKDMADNPSKWKGRKVLFV
1157

Query: 361  HTGGLLGLYDKVDQMASLMGNWSRMDVSESVPRKDGVGKMF 401
             HTGGLLGLYDKVDQM+SL G+W RMD+ ESVPRKDG GKMF
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<110> BASF PLant Science GmbH
Sarria-Millan, Rodrigo
Garr, Eric R
Haertel, Jamie
Allen, Damian
McKersie, Bryan

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Leu Glu Leu Ala Arg Arg Ser Met Ser Ala Thr Ser Val Pro Ser Met
          15                  20                  25
gcg gat ttt ctc acc aaa aaa cct tac tct cct cct tct tgg gct tct     147
Ala Asp Phe Leu Thr Lys Lys Pro Tyr Ser Pro Pro Ser Trp Ala Ser
      30                  35                  40
cat ctt cgt ccg ctt cct tct cac act ttc tcc ctc gct cac ctt cct     195
His Leu Arg Pro Leu Pro Ser His Thr Phe Ser Leu Ala His Leu Pro
45                    50                  55                  60
act ccg atc cat cga tgg aat ctt cct ggt ctt cct aat ggc aca gaa     243
Thr Pro Ile His Arg Trp Asn Leu Pro Gly Leu Pro Asn Gly Thr Glu
                  65                  70                  75
ctc tgg atc aag cga gat gat ttc acc gga atg gaa ttg agt gga aac     291
Leu Trp Ile Lys Arg Asp Asp Phe Thr Gly Met Glu Leu Ser Gly Asn
              80                  85                  90
aaa gta cga aaa ctc gaa ttc tta atg gcg gaa gct gtt gat caa cac     339
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          95                  100                 105
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Ala Asp Thr Val Ile Thr Ile Gly Gly Ile Gln Ser Asn His Cys Arg
      110                 115                 120
gct aca gcc act gca tct aac tat ctt aat ctc aat tct cat ctt att     435
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125                   130                 135                 140
ctc cgt act tcc aag ctt ctt gct gat gaa gat cct gga ttg gtt ggg     483
Leu Arg Thr Ser Lys Leu Leu Ala Asp Glu Asp Pro Gly Leu Val Gly
                  145                 150                 155
aat ctc ctt gtc gag cgt ctc gtt gga gct aat gtt cat cta atc tct     531
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        175                 180                 185
aaa gag aaa ctg gaa aaa gaa gga aag aaa ccc tat gtt att cca gtc       627
Lys Glu Lys Leu Glu Lys Glu Gly Lys Lys Pro Tyr Val Ile Pro Val
    190                 195                 200
ggt gga tcg aac tct ttg gga act tgg ggt tat ata gaa gca gca agg       675
Gly Gly Ser Asn Ser Leu Gly Thr Trp Gly Tyr Ile Glu Ala Ala Arg
205                 210                 215                 220
gaa att gag gag cag ctg aat tat aga ccc gat gac ctg aaa ttt gat       723
Glu Ile Glu Glu Gln Leu Asn Tyr Arg Pro Asp Asp Leu Lys Phe Asp
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gat att gtg gta gca tgt ggc agt ggt ggt aca att gct ggt att tca       771
Asp Ile Val Val Ala Cys Gly Ser Gly Gly Thr Ile Ala Gly Ile Ser
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ttg ggg tct tgg ttg gga gct cta aaa gcc aag gtt cat gct ttc tcg       819
Leu Gly Ser Trp Leu Gly Ala Leu Lys Ala Lys Val His Ala Phe Ser
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gtt tgc gat gat cct gat tac ttc tat gac ttt gtc caa ggg ctt ctg       867
Val Cys Asp Asp Pro Asp Tyr Phe Tyr Asp Phe Val Gln Gly Leu Leu
    270                 275                 280
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Asp Gly Leu His Ala Gly Val Asn Ser Arg Asp Ile Val Asn Ile His
285                 290                 295                 300
aat gcc aaa gga aaa gga tat gcc atg aac acg tca gag gag ctt gag       963
Asn Ala Lys Gly Lys Gly Tyr Ala Met Asn Thr Ser Glu Glu Leu Glu
                305                 310                 315
ttt gta aag aaa gta gca agt tca act ggt gtt att ctt gat ccg gtt      1011
Phe Val Lys Lys Val Ala Ser Ser Thr Gly Val Ile Leu Asp Pro Val
            320                 325                 330
tac agt ggg aaa gct gcg tat ggt ttg ata aat gag atc acc aaa gat      1059
Tyr Ser Gly Lys Ala Ala Tyr Gly Leu Ile Asn Glu Ile Thr Lys Asp
        335                 340                 345
ccc aaa tgt tgg gag gga agg aag ata ttg ttc ata cac act ggt ggg      1107
Pro Lys Cys Trp Glu Gly Arg Lys Ile Leu Phe Ile His Thr Gly Gly
    350                 355                 360
ctt ctt ggg ttg tat gat aag gtt gat caa atg gca tct ctg atg ggt      1155
Leu Leu Gly Leu Tyr Asp Lys Val Asp Gln Met Ala Ser Leu Met Gly
365                 370                 375                 380
aat tgg tcc cgg atg gat gtt tca gaa tcc gtt cca aga aaa gat ggt      1203
Asn Trp Ser Arg Met Asp Val Ser Glu Ser Val Pro Arg Lys Asp Gly
                385                 390                 395
gtt ggg aaa atg ttc tag cacaacaaaa tctgttaatt aaccc                 1246
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            20                  25                  30
Thr Lys Lys Pro Tyr Ser Pro Pro Ser Trp Ala Ser His Leu Arg Pro
        35                  40                  45
Leu Pro Ser His Thr Phe Ser Leu Ala His Leu Pro Thr Pro Ile His
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    50                  55                  60
Arg Trp Asn Leu Pro Gly Leu Pro Asn Gly Thr Glu Leu Trp Ile Lys
65                  70                  75                  80
Arg Asp Asp Phe Thr Gly Met Glu Leu Ser Gly Asn Lys Val Arg Lys
                85                  90                  95
Leu Glu Phe Leu Met Ala Glu Ala Val Asp Gln His Ala Asp Thr Val
            100                 105                 110
Ile Thr Ile Gly Gly Ile Gln Ser Asn His Cys Arg Ala Thr Ala Thr
        115                 120                 125
Ala Ser Asn Tyr Leu Asn Leu Asn Ser His Leu Ile Leu Arg Thr Ser
    130                 135                 140
Lys Leu Leu Ala Asp Glu Asp Pro Gly Leu Val Gly Asn Leu Leu Val
145                 150                 155                 160
Glu Arg Leu Val Gly Ala Asn Val His Leu Ile Ser Lys Glu Glu Tyr
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Ser Ser Ile Gly Ser Glu Ala Leu Thr Asn Ala Leu Lys Glu Lys Leu
            180                 185                 190
Glu Lys Glu Gly Lys Lys Pro Tyr Val Ile Pro Val Gly Gly Ser Asn
        195                 200                 205
Ser Leu Gly Thr Trp Gly Tyr Ile Glu Ala Ala Arg Glu Ile Glu Glu
    210                 215                 220
Gln Leu Asn Tyr Arg Pro Asp Asp Leu Lys Phe Asp Asp Ile Val Val
225                 230                 235                 240
Ala Cys Gly Ser Gly Gly Thr Ile Ala Gly Ile Ser Leu Gly Ser Trp
                245                 250                 255
Leu Gly Ala Leu Lys Ala Lys Val His Ala Phe Ser Val Cys Asp Asp
            260                 265                 270
Pro Asp Tyr Phe Tyr Asp Phe Val Gln Gly Leu Leu Asp Gly Leu His
        275                 280                 285
Ala Gly Val Asn Ser Arg Asp Ile Val Asn Ile His Asn Ala Lys Gly
    290                 295                 300
Lys Gly Tyr Ala Met Asn Thr Ser Glu Glu Leu Glu Phe Val Lys Lys
305                 310                 315                 320
Val Ala Ser Ser Thr Gly Val Ile Leu Asp Pro Val Tyr Ser Gly Lys
                325                 330                 335
Ala Ala Tyr Gly Leu Ile Asn Glu Ile Thr Lys Asp Pro Lys Cys Trp
            340                 345                 350
Glu Gly Arg Lys Ile Leu Phe Ile His Thr Gly Gly Leu Leu Gly Leu
        355                 360                 365
Tyr Asp Lys Val Asp Gln Met Ala Ser Leu Met Gly Asn Trp Ser Arg
    370                 375                 380
Met Asp Val Ser Glu Ser Val Pro Arg Lys Asp Gly Val Gly Lys Met
385                 390                 395                 400
Phe
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<210> 3
<211> 284
<212> PRT
<213> Arabidopsis thaliana

<400> 3

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

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

<210> 4
<211> 1083
<212> DNA
<213> Escherichia coli

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

<400> 4

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atg aca aaa aag ggc gct ttc act agc gcc ttt ttt att tac gcg ttt      48
Met Thr Lys Lys Gly Ala Phe Thr Ser Ala Phe Phe Ile Tyr Ala Phe
1               5                   10                  15
tca gcg tgc ata ata aga aaa tca caa caa cac aca tcg gag gct gtt      96
Ser Ala Cys Ile Ile Arg Lys Ser Gln Gln His Thr Ser Glu Ala Val
            20                  25                  30
atg cca ctg cat aat tta acc cgt ttt cca cgg ctg gag ttt atc ggc     144
Met Pro Leu His Asn Leu Thr Arg Phe Pro Arg Leu Glu Phe Ile Gly
        35                  40                  45
gcg cca acg ccg ctc gaa tat ctg ccg cgc ttt tct gat tat cta gga     192
Ala Pro Thr Pro Leu Glu Tyr Leu Pro Arg Phe Ser Asp Tyr Leu Gly
    50                  55                  60
cgg gaa att ttc atc aaa cgg gat gac gtc acc ccc atg gca atg ggc     240
Arg Glu Ile Phe Ile Lys Arg Asp Asp Val Thr Pro Met Ala Met Gly
65                  70                  75                  80
ggc aat aaa tta cgt aag ctg gaa ttt ctc gcg gca gat gct ctg cgt     288
Gly Asn Lys Leu Arg Lys Leu Glu Phe Leu Ala Ala Asp Ala Leu Arg
                85                  90                  95
gaa ggt gcc gat acg ctg att act gcc ggg gcg atc cag tct aac cat     336
Glu Gly Ala Asp Thr Leu Ile Thr Ala Gly Ala Ile Gln Ser Asn His
            100                 105                 110
gtg cgg cag act gcc gca gtc gct gcc aaa ctc ggt ctg cac tgc gtg     384
Val Arg Gln Thr Ala Ala Val Ala Ala Lys Leu Gly Leu His Cys Val
```

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

<210> 5
<211> 360
<212> PRT
<213> Escherichia coli

<400> 5

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Met Thr Lys Lys Gly Ala Phe Thr Ser Ala Phe Phe Ile Tyr Ala Phe
1               5                   10                  15
Ser Ala Cys Ile Ile Arg Lys Ser Gln Gln His Thr Ser Glu Ala Val
            20                  25                  30
Met Pro Leu His Asn Leu Thr Arg Phe Pro Arg Leu Glu Phe Ile Gly
        35                  40                  45
Ala Pro Thr Pro Leu Glu Tyr Leu Pro Arg Phe Ser Asp Tyr Leu Gly
    50                  55                  60
```

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

<210> 6
<211> 893
<212> DNA
<213> Oryza sativa

<220>
<221> CDS
<222> (79)..(702)

<400> 6

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gctgctgccc cgacgcgctg ctcgctgccc cactctctcc ccattccccc ccacgccgcc      60

gccgccgccg ccgcgtgg atg gcc gga gtt tcc gcc gcc tcc gcc gcc ggg        111
                       Met Ala Gly Val Ser Ala Ala Ser Ala Ala Gly
                       1               5                   10
aag atc ggg agc ttc ctc tcc aag agg ccg tac gcg ccg ccg tcc tgg        159
Lys Ile Gly Ser Phe Leu Ser Lys Arg Pro Tyr Ala Pro Pro Ser Trp
            15                  20                  25
gcc tcg cac ctg tcc ccc gcc ccc tcg cag acc ttc tcg ctc ggc cat        207
Ala Ser His Leu Ser Pro Ala Pro Ser Gln Thr Phe Ser Leu Gly His
        30                  35                  40
ttc ccg acg ccg atc cac aag tgg aat ctg ccc aat ttg ccg aat ggc        255
```

```
Phe Pro Thr Pro Ile His Lys Trp Asn Leu Pro Asn Leu Pro Asn Gly
    45                  50                  55
acg gag gtg tgg atc aag cga gac gac atc tca ggc atg cag ttg agc      303
Thr Glu Val Trp Ile Lys Arg Asp Asp Ile Ser Gly Met Gln Leu Ser
60                  65                  70                  75
ggg aac aag gtc cgg aag ctc gag ttc ctg atg gca gat gcc gtc gcg      351
Gly Asn Lys Val Arg Lys Leu Glu Phe Leu Met Ala Asp Ala Val Ala
                80                  85                  90
cag ggc gct gac tgc gtt ata act gta ggt ggc atc cag agc aat cac      399
Gln Gly Ala Asp Cys Val Ile Thr Val Gly Gly Ile Gln Ser Asn His
        95                  100                 105
tgc cgt gcc acc gca gtg gct gca aag tat ata aat ctt gat tgt tat      447
Cys Arg Ala Thr Ala Val Ala Ala Lys Tyr Ile Asn Leu Asp Cys Tyr
    110                 115                 120
ctg ata ctg cgc aca tcc aag ctt ctt gtg gat aag gac cct ggt ttg      495
Leu Ile Leu Arg Thr Ser Lys Leu Leu Val Asp Lys Asp Pro Gly Leu
125                 130                 135
gtt ggg aat ctc ctt gtt gag aga ttg gtg gga gcg cat att gat ctt      543
Val Gly Asn Leu Leu Val Glu Arg Leu Val Gly Ala His Ile Asp Leu
140                 145                 150                 155
gtt tca aaa gaa gaa tat gga aaa att ggc agt gtg gct tta gcg gac      591
Val Ser Lys Glu Glu Tyr Gly Lys Ile Gly Ser Val Ala Leu Ala Asp
                160                 165                 170
ttg ctg aaa aag aag ctt ttg gaa gaa ggc cga aaa cca tat gtt att      639
Leu Leu Lys Lys Lys Leu Leu Glu Glu Gly Arg Lys Pro Tyr Val Ile
            175                 180                 185
cct gtt ggt gga tca aac tct cta gga act tgg tat tgt ttt ctg ttc      687
Pro Val Gly Gly Ser Asn Ser Leu Gly Thr Trp Tyr Cys Phe Leu Phe
        190                 195                 200
aat cct aac tat tgaaccattt ttgcattttc aatttctttg tgcgtttata          739
Asn Pro Asn Tyr
    205
gcatactttg aatattcctc agggactatt attattcatg gattggtgtt tgccatcagt    799

ctatcagaaa agaagagatt agtttgtatt tgaataaaca ttagggcatc actttttttt    859

ggcaaatttc taatggtcaa tatactatgt tgga                               893


<210> 7
<211> 207
<212> PRT
<213> Oryza sativa

<400> 7
Met Ala Gly Val Ser Ala Ala Ser Ala Ala Gly Lys Ile Gly Ser Phe
1               5                   10                  15
Leu Ser Lys Arg Pro Tyr Ala Pro Pro Ser Trp Ala Ser His Leu Ser
            20                  25                  30
Pro Ala Pro Ser Gln Thr Phe Ser Leu Gly His Phe Pro Thr Pro Ile
        35                  40                  45
His Lys Trp Asn Leu Pro Asn Leu Pro Asn Gly Thr Glu Val Trp Ile
    50                  55                  60
Lys Arg Asp Asp Ile Ser Gly Met Gln Leu Ser Gly Asn Lys Val Arg
65                  70                  75                  80
Lys Leu Glu Phe Leu Met Ala Asp Ala Val Ala Gln Gly Ala Asp Cys
                85                  90                  95
Val Ile Thr Val Gly Gly Ile Gln Ser Asn His Cys Arg Ala Thr Ala
            100                 105                 110
Val Ala Ala Lys Tyr Ile Asn Leu Asp Cys Tyr Leu Ile Leu Arg Thr
```

```
        115                 120                 125
Ser Lys Leu Leu Val Asp Lys Asp Pro Gly Leu Val Gly Asn Leu Leu
    130                 135                 140
Val Glu Arg Leu Val Gly Ala His Ile Asp Leu Val Ser Lys Glu Glu
145                 150                 155                 160
Tyr Gly Lys Ile Gly Ser Val Ala Leu Ala Asp Leu Leu Lys Lys Lys
                165                 170                 175
Leu Leu Glu Glu Gly Arg Lys Pro Tyr Val Ile Pro Val Gly Gly Ser
            180                 185                 190
Asn Ser Leu Gly Thr Trp Tyr Cys Phe Leu Phe Asn Pro Asn Tyr
        195                 200                 205
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<210> 8
<211> 1455
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (85)..(1272)

<400> 8

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cattgggaac ctcgagtccg gacggcgact ctcccactcc tctgtcgctt ccgccgacac      60

ctgagtcttg tcgctgccgc cggg atg gcc gga gtc acc gcc acc ggg atg          111
                          Met Ala Gly Val Thr Ala Thr Gly Met
                          1               5
gcc gga gtt ccc gcc acc ttc tcc tca gcc acc gct cag atc ggg ggc        159
Ala Gly Val Pro Ala Thr Phe Ser Ser Ala Thr Ala Gln Ile Gly Gly
10                  15                  20                  25
ttc ctc tcg aag aag cct tac gcg ccg ccg ttg tgg gcc acg cac ctc        207
Phe Leu Ser Lys Lys Pro Tyr Ala Pro Pro Leu Trp Ala Thr His Leu
                30                  35                  40
tcc ccc atg cct tgc cat acc ttc tcg ctc ggc cat ttc cca aca ccg        255
Ser Pro Met Pro Cys His Thr Phe Ser Leu Gly His Phe Pro Thr Pro
            45                  50                  55
att cac aag tgg aat ctg ccc aat ttg ccg gaa gga acg gaa gtg tgg        303
Ile His Lys Trp Asn Leu Pro Asn Leu Pro Glu Gly Thr Glu Val Trp
        60                  65                  70
atc aag cga gac gat tta tca ggc atg cag ttg agt gga aac aag gtc        351
Ile Lys Arg Asp Asp Leu Ser Gly Met Gln Leu Ser Gly Asn Lys Val
    75                  80                  85
cgg aag ctg gag ttc ttg atg gca gat gcc gta gca caa ggc gca gac        399
Arg Lys Leu Glu Phe Leu Met Ala Asp Ala Val Ala Gln Gly Ala Asp
90                  95                  100                 105
tgc gtt att act gtt ggg ggt ata cag agt aac cac tgc cgt gcc aca        447
Cys Val Ile Thr Val Gly Gly Ile Gln Ser Asn His Cys Arg Ala Thr
                110                 115                 120
gcc gtg gct gct aag tat ctc aat ctt gat tgc tac ctg ata cta cgt        495
Ala Val Ala Ala Lys Tyr Leu Asn Leu Asp Cys Tyr Leu Ile Leu Arg
            125                 130                 135
acc tcc aag ctt ctt gtg gat aag gac cct ggt ttg gtt ggc aat ctt        543
Thr Ser Lys Leu Leu Val Asp Lys Asp Pro Gly Leu Val Gly Asn Leu
        140                 145                 150
ctt gtc gag aga cta gtt ggg gca cac gtt gat ctt gtg tca aaa gaa        591
Leu Val Glu Arg Leu Val Gly Ala His Val Asp Leu Val Ser Lys Glu
    155                 160                 165
gaa tat gga aaa att ggt agt gtg gct tta gct gac ctg ctg aaa aaa        639
Glu Tyr Gly Lys Ile Gly Ser Val Ala Leu Ala Asp Leu Leu Lys Lys
170                 175                 180                 185
agg ctt ctg gaa gaa ggg agg aag ccg tat gtg att cct gtt ggt gga        687
```

```
Arg Leu Leu Glu Glu Gly Arg Lys Pro Tyr Val Ile Pro Val Gly Gly
                190                 195                 200
tca aac tca ttg gga act tgg gga tat att gag gca ata agg gag att      735
Ser Asn Ser Leu Gly Thr Trp Gly Tyr Ile Glu Ala Ile Arg Glu Ile
            205                 210                 215
gag cag caa att cag caa tct tct gat gtt cag ttt gat gat att gtt      783
Glu Gln Gln Ile Gln Gln Ser Ser Asp Val Gln Phe Asp Asp Ile Val
        220                 225                 230
gtt gca tgt ggc agt ggt gga acc att gct ggc ctt gct tta gga tcc      831
Val Ala Cys Gly Ser Gly Gly Thr Ile Ala Gly Leu Ala Leu Gly Ser
    235                 240                 245
aga ttg agc agc tta aat aca aaa gtt cat gca ttc tct gtt tgt gat      879
Arg Leu Ser Ser Leu Asn Thr Lys Val His Ala Phe Ser Val Cys Asp
250                 255                 260                 265
gac cct gaa tac ttc tat gac tat gtc caa ggc ctg att gat gga ctt      927
Asp Pro Glu Tyr Phe Tyr Asp Tyr Val Gln Gly Leu Ile Asp Gly Leu
                270                 275                 280
aat tct ggt ttg gat tca cat gat ata gtt agc atc gaa aat gct aag      975
Asn Ser Gly Leu Asp Ser His Asp Ile Val Ser Ile Glu Asn Ala Lys
            285                 290                 295
ggg tta ggc tat gcc atg aac aca gct gag gag ctt aag ttt gtc aaa     1023
Gly Leu Gly Tyr Ala Met Asn Thr Ala Glu Glu Leu Lys Phe Val Lys
        300                 305                 310
gac ata gct gca tca aca ggc att gtc ctt gat cca gtc tac agt ggg     1071
Asp Ile Ala Ala Ser Thr Gly Ile Val Leu Asp Pro Val Tyr Ser Gly
    315                 320                 325
aag gcg gtt tat ggt ttg cta aaa gac atg gct ggc aat cca gcc aaa     1119
Lys Ala Val Tyr Gly Leu Leu Lys Asp Met Ala Gly Asn Pro Ala Lys
330                 335                 340                 345
tgg aaa ggt cga aaa gtt ctg ttt atc cac aca ggt ggt ctt ctt ggg     1167
Trp Lys Gly Arg Lys Val Leu Phe Ile His Thr Gly Gly Leu Leu Gly
                350                 355                 360
ttg tat gat aag gct gac cag ttg tca tct ttg gct ggg agc tgg cgc     1215
Leu Tyr Asp Lys Ala Asp Gln Leu Ser Ser Leu Ala Gly Ser Trp Arg
            365                 370                 375
aga atg gat ctt gaa gat tct gtt cca cgc aaa gat ggc act ggt aag     1263
Arg Met Asp Leu Glu Asp Ser Val Pro Arg Lys Asp Gly Thr Gly Lys
        380                 385                 390
atg ttc tgatcagtat ggtccatgtg attccatgat ggctcattct tgcaaacatt      1319
Met Phe
    395
gtatccatta cagagttatt actcttaaat ttgtgcaaga aaatgcagaa tagatggttc   1379

acattgtata gaacactgat gcaatttaag aataaagcac atctttctgc cctttaaaaa   1439

aaaaaaacaa caaaaa                                                   1455
```

<210> 9
<211> 395
<212> PRT
<213> Zea mays

<400> 9

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Met Ala Gly Val Thr Ala Thr Gly Met Ala Gly Val Pro Ala Thr Phe
1               5                   10                  15
Ser Ser Ala Thr Ala Gln Ile Gly Gly Phe Leu Ser Lys Lys Pro Tyr
            20                  25                  30
Ala Pro Pro Leu Trp Ala Thr His Leu Ser Pro Met Pro Cys His Thr
        35                  40                  45
```

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

<210> 10
<211> 987
<212> DNA
<213> Escherichia coli W3110

<220>
<221> CDS
<222> (1)..(987)
<223> transl_table=11

<400> 10
atg cca ctg cat aat tta acc cgt ttt cca cgg ctg gag ttt atc ggc      48
Met Pro Leu His Asn Leu Thr Arg Phe Pro Arg Leu Glu Phe Ile Gly
1               5                   10                  15
gcg cca acg ccg ctc gaa tat ctg ccg cgc ttt tct gat tat cta gga      96
Ala Pro Thr Pro Leu Glu Tyr Leu Pro Arg Phe Ser Asp Tyr Leu Gly
```

```
            20                  25                  30
cgg gaa att ttc atc aaa cgg gat gac gtc acc ccc atg gca atg ggc       144
Arg Glu Ile Phe Ile Lys Arg Asp Asp Val Thr Pro Met Ala Met Gly
        35                  40                  45
ggc aat aaa tta cgt aag ctg gaa ttt ctc gcg gca gat gct ctg cgt       192
Gly Asn Lys Leu Arg Lys Leu Glu Phe Leu Ala Ala Asp Ala Leu Arg
    50                  55                  60
gaa ggt gcc gat acg ctg att act gcc ggg gcg atc cag tct aac cat       240
Glu Gly Ala Asp Thr Leu Ile Thr Ala Gly Ala Ile Gln Ser Asn His
65                  70                  75                  80
gtg cgg cag act gcc gca gtc gct gcc aaa ctc ggt ctg cac tgc gtg       288
Val Arg Gln Thr Ala Ala Val Ala Ala Lys Leu Gly Leu His Cys Val
                85                  90                  95
gcg ctg ctg gaa aat cct att ggc aca acc gca gaa aac tat tta acc       336
Ala Leu Leu Glu Asn Pro Ile Gly Thr Thr Ala Glu Asn Tyr Leu Thr
            100                 105                 110
aac ggc aat cgc ttg ttg ctg gat ctg ttc aat acc cag att gaa atg       384
Asn Gly Asn Arg Leu Leu Leu Asp Leu Phe Asn Thr Gln Ile Glu Met
        115                 120                 125
tgc gac gca ctg acc gat ccc aat gcc caa ctg gaa gag ctg gcg acg       432
Cys Asp Ala Leu Thr Asp Pro Asn Ala Gln Leu Glu Glu Leu Ala Thr
    130                 135                 140
cga gtc gaa gca caa ggc ttt cgc ccg tat gtc att ccg gtt ggc ggt       480
Arg Val Glu Ala Gln Gly Phe Arg Pro Tyr Val Ile Pro Val Gly Gly
145                 150                 155                 160
tct aat gct ctt ggc gcg cta ggt tat gtg gag agt gcg ctg gaa atc       528
Ser Asn Ala Leu Gly Ala Leu Gly Tyr Val Glu Ser Ala Leu Glu Ile
                165                 170                 175
gcg caa cag tgt gaa ggg gcg gtt aat att tca tcg gtg gta gtc gca       576
Ala Gln Gln Cys Glu Gly Ala Val Asn Ile Ser Ser Val Val Val Ala
            180                 185                 190
tcg ggc agt gcc gga act cac gcc gga ctg gct gtt ggg ctg gaa cac       624
Ser Gly Ser Ala Gly Thr His Ala Gly Leu Ala Val Gly Leu Glu His
        195                 200                 205
ctg atg cct gaa agc gaa ctg att ggc gtg acc gtg tcg cgt tcc gtt       672
Leu Met Pro Glu Ser Glu Leu Ile Gly Val Thr Val Ser Arg Ser Val
    210                 215                 220
gcc gat caa ttg ccg aaa gtg gtt aac cta caa cag gcg att gcg aaa       720
Ala Asp Gln Leu Pro Lys Val Val Asn Leu Gln Gln Ala Ile Ala Lys
225                 230                 235                 240
gaa ctg gag ctg acc gca tca gcg gaa att tta ctc tgg gat gac tat       768
Glu Leu Glu Leu Thr Ala Ser Ala Glu Ile Leu Leu Trp Asp Asp Tyr
                245                 250                 255
ttt gca cct ggc tac ggc gtg ccg aac gac gaa ggc atg gaa gca gtg       816
Phe Ala Pro Gly Tyr Gly Val Pro Asn Asp Glu Gly Met Glu Ala Val
            260                 265                 270
aaa ttg ctg gcg cgg ctg gaa ggc att ctg ctt gat cct gtg tat acc       864
Lys Leu Leu Ala Arg Leu Glu Gly Ile Leu Leu Asp Pro Val Tyr Thr
        275                 280                 285
gga aaa gcg atg gcg ggg ctg att gac ggt atc agt cag aaa cgc ttc       912
Gly Lys Ala Met Ala Gly Leu Ile Asp Gly Ile Ser Gln Lys Arg Phe
    290                 295                 300
aaa gat gaa ggg ccg att ctg ttt att cat acc ggc ggt gcg cct gcg       960
Lys Asp Glu Gly Pro Ile Leu Phe Ile His Thr Gly Gly Ala Pro Ala
305                 310                 315                 320
ctg ttc gcc tat cat ccc cac gtt tag                                  987
Leu Phe Ala Tyr His Pro His Val
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<210> 11
<211> 328

<212> PRT
<213> Escherichia coli W3110

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

<210> 12
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<212> DNA
<213> Pyrococcus horikoshii OT3

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<222> (1)..(987)
<223> transl_table=11

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agg gtt gag tta atc ccc tgg gag aca ccc ata cag tac ctt cct aac      96
Arg Val Glu Leu Ile Pro Trp Glu Thr Pro Ile Gln Tyr Leu Pro Asn
            20                  25                  30
ata agt aga gaa ata gga gcc gac gta tat atc aaa agg gat gat cta     144
Ile Ser Arg Glu Ile Gly Ala Asp Val Tyr Ile Lys Arg Asp Asp Leu
        35                  40                  45
act ggt ctc gga att ggg ggg aat aaa ata agg aag ctc gaa tat ctc     192
Thr Gly Leu Gly Ile Gly Gly Asn Lys Ile Arg Lys Leu Glu Tyr Leu
    50                  55                  60
ctg ggt gac gct ctc tct aaa gga gca gac gtc gta ata act gtg gga     240
Leu Gly Asp Ala Leu Ser Lys Gly Ala Asp Val Val Ile Thr Val Gly
65                  70                  75                  80
gca gtg cat tcc aat cat gca ttc gtt act gga cta gcc gcc aag aaa     288
Ala Val His Ser Asn His Ala Phe Val Thr Gly Leu Ala Ala Lys Lys
                85                  90                  95
ctt ggg ctt gat gca atc cta gtt tta agg ggg aag gaa gag ctg aaa     336
Leu Gly Leu Asp Ala Ile Leu Val Leu Arg Gly Lys Glu Glu Leu Lys
            100                 105                 110
gga aac tac ctt cta gat aag atc atg ggc atc gaa aca agg gtg tat     384
Gly Asn Tyr Leu Leu Asp Lys Ile Met Gly Ile Glu Thr Arg Val Tyr
        115                 120                 125
gat gca aag gac tcc ttt gag ctc atg aag tat gct gag gag atc gcg     432
Asp Ala Lys Asp Ser Phe Glu Leu Met Lys Tyr Ala Glu Glu Ile Ala
    130                 135                 140
gag gaa ttg aaa aga gag ggt agg aag ccc tat gtt att cca ccg gga     480
Glu Glu Leu Lys Arg Glu Gly Arg Lys Pro Tyr Val Ile Pro Pro Gly
145                 150                 155                 160
gga gca tcc cca ata ggg acg ctt ggt tac gtt agg gcc gtt gga gag     528
Gly Ala Ser Pro Ile Gly Thr Leu Gly Tyr Val Arg Ala Val Gly Glu
                165                 170                 175
att gca acg cag agc gaa gtt aaa ttc gat agc ata gtt gta gca gct     576
Ile Ala Thr Gln Ser Glu Val Lys Phe Asp Ser Ile Val Val Ala Ala
            180                 185                 190
gga agt gga ggt acg ctt gca gga tta tcc ctg ggc ttg tcg atc ctt     624
Gly Ser Gly Gly Thr Leu Ala Gly Leu Ser Leu Gly Leu Ser Ile Leu
        195                 200                 205
aat gaa gat att aga ccc gta gga atc gca gtt ggt aga ttc ggt gaa     672
Asn Glu Asp Ile Arg Pro Val Gly Ile Ala Val Gly Arg Phe Gly Glu
    210                 215                 220
gta atg act agt aag ctg gac aac tta att aaa gaa gct gcg gag tta     720
Val Met Thr Ser Lys Leu Asp Asn Leu Ile Lys Glu Ala Ala Glu Leu
225                 230                 235                 240
ctt gga gta aag gtt gag gta agg ccg gag tta tac gac tac agc ttt     768
Leu Gly Val Lys Val Glu Val Arg Pro Glu Leu Tyr Asp Tyr Ser Phe
                245                 250                 255
gga gag tac ggt aag ata acc ggt gaa gtt gct caa att ata agg aaa     816
Gly Glu Tyr Gly Lys Ile Thr Gly Glu Val Ala Gln Ile Ile Arg Lys
            260                 265                 270
gtt gga acg agg gaa gga ata ata ctg gat ccc gta tat acg ggg aag     864
Val Gly Thr Arg Glu Gly Ile Ile Leu Asp Pro Val Tyr Thr Gly Lys
        275                 280                 285
gca ttc tat ggg ctc gtt gat cta gct agg aaa ggg gag ttg ggg gag     912
Ala Phe Tyr Gly Leu Val Asp Leu Ala Arg Lys Gly Glu Leu Gly Glu
    290                 295                 300
aag att ctc ttt atc cat act gga ggg ata tcg gga acg ttc cac tat     960
Lys Ile Leu Phe Ile His Thr Gly Gly Ile Ser Gly Thr Phe His Tyr
305                 310                 315                 320
ggt gac aaa ctt ttg tca cta ctt tag                                 987
Gly Asp Lys Leu Leu Ser Leu Leu
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<210> 13
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<213> Pyrococcus horikoshii OT3

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20 25 30
Ile Ser Arg Glu Ile Gly Ala Asp Val Tyr Ile Lys Arg Asp Asp Leu
35 40 45
Thr Gly Leu Gly Ile Gly Gly Asn Lys Ile Arg Lys Leu Glu Tyr Leu
50 55 60
Leu Gly Asp Ala Leu Ser Lys Gly Ala Asp Val Val Ile Thr Val Gly
65 70 75 80
Ala Val His Ser Asn His Ala Phe Val Thr Gly Leu Ala Ala Lys Lys
85 90 95
Leu Gly Leu Asp Ala Ile Leu Val Leu Arg Gly Lys Glu Glu Leu Lys
100 105 110
Gly Asn Tyr Leu Leu Asp Lys Ile Met Gly Ile Glu Thr Arg Val Tyr
115 120 125
Asp Ala Lys Asp Ser Phe Glu Leu Met Lys Tyr Ala Glu Glu Ile Ala
130 135 140
Glu Glu Leu Lys Arg Glu Gly Arg Lys Pro Tyr Val Ile Pro Pro Gly
145 150 155 160
Gly Ala Ser Pro Ile Gly Thr Leu Gly Tyr Val Arg Ala Val Gly Glu
165 170 175
Ile Ala Thr Gln Ser Glu Val Lys Phe Asp Ser Ile Val Val Ala Ala
180 185 190
Gly Ser Gly Gly Thr Leu Ala Gly Leu Ser Leu Gly Leu Ser Ile Leu
195 200 205
Asn Glu Asp Ile Arg Pro Val Gly Ile Ala Val Gly Arg Phe Gly Glu
210 215 220

Val Met Thr Ser Lys Leu Asp Asn Leu Ile Lys Glu Ala Ala Glu Leu
225 230 235 240
Leu Gly Val Lys Val Glu Val Arg Pro Glu Leu Tyr Asp Tyr Ser Phe
245 250 255
Gly Glu Tyr Gly Lys Ile Thr Gly Glu Val Ala Gln Ile Ile Arg Lys
260 265 270
Val Gly Thr Arg Glu Gly Ile Ile Leu Asp Pro Val Tyr Thr Gly Lys
275 280 285
Ala Phe Tyr Gly Leu Val Asp Leu Ala Arg Lys Gly Glu Leu Gly Glu
290 295 300
Lys Ile Leu Phe Ile His Thr Gly Gly Ile Ser Gly Thr Phe His Tyr
305 310 315 320
Gly Asp Lys Leu Leu Ser Leu Leu
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<212> DNA
<213> Campylobacter jejuni subsp. jejuni NCTC 11168

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1               5                   10                  15
gga ttt gaa ttt tat att aaa aga gat gat tta tta ggg gaa att aat       96
Gly Phe Glu Phe Tyr Ile Lys Arg Asp Asp Leu Leu Gly Glu Ile Asn
            20                  25                  30
gga aat aaa gct agg aaa ctt gct ttt tat atc cat caa aga tat cct      144
Gly Asn Lys Ala Arg Lys Leu Ala Phe Tyr Ile His Gln Arg Tyr Pro
        35                  40                  45
aaa aat caa tct ttt gta agt tat gga gga agc caa agt aat gct ttg      192
Lys Asn Gln Ser Phe Val Ser Tyr Gly Gly Ser Gln Ser Asn Ala Leu
    50                  55                  60
gcg gca tta agt att ttt gct aaa caa aga tca tat aag ctt gtt ttt      240
Ala Ala Leu Ser Ile Phe Ala Lys Gln Arg Ser Tyr Lys Leu Val Phe
65                  70                  75                  80
gct tgt gaa aaa att tct act ttt ctt aag aat aat cct tgt gga aac      288
Ala Cys Glu Lys Ile Ser Thr Phe Leu Lys Asn Asn Pro Cys Gly Asn
                85                  90                  95
tat gct tta gct tta gaa aat ggt gtt gat ttt gta gaa aat atc cat      336
Tyr Ala Leu Ala Leu Glu Asn Gly Val Asp Phe Val Glu Asn Ile His
            100                 105                 110
tct tta tcc tta aag caa ttt gct ttg tct ttg tgt aaa aaa gat gat      384
Ser Leu Ser Leu Lys Gln Phe Ala Leu Ser Leu Cys Lys Lys Asp Asp
        115                 120                 125
gtt ttt ata gaa caa ggt ata gct aat tta gaa gct caa tat ggc tat      432
Val Phe Ile Glu Gln Gly Ile Ala Asn Leu Glu Ala Gln Tyr Gly Tyr
    130                 135                 140
atg gaa ctt gct caa gaa att caa atg caa agt caa agt tta aag ctt      480
Met Glu Leu Ala Gln Glu Ile Gln Met Gln Ser Gln Ser Leu Lys Leu
145                 150                 155                 160
gat ttt gat att ttt tta cct tcg ggt aca ggc act tcg gca gct ttt      528
Asp Phe Asp Ile Phe Leu Pro Ser Gly Thr Gly Thr Ser Ala Ala Phe
                165                 170                 175
ttg gca aag tat tct aaa ttt aaa gta ttt act tgc gct tgt gta ggt      576

Leu Ala Lys Tyr Ser Lys Phe Lys Val Phe Thr Cys Ala Cys Val Gly
            180                 185                 190
gat att aaa tat ctt aaa aaa caa att tta aca tta gat cca agc tat      624
Asp Ile Lys Tyr Leu Lys Lys Gln Ile Leu Thr Leu Asp Pro Ser Tyr
        195                 200                 205
gat ttt tca aat tta gaa ttt tta aca agt gat aaa aaa tat cac ttt      672
Asp Phe Ser Asn Leu Glu Phe Leu Thr Ser Asp Lys Lys Tyr His Phe
    210                 215                 220
gct aag ccg tat aaa gaa ttt tat gag ctt tat atg gat tta aag tta      720
Ala Lys Pro Tyr Lys Glu Phe Tyr Glu Leu Tyr Met Asp Leu Lys Leu
225                 230                 235                 240
aag tgc aat ata gaa ttt gac ttg ttg tat gat att tta gga tta agt      768
Lys Cys Asn Ile Glu Phe Asp Leu Leu Tyr Asp Ile Leu Gly Leu Ser
                245                 250                 255
ata gca tta aaa caa gag tgg aaa aaa cca ttg ctt tat ata cat caa      816
Ile Ala Leu Lys Gln Glu Trp Lys Lys Pro Leu Leu Tyr Ile His Gln
            260                 265                 270
ggt gga att tta gga aat tcc act atg tta gag aga tat aaa ttt aaa      864
Gly Gly Ile Leu Gly Asn Ser Thr Met Leu Glu Arg Tyr Lys Phe Lys
        275                 280                 285
aaa tca gtt taa                                                     876
Lys Ser Val
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<210> 15

<211> 291
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Gly Asn Lys Ala Arg Lys Leu Ala Phe Tyr Ile His Gln Arg Tyr Pro
35 40 45
Lys Asn Gln Ser Phe Val Ser Tyr Gly Gly Ser Gln Ser Asn Ala Leu
50 55 60
Ala Ala Leu Ser Ile Phe Ala Lys Gln Arg Ser Tyr Lys Leu Val Phe
65 70 75 80
Ala Cys Glu Lys Ile Ser Thr Phe Leu Lys Asn Asn Pro Cys Gly Asn
85 90 95
Tyr Ala Leu Ala Leu Glu Asn Gly Val Asp Phe Val Glu Asn Ile His
100 105 110
Ser Leu Ser Leu Lys Gln Phe Ala Leu Ser Leu Cys Lys Lys Asp Asp
115 120 125
Val Phe Ile Glu Gln Gly Ile Ala Asn Leu Glu Ala Gln Tyr Gly Tyr
130 135 140
Met Glu Leu Ala Gln Glu Ile Gln Met Gln Ser Gln Ser Leu Lys Leu
145 150 155 160
Asp Phe Asp Ile Phe Leu Pro Ser Gly Thr Gly Thr Ser Ala Ala Phe
165 170 175
Leu Ala Lys Tyr Ser Lys Phe Lys Val Phe Thr Cys Ala Cys Val Gly
180 185 190
Asp Ile Lys Tyr Leu Lys Lys Gln Ile Leu Thr Leu Asp Pro Ser Tyr
195 200 205
Asp Phe Ser Asn Leu Glu Phe Leu Thr Ser Asp Lys Lys Tyr His Phe
210 215 220
Ala Lys Pro Tyr Lys Glu Phe Tyr Glu Leu Tyr Met Asp Leu Lys Leu
225 230 235 240
Lys Cys Asn Ile Glu Phe Asp Leu Leu Tyr Asp Ile Leu Gly Leu Ser
245 250 255
Ile Ala Leu Lys Gln Glu Trp Lys Lys Pro Leu Leu Tyr Ile His Gln
260 265 270
Gly Gly Ile Leu Gly Asn Ser Thr Met Leu Glu Arg Tyr Lys Phe Lys
275 280 285
Lys Ser Val
290

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<212> DNA
<213> Escherichia coli O157:H7 EDL933

<220>
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tca gcg tgc ata atg aga aaa tca caa caa cac aca tcg gag gct gtt 96
Ser Ala Cys Ile Met Arg Lys Ser Gln Gln His Thr Ser Glu Ala Val
20 25 30

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atg cca ctg cat aat tta acc cgt ttt cca cgg ctg gag ttt atc ggc      144
Met Pro Leu His Asn Leu Thr Arg Phe Pro Arg Leu Glu Phe Ile Gly
        35                  40                  45
gcg cca acg ccg ctc gaa tat ctg ccg cgc ttt tct gat tat cta gga      192
Ala Pro Thr Pro Leu Glu Tyr Leu Pro Arg Phe Ser Asp Tyr Leu Gly
    50                  55                  60
cgg gaa att ttc atc aaa cgg gat gac gtc acc ccc atg gca atg ggc      240
Arg Glu Ile Phe Ile Lys Arg Asp Asp Val Thr Pro Met Ala Met Gly
65                  70                  75                  80
ggc aat aaa tta cgt aag cta gaa ttt ctc gcg gca gat gct ctg cgt      288
Gly Asn Lys Leu Arg Lys Leu Glu Phe Leu Ala Ala Asp Ala Leu Arg
                85                  90                  95
gaa ggt gcc gat acg ctg att act gcc ggg gcg atc cag tct aac cat      336
Glu Gly Ala Asp Thr Leu Ile Thr Ala Gly Ala Ile Gln Ser Asn His
            100                 105                 110
gtg cgg cag act gcc gca gtc gct gcc aaa ctc ggt ctg cac tgc gtg      384
Val Arg Gln Thr Ala Ala Val Ala Ala Lys Leu Gly Leu His Cys Val
        115                 120                 125
gcg ctg ctg gaa aat cct att ggc aca acc gca gaa aac tat tta acc      432
Ala Leu Leu Glu Asn Pro Ile Gly Thr Thr Ala Glu Asn Tyr Leu Thr
    130                 135                 140
aac ggc aat cgc ttg ttg ctg gat ctg ttc aat acc cag att gaa atg      480
Asn Gly Asn Arg Leu Leu Leu Asp Leu Phe Asn Thr Gln Ile Glu Met
145                 150                 155                 160
tgc gac gca ctg acc gat ccc aat gcc caa ctg gaa gag ctg gcg acg      528
Cys Asp Ala Leu Thr Asp Pro Asn Ala Gln Leu Glu Glu Leu Ala Thr
                165                 170                 175
cga gtc gaa gca caa ggc ttt cgc ccg tat gtc att ccg gtt ggc ggt      576
Arg Val Glu Ala Gln Gly Phe Arg Pro Tyr Val Ile Pro Val Gly Gly
            180                 185                 190
tct aat gct ctt ggc gcg cta ggt tat gtg gag agt gcg ctg gaa atc      624
Ser Asn Ala Leu Gly Ala Leu Gly Tyr Val Glu Ser Ala Leu Glu Ile
        195                 200                 205
gcg caa cag tgt gaa ggg gcg gtt aat att tca tcg gtg gta gtc gca      672
Ala Gln Gln Cys Glu Gly Ala Val Asn Ile Ser Ser Val Val Val Ala
    210                 215                 220
tcg ggc agt gcc gga act cac gcc gga ctg gct gtt ggg ctg gaa cac      720
Ser Gly Ser Ala Gly Thr His Ala Gly Leu Ala Val Gly Leu Glu His
225                 230                 235                 240
ctg atg cct gaa agc gaa ctg att ggc gtg acc gtg tcg cgt tcc gtt      768
Leu Met Pro Glu Ser Glu Leu Ile Gly Val Thr Val Ser Arg Ser Val
                245                 250                 255
gcc gat caa ttg ccg aaa gtg gtt aac cta caa cag gcg att gcg aaa      816
Ala Asp Gln Leu Pro Lys Val Val Asn Leu Gln Gln Ala Ile Ala Lys
            260                 265                 270
gaa ctg gag ctg acc gca tca gtg gaa att tta ctc tgg gat gac tat      864
Glu Leu Glu Leu Thr Ala Ser Val Glu Ile Leu Leu Trp Asp Asp Tyr
        275                 280                 285
ttt gca cct ggc tac ggc gtg ccg aac gac gaa ggc atg gaa gca gtg      912
Phe Ala Pro Gly Tyr Gly Val Pro Asn Asp Glu Gly Met Glu Ala Val
    290                 295                 300
aaa ttg ctg gcg cgg ctg gaa ggc att ctg ctt gat cct gtg tat acc      960
Lys Leu Leu Ala Arg Leu Glu Gly Ile Leu Leu Asp Pro Val Tyr Thr
305                 310                 315                 320
gga aaa gcg atg gcg ggt ctg att gac ggt atc agt cag aaa cgc ttc     1008
Gly Lys Ala Met Ala Gly Leu Ile Asp Gly Ile Ser Gln Lys Arg Phe
                325                 330                 335
aaa gat gaa ggg ccg att ctg ttt att cat acc ggc ggc gcg cct gcg     1056
Lys Asp Glu Gly Pro Ile Leu Phe Ile His Thr Gly Gly Ala Pro Ala
            340                 345                 350
ctg ttc gcc tat cat ccc cac gtt tag                                1083
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Leu Phe Ala Tyr His Pro His Val

355 360

<210> 17
<211> 360
<212> PRT
<213> Escherichia coli O157:H7 EDL933

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

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<212> DNA
<213> Caulobacter crescentus CB15

<220>
<221> CDS
<222> (1)..(1002)
<223> transl_table=11

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

```
tcg ggc aag gcg atg aag ggg ctg atc gac cag gcc cgc aaa ggc gcg        912
Ser Gly Lys Ala Met Lys Gly Leu Ile Asp Gln Ala Arg Lys Gly Ala
    290                 295                 300
ttc aag ggc gag cgg gtc gtc ttc ctg cac acc ggc ggc gcc cag ggc        960

Phe Lys Gly Glu Arg Val Val Phe Leu His Thr Gly Gly Ala Gln Gly
305                 310                 315                 320
ctg ttc ggc tat cag acg gtg ctc gag ccg gcg ctg gga tag                1002
Leu Phe Gly Tyr Gln Thr Val Leu Glu Pro Ala Leu Gly
                325                 330
```

<210> 19
<211> 333
<212> PRT
<213> Caulobacter crescentus CB15

<400> 19

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

<211> 987
<212> DNA
<213> Salmonella enterica subsp. enterica serovar Typhi str. CT18

<220>
<221> CDS
<222> (1)..(987)
<223> transl_table=11

<400> 20

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

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aaa ctg ctg gcg aac ctg gag ggg gtg ctg ctg gat ccg gta tat acc       864
Lys Leu Leu Ala Asn Leu Glu Gly Val Leu Leu Asp Pro Val Tyr Thr
        275                 280                 285
ggt aaa gcg atg gcg ggt ctg ata gat ggc atc agc cag aaa cgc ttt       912
Gly Lys Ala Met Ala Gly Leu Ile Asp Gly Ile Ser Gln Lys Arg Phe
    290                 295                 300
aac gat gac ggg ccg att ctc ttt att cat acc ggt ggg gcg cct gcg       960
Asn Asp Asp Gly Pro Ile Leu Phe Ile His Thr Gly Gly Ala Pro Ala
305                 310                 315                 320
ctg ttt gcc tac cat cct cat gta taa                                  987
Leu Phe Ala Tyr His Pro His Val
                325
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<210> 21
<211> 328
<212> PRT
<213> Salmonella enterica subsp. enterica serovar Typhi str. CT18

<400> 21

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

<210> 22
<211> 987
<212> DNA
<213> Salmonella typhimurium LT2

<220>
<221> CDS
<222> (1)..(987)
<223> transl_table=11

<400> 22

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

```
Phe Ala Pro Gly Tyr Gly Val Pro Asn Asp Ala Gly Met Glu Ala Val
            260                 265                 270
aaa ctg ctg gcg agc ctg gag ggg gtg ctg ctg gat ccg gta tat acc      864
Lys Leu Leu Ala Ser Leu Glu Gly Val Leu Leu Asp Pro Val Tyr Thr
        275                 280                 285
ggt aaa gcg atg gcg ggt ctg ata gac ggc atc agc cag aaa cgc ttt      912
Gly Lys Ala Met Ala Gly Leu Ile Asp Gly Ile Ser Gln Lys Arg Phe
    290                 295                 300
aac gat gac ggg ccg att ctc ttt att cac acc ggt ggg gcg cct gcg      960
Asn Asp Asp Gly Pro Ile Leu Phe Ile His Thr Gly Gly Ala Pro Ala
305                 310                 315                 320
ctg ttt gcc tac cat cct cat gta taa                                 987
Leu Phe Ala Tyr His Pro His Val
                325
```

<210> 23
<211> 328
<212> PRT
<213> Salmonella typhimurium LT2

<400> 23

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

<210> 24
<211> 948
<212> DNA
<213> Nostoc sp. PCC 7120

<220>
<221> CDS
<222> (1)..(948)
<223> transl_table=11

<400> 24
atg tca ttg acc ttt gtt cct ccg cca ata caa aaa atc aat agt gag 48
Met Ser Leu Thr Phe Val Pro Pro Pro Ile Gln Lys Ile Asn Ser Glu
1 5 10 15
att gct aat aat gct ggt gta gaa att tat gta tta cgc ctt gat tta 96
Ile Ala Asn Asn Ala Gly Val Glu Ile Tyr Val Leu Arg Leu Asp Leu
20 25 30
atg cac ccg tgg gta aac ggt aat aag tgg tac aag ctg aaa tac aat 144
Met His Pro Trp Val Asn Gly Asn Lys Trp Tyr Lys Leu Lys Tyr Asn
35 40 45
ctc tta gaa gct aag gag aaa agt tac aca aaa tta ctc acc ttt ggt 192
Leu Leu Glu Ala Lys Glu Lys Ser Tyr Thr Lys Leu Leu Thr Phe Gly
50 55 60
ggt gca tat tct aat cac atc ttc gct act gcc gca gca ggt aat ctt 240
Gly Ala Tyr Ser Asn His Ile Phe Ala Thr Ala Ala Ala Gly Asn Leu
65 70 75 80
tta gga ttc cag act att ggt ata att cgt ggg gaa gaa acc tta ccc 288
Leu Gly Phe Gln Thr Ile Gly Ile Ile Arg Gly Glu Glu Thr Leu Pro
85 90 95
tta aat ccc aca cta agt ttt gca acg caa caa ggt atg cag ctt gtc 336
Leu Asn Pro Thr Leu Ser Phe Ala Thr Gln Gln Gly Met Gln Leu Val
100 105 110
tat gtg gac agg gaa acc tat cga caa cga aac agc acc aca tta cac 384
Tyr Val Asp Arg Glu Thr Tyr Arg Gln Arg Asn Ser Thr Thr Leu His
115 120 125
aca gac cta agg aaa cgc ttt ggt gag gta ttt atc att cca gaa ggt 432
Thr Asp Leu Arg Lys Arg Phe Gly Glu Val Phe Ile Ile Pro Glu Gly
130 135 140
ggt agt aat ttg aat ggt gtg cgt ggt tgt cta gaa ata ata agt gcc 480
Gly Ser Asn Leu Asn Gly Val Arg Gly Cys Leu Glu Ile Ile Ser Ala
145 150 155 160
gca aca caa gta ttt gat att gtt tgt gta gct tgt ggt aca gcc acc 528
Ala Thr Gln Val Phe Asp Ile Val Cys Val Ala Cys Gly Thr Ala Thr
165 170 175
acc cta gca ggt atc gct ctg gca ctg gaa cct cag caa cgt gtg att 576
Thr Leu Ala Gly Ile Ala Leu Ala Leu Glu Pro Gln Gln Arg Val Ile
180 185 190
ggt ttt cct gtc tta aaa aat ggg ggt ttt tta gca cag gat att gct 624
Gly Phe Pro Val Leu Lys Asn Gly Gly Phe Leu Ala Gln Asp Ile Ala
195 200 205
cag tta atg aag aat tat gtc gcg gcg ggg ttg ccc att tca tct agt 672
Gln Leu Met Lys Asn Tyr Val Ala Ala Gly Leu Pro Ile Ser Ser Ser
210 215 220
tct ccc gcc tct tgg gaa tta gtt tgc gat tac cat ttt ggc ggt tac 720
Ser Pro Ala Ser Trp Glu Leu Val Cys Asp Tyr His Phe Gly Gly Tyr
225 230 235 240
gcc aag gtg aaa gat gat ctc ata ctg ttc agt cac cag ttt acc caa 768
Ala Lys Val Lys Asp Asp Leu Ile Leu Phe Ser His Gln Phe Thr Gln

```
                245                 250                 255
agc tac ggc gta cct ctt gat tac gtg tat aca gcg aaa atg ttt tac       816
Ser Tyr Gly Val Pro Leu Asp Tyr Val Tyr Thr Ala Lys Met Phe Tyr
            260                 265                 270
ggc gta atg gac ttg tta aag caa aga tat ttt acg aaa ggt gat ggt       864
Gly Val Met Asp Leu Leu Lys Gln Arg Tyr Phe Thr Lys Gly Asp Gly
        275                 280                 285
ctc cga ccg acc gta ggt cat cgt atc tta atg att cac acg ggt ggc       912
Leu Arg Pro Thr Val Gly His Arg Ile Leu Met Ile His Thr Gly Gly
    290                 295                 300
tta cag gga aat atc ggg atg agt gaa cga ttg taa                       948
Leu Gln Gly Asn Ile Gly Met Ser Glu Arg Leu
305                 310                 315
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<210> 25
<211> 315
<212> PRT
<213> Nostoc sp. PCC 7120

<400> 25

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

Ala Thr Gln Val Phe Asp Ile Val Cys Val Ala Cys Gly Thr Ala Thr
                165                 170                 175
Thr Leu Ala Gly Ile Ala Leu Ala Leu Glu Pro Gln Gln Arg Val Ile
            180                 185                 190
Gly Phe Pro Val Leu Lys Asn Gly Gly Phe Leu Ala Gln Asp Ile Ala
        195                 200                 205
Gln Leu Met Lys Asn Tyr Val Ala Ala Gly Leu Pro Ile Ser Ser Ser
    210                 215                 220
Ser Pro Ala Ser Trp Glu Leu Val Cys Asp Tyr His Phe Gly Gly Tyr
225                 230                 235                 240
Ala Lys Val Lys Asp Asp Leu Ile Leu Phe Ser His Gln Phe Thr Gln
                245                 250                 255
Ser Tyr Gly Val Pro Leu Asp Tyr Val Tyr Thr Ala Lys Met Phe Tyr
            260                 265                 270
Gly Val Met Asp Leu Leu Lys Gln Arg Tyr Phe Thr Lys Gly Asp Gly
        275                 280                 285
Leu Arg Pro Thr Val Gly His Arg Ile Leu Met Ile His Thr Gly Gly
    290                 295                 300
Leu Gln Gly Asn Ile Gly Met Ser Glu Arg Leu
```

305 310 315

<210> 26
<211> 1065
<212> DNA
<213> Pyrococcus furiosus DSM 3638

<220>
<221> CDS
<222> (1)..(1065)
<223> transl_table=11

<400> 26

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

```
                245                 250                 255
gaa ctt gca aaa gca act gga gag ttc atc gga gtg aaa aat tta aag       816
Glu Leu Ala Lys Ala Thr Gly Glu Phe Ile Gly Val Lys Asn Leu Lys
            260                 265                 270
cta aaa att gag ctc tat gat tac agc ttt gga gaa tat gga aaa ata       864
Leu Lys Ile Glu Leu Tyr Asp Tyr Ser Phe Gly Glu Tyr Gly Lys Ile
        275                 280                 285
aca agg gaa gtt gca gaa acc att agg cta gtc gga aca aaa gaa ggg       912
Thr Arg Glu Val Ala Glu Thr Ile Arg Leu Val Gly Thr Lys Glu Gly
    290                 295                 300
gta atc tta gac cct gtc tat act gga aaa gca ttc tac gga tta ctt       960
Val Ile Leu Asp Pro Val Tyr Thr Gly Lys Ala Phe Tyr Gly Leu Leu
305                 310                 315                 320
gat ctc gct aaa aaa gga gaa tta ggg gag aaa ata ctg ttt att cac      1008
Asp Leu Ala Lys Lys Gly Glu Leu Gly Glu Lys Ile Leu Phe Ile His
                325                 330                 335
acc gga gga atc tct gga aca ttc cat tat ggg gac aag ata ctc tca      1056
Thr Gly Gly Ile Ser Gly Thr Phe His Tyr Gly Asp Lys Ile Leu Ser
            340                 345                 350
ttc ctt tag                                                         1065
Phe Leu
```

<210> 27
<211> 354
<212> PRT
<213> Pyrococcus furiosus DSM 3638

<400> 27

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

```
Glu Leu Ala Lys Ala Thr Gly Glu Phe Ile Gly Val Lys Asn Leu Lys
            260                 265                 270
Leu Lys Ile Glu Leu Tyr Asp Tyr Ser Phe Gly Glu Tyr Gly Lys Ile
        275                 280                 285
Thr Arg Glu Val Ala Glu Thr Ile Arg Leu Val Gly Thr Lys Glu Gly
    290                 295                 300
Val Ile Leu Asp Pro Val Tyr Thr Gly Lys Ala Phe Tyr Gly Leu Leu
305                 310                 315                 320
Asp Leu Ala Lys Lys Gly Glu Leu Gly Glu Lys Ile Leu Phe Ile His
                325                 330                 335
Thr Gly Gly Ile Ser Gly Thr Phe His Tyr Gly Asp Lys Ile Leu Ser
            340                 345                 350
Phe Leu
```

<210> 28
<211> 1020
<212> DNA
<213> Yersinia pestis KIM

<220>
<221> CDS
<222> (1)..(1020)
<223> transl_table=11

<400> 28

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

```
            180                 185                 190
aat gtt gcg ttt agt tcg gtc gtc gtg gcc tct ggc agt gcg gga aca       624
Asn Val Ala Phe Ser Ser Val Val Val Ala Ser Gly Ser Ala Gly Thr
        195                 200                 205
cat gca gga ttg gcg gtt ggt cta cag cag ttg tta ccc gat gcg gaa       672
His Ala Gly Leu Ala Val Gly Leu Gln Gln Leu Leu Pro Asp Ala Glu
    210                 215                 220
tta atc ggt gtg acg gta tca cgt agt gcc gat gaa cag cgg cct aaa       720
Leu Ile Gly Val Thr Val Ser Arg Ser Ala Asp Glu Gln Arg Pro Lys
225                 230                 235                 240
gtg gca cag att caa caa gcg ttg gcg aca tca tta ggg atg acg gac       768
Val Ala Gln Ile Gln Gln Ala Leu Ala Thr Ser Leu Gly Met Thr Asp
                245                 250                 255
cca ttg gca aaa atc acc ttg tgg gat agt tat ttt gcc ccg caa tat       816
Pro Leu Ala Lys Ile Thr Leu Trp Asp Ser Tyr Phe Ala Pro Gln Tyr
            260                 265                 270
ggg atg cca aac gaa gag ggg ata gcg gct att aag ctc ttg gca aga       864
Gly Met Pro Asn Glu Glu Gly Ile Ala Ala Ile Lys Leu Leu Ala Arg
        275                 280                 285
ctg gaa gga ata ttg ttg gac cct gtg tat acc ggt aag gcg atg gcg       912
Leu Glu Gly Ile Leu Leu Asp Pro Val Tyr Thr Gly Lys Ala Met Ala
    290                 295                 300
ggc tta ctt gat ggt att gaa cag caa aaa ttc tgc gac aaa ggg cca       960
Gly Leu Leu Asp Gly Ile Glu Gln Gln Lys Phe Cys Asp Lys Gly Pro
305                 310                 315                 320
att tta ttt atc cac act ggc ggg gca cct gcg ctg ttt gct tat cat      1008
Ile Leu Phe Ile His Thr Gly Gly Ala Pro Ala Leu Phe Ala Tyr His
                325                 330                 335
ccg cag gtg tag                                                     1020
Pro Gln Val
```

<210> 29
<211> 339
<212> PRT
<213> Yersinia pestis KIM

<400> 29

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

```
            180                 185                 190
Asn Val Ala Phe Ser Ser Val Val Val Ala Ser Gly Ser Ala Gly Thr
        195                 200                 205
His Ala Gly Leu Ala Val Gly Leu Gln Gln Leu Leu Pro Asp Ala Glu
    210                 215                 220
Leu Ile Gly Val Thr Val Ser Arg Ser Ala Asp Glu Gln Arg Pro Lys
225                 230                 235                 240
Val Ala Gln Ile Gln Gln Ala Leu Ala Thr Ser Leu Gly Met Thr Asp
                245                 250                 255
Pro Leu Ala Lys Ile Thr Leu Trp Asp Ser Tyr Phe Ala Pro Gln Tyr
            260                 265                 270
Gly Met Pro Asn Glu Glu Gly Ile Ala Ala Ile Lys Leu Leu Ala Arg
        275                 280                 285
Leu Glu Gly Ile Leu Leu Asp Pro Val Tyr Thr Gly Lys Ala Met Ala
    290                 295                 300
Gly Leu Leu Asp Gly Ile Glu Gln Gln Lys Phe Cys Asp Lys Gly Pro
305                 310                 315                 320
Ile Leu Phe Ile His Thr Gly Gly Ala Pro Ala Leu Phe Ala Tyr His
                325                 330                 335
Pro Gln Val
```

<210> 30
<211> 1083
<212> DNA
<213> Shigella flexneri 2a str. 301

<220>
<221> CDS
<222> (1)..(1083)
<223> transl_table=11

<400> 30

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atg aca aaa aag ggc gct ttc act agc gcc ttt ttt att tac gcg ttt      48
Met Thr Lys Lys Gly Ala Phe Thr Ser Ala Phe Phe Ile Tyr Ala Phe
1               5                   10                  15
tca gcg tgc ata ata aga aaa tca caa caa cac aca tcg gag gct gtt      96
Ser Ala Cys Ile Ile Arg Lys Ser Gln Gln His Thr Ser Glu Ala Val
            20                  25                  30
atg cca ctg cat aat tta acc cgt ttt cca cgg ttg gag ttt atc ggc     144
Met Pro Leu His Asn Leu Thr Arg Phe Pro Arg Leu Glu Phe Ile Gly
        35                  40                  45
gcg cca acg ccg ctc gaa tat ctg ccg cgc ttt tct gat tat ctt gga     192
Ala Pro Thr Pro Leu Glu Tyr Leu Pro Arg Phe Ser Asp Tyr Leu Gly
    50                  55                  60
cgg gaa att ttc atc aaa cgg gat gag gtc acc ccc atg gca atg ggc     240

Arg Glu Ile Phe Ile Lys Arg Asp Glu Val Thr Pro Met Ala Met Gly
65                  70                  75                  80
ggc aat aaa tta cgt aag ctg gaa ttt ctc gcg gca gat gcc ctg cgc     288
Gly Asn Lys Leu Arg Lys Leu Glu Phe Leu Ala Ala Asp Ala Leu Arg
                85                  90                  95
gaa ggt gcc gat acg ctg att act gcc ggc gcg atc cag tct aac cat     336
Glu Gly Ala Asp Thr Leu Ile Thr Ala Gly Ala Ile Gln Ser Asn His
            100                 105                 110
gtg cgc cag act gcc gca gtc gcg gcg aaa ctc ggt ctg cac tgc gtg     384
Val Arg Gln Thr Ala Ala Val Ala Ala Lys Leu Gly Leu His Cys Val
        115                 120                 125
gcg ctg ctg gaa aat cct att ggc aca acc gca gaa aac tat tta acc     432
Ala Leu Leu Glu Asn Pro Ile Gly Thr Thr Ala Glu Asn Tyr Leu Thr
    130                 135                 140
```

```
aac ggc aat cgt ttg ttg ctg gat ctg ttc aat acc cag att gaa atg       480
Asn Gly Asn Arg Leu Leu Leu Asp Leu Phe Asn Thr Gln Ile Glu Met
145                 150                 155                 160
tgc gac gca ctg acc gat ccc aat gcc caa ctg gaa gaa ctg gcg acg       528
Cys Asp Ala Leu Thr Asp Pro Asn Ala Gln Leu Glu Glu Leu Ala Thr
                165                 170                 175
cga gtc gaa gca caa ggc ttt cgc ccg tat gtc att ccg gtt ggc ggt       576
Arg Val Glu Ala Gln Gly Phe Arg Pro Tyr Val Ile Pro Val Gly Gly
            180                 185                 190
tct aat gct ctt ggc gcg cta ggt tat gtg gag agt gcg ctg gaa atc       624
Ser Asn Ala Leu Gly Ala Leu Gly Tyr Val Glu Ser Ala Leu Glu Ile
        195                 200                 205
gcg caa cag tgt gaa ggg gcg gtt aat att tcg tcg gtg gta gtc gca       672
Ala Gln Gln Cys Glu Gly Ala Val Asn Ile Ser Ser Val Val Val Ala
    210                 215                 220
tcg ggc agt gcc gga act cac gcc gga ctg gct gtt ggg ctg gaa cac       720
Ser Gly Ser Ala Gly Thr His Ala Gly Leu Ala Val Gly Leu Glu His
225                 230                 235                 240
ctg atg cct gaa agc gaa ctg att ggc gtg acc gtg tcg cgt tcc gtt       768
Leu Met Pro Glu Ser Glu Leu Ile Gly Val Thr Val Ser Arg Ser Val
                245                 250                 255
gcc gat caa ttg ccg aaa gtg gtt aac cta caa cag gcg att gcg aaa       816
Ala Asp Gln Leu Pro Lys Val Val Asn Leu Gln Gln Ala Ile Ala Lys
            260                 265                 270
gaa ctg gag ctg acc gca tca gcg gaa att tta ctc tgg gat gac tat       864
Glu Leu Glu Leu Thr Ala Ser Ala Glu Ile Leu Leu Trp Asp Asp Tyr
        275                 280                 285
ttt gca cct ggc tac ggc gtg ccg aac gac gaa ggc atg gaa gca gtg       912
Phe Ala Pro Gly Tyr Gly Val Pro Asn Asp Glu Gly Met Glu Ala Val
    290                 295                 300
aaa ttg ctg gcg cgt ctg gaa ggc att ctg ctt gat cct gtg tat acc       960
Lys Leu Leu Ala Arg Leu Glu Gly Ile Leu Leu Asp Pro Val Tyr Thr
305                 310                 315                 320
gga aaa gcg atg gcg ggg ctg att gac ggt atc agt cag aaa cgc ttc      1008
Gly Lys Ala Met Ala Gly Leu Ile Asp Gly Ile Ser Gln Lys Arg Phe
                325                 330                 335
aaa gat gaa ggg ccg att ctg ttt att cat acc ggc ggc gcg cct gcg      1056
Lys Asp Glu Gly Pro Ile Leu Phe Ile His Thr Gly Gly Ala Pro Ala
            340                 345                 350
ctg ttc gcc tat cat ccc cac gtt tag                                 1083
Leu Phe Ala Tyr His Pro His Val
        355                 360
```

<210> 31
<211> 360
<212> PRT
<213> Shigella flexneri 2a str. 301

<400> 31

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

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

<210> 32
<211> 894
<212> DNA
<213> Pseudomonas putida KT2440

<220>
<221> CDS
<222> (1)..(894)
<223> transl_table=11

<400> 32

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atg cat gta ttc gac ctc ccc caa gcc ccg ctg cat ttt ctg gac ttg       48
Met His Val Phe Asp Leu Pro Gln Ala Pro Leu His Phe Leu Asp Leu
1               5                   10                  15
ccc tgg ctg gaa caa gcc cag gtc cag gcc gcc act ctg cgc ctg gac       96
Pro Trp Leu Glu Gln Ala Gln Val Gln Ala Ala Thr Leu Arg Leu Asp
            20                  25                  30
ctg atc gac ccg ctg atc agc ggc aac aag tgg ttc aaa cta cgc cac      144
Leu Ile Asp Pro Leu Ile Ser Gly Asn Lys Trp Phe Lys Leu Arg His
        35                  40                  45
cac ctg caa cag gcc ggc gcc agc aac gct cca ggc ctg atc agc ctc      192
His Leu Gln Gln Ala Gly Ala Ser Asn Ala Pro Gly Leu Ile Ser Leu
    50                  55                  60
ggc ggt aac cat tcc aac cat ctg cac gcc ttg gcc gct gcc ggc aag      240
Gly Gly Asn His Ser Asn His Leu His Ala Leu Ala Ala Ala Gly Lys
65                  70                  75                  80
```

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

Ala Gly Leu Phe Lys Pro Gly Ser Arg Leu Ile Phe Val His Thr Gly
        275                 280                 285
ggc ctg cag ggg cga cgc ggt tac ttg taa                                894
Gly Leu Gln Gly Arg Arg Gly Tyr Leu
    290                 295
```

<210> 33
<211> 297
<212> PRT
<213> Pseudomonas putida KT2440

<400> 33

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

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

<210> 34
<211> 987
<212> DNA
<213> Escherichia coli CFT073

<220>
<221> CDS
<222> (1)..(987)
<223> transl_table=11

<400> 34

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atg cca ctg cat aat tta acc cgt ttt cca cgg ctg gag ttt atc ggc       48
Met Pro Leu His Asn Leu Thr Arg Phe Pro Arg Leu Glu Phe Ile Gly
1               5                   10                  15
gcg cca acg ccg ctc gaa tat ctg ccg cgc ttt tct gat tat ctt gga       96
Ala Pro Thr Pro Leu Glu Tyr Leu Pro Arg Phe Ser Asp Tyr Leu Gly
            20                  25                  30
cgg gaa att ttc atc aaa cgg gat gac gtc act ccc atg gca atg ggc      144
Arg Glu Ile Phe Ile Lys Arg Asp Asp Val Thr Pro Met Ala Met Gly
        35                  40                  45
ggc aat aaa tta cgt aag ctg gaa ttt ctc gcg gca gat gct ctg cgt      192
Gly Asn Lys Leu Arg Lys Leu Glu Phe Leu Ala Ala Asp Ala Leu Arg
    50                  55                  60
gaa ggt gcc gat acg ctg att act gcc ggg gcg atc cag tct aac cat      240
Glu Gly Ala Asp Thr Leu Ile Thr Ala Gly Ala Ile Gln Ser Asn His
65                  70                  75                  80
gtg cgc cag act gcc gca gtt gcg gcg aaa ctc ggt ctg cac tgc gtg      288
Val Arg Gln Thr Ala Ala Val Ala Ala Lys Leu Gly Leu His Cys Val
                85                  90                  95
gcg ctg ctg gaa aat cct att ggc aca acc gca gaa aac tat tta acc      336
Ala Leu Leu Glu Asn Pro Ile Gly Thr Thr Ala Glu Asn Tyr Leu Thr
            100                 105                 110
aac ggc aat cgt ttg ttg ctg gat ctg ttc aat acc cag att gaa atg      384
```

```
Asn Gly Asn Arg Leu Leu Leu Asp Leu Phe Asn Thr Gln Ile Glu Met
        115                 120                 125
tgc gac gca ctg acc gat ccc aat gcc caa ctg gaa gtg ctg gcg acg      432
Cys Asp Ala Leu Thr Asp Pro Asn Ala Gln Leu Glu Val Leu Ala Thr
    130                 135                 140
cga gtc gaa gca caa ggc ttt cgc ccg tat gtc att ccg gtt ggc ggt      480
Arg Val Glu Ala Gln Gly Phe Arg Pro Tyr Val Ile Pro Val Gly Gly
145                 150                 155                 160
tct aat gct ttg ggc gcg ctg ggt tat gtg gag agt gcg ctg gaa att      528
Ser Asn Ala Leu Gly Ala Leu Gly Tyr Val Glu Ser Ala Leu Glu Ile
                165                 170                 175
gcg caa cag tgt gaa ggg gca gtt aat att tcg tcg gtg gtg gtc gcg      576
Ala Gln Gln Cys Glu Gly Ala Val Asn Ile Ser Ser Val Val Val Ala
            180                 185                 190
tcg ggc agt gcc gga act cac gcc gga ctg gct gtt ggg ctg gaa cac      624
Ser Gly Ser Ala Gly Thr His Ala Gly Leu Ala Val Gly Leu Glu His
        195                 200                 205
ctg atg cct gaa agc gaa ctg att ggc gtg act gtg tcg cgt tct gtt      672
Leu Met Pro Glu Ser Glu Leu Ile Gly Val Thr Val Ser Arg Ser Val
    210                 215                 220
gcc gat caa ttg ccg aaa gtg gtt aac ctc caa cag gcg att gcg aaa      720
Ala Asp Gln Leu Pro Lys Val Val Asn Leu Gln Gln Ala Ile Ala Lys
225                 230                 235                 240
gaa ctg gag ctg acc gca tca gcg gaa att tta ctc tgg gat gac tat      768
Glu Leu Glu Leu Thr Ala Ser Ala Glu Ile Leu Leu Trp Asp Asp Tyr
                245                 250                 255
ttt gca cct ggc tac ggc gtg ccg aac gac gaa ggc atg gaa gca gtg      816
Phe Ala Pro Gly Tyr Gly Val Pro Asn Asp Glu Gly Met Glu Ala Val
            260                 265                 270
aaa ttg ctg gcg cgg ctg gaa ggc att ctg ctt gat cct gtg tat acc      864
Lys Leu Leu Ala Arg Leu Glu Gly Ile Leu Leu Asp Pro Val Tyr Thr
        275                 280                 285
gga aaa gcg atg gcg ggg ctg att gac ggt atc agt cag aaa cgc ttc      912
Gly Lys Ala Met Ala Gly Leu Ile Asp Gly Ile Ser Gln Lys Arg Phe
    290                 295                 300
aaa gat gaa ggg ccg att ttg ttt att cat acc ggc ggt gcg cct gcg      960
Lys Asp Glu Gly Pro Ile Leu Phe Ile His Thr Gly Gly Ala Pro Ala
305                 310                 315                 320
ctg ttc gcc tat cat ccc cac gtt tag                                 987
Leu Phe Ala Tyr His Pro His Val
                325
```

<210> 35
<211> 328
<212> PRT
<213> Escherichia coli CFT073

<400> 35

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

```
            100                 105                 110
Asn Gly Asn Arg Leu Leu Leu Asp Leu Phe Asn Thr Gln Ile Glu Met
        115                 120                 125
Cys Asp Ala Leu Thr Asp Pro Asn Ala Gln Leu Glu Val Leu Ala Thr
    130                 135                 140
Arg Val Glu Ala Gln Gly Phe Arg Pro Tyr Val Ile Pro Val Gly Gly
145                 150                 155                 160
Ser Asn Ala Leu Gly Ala Leu Gly Tyr Val Glu Ser Ala Leu Glu Ile
                165                 170                 175
Ala Gln Gln Cys Glu Gly Ala Val Asn Ile Ser Ser Val Val Val Ala
            180                 185                 190
Ser Gly Ser Ala Gly Thr His Ala Gly Leu Ala Val Gly Leu Glu His
        195                 200                 205
Leu Met Pro Glu Ser Glu Leu Ile Gly Val Thr Val Ser Arg Ser Val
    210                 215                 220
Ala Asp Gln Leu Pro Lys Val Val Asn Leu Gln Gln Ala Ile Ala Lys
225                 230                 235                 240
Glu Leu Glu Leu Thr Ala Ser Ala Glu Ile Leu Leu Trp Asp Asp Tyr
                245                 250                 255
Phe Ala Pro Gly Tyr Gly Val Pro Asn Asp Glu Gly Met Glu Ala Val
            260                 265                 270
Lys Leu Leu Ala Arg Leu Glu Gly Ile Leu Leu Asp Pro Val Tyr Thr
        275                 280                 285
Gly Lys Ala Met Ala Gly Leu Ile Asp Gly Ile Ser Gln Lys Arg Phe
    290                 295                 300
Lys Asp Glu Gly Pro Ile Leu Phe Ile His Thr Gly Gly Ala Pro Ala
305                 310                 315                 320
Leu Phe Ala Tyr His Pro His Val
                325
```

<210> 36
<211> 999
<212> DNA
<213> Pseudomonas syringae pv. tomato str. DC3000

<220>
<221> CDS
<222> (1)..(999)
<223> transl_table=11

<400> 36

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atg atc aaa aat cag ctt gcc cgc ttc aat cgt ctg gac ttg atc agc      48
Met Ile Lys Asn Gln Leu Ala Arg Phe Asn Arg Leu Asp Leu Ile Ser
1               5                   10                  15
gcg cca acg gcc ctg gaa aag ctt gag cgc ctg tcg ctg tgg gca gat      96
Ala Pro Thr Ala Leu Glu Lys Leu Glu Arg Leu Ser Leu Trp Ala Asp
            20                  25                  30
cgc gac atc tac atc aag cgt gat gac acc acc acg ctc gcg ctg ggc     144
Arg Asp Ile Tyr Ile Lys Arg Asp Asp Thr Thr Thr Leu Ala Leu Gly
        35                  40                  45
ggc aac aag gtg cgc aag ctt gaa tac ctg gcc gcc gat gcg ctg gct     192
Gly Asn Lys Val Arg Lys Leu Glu Tyr Leu Ala Ala Asp Ala Leu Ala
    50                  55                  60
cag ggt gcc gac aca ctg atc acg gcc ggc gca atc cag tcc aac cat     240
Gln Gly Ala Asp Thr Leu Ile Thr Ala Gly Ala Ile Gln Ser Asn His
65                  70                  75                  80
gta cgc cag acg gca gcc ctg gcg gcg cgg ctg ggg ctg ggc tgc gtg     288
Val Arg Gln Thr Ala Ala Leu Ala Ala Arg Leu Gly Leu Gly Cys Val
                85                  90                  95
gcc ctg ctg gaa aac ccc atc ggc acc gaa gac ccg agt tac ctg aaa     336
Ala Leu Leu Glu Asn Pro Ile Gly Thr Glu Asp Pro Ser Tyr Leu Lys
```

```
            100                 105                 110
aac ggc aac cgc ctg ctg ctg gaa ctg ttc gat gcc aag gtc gag ctg       384
Asn Gly Asn Arg Leu Leu Leu Glu Leu Phe Asp Ala Lys Val Glu Leu
        115                 120                 125
gtc gaa aac ctc gat aac gcc gac gac cag ttg cat gcc ttg gct gcg       432
Val Glu Asn Leu Asp Asn Ala Asp Asp Gln Leu His Ala Leu Ala Ala
    130                 135                 140
cgc ctg cgc tcc agc ggc aag aag ccg tat ctg gtg cct atc ggt ggc       480
Arg Leu Arg Ser Ser Gly Lys Lys Pro Tyr Leu Val Pro Ile Gly Gly
145                 150                 155                 160
tca agc ccg gtt ggt gca ctg ggg tat gtc cgc gcc ggg ctg gaa ctc       528
Ser Ser Pro Val Gly Ala Leu Gly Tyr Val Arg Ala Gly Leu Glu Leu
                165                 170                 175
gcc gag cag atc aaa cag acc ggt atc gac ttt gcg gcc gtg gtg ctg       576
Ala Glu Gln Ile Lys Gln Thr Gly Ile Asp Phe Ala Ala Val Val Leu
            180                 185                 190
gca tcg ggc agt gcg ggt acg cac agc ggc ctg gcg ttg gcg ctg gct       624
Ala Ser Gly Ser Ala Gly Thr His Ser Gly Leu Ala Leu Ala Leu Ala
        195                 200                 205
cat gag ttg ccg cag ttg ccg gtg gtc ggc gtg acc gtg tcg cgc agt       672
His Glu Leu Pro Gln Leu Pro Val Val Gly Val Thr Val Ser Arg Ser
    210                 215                 220
gaa gaa gcg cag ttg ccc aaa gtg caa ggc ctc gcc gag cgc acc gcg       720
Glu Glu Ala Gln Leu Pro Lys Val Gln Gly Leu Ala Glu Arg Thr Ala
225                 230                 235                 240
caa ctg ctc gat atc gcc ctg ccg gag cac ttc aag gtc gaa ctg tgg       768
Gln Leu Leu Asp Ile Ala Leu Pro Glu His Phe Lys Val Glu Leu Trp
                245                 250                 255
gac gag tat ttc gcc ccg cgc tac ggc gag cca aac gcc ggt acg ctg       816
Asp Glu Tyr Phe Ala Pro Arg Tyr Gly Glu Pro Asn Ala Gly Thr Leu
            260                 265                 270
gca gcg atc aaa ctg gtg gcc agc cag gaa ggc ctg ttg ctg gac ccg       864
Ala Ala Ile Lys Leu Val Ala Ser Gln Glu Gly Leu Leu Leu Asp Pro
        275                 280                 285
gtc tac acc ggc aag gcc atg tcc ggc ctg ctg gac ggt atc ggc cgt       912
Val Tyr Thr Gly Lys Ala Met Ser Gly Leu Leu Asp Gly Ile Gly Arg
    290                 295                 300
caa cgc ttc aac gac ggg ccg ttg ata ttc ctg cac acc ggt ggc gcg       960
Gln Arg Phe Asn Asp Gly Pro Leu Ile Phe Leu His Thr Gly Gly Ala
305                 310                 315                 320
cct gcg ttg ttc gct tat ccg gat gcg ttt gac cag tga                   999
Pro Ala Leu Phe Ala Tyr Pro Asp Ala Phe Asp Gln
                325                 330
```

<210> 37
<211> 332
<212> PRT
<213> Pseudomonas syringae pv. tomato str. DC3000

<400> 37

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

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

<210> 38
<211> 981
<212> DNA
<213> Streptomyces avermitilis MA-4680

<220>
<221> CDS
<222> (1)..(981)
<223> transl_table=11

<400> 38

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atg agt gac aag atc gcc ctg tcg acg tgg ccc aca ccg ctg gag ccc       48
Met Ser Asp Lys Ile Ala Leu Ser Thr Trp Pro Thr Pro Leu Glu Pro
1               5                   10                  15
atg ccc cgt ctg gcg gcg gca ctg ggc ctc ggc gag aac gac ctc tgg       96
Met Pro Arg Leu Ala Ala Ala Leu Gly Leu Gly Glu Asn Asp Leu Trp
            20                  25                  30
atc aaa cgg gac gac ctc atc ggc ctg ggc ggc ggt ggc aac aag gtc      144
Ile Lys Arg Asp Asp Leu Ile Gly Leu Gly Gly Gly Gly Asn Lys Val
        35                  40                  45

cgc aaa ctg gaa tgg acc gtc ggc gcc gcc ctc gcg gca ggc gcg gac      192
Arg Lys Leu Glu Trp Thr Val Gly Ala Ala Leu Ala Ala Gly Ala Asp
    50                  55                  60
acc ctg gtc acc acc ggc gcc gcg cag agc aac cac gcc cgc ctc acc      240
Thr Leu Val Thr Thr Gly Ala Ala Gln Ser Asn His Ala Arg Leu Thr
65                  70                  75                  80
gcg gcc gcc ggc gcc cgc ctg gga ctc gac gtc gta ctc gtc ttc ccc      288
Ala Ala Ala Gly Ala Arg Leu Gly Leu Asp Val Val Leu Val Phe Pro
```

```
                85                  90                  95
ggc act ccc gac agc gcc acg cac ggc tcc ggc aac ctc gtt ctc gac      336
Gly Thr Pro Asp Ser Ala Thr His Gly Ser Gly Asn Leu Val Leu Asp
            100                 105                 110
agc ctc ttc gga gcc agg gtc cac tgg gcc gga gac ggc ggc ccg agc      384
Ser Leu Phe Gly Ala Arg Val His Trp Ala Gly Asp Gly Gly Pro Ser
        115                 120                 125
acg atg ggt gac gtc gcc gac gag gtc tgc cgg cag ctg cgc cgc gat      432
Thr Met Gly Asp Val Ala Asp Glu Val Cys Arg Gln Leu Arg Arg Asp
    130                 135                 140
gga gca cgc cct cat ctc atc ccc ttc ggg ggg tca agt ccc ctc ggg      480
Gly Ala Arg Pro His Leu Ile Pro Phe Gly Gly Ser Ser Pro Leu Gly
145                 150                 155                 160
gcg cgg gga tac gtg gaa ggc ggc gag gaa ctg cgc tcc caa ctg ccc      528
Ala Arg Gly Tyr Val Glu Gly Gly Glu Glu Leu Arg Ser Gln Leu Pro
                165                 170                 175
gac gtg gac cac gtc gtg gtc gcc ctc ggt tcc ggc ggc acc atg gcg      576
Asp Val Asp His Val Val Val Ala Leu Gly Ser Gly Gly Thr Met Ala
            180                 185                 190
gga ctg gtc ggc gca ctc ggg gag caa cgc gtc ctc ggc gtt cac tgc      624
Gly Leu Val Gly Ala Leu Gly Glu Gln Arg Val Leu Gly Val His Cys
        195                 200                 205
ggg gcg gtg gca gag ccg gcc gcc acc gtc gcc gac ctc gcg ggc cca      672
Gly Ala Val Ala Glu Pro Ala Ala Thr Val Ala Asp Leu Ala Gly Pro
    210                 215                 220
ctc acc cgc cgc agc atc acc ccg gaa tcc ctg cgc ctt cgc acc gac      720
Leu Thr Arg Arg Ser Ile Thr Pro Glu Ser Leu Arg Leu Arg Thr Asp
225                 230                 235                 240
cag gtg ggt gcg gga tac gga gtg ctt cat gag ccg gtc ctg gaa gcg      768
Gln Val Gly Ala Gly Tyr Gly Val Leu His Glu Pro Val Leu Glu Ala
                245                 250                 255
atg cga acc gcc gca ggc acc gag ggc atc gtc ctg gat ccg gtc tac      816
Met Arg Thr Ala Ala Gly Thr Glu Gly Ile Val Leu Asp Pro Val Tyr
            260                 265                 270
agc ggg cgc gcc atg gcc ggc ctg atc gcc gcg gtg cgg gac ggc gac      864
Ser Gly Arg Ala Met Ala Gly Leu Ile Ala Ala Val Arg Asp Gly Asp
        275                 280                 285
atc cgc ccg gcc cag cgc acc gta ttt ctt cac acc ggg ggg ctc ccg      912
Ile Arg Pro Ala Gln Arg Thr Val Phe Leu His Thr Gly Gly Leu Pro
    290                 295                 300
ggc ctg ttc ggg cat acg gag acc gtg cag cgc tcc gtc agc acc ctg      960
Gly Leu Phe Gly His Thr Glu Thr Val Gln Arg Ser Val Ser Thr Leu
305                 310                 315                 320
cgc tcc tac gag gtc gag tga                                          981
Arg Ser Tyr Glu Val Glu
                325
```

<210> 39
<211> 326
<212> PRT
<213> Streptomyces avermitilis MA-4680

<400> 39

```
Met Ser Asp Lys Ile Ala Leu Ser Thr Trp Pro Thr Pro Leu Glu Pro
1               5                   10                  15
Met Pro Arg Leu Ala Ala Ala Leu Gly Leu Gly Glu Asn Asp Leu Trp
            20                  25                  30
Ile Lys Arg Asp Asp Leu Ile Gly Leu Gly Gly Gly Gly Asn Lys Val
        35                  40                  45
Arg Lys Leu Glu Trp Thr Val Gly Ala Ala Leu Ala Ala Gly Ala Asp
    50                  55                  60
```

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

<210> 40
<211> 936
<212> DNA
<213> Streptomyces avermitilis MA-4680

<220>
<221> CDS
<222> (1)..(936)
<223> transl_table=11

<400> 40

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gtg tcc gac aat ggt ggg gtg acc ggc ccc gac gtc ccc gaa gcg ctc       48
Met Ser Asp Asn Gly Gly Val Thr Gly Pro Asp Val Pro Glu Ala Leu
1               5                   10                  15
gac ctc gcc gcc ctg cga ccg cgc ctg ccg tcg ccg gtg cag gcg gtc       96
Asp Leu Ala Ala Leu Arg Pro Arg Leu Pro Ser Pro Val Gln Ala Val
            20                  25                  30
gac gac gag cgc ttc gca cgg cac ggg gtc cgg ctc ctg ctc aag cgg      144
Asp Asp Glu Arg Phe Ala Arg His Gly Val Arg Leu Leu Leu Lys Arg
        35                  40                  45
gac gac ctg atc cac ccg gac ctc atc ggc aac aag tgg cgc aag ctc      192
Asp Asp Leu Ile His Pro Asp Leu Ile Gly Asn Lys Trp Arg Lys Leu
    50                  55                  60
gcg ccg aac ctc cgg gcc gcg gcg ggc cgc ccg ctc gtc acc ttc ggc      240
Ala Pro Asn Leu Arg Ala Ala Ala Gly Arg Pro Leu Val Thr Phe Gly
65                  70                  75                  80
```

```
ggt gcg tac tcg aac cac ctg cga gcg acg gcc gcc gcg ggc cgc ctc       288
Gly Ala Tyr Ser Asn His Leu Arg Ala Thr Ala Ala Ala Gly Arg Leu
                85                  90                  95
ctg ggg ctg gcc acg atc ggc gtg gtc cgc ggc cag gag ctg gcc gac       336
Leu Gly Leu Ala Thr Ile Gly Val Val Arg Gly Gln Glu Leu Ala Asp
            100                 105                 110
cgt ccg ctg aac ccc tcc ctc acc cgg tgc gcg gcc gac ggc atg cgg       384
Arg Pro Leu Asn Pro Ser Leu Thr Arg Cys Ala Ala Asp Gly Met Arg
        115                 120                 125
ctg cac ttc gtg gac cgg tcg acg tac cgc cgc aag acc gaa ccg ggg       432
Leu His Phe Val Asp Arg Ser Thr Tyr Arg Arg Lys Thr Glu Pro Gly
    130                 135                 140
acg ctg gcc gcg atc ctg cgc gcg gtg gcc gcc gag gac gcg tac gtc       480
Thr Leu Ala Ala Ile Leu Arg Ala Val Ala Ala Glu Asp Ala Tyr Val
145                 150                 155                 160
gtg ccc gaa ggc ggc agc aac tcc cct gcc gta cgc ggc tgc cgc gcc       528
Val Pro Glu Gly Gly Ser Asn Ser Pro Ala Val Arg Gly Cys Arg Ala
                165                 170                 175
ctc ggc gag gag ctg cgc ggg cac gcc gac gtc gtc gcc ctc gcc tgc       576
Leu Gly Glu Glu Leu Arg Gly His Ala Asp Val Val Ala Leu Ala Cys
            180                 185                 190
ggc acc ggc ggc acg ctc gcg ggc ctg gcc gcc ggc ctc ggc ccc ggc       624
Gly Thr Gly Gly Thr Leu Ala Gly Leu Ala Ala Gly Leu Gly Pro Gly
        195                 200                 205
cag cgg gcg ctg ggc gtc ccg gtc ctc aag ggc gac ttc ctg acc gcc       672
Gln Arg Ala Leu Gly Val Pro Val Leu Lys Gly Asp Phe Leu Thr Ala
    210                 215                 220
gag gtc acc gcg ctc cag gag cgg gcg ttc ggc ggc cgc cag ggc gcc       720
Glu Val Thr Ala Leu Gln Glu Arg Ala Phe Gly Gly Arg Gln Gly Ala
225                 230                 235                 240
tgg tcc ctg gac gac cgc ttc cac ttc ggc ggc tac gcc cgt acc tct       768
Trp Ser Leu Asp Asp Arg Phe His Phe Gly Gly Tyr Ala Arg Thr Ser
                245                 250                 255
ccc ggc ctc cac gcg ttc gcg gcg gac ttc gag cgg cga cac gga ctg       816
Pro Gly Leu His Ala Phe Ala Ala Asp Phe Glu Arg Arg His Gly Leu
            260                 265                 270
ccg gtg gaa cgt ctc tat gtc gcc aag atg ctg tac gga ctt gtc gcc       864
Pro Val Glu Arg Leu Tyr Val Ala Lys Met Leu Tyr Gly Leu Val Ala
        275                 280                 285
ctg gcc gaa gag ggc ggg ttc gcc cgc ggc acg acc gtc gcg gcc gtc       912
Leu Ala Glu Glu Gly Gly Phe Ala Arg Gly Thr Thr Val Ala Ala Val
    290                 295                 300
atc acc gga cgg ccg ctc ggc tga                                      936
Ile Thr Gly Arg Pro Leu Gly
305                 310
```

<210> 41
<211> 311
<212> PRT
<213> Streptomyces avermitilis MA-4680

<400> 41

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

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

<210> 42
<211> 996
<212> DNA
<213> Bacillus cereus ATCC 14579

<220>
<221> CDS
<222> (1)..(996)
<223> transl_table=11

<400> 42

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atg aat tta gct aaa ttc ccg aga aaa aaa tat aca gaa tca tat aca       48
Met Asn Leu Ala Lys Phe Pro Arg Lys Lys Tyr Thr Glu Ser Tyr Thr
1               5                   10                  15
cca att gaa aag tta aac aat ttt tct gaa gca ctt ggt ggt ccg act       96
Pro Ile Glu Lys Leu Asn Asn Phe Ser Glu Ala Leu Gly Gly Pro Thr
            20                  25                  30
att tat ttt aaa cga gat gat tta ctt ggt tta aca gcc ggt ggc aat      144
Ile Tyr Phe Lys Arg Asp Asp Leu Leu Gly Leu Thr Ala Gly Gly Asn
        35                  40                  45
aag acg aga aag tta gaa ttt tta gtt gca gat gca cag gaa aat ggt      192
Lys Thr Arg Lys Leu Glu Phe Leu Val Ala Asp Ala Gln Glu Asn Gly
    50                  55                  60
gca gat acg tta att aca gct ggt ggt att cag tca aat cat tgc cgc      240
Ala Asp Thr Leu Ile Thr Ala Gly Gly Ile Gln Ser Asn His Cys Arg
65                  70                  75                  80
ctg aca ctt gct gct gcg gta aaa gaa aaa atg aaa tgt atc ctt gta      288
Leu Thr Leu Ala Ala Ala Val Lys Glu Lys Met Lys Cys Ile Leu Val
                85                  90                  95
```

```
tta gag gaa ggg ctt gag aca gaa gag aag aga gac ttt aac gga aac       336
Leu Glu Glu Gly Leu Glu Thr Glu Glu Lys Arg Asp Phe Asn Gly Asn
            100                 105                 110
tat ttc tta tat cac tta tta ggt gct gaa aac gtc att gtt gta ccg       384
Tyr Phe Leu Tyr His Leu Leu Gly Ala Glu Asn Val Ile Val Val Pro
        115                 120                 125
aac gga gca gac ctg atg gaa gaa atg cat aaa gta gca aaa gaa gta       432
Asn Gly Ala Asp Leu Met Glu Glu Met His Lys Val Ala Lys Glu Val
    130                 135                 140
agt gaa aaa gga aat aca cca tat gta att cca gtt ggt gga tca aac       480
Ser Glu Lys Gly Asn Thr Pro Tyr Val Ile Pro Val Gly Gly Ser Asn
145                 150                 155                 160
cct aca ggc gct atg gga tac gtt gct tgt gcg caa gaa att atg gcg       528
Pro Thr Gly Ala Met Gly Tyr Val Ala Cys Ala Gln Glu Ile Met Ala
                165                 170                 175
caa tca ttt gag caa gga att gat ttc agt tca gtt gtt tgt gta agt       576
Gln Ser Phe Glu Gln Gly Ile Asp Phe Ser Ser Val Val Cys Val Ser
            180                 185                 190
ggt agc ggc ggt atg cat gct ggt tta att act ggt ttt tct gga aca       624
Gly Ser Gly Gly Met His Ala Gly Leu Ile Thr Gly Phe Ser Gly Thr
        195                 200                 205
caa agc cat att cct gta atc ggg att aat gta agt aga gga aaa gct       672
Gln Ser His Ile Pro Val Ile Gly Ile Asn Val Ser Arg Gly Lys Ala
    210                 215                 220
gag caa gaa gag aaa gta gca aaa ctt gta gat gaa act tca gca cat       720
Glu Gln Glu Glu Lys Val Ala Lys Leu Val Asp Glu Thr Ser Ala His
225                 230                 235                 240
gtt ggt att cca aac ttt atc tcg cgc gac gct gtt acg tgc ttt gat       768
Val Gly Ile Pro Asn Phe Ile Ser Arg Asp Ala Val Thr Cys Phe Asp
                245                 250                 255
gaa tat gta gga cca ggc tat gcg tta cca acg ccg gaa atg gta gag       816

Glu Tyr Val Gly Pro Gly Tyr Ala Leu Pro Thr Pro Glu Met Val Glu
            260                 265                 270
gca gtt cag tta ctt gcg aaa aca gaa ggt att tta ctt gat cca gtg       864
Ala Val Gln Leu Leu Ala Lys Thr Glu Gly Ile Leu Leu Asp Pro Val
        275                 280                 285
tat aca ggt aag gca gta gcg gga tta atc gac tta att aga aaa ggt       912
Tyr Thr Gly Lys Ala Val Ala Gly Leu Ile Asp Leu Ile Arg Lys Gly
    290                 295                 300
aat ttt aat aag gaa gac aat att tta ttc gta cat tca ggt ggt tca       960
Asn Phe Asn Lys Glu Asp Asn Ile Leu Phe Val His Ser Gly Gly Ser
305                 310                 315                 320
cca gct tta tat gcg aat act tct tta ttt gtg taa                       996
Pro Ala Leu Tyr Ala Asn Thr Ser Leu Phe Val
                325                 330
```

<210> 43
<211> 331
<212> PRT
<213> Bacillus cereus ATCC 14579

```
<400> 43
Met Asn Leu Ala Lys Phe Pro Arg Lys Lys Tyr Thr Glu Ser Tyr Thr
1               5                   10                  15
Pro Ile Glu Lys Leu Asn Asn Phe Ser Glu Ala Leu Gly Gly Pro Thr
            20                  25                  30
Ile Tyr Phe Lys Arg Asp Asp Leu Leu Gly Leu Thr Ala Gly Gly Asn
        35                  40                  45
Lys Thr Arg Lys Leu Glu Phe Leu Val Ala Asp Ala Gln Glu Asn Gly
    50                  55                  60
```

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

<210> 44
<211> 996
<212> DNA
<213> Bacillus anthracis str. Ames

<220>
<221> CDS
<222> (1)..(996)
<223> transl_table=11

<400> 44

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atg aat tta gct aaa ttc ccg aga aaa aaa tat aca gag tca tat aca      48
Met Asn Leu Ala Lys Phe Pro Arg Lys Lys Tyr Thr Glu Ser Tyr Thr
1               5                   10                  15
cca att gaa aaa tta aac aat ttt tca gaa gca ctt ggt ggg ccg act      96
Pro Ile Glu Lys Leu Asn Asn Phe Ser Glu Ala Leu Gly Gly Pro Thr
            20                  25                  30
att tat ttt aaa cga gat gat tta ctt ggt tta aca gct ggt ggt aat     144
Ile Tyr Phe Lys Arg Asp Asp Leu Leu Gly Leu Thr Ala Gly Gly Asn
        35                  40                  45
aag acg aga aag tta gag ttt tta gtt gcg gat gca cag gca aag ggt     192
Lys Thr Arg Lys Leu Glu Phe Leu Val Ala Asp Ala Gln Ala Lys Gly
    50                  55                  60
gca gat acg tta att aca gct ggt ggt att cag tca aat cat tgc cgc     240
Ala Asp Thr Leu Ile Thr Ala Gly Gly Ile Gln Ser Asn His Cys Arg
65                  70                  75                  80
```

```
cta aca ctt gca gcg gcg gta aaa gaa aaa atg aaa tgt atc ctt gta       288
Leu Thr Leu Ala Ala Ala Val Lys Glu Lys Met Lys Cys Ile Leu Val
                85                  90                  95
tta gaa gaa ggg ctt gag cca gaa gag aag cca gac ttt aat gga aac       336
Leu Glu Glu Gly Leu Glu Pro Glu Glu Lys Pro Asp Phe Asn Gly Asn
            100                 105                 110
tat ttc tta tat cat tta cta ggt gct gaa aat gtc att gtt gta ccg       384
Tyr Phe Leu Tyr His Leu Leu Gly Ala Glu Asn Val Ile Val Val Pro
        115                 120                 125
aac gga gca gat ctt atg gaa gag atg cat aaa gcc gcg aaa gaa gtt       432
Asn Gly Ala Asp Leu Met Glu Glu Met His Lys Ala Ala Lys Glu Val
    130                 135                 140
agt gaa aaa ggg aat aca cca tat gtc att ccg gtc ggt gga tcg aat       480
Ser Glu Lys Gly Asn Thr Pro Tyr Val Ile Pro Val Gly Gly Ser Asn
145                 150                 155                 160
cct act gga gca atg gga tac gtt gct tgt gcg caa gaa att ata gcg       528
Pro Thr Gly Ala Met Gly Tyr Val Ala Cys Ala Gln Glu Ile Ile Ala
                165                 170                 175
caa tca ttt gac caa gga att gat ttc agt tca gtc gtt tgc gta agt       576
Gln Ser Phe Asp Gln Gly Ile Asp Phe Ser Ser Val Val Cys Val Ser
            180                 185                 190
ggt agc ggc ggt atg cac gct ggt tta att aca ggt ttt gct gga aca       624
Gly Ser Gly Gly Met His Ala Gly Leu Ile Thr Gly Phe Ala Gly Thr
        195                 200                 205
caa agt aac atc cct gta atc gga att aac gta agt aga gga aaa gca       672
Gln Ser Asn Ile Pro Val Ile Gly Ile Asn Val Ser Arg Gly Lys Ala
    210                 215                 220
gag caa gaa gag aaa gta gca aaa ctt gta gat gaa acg tca gct cat       720
Glu Gln Glu Glu Lys Val Ala Lys Leu Val Asp Glu Thr Ser Ala His
225                 230                 235                 240

gtt ggt att cca aac ttt atc ccg cgc gaa gcg gtt aca tgc ttt gat       768
Val Gly Ile Pro Asn Phe Ile Pro Arg Glu Ala Val Thr Cys Phe Asp
                245                 250                 255
gaa tat gta gga ccg ggt tac gcg tta cca acg cca gaa atg gtg gaa       816
Glu Tyr Val Gly Pro Gly Tyr Ala Leu Pro Thr Pro Glu Met Val Glu
            260                 265                 270
gca gtg cag ctg tta gca aaa aca gaa ggt att tta ctt gat cca gta       864
Ala Val Gln Leu Leu Ala Lys Thr Glu Gly Ile Leu Leu Asp Pro Val
        275                 280                 285
tat aca ggt aaa gca gta gcg gga tta atc gac tta att aga aaa ggt       912
Tyr Thr Gly Lys Ala Val Ala Gly Leu Ile Asp Leu Ile Arg Lys Gly
    290                 295                 300
aca ttt aat aaa gag gat aac att tta ttc gta cat tca ggt ggt tca       960
Thr Phe Asn Lys Glu Asp Asn Ile Leu Phe Val His Ser Gly Gly Ser
305                 310                 315                 320
cca gct tta tat gcg aat aca tct tta ttc gcg taa                       996
Pro Ala Leu Tyr Ala Asn Thr Ser Leu Phe Ala
                325                 330
```

<210> 45
<211> 331
<212> PRT
<213> Bacillus anthracis str. Ames

<400> 45

```
Met Asn Leu Ala Lys Phe Pro Arg Lys Lys Tyr Thr Glu Ser Tyr Thr
1               5                  10                  15
Pro Ile Glu Lys Leu Asn Asn Phe Ser Glu Ala Leu Gly Gly Pro Thr
            20                  25                  30
Ile Tyr Phe Lys Arg Asp Asp Leu Leu Gly Leu Thr Ala Gly Gly Asn
```

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

        275                 280                 285
Tyr Thr Gly Lys Ala Val Ala Gly Leu Ile Asp Leu Ile Arg Lys Gly
    290                 295                 300
Thr Phe Asn Lys Glu Asp Asn Ile Leu Phe Val His Ser Gly Gly Ser
305                 310                 315                 320
Pro Ala Leu Tyr Ala Asn Thr Ser Leu Phe Ala
                325                 330
```

<210> 46
<211> 1026
<212> DNA
<213> Bordetella bronchiseptica RB50

<220>
<221> CDS
<222> (1)..(1026)
<223> transl_table=11

<400> 46

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atg cta cat ctt gcc aag ttt ccc cgc ata aaa ctc ggg cac ttc ccc       48
Met Leu His Leu Ala Lys Phe Pro Arg Ile Lys Leu Gly His Phe Pro
1               5                   10                  15
acc ccg ctc gaa ttc atg ccc aac ctg acc cgc cac ctg ggc gga ccg       96
Thr Pro Leu Glu Phe Met Pro Asn Leu Thr Arg His Leu Gly Gly Pro
            20                  25                  30
aac ctc tac atc aag cgc gac gac tgc acc ggc ctg gcc acc ggc ggc      144
Asn Leu Tyr Ile Lys Arg Asp Asp Cys Thr Gly Leu Ala Thr Gly Gly
        35                  40                  45
aac aag acg cgc aaa ctg gag ttt ctg gtg gcc cag gcc gtt gcg caa      192
Asn Lys Thr Arg Lys Leu Glu Phe Leu Val Ala Gln Ala Val Ala Gln
```

```
    50                  55                  60
ggg gcg gat acg ctg atc acc cag ggc gcc gtc cag tcc aac cac gcg       240
Gly Ala Asp Thr Leu Ile Thr Gln Gly Ala Val Gln Ser Asn His Ala
65                  70                  75                  80
cgc cag acc gcc gcg gcc gcc gcg cgc gtc ggc atg aag tgc aag atc       288
Arg Gln Thr Ala Ala Ala Ala Ala Arg Val Gly Met Lys Cys Lys Ile
                85                  90                  95
ctc ctg gaa gag cgt gtc ccg cat ccg gac gat gac tac tcc cac tcc       336
Leu Leu Glu Glu Arg Val Pro His Pro Asp Asp Asp Tyr Ser His Ser
            100                 105                 110
ggc aac gtc atg ctc gac ggc ctg atg gac ggc gag atc gtc gcg cgc       384
Gly Asn Val Met Leu Asp Gly Leu Met Asp Gly Glu Ile Val Ala Arg
        115                 120                 125
ctg ccc gcc ggc acc gac atg cag cag gcc atg gaa gac ctg gcc cgc       432
Leu Pro Ala Gly Thr Asp Met Gln Gln Ala Met Glu Asp Leu Ala Arg
    130                 135                 140
gaa ctg gcc ggg cgc ggc agc aag ccc tac gtc atc gcc ggc ggc ggc       480
Glu Leu Ala Gly Arg Gly Ser Lys Pro Tyr Val Ile Ala Gly Gly Gly
145                 150                 155                 160
tcg acc ccg gtc ggc gcg ctg gga tac gtg gcc tgc gcg cag gag ctg       528
Ser Thr Pro Val Gly Ala Leu Gly Tyr Val Ala Cys Ala Gln Glu Leu
                165                 170                 175
ctg cac caa tcg ttc gaa acc ggg ctg cgc atc gac cat gtc gtg cac       576
Leu His Gln Ser Phe Glu Thr Gly Leu Arg Ile Asp His Val Val His
            180                 185                 190
gcg acc ggc agc gcc ggc acg cag gcc ggg ctg gtg gtc ggg ctg cgc       624
Ala Thr Gly Ser Ala Gly Thr Gln Ala Gly Leu Val Val Gly Leu Arg
        195                 200                 205
gcc ggc aac agc ggc att ccg gtc tac ggc atc agc gtg cgg gcg ccc       672
Ala Gly Asn Ser Gly Ile Pro Val Tyr Gly Ile Ser Val Arg Ala Pro
    210                 215                 220
aag ccc agg cag gaa gaa aac gtc tgg aag ctg gtg cag tcc acg gtc       720
Lys Pro Arg Gln Glu Glu Asn Val Trp Lys Leu Val Gln Ser Thr Val
225                 230                 235                 240
gat tac atg ggc ctg ccc gcc agc gcg gtg gag cgc gcc gac gtg gtg       768
Asp Tyr Met Gly Leu Pro Ala Ser Ala Val Glu Arg Ala Asp Val Val
                245                 250                 255
gcc aat tcc gac tac gtc ggc gag gga tat ggc atc tcc acc gac gcg       816
Ala Asn Ser Asp Tyr Val Gly Glu Gly Tyr Gly Ile Ser Thr Asp Ala
            260                 265                 270
atg atc gag gcg gtg cac atg acc gcc gca ctg gaa gcc atc ctg ctg       864
Met Ile Glu Ala Val His Met Thr Ala Ala Leu Glu Ala Ile Leu Leu
        275                 280                 285
gac ccc gtc tac tcg ggc aaa ggc atg gcc ggc ctg atc gga ttg atc       912
Asp Pro Val Tyr Ser Gly Lys Gly Met Ala Gly Leu Ile Gly Leu Ile
    290                 295                 300
cgt tcg ggt cat ttc aag cag ggc gag aac gta gtg ttc gtt cac acg       960
Arg Ser Gly His Phe Lys Gln Gly Glu Asn Val Val Phe Val His Thr
305                 310                 315                 320
gga ggc gca gta ggc ctg ttc ggt tac cgc cgc gca ttc gaa ggc ctg      1008
Gly Gly Ala Val Gly Leu Phe Gly Tyr Arg Arg Ala Phe Glu Gly Leu
                325                 330                 335
cct cca ttg gcc gcc tag                                             1026
Pro Pro Leu Ala Ala
            340
```

<210> 47
<211> 341
<212> PRT
<213> Bordetella bronchiseptica RB50

<400> 47
Met Leu His Leu Ala Lys Phe Pro Arg Ile Lys Leu Gly His Phe Pro
1 5 10 15
Thr Pro Leu Glu Phe Met Pro Asn Leu Thr Arg His Leu Gly Gly Pro
20 25 30
Asn Leu Tyr Ile Lys Arg Asp Asp Cys Thr Gly Leu Ala Thr Gly Gly
35 40 45
Asn Lys Thr Arg Lys Leu Glu Phe Leu Val Ala Gln Ala Val Ala Gln
50 55 60
Gly Ala Asp Thr Leu Ile Thr Gln Gly Ala Val Gln Ser Asn His Ala
65 70 75 80
Arg Gln Thr Ala Ala Ala Ala Ala Arg Val Gly Met Lys Cys Lys Ile
85 90 95
Leu Leu Glu Glu Arg Val Pro His Pro Asp Asp Asp Tyr Ser His Ser
100 105 110
Gly Asn Val Met Leu Asp Gly Leu Met Asp Gly Glu Ile Val Ala Arg
115 120 125
Leu Pro Ala Gly Thr Asp Met Gln Gln Ala Met Glu Asp Leu Ala Arg
130 135 140
Glu Leu Ala Gly Arg Gly Ser Lys Pro Tyr Val Ile Ala Gly Gly Gly
145 150 155 160
Ser Thr Pro Val Gly Ala Leu Gly Tyr Val Ala Cys Ala Gln Glu Leu
165 170 175
Leu His Gln Ser Phe Glu Thr Gly Leu Arg Ile Asp His Val Val His
180 185 190
Ala Thr Gly Ser Ala Gly Thr Gln Ala Gly Leu Val Val Gly Leu Arg
195 200 205
Ala Gly Asn Ser Gly Ile Pro Val Tyr Gly Ile Ser Val Arg Ala Pro
210 215 220
Lys Pro Arg Gln Glu Glu Asn Val Trp Lys Leu Val Gln Ser Thr Val
225 230 235 240
Asp Tyr Met Gly Leu Pro Ala Ser Ala Val Glu Arg Ala Asp Val Val
245 250 255
Ala Asn Ser Asp Tyr Val Gly Glu Gly Tyr Gly Ile Ser Thr Asp Ala
260 265 270
Met Ile Glu Ala Val His Met Thr Ala Ala Leu Glu Ala Ile Leu Leu
275 280 285
Asp Pro Val Tyr Ser Gly Lys Gly Met Ala Gly Leu Ile Gly Leu Ile
290 295 300
Arg Ser Gly His Phe Lys Gln Gly Glu Asn Val Val Phe Val His Thr
305 310 315 320
Gly Gly Ala Val Gly Leu Phe Gly Tyr Arg Arg Ala Phe Glu Gly Leu
325 330 335
Pro Pro Leu Ala Ala
340

<210> 48
<211> 1224
<212> DNA
<213> Oryza sativa (japonica cultivar-group)

<220>
<221> CDS
<222> (1)..(1224)

<400> 48
atg cgg cca tcg ccg gcg ctc gcc ggc ggc ggc agg acg gtc gca aat 48
Met Arg Pro Ser Pro Ala Leu Ala Gly Gly Gly Arg Thr Val Ala Asn
1 5 10 15
ctt ctc tcc gcc acg gag tgg atg ctt cct tct ccg gcc acc caa gtc 96
Leu Leu Ser Ala Thr Glu Trp Met Leu Pro Ser Pro Ala Thr Gln Val

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

```
atc ctg ttg gat cca atg tac acc tta gct ggt tgg gag caa gct gtg       1104
Ile Leu Leu Asp Pro Met Tyr Thr Leu Ala Gly Trp Glu Gln Ala Val
        355                 360                 365
gat cta tgt gtt gga gac agt aga acc aaa gtg gtg atg atc cat acg       1152
Asp Leu Cys Val Gly Asp Ser Arg Thr Lys Val Val Met Ile His Thr
    370                 375                 380
gga gga acg ctt ggc ttc tgc gga ttg gcg cag cgg tac tca tcg cac       1200
Gly Gly Thr Leu Gly Phe Cys Gly Leu Ala Gln Arg Tyr Ser Ser His
385                 390                 395                 400
ttc acc tcg gat gag caa act tag                                      1224
Phe Thr Ser Asp Glu Gln Thr
                405
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<210> 49
<211> 407
<212> PRT
<213> Oryza sativa (japonica cultivar-group)

<400> 49

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

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

```
Leu Val Glu Trp Val Glu Arg Phe Ser Pro Arg Arg Phe Gly Lys Val
                325                 330                 335
Leu Asn Gly Glu Ile Ala Leu Cys Arg Gln Ile Ala Gln Gln Thr Gly
            340                 345                 350
Ile Leu Leu Asp Pro Met Tyr Thr Leu Ala Gly Trp Glu Gln Ala Val
        355                 360                 365
Asp Leu Cys Val Gly Asp Ser Arg Thr Lys Val Val Met Ile His Thr
    370                 375                 380
Gly Gly Thr Leu Gly Phe Cys Gly Leu Ala Gln Arg Tyr Ser Ser His
385                 390                 395                 400
Phe Thr Ser Asp Glu Gln Thr
                405
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<210> 50
<211> 996
<212> DNA
<213> Bacillus cereus ATCC 10987

<220>
<221> CDS
<222> (1)..(996)
<223> transl_table=11

<400> 50

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atg aat tta gct aaa ttc cct aga aaa aaa tat acc gaa tca tat aca       48
Met Asn Leu Ala Lys Phe Pro Arg Lys Lys Tyr Thr Glu Ser Tyr Thr
1               5                   10                  15
cca att gaa aaa tta aac aat ttt tct gaa gca ctt ggt ggg ccg act       96
Pro Ile Glu Lys Leu Asn Asn Phe Ser Glu Ala Leu Gly Gly Pro Thr
            20                  25                  30
att tat ttt aaa cga gat gat tta ctt ggt tta aca gct ggt ggt aat      144
Ile Tyr Phe Lys Arg Asp Asp Leu Leu Gly Leu Thr Ala Gly Gly Asn
        35                  40                  45
aag acg aga aag tta gag ttt cta gtt gcg gat gcg cag gta aag ggt      192
Lys Thr Arg Lys Leu Glu Phe Leu Val Ala Asp Ala Gln Val Lys Gly
    50                  55                  60
gca gat acg tta att aca gct ggc ggc att caa tca aat cat tgc cgc      240
Ala Asp Thr Leu Ile Thr Ala Gly Gly Ile Gln Ser Asn His Cys Arg
65                  70                  75                  80
cta aca ctt gca gct gcg gta aaa gaa aaa atg aaa tgt att ctt gta      288
Leu Thr Leu Ala Ala Ala Val Lys Glu Lys Met Lys Cys Ile Leu Val
                85                  90                  95
tta gaa gaa ggg ctt gag cca gaa gag aag cca gat ttt aac gga aac      336
Leu Glu Glu Gly Leu Glu Pro Glu Glu Lys Pro Asp Phe Asn Gly Asn
            100                 105                 110
tat ttc tta tat cat tta cta ggt gct gaa aat gtc att gtt gta cga      384
Tyr Phe Leu Tyr His Leu Leu Gly Ala Glu Asn Val Ile Val Val Arg
        115                 120                 125
aac gga gca gat ctt atg gaa gag atg cat aaa gtc gcg aaa gaa gtt      432
Asn Gly Ala Asp Leu Met Glu Glu Met His Lys Val Ala Lys Glu Val
    130                 135                 140
agt gaa aaa ggt agt aca cca tat gta att ccg gtt ggt gga tca aat      480
Ser Glu Lys Gly Ser Thr Pro Tyr Val Ile Pro Val Gly Gly Ser Asn
145                 150                 155                 160
cct act ggc gca atg ggg tac gtt gct tgt gcg caa gaa att atg gcg      528
Pro Thr Gly Ala Met Gly Tyr Val Ala Cys Ala Gln Glu Ile Met Ala
                165                 170                 175
caa tca ttt gac caa gga att gat ttc agt tca gtc gtt tgc gta agt      576
Gln Ser Phe Asp Gln Gly Ile Asp Phe Ser Ser Val Val Cys Val Ser
            180                 185                 190
ggt agc ggc ggt atg cac gct ggt tta att act ggt ttt gct gga aca      624
```

```
Gly Ser Gly Gly Met His Ala Gly Leu Ile Thr Gly Phe Ala Gly Thr
        195                 200                 205
caa agt aac att cca gta atc ggc att aac gta agt aga gga aaa gca       672
Gln Ser Asn Ile Pro Val Ile Gly Ile Asn Val Ser Arg Gly Lys Ala
    210                 215                 220
gag caa gaa gag aaa gta gca aaa ctt gta gat gaa acg tca gct cac       720
Glu Gln Glu Glu Lys Val Ala Lys Leu Val Asp Glu Thr Ser Ala His
225                 230                 235                 240
gtt ggt att cca aac ttt atc ccg cgc gaa gct gtt aca tgc ttt gat       768
Val Gly Ile Pro Asn Phe Ile Pro Arg Glu Ala Val Thr Cys Phe Asp
                245                 250                 255
gaa tat gta gga cca ggt tat gcg tta cca acg ccg gaa atg gtg gaa       816
Glu Tyr Val Gly Pro Gly Tyr Ala Leu Pro Thr Pro Glu Met Val Glu
            260                 265                 270
gca gtg caa tta ctt gcg aaa aca gaa ggt att tta ctg gat cca gtg       864
Ala Val Gln Leu Leu Ala Lys Thr Glu Gly Ile Leu Leu Asp Pro Val
        275                 280                 285
tat aca ggt aaa gca gta gcg ggg cta atc gac tta att aga aaa ggt       912
Tyr Thr Gly Lys Ala Val Ala Gly Leu Ile Asp Leu Ile Arg Lys Gly
    290                 295                 300
aca ttt aaa aaa gaa gac aac att tta ttc gta cat tca ggt ggt tca       960
Thr Phe Lys Lys Glu Asp Asn Ile Leu Phe Val His Ser Gly Gly Ser
305                 310                 315                 320
cca gct tta tat gcg aat acg tct tta ttt gtg taa                      996
Pro Ala Leu Tyr Ala Asn Thr Ser Leu Phe Val
                325                 330
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<210> 51
<211> 331
<212> PRT
<213> Bacillus cereus ATCC 10987

<400> 51

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

```
Glu Gln Glu Glu Lys Val Ala Lys Leu Val Asp Glu Thr Ser Ala His
225                 230                 235                 240
Val Gly Ile Pro Asn Phe Ile Pro Arg Glu Ala Val Thr Cys Phe Asp
                245                 250                 255
Glu Tyr Val Gly Pro Gly Tyr Ala Leu Pro Thr Pro Glu Met Val Glu
            260                 265                 270
Ala Val Gln Leu Leu Ala Lys Thr Glu Gly Ile Leu Leu Asp Pro Val
        275                 280                 285
Tyr Thr Gly Lys Ala Val Ala Gly Leu Ile Asp Leu Ile Arg Lys Gly
    290                 295                 300
Thr Phe Lys Lys Glu Asp Asn Ile Leu Phe Val His Ser Gly Gly Ser
305                 310                 315                 320
Pro Ala Leu Tyr Ala Asn Thr Ser Leu Phe Val
                325                 330
```

<210> 52
<211> 1206
<212> DNA
<213> Magnaporthe grisea 70-15

<220>
<221> CDS
<222> (1)..(1206)

<400> 52

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atg agc acc aac gat atc aag ctc cct gag cca ttt gcg agc att cct       48
Met Ser Thr Asn Asp Ile Lys Leu Pro Glu Pro Phe Ala Ser Ile Pro
1               5                   10                  15
cgg gaa act ttt cta ttt ggc ccc tcg ccc ata cag cac ctg gaa cgc       96
Arg Glu Thr Phe Leu Phe Gly Pro Ser Pro Ile Gln His Leu Glu Arg
            20                  25                  30
atc tca gaa gca cta ggc ggc aag gtg aac gtt tac gca aag cgt gat      144
Ile Ser Glu Ala Leu Gly Gly Lys Val Asn Val Tyr Ala Lys Arg Asp
        35                  40                  45
gac tgc aat tcg ggt ttg gca tat ggc ggc aac aag acg cgg aag cta      192
Asp Cys Asn Ser Gly Leu Ala Tyr Gly Gly Asn Lys Thr Arg Lys Leu
    50                  55                  60
gaa tac ctc gcg gca gaa gcc aag gcg cag ggc gct gac aca ctc gtg      240
Glu Tyr Leu Ala Ala Glu Ala Lys Ala Gln Gly Ala Asp Thr Leu Val
65                  70                  75                  80
tcc att ggc ggc gtg caa tca aac cac acg cgc cag gtc gcg gcc gtc      288
Ser Ile Gly Gly Val Gln Ser Asn His Thr Arg Gln Val Ala Ala Val
                85                  90                  95
tcg acc aag ctc ggg ctc aag gct gtc ctg gtg cag gag cac tgg gtg      336
Ser Thr Lys Leu Gly Leu Lys Ala Val Leu Val Gln Glu His Trp Val

            100                 105                 110
ccc gac tgg tcg gat ccg gtg tac ggc aag gtg ggc aac atc cag ctg      384
Pro Asp Trp Ser Asp Pro Val Tyr Gly Lys Val Gly Asn Ile Gln Leu
        115                 120                 125
tcg cgg ctg atg ggc gcc gac gtc aag ctg gac ccg tcc ggg ttc ggc      432
Ser Arg Leu Met Gly Ala Asp Val Lys Leu Asp Pro Ser Gly Phe Gly
    130                 135                 140
atc gag cac aag aac tcg ctc gcg gcg gcg gtg gcg gag ctg cag tcg      480
Ile Glu His Lys Asn Ser Leu Ala Ala Ala Val Ala Glu Leu Gln Ser
145                 150                 155                 160
cag ggg aga agg ccg tac gcg atc ccg gcg ggg gcc agc gac cac ccg      528
Gln Gly Arg Arg Pro Tyr Ala Ile Pro Ala Gly Ala Ser Asp His Pro
                165                 170                 175
ctc ggc ggg ctg ggc ttc gcg cgc tgg gcg ttc gag gtc gag gag cag      576
Leu Gly Gly Leu Gly Phe Ala Arg Trp Ala Phe Glu Val Glu Glu Gln
```

```
            180                 185                 190
gag cgg cag atg ggc gtc ttc ttc gac acg gtg att gtg tgc gcc gtc       624
Glu Arg Gln Met Gly Val Phe Phe Asp Thr Val Ile Val Cys Ala Val
        195                 200                 205
acg ggc tcg acc atg gcg ggc atg gtg gcc ggg ttc aag ctg gcg cag       672
Thr Gly Ser Thr Met Ala Gly Met Val Ala Gly Phe Lys Leu Ala Gln
    210                 215                 220
aaa aag tgc ggg tcc aag ccg cgg cgc gtc atc ggc atc gac gcc tcg       720
Lys Lys Cys Gly Ser Lys Pro Arg Arg Val Ile Gly Ile Asp Ala Ser
225                 230                 235                 240
gcc acg gtg ccg cag acc aag gag cag gtg ctg cgc atc gcg cag gtg       768
Ala Thr Val Pro Gln Thr Lys Glu Gln Val Leu Arg Ile Ala Gln Val
                245                 250                 255
acg ggc cgc aag att ggc ctc gag gac ggc gtc gac aac gtc acg acc       816
Thr Gly Arg Lys Ile Gly Leu Glu Asp Gly Val Asp Asn Val Thr Thr
            260                 265                 270
gag gac gtc gag ctg gac gac cgc tac cac gcc ggc atc tac ggc gtc       864
Glu Asp Val Glu Leu Asp Asp Arg Tyr His Ala Gly Ile Tyr Gly Val
        275                 280                 285
ccg gac cag cag acc aag gac gcc atc cgc ttc ggg gcc agc acc gag       912
Pro Asp Gln Gln Thr Lys Asp Ala Ile Arg Phe Gly Ala Ser Thr Glu
    290                 295                 300
gcc ttc atc acc gat ccc gtc tat gag ggt aag agc ttg gcc ggc atg       960
Ala Phe Ile Thr Asp Pro Val Tyr Glu Gly Lys Ser Leu Ala Gly Met
305                 310                 315                 320
atg gac atg att cgc aaa ggg gag atc aag ccc ggg agc aac gtc ttg      1008
Met Asp Met Ile Arg Lys Gly Glu Ile Lys Pro Gly Ser Asn Val Leu
                325                 330                 335
tat gcg cac ttg ggc ggc cag ctt gcg ctc aat gcg tac tct gac ata      1056
Tyr Ala His Leu Gly Gly Gln Leu Ala Leu Asn Ala Tyr Ser Asp Ile
            340                 345                 350
ttc att gtg cat cgt cgt caa tct tct ctg ggt aat ccc atg gcc aac      1104
Phe Ile Val His Arg Arg Gln Ser Ser Leu Gly Asn Pro Met Ala Asn
        355                 360                 365
cca tgg cca aaa cac gct atg cac ttg gct gaa tac tct ccg gcc aat      1152
Pro Trp Pro Lys His Ala Met His Leu Ala Glu Tyr Ser Pro Ala Asn
    370                 375                 380
act tgg tgg tgg tca aaa gcc aca atg tgc gga tgc aag aaa cat acc      1200
Thr Trp Trp Trp Ser Lys Ala Thr Met Cys Gly Cys Lys Lys His Thr
385                 390                 395                 400
ctc tga                                                             1206
Leu
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<210> 53
<211> 401
<212> PRT
<213> Magnaporthe grisea 70-15

<400> 53

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

```
                85                  90                  95
Ser Thr Lys Leu Gly Leu Lys Ala Val Leu Val Gln Glu His Trp Val
            100                 105                 110
Pro Asp Trp Ser Asp Pro Val Tyr Gly Lys Val Gly Asn Ile Gln Leu
        115                 120                 125
Ser Arg Leu Met Gly Ala Asp Val Lys Leu Asp Pro Ser Gly Phe Gly
    130                 135                 140
Ile Glu His Lys Asn Ser Leu Ala Ala Ala Val Ala Glu Leu Gln Ser
145                 150                 155                 160
Gln Gly Arg Arg Pro Tyr Ala Ile Pro Ala Gly Ala Ser Asp His Pro
                165                 170                 175
Leu Gly Gly Leu Gly Phe Ala Arg Trp Ala Phe Glu Val Glu Glu Gln
            180                 185                 190
Glu Arg Gln Met Gly Val Phe Phe Asp Thr Val Ile Val Cys Ala Val
        195                 200                 205
Thr Gly Ser Thr Met Ala Gly Met Val Ala Gly Phe Lys Leu Ala Gln
    210                 215                 220
Lys Lys Cys Gly Ser Lys Pro Arg Arg Val Ile Gly Ile Asp Ala Ser
225                 230                 235                 240
Ala Thr Val Pro Gln Thr Lys Glu Gln Val Leu Arg Ile Ala Gln Val
                245                 250                 255
Thr Gly Arg Lys Ile Gly Leu Glu Asp Gly Val Asp Asn Val Thr Thr
            260                 265                 270
Glu Asp Val Glu Leu Asp Asp Arg Tyr His Ala Gly Ile Tyr Gly Val
        275                 280                 285
Pro Asp Gln Gln Thr Lys Asp Ala Ile Arg Phe Gly Ala Ser Thr Glu
    290                 295                 300
Ala Phe Ile Thr Asp Pro Val Tyr Glu Gly Lys Ser Leu Ala Gly Met
305                 310                 315                 320
Met Asp Met Ile Arg Lys Gly Glu Ile Lys Pro Gly Ser Asn Val Leu
                325                 330                 335
Tyr Ala His Leu Gly Gly Gln Leu Ala Leu Asn Ala Tyr Ser Asp Ile
            340                 345                 350
Phe Ile Val His Arg Arg Gln Ser Ser Leu Gly Asn Pro Met Ala Asn
        355                 360                 365
Pro Trp Pro Lys His Ala Met His Leu Ala Glu Tyr Ser Pro Ala Asn
    370                 375                 380
Thr Trp Trp Trp Ser Lys Ala Thr Met Cys Gly Cys Lys Lys His Thr
385                 390                 395                 400
Leu
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<210> 54
<211> 984
<212> DNA
<213> Gibberella zeae PH-1

<220>
<221> CDS
<222> (1)..(984)

<400> 54

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atg gtc act ctt ccg tca cct ttt agc gac atc gat cgt gtc cag ctg       48
Met Val Thr Leu Pro Ser Pro Phe Ser Asp Ile Asp Arg Val Gln Leu
1               5                   10                  15
ttg ttc aat cgc ccc aca gac att gaa ccg ctc tcc cgt ctc aca gaa       96
Leu Phe Asn Arg Pro Thr Asp Ile Glu Pro Leu Ser Arg Leu Thr Glu
            20                  25                  30
tct gtc aat aat aac gtc aag cta tgg ata gct cgt gaa gat cgc aat      144
Ser Val Asn Asn Asn Val Lys Leu Trp Ile Ala Arg Glu Asp Arg Asn
        35                  40                  45
```

```
tca ggt ctc gca ttc gct gga aac aag gtt cgc aag ctt gaa tat gtg       192
Ser Gly Leu Ala Phe Ala Gly Asn Lys Val Arg Lys Leu Glu Tyr Val
    50                  55                  60
cta gca gat gct ctt gcc caa gga gca gac acc gtt gtg act aca ggt       240
Leu Ala Asp Ala Leu Ala Gln Gly Ala Asp Thr Val Val Thr Thr Gly
65                  70                  75                  80
ggc atc cag tca aac cac atg tgt caa acc tct gct gct gct gct cga       288
Gly Ile Gln Ser Asn His Met Cys Gln Thr Ser Ala Ala Ala Ala Arg
                85                  90                  95
ctt ggc ctc aaa gtc gct ctt tat cct gcg gac cgt gtt gct tcg aat       336
Leu Gly Leu Lys Val Ala Leu Tyr Pro Ala Asp Arg Val Ala Ser Asn
            100                 105                 110
gac gcc gag tac aaa tat ttg ggc aat ata cag gca aac gcc att ctc       384
Asp Ala Glu Tyr Lys Tyr Leu Gly Asn Ile Gln Ala Asn Ala Ile Leu
        115                 120                 125
ggt gcc gag acg ttt ccg gtc gac aca gct gaa gag act gtt atc acg       432
Gly Ala Glu Thr Phe Pro Val Asp Thr Ala Glu Glu Thr Val Ile Thr
    130                 135                 140
act ctt aaa gat cgt ggc caa aaa ccc tac tcc att cct ccc gga gct       480
Thr Leu Lys Asp Arg Gly Gln Lys Pro Tyr Ser Ile Pro Pro Gly Ala
145                 150                 155                 160
agc tcc cat ccc ctt gga ggc ctt ggc tat gct cgc tgg gcg ttt gaa       528
Ser Ser His Pro Leu Gly Gly Leu Gly Tyr Ala Arg Trp Ala Phe Glu
                165                 170                 175
ttg cta gag caa gaa aag aag atc ggc gtg acc ttt gat acc ata gca       576
Leu Leu Glu Gln Glu Lys Lys Ile Gly Val Thr Phe Asp Thr Ile Ala
            180                 185                 190
ctc gtt gca ggg tct tgc tct acc cta gga ggt tta ctc gcc gga ttg       624
Leu Val Ala Gly Ser Cys Ser Thr Leu Gly Gly Leu Leu Ala Gly Leu
        195                 200                 205
aag ctt gca caa aaa gag caa att cca ggt tcc aag aaa cgc ctt att       672
Lys Leu Ala Gln Lys Glu Gln Ile Pro Gly Ser Lys Lys Arg Leu Ile
    210                 215                 220
gga ttt tcg gtt ctg cac aag tct aag aag gat gtc gaa gca ctg gtt       720
Gly Phe Ser Val Leu His Lys Ser Lys Lys Asp Val Glu Ala Leu Val
225                 230                 235                 240
ctc aaa aca tcc cga acc aca gca tca aag att gga att tca ccc aac       768
Leu Lys Thr Ser Arg Thr Thr Ala Ser Lys Ile Gly Ile Ser Pro Asn
                245                 250                 255
gag ata acc gca gac gat ttc gag att aat act tcc tat ata ggt gat       816
Glu Ile Thr Ala Asp Asp Phe Glu Ile Asn Thr Ser Tyr Ile Gly Asp
            260                 265                 270
ggg tac ggg caa ctc aat gac tcc aca gct gag gcg atg aag aag cta       864
Gly Tyr Gly Gln Leu Asn Asp Ser Thr Ala Glu Ala Met Lys Lys Leu
        275                 280                 285
gca agg aag gaa ggt atc ctg acc gac cct gtt tac acc ggc aag gcg       912
Ala Arg Lys Glu Gly Ile Leu Thr Asp Pro Val Tyr Thr Gly Lys Ala
    290                 295                 300
ttt act ggc ttg ctt gat ctt gcc aag aca gga tat ttg aac gta tct       960
Phe Thr Gly Leu Leu Asp Leu Ala Lys Thr Gly Tyr Leu Asn Val Ser
305                 310                 315                 320
acg acc att gtt cta aac atc taa                                      984
Thr Thr Ile Val Leu Asn Ile
                325
```

<210> 55
<211> 327
<212> PRT
<213> Gibberella zeae PH-1

<400> 55

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        115                 120                 125
Gly Ala Glu Thr Phe Pro Val Asp Thr Ala Glu Glu Thr Val Ile Thr
    130                 135                 140
Thr Leu Lys Asp Arg Gly Gln Lys Pro Tyr Ser Ile Pro Pro Gly Ala
145                 150                 155                 160
Ser Ser His Pro Leu Gly Gly Leu Gly Tyr Ala Arg Trp Ala Phe Glu
                165                 170                 175
Leu Leu Glu Gln Glu Lys Lys Ile Gly Val Thr Phe Asp Thr Ile Ala
            180                 185                 190
Leu Val Ala Gly Ser Cys Ser Thr Leu Gly Gly Leu Leu Ala Gly Leu
        195                 200                 205
Lys Leu Ala Gln Lys Glu Gln Ile Pro Gly Ser Lys Lys Arg Leu Ile
    210                 215                 220
Gly Phe Ser Val Leu His Lys Ser Lys Lys Asp Val Glu Ala Leu Val
225                 230                 235                 240
Leu Lys Thr Ser Arg Thr Thr Ala Ser Lys Ile Gly Ile Ser Pro Asn
                245                 250                 255
Glu Ile Thr Ala Asp Asp Phe Glu Ile Asn Thr Ser Tyr Ile Gly Asp
            260                 265                 270
Gly Tyr Gly Gln Leu Asn Asp Ser Thr Ala Glu Ala Met Lys Lys Leu
        275                 280                 285
Ala Arg Lys Glu Gly Ile Leu Thr Asp Pro Val Tyr Thr Gly Lys Ala
    290                 295                 300
Phe Thr Gly Leu Leu Asp Leu Ala Lys Thr Gly Tyr Leu Asn Val Ser
305                 310                 315                 320
Thr Thr Ile Val Leu Asn Ile
                325
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<210> 56
<211> 1158
<212> DNA
<213> Oryza sativa (japonica cultivar-group)

<220>
<221> CDS
<222> (1)..(1158)

<400> 56

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atg gcc gga gtt tcc gcc gcc tcc gcc gcc ggg aag atc ggg agc ttc      48
Met Ala Gly Val Ser Ala Ala Ser Ala Ala Gly Lys Ile Gly Ser Phe
1               5                   10                  15
ctc tcc aag agg ccg tac gcg ccg ccg tcc tgg gcc tcg cac ctg tcc      96
Leu Ser Lys Arg Pro Tyr Ala Pro Pro Ser Trp Ala Ser His Leu Ser
            20                  25                  30
ccc gcc ccc tcg cag acc ttc tcg ctc ggc cat ttc ccg acg ccg atc     144
Pro Ala Pro Ser Gln Thr Phe Ser Leu Gly His Phe Pro Thr Pro Ile
        35                  40                  45
cac aag tgg aat ctg ccc aat ttg ccg aat ggc acg gag gtg tgg atc     192
His Lys Trp Asn Leu Pro Asn Leu Pro Asn Gly Thr Glu Val Trp Ile
    50                  55                  60
aag cga gac gac atc tca ggc atg cag ttg agc ggg aac aag gtc cgg     240
Lys Arg Asp Asp Ile Ser Gly Met Gln Leu Ser Gly Asn Lys Val Arg
65                  70                  75                  80
aag ctc gag ttc ctg atg gca gat gcc gtc gcg cag ggc gct gac tgc     288
Lys Leu Glu Phe Leu Met Ala Asp Ala Val Ala Gln Gly Ala Asp Cys
                85                  90                  95
gtt ata act gta ggt ggc atc cag agc aat cac tgc cgt gcc acc gca     336
Val Ile Thr Val Gly Gly Ile Gln Ser Asn His Cys Arg Ala Thr Ala
            100                 105                 110
gtg gct gca aag tat ata aat ctt gat tgt tat ctg ata ctg cgc aca     384
Val Ala Ala Lys Tyr Ile Asn Leu Asp Cys Tyr Leu Ile Leu Arg Thr
```

```
        35                  40                  45
cac aag tgg aat ctg ccc aat ttg ccg aat ggc acg gag gtg tgg atc      192
His Lys Trp Asn Leu Pro Asn Leu Pro Asn Gly Thr Glu Val Trp Ile
    50                  55                  60
aag cga gac gac atc tca ggc atg cag ttg agc ggg aac aag gtc cgg      240
Lys Arg Asp Asp Ile Ser Gly Met Gln Leu Ser Gly Asn Lys Val Arg
65                  70                  75                  80
aag ctc gag ttc ctg atg gca gat gcc gtc gcg cag ggc gct gac tgc      288
Lys Leu Glu Phe Leu Met Ala Asp Ala Val Ala Gln Gly Ala Asp Cys
                85                  90                  95
gtt ata act gta ggt ggc atc cag agc aat cac tgc cgt gcc acc gca      336
Val Ile Thr Val Gly Gly Ile Gln Ser Asn His Cys Arg Ala Thr Ala
            100                 105                 110
gtg gct gca aag tat ata aat ctt gat tgt tat ctg ata ctg cgc aca      384
Val Ala Ala Lys Tyr Ile Asn Leu Asp Cys Tyr Leu Ile Leu Arg Thr
        115                 120                 125
tcc aag ctt ctt gtg gat aag gac cct ggt ttg gtt ggg aat ctc ctt      432
Ser Lys Leu Leu Val Asp Lys Asp Pro Gly Leu Val Gly Asn Leu Leu
    130                 135                 140
gtt gag aga ttg gtg gga gcg cat att gat ctt gtt tca aaa gaa gaa      480
Val Glu Arg Leu Val Gly Ala His Ile Asp Leu Val Ser Lys Glu Glu
145                 150                 155                 160
tat gga aaa att ggc agt gtg gct tta gcg gac ttg ctg aaa aag aag      528
Tyr Gly Lys Ile Gly Ser Val Ala Leu Ala Asp Leu Leu Lys Lys Lys
                165                 170                 175
ctt ttg gaa gaa ggc cga aaa cca tat gtt att cct gtt ggt gga tca      576
Leu Leu Glu Glu Gly Arg Lys Pro Tyr Val Ile Pro Val Gly Gly Ser
            180                 185                 190
aac tct cta gga act tgg gga tat ata gaa gca ata agg gag att gaa      624
Asn Ser Leu Gly Thr Trp Gly Tyr Ile Glu Ala Ile Arg Glu Ile Glu
        195                 200                 205
cat caa att cag ata tca ggt gat gtt cag ttt gac gac att gtt gtt      672
His Gln Ile Gln Ile Ser Gly Asp Val Gln Phe Asp Asp Ile Val Val
    210                 215                 220
gca tgt ggc agc ggt gga acc att gct ggt ctt gct tta gga tca aaa      720
Ala Cys Gly Ser Gly Gly Thr Ile Ala Gly Leu Ala Leu Gly Ser Lys
225                 230                 235                 240
ttg agt agc tta aag gca aaa gtc cat gct ttc tct gtt tgt gat gat      768
Leu Ser Ser Leu Lys Ala Lys Val His Ala Phe Ser Val Cys Asp Asp
                245                 250                 255
cct gga tat ttc cat tcc tat gtt caa gac ctg att gat gga ctt cat      816
Pro Gly Tyr Phe His Ser Tyr Val Gln Asp Leu Ile Asp Gly Leu His
            260                 265                 270
tct gat ttg cgt tca cat gat tta gtc aac att gaa aat gct aag ggc      864
Ser Asp Leu Arg Ser His Asp Leu Val Asn Ile Glu Asn Ala Lys Gly
        275                 280                 285
tta ggt tat gcc atg aac aca gct gag gag ctt aag ttt gtt aaa gat      912
Leu Gly Tyr Ala Met Asn Thr Ala Glu Glu Leu Lys Phe Val Lys Asp
    290                 295                 300
ata gct aca gca aca ggc att gtc ctt gat cca gtc tac agt gga aag      960
Ile Ala Thr Ala Thr Gly Ile Val Leu Asp Pro Val Tyr Ser Gly Lys
305                 310                 315                 320
gca gca tat gga atg ctg aaa gac atg ggt gct aat cca gct aag tgg     1008
Ala Ala Tyr Gly Met Leu Lys Asp Met Gly Ala Asn Pro Ala Lys Trp
                325                 330                 335
gaa ggg cga aaa att ctt ttt gta cat aca ggt ggt ctt ctt ggt ttg     1056
Glu Gly Arg Lys Ile Leu Phe Val His Thr Gly Gly Leu Leu Gly Leu
            340                 345                 350
tat gat aag gtt gat gag tta tca tct ttg agt ggg agt tgg cgc aga     1104
Tyr Asp Lys Val Asp Glu Leu Ser Ser Leu Ser Gly Ser Trp Arg Arg
        355                 360                 365
```

```
atg gat ctt gaa gaa tct gtt cca cgc aaa gat gga act ggt aag atg      1152
Met Asp Leu Glu Glu Ser Val Pro Arg Lys Asp Gly Thr Gly Lys Met
    370                 375                 380
ttc tga                                                            1158
Phe
385
```

<210> 57
<211> 385
<212> PRT
<213> Oryza sativa (japonica cultivar-group)

<400> 57

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

Phe
385

<210> 58
<211> 1011
<212> DNA
<213> Aspergillus nidulans FGSC A4

<220>
<221> CDS
<222> (1)..(1011)

<400> 58

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

```
ttc aca ggt gtc aag ata ggt ttg gac gag gag gat atc acg gcg gag       816
Phe Thr Gly Val Lys Ile Gly Leu Asp Glu Glu Asp Ile Thr Ala Glu
            260                 265                 270
gat gtg ata tta gat gat cgg tat cac gct ggt gtg tat ggg att cca       864
Asp Val Ile Leu Asp Asp Arg Tyr His Ala Gly Val Tyr Gly Ile Pro
        275                 280                 285
gat gag gcg acc att gag gcg atc aag ttt ggg gcc agg act gag gct       912
Asp Glu Ala Thr Ile Glu Ala Ile Lys Phe Gly Ala Arg Thr Glu Ala
    290                 295                 300
ttc att acg gat cct gtg tat gaa ggg aag agc ctg aat ggg atg atg       960
Phe Ile Thr Asp Pro Val Tyr Glu Gly Lys Ser Leu Asn Gly Met Met
305                 310                 315                 320
gat atg ggt tta ttg tct tgc tgc cgg att gta ttc aga gta aag tcg      1008
Asp Met Gly Leu Leu Ser Cys Cys Arg Ile Val Phe Arg Val Lys Ser
                325                 330                 335
tag                                                                 1011
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<210> 59
<211> 336
<212> PRT
<213> Aspergillus nidulans FGSC A4

<400> 59

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

```
Asp Glu Ala Thr Ile Glu Ala Ile Lys Phe Gly Ala Arg Thr Glu Ala
    290                 295                 300
Phe Ile Thr Asp Pro Val Tyr Glu Gly Lys Ser Leu Asn Gly Met Met
305                 310                 315                 320
Asp Met Gly Leu Leu Ser Cys Cys Arg Ile Val Phe Arg Val Lys Ser
                325                 330                 335

<210> 60
<211> 1200
<212> DNA
<213> Aspergillus fumigatus Af293

<220>
<221> CDS
<222> (1)..(1200)

<400> 60
atg gca gtc cct cta ccg gca gct ttt gct cag att cct cgg tat cct       48
Met Ala Val Pro Leu Pro Ala Ala Phe Ala Gln Ile Pro Arg Tyr Pro
1               5                   10                  15
ctt cta tac cct cat cct tcc ccg atc cac ccc ctc aca ctt cta tcc       96
Leu Leu Tyr Pro His Pro Ser Pro Ile His Pro Leu Thr Leu Leu Ser
            20                  25                  30
aca tac ctc aac aac agc cgc aac aat aat acg gcc aaa aca ccg tat      144
Thr Tyr Leu Asn Asn Ser Arg Asn Asn Asn Thr Ala Lys Thr Pro Tyr
        35                  40                  45
atc tcc ctc tac gcc aaa cga gaa gac cac tct tcc cca ctc gcc tgc      192
Ile Ser Leu Tyr Ala Lys Arg Glu Asp His Ser Ser Pro Leu Ala Cys
    50                  55                  60
gca ggg aac aaa tac cgc aag ctt gaa tac att atc ccc gac atc cgg      240
Ala Gly Asn Lys Tyr Arg Lys Leu Glu Tyr Ile Ile Pro Asp Ile Arg
65                  70                  75                  80
gcc tct cac agc gcc ccc aat gaa ccc cca cca acc ctc gtc act gag      288

Ala Ser His Ser Ala Pro Asn Glu Pro Pro Pro Thr Leu Val Thr Glu
                85                  90                  95
ggc gcc atc cag agc aac cac acc gtg cag gtc gcc gcg gta gcg aaa      336
Gly Ala Ile Gln Ser Asn His Thr Val Gln Val Ala Ala Val Ala Lys
            100                 105                 110
cga ctc ggc ctc gag gca gtc gtc atc ctt cac aaa ggc aca ggc ggc      384
Arg Leu Gly Leu Glu Ala Val Val Ile Leu His Lys Gly Thr Gly Gly
        115                 120                 125
ggt cta gcc gcc tca acc gat aaa gtc tcg ttc ctg cgc acg gga aac      432
Gly Leu Ala Ala Ser Thr Asp Lys Val Ser Phe Leu Arg Thr Gly Asn
    130                 135                 140
ccg caa gtc gtc cgt ctc ctg ggg gcg gag gtg agg atg ctg gag tcg      480
Pro Gln Val Val Arg Leu Leu Gly Ala Glu Val Arg Met Leu Glu Ser
145                 150                 155                 160
tcg act gtt ccc gca gac ggg gat aag gat ccg att cct ggg att ctg      528
Ser Thr Val Pro Ala Asp Gly Asp Lys Asp Pro Ile Pro Gly Ile Leu
                165                 170                 175
gag gag tta cgc gcg cag ggc aag gcg ccg tat tgg atc cct tcc ggg      576
Glu Glu Leu Arg Ala Gln Gly Lys Ala Pro Tyr Trp Ile Pro Ser Gly
            180                 185                 190
gca agt ctg cat cct ctc ggt gga ttg ggg tat gcg cgc tgt gcg ttt      624
Ala Ser Leu His Pro Leu Gly Gly Leu Gly Tyr Ala Arg Cys Ala Phe
        195                 200                 205
gag att gcg ata cag gag cag gcg caa ggt ttg gat ggg agt ggg cgc      672
Glu Ile Ala Ile Gln Glu Gln Ala Gln Gly Leu Asp Gly Ser Gly Arg
    210                 215                 220
ttt gat tat atc ttc gtt gcg tgc ggg agt ggc agt acg gtg ggc ggt      720
```

```
Phe Asp Tyr Ile Phe Val Ala Cys Gly Ser Gly Ser Thr Val Gly Gly
225                 230                 235                 240
ttg atc gcc ggg ctg aag ctg ttg gag aag aag gaa ggc aga acc tgg       768
Leu Ile Ala Gly Leu Lys Leu Leu Glu Lys Lys Glu Gly Arg Thr Trp
                245                 250                 255
ttg agc aaa cca cct cgg caa gtc att ggg atc ttg act tcg cct acc       816
Leu Ser Lys Pro Pro Arg Gln Val Ile Gly Ile Leu Thr Ser Pro Thr
            260                 265                 270
aag cct cag gag tac cat gaa gag cgg gta ctc acc ttt gcg cgt cgc       864
Lys Pro Gln Glu Tyr His Glu Glu Arg Val Leu Thr Phe Ala Arg Arg
        275                 280                 285
gca gct gct ctt att ggg ttg gat gcc gaa aag gac att tct atg gat       912
Ala Ala Ala Leu Ile Gly Leu Asp Ala Glu Lys Asp Ile Ser Met Asp
    290                 295                 300
gat gtt cgg ctt gat gat cgg ttc gct ggc acc gca tat ggc gtt cta       960
Asp Val Arg Leu Asp Asp Arg Phe Ala Gly Thr Ala Tyr Gly Val Leu
305                 310                 315                 320
gac gcc cag aca agc acg gcg ctg gac tta atg gcg aaa aag gag gca      1008
Asp Ala Gln Thr Ser Thr Ala Leu Asp Leu Met Ala Lys Lys Glu Ala
                325                 330                 335
gta atg cta gat ccc gta tat act tca aag gtc gta cgg gga ctc ttg      1056
Val Met Leu Asp Pro Val Tyr Thr Ser Lys Val Val Arg Gly Leu Leu
            340                 345                 350
cac tgg gta cag caa gag gag ctg gca aag gac tgg tca ctt cgt ctg      1104
His Trp Val Gln Gln Glu Glu Leu Ala Lys Asp Trp Ser Leu Arg Leu
        355                 360                 365
gga gat cga gaa cgt ccc gac tgc atg aat gtg ctt ttc atc cac act      1152
Gly Asp Arg Glu Arg Pro Asp Cys Met Asn Val Leu Phe Ile His Thr
    370                 375                 380
gga gga cag gct gcg tta ggc gcc tac gca gac atg gtc gaa tta          1197
Gly Gly Gln Ala Ala Leu Gly Ala Tyr Ala Asp Met Val Glu Leu
385                 390                 395
tag                                                                 1200
```

<210> 61
<211> 399
<212> PRT
<213> Aspergillus fumigatus Af293

<400> 61

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

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

<210> 62
<211> 1053
<212> DNA
<213> Aspergillus fumigatus Af293

<220>
<221> CDS
<222> (1)..(1053)

<400> 62

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atg acc cta gaa atc ccc ctc cca gaa ccc ttc gcc tcc atc ccc cgc       48
Met Thr Leu Glu Ile Pro Leu Pro Glu Pro Phe Ala Ser Ile Pro Arg
1               5                   10                  15
tac acc ctc acc ctc ggc ccc tcc ccc atc cac ctc ctc ccc aac acc       96
Tyr Thr Leu Thr Leu Gly Pro Ser Pro Ile His Leu Leu Pro Asn Thr
            20                  25                  30
tcc gcc gat ttg cac acc acc atc tac gcc aag cgc gag gac ctc aac      144
Ser Ala Asp Leu His Thr Thr Ile Tyr Ala Lys Arg Glu Asp Leu Asn
        35                  40                  45
tcc gcc ctc gcc tac ggc ggc aac aaa acc cgc aaa ctc gag tat ctt      192
Ser Ala Leu Ala Tyr Gly Gly Asn Lys Thr Arg Lys Leu Glu Tyr Leu
    50                  55                  60
ctc gcg gac gcc ctc gcc caa aac gcc acg acc ctg ctc tcc atc ggc      240
Leu Ala Asp Ala Leu Ala Gln Asn Ala Thr Thr Leu Leu Ser Ile Gly
65                  70                  75                  80
ggc gtc caa tcc aac cac acc cgt cag gtc gcc gcc gcc gca cac           288
Gly Val Gln Ser Asn His Thr Arg Gln Val Ala Ala Ala Ala His
                85                  90                  95
gcc ggc ctc acc gcc cgt ctc gtg cag gag cac tgg gtc gac tgg aac       336
```

```
Ala Gly Leu Thr Ala Arg Leu Val Gln Glu His Trp Val Asp Trp Asn
            100                 105                 110
gac gcc cat tac gac cag gta ggc aat atc cag ctg tcg cgg ctg atg       384
Asp Ala His Tyr Asp Gln Val Gly Asn Ile Gln Leu Ser Arg Leu Met
        115                 120                 125
ggc gcg gat gtg cgg ctg cat cca gcg ggg ttc ggc atc gag cat aaa       432
Gly Ala Asp Val Arg Leu His Pro Ala Gly Phe Gly Ile Glu His Lys
    130                 135                 140
gag agt ctg cgc cag ttg ctg ggc gag tgc gag gcg cgc ggc gag cgc       480
Glu Ser Leu Arg Gln Leu Leu Gly Glu Cys Glu Ala Arg Gly Glu Arg
145                 150                 155                 160
gcg tac tac atc ccg gcg ggt gcg tct gac cat ccg ctc ggc ggg ctg       528
Ala Tyr Tyr Ile Pro Ala Gly Ala Ser Asp His Pro Leu Gly Gly Leu
                165                 170                 175
ggg ttt gcg cgg tgg gcg ttt gag gtg gcg atg cag gag cgc gag atg       576
Gly Phe Ala Arg Trp Ala Phe Glu Val Ala Met Gln Glu Arg Glu Met
            180                 185                 190
ggg gtg ttc ttc gat gtg gtg gtg gtg tgt gcg gtg acg ggg agt acg       624
Gly Val Phe Phe Asp Val Val Val Val Cys Ala Val Thr Gly Ser Thr
        195                 200                 205
ttt gcg ggc atg att gct ggg ttt aag ttg ctg gag cgg gtg cag cct       672
Phe Ala Gly Met Ile Ala Gly Phe Lys Leu Leu Glu Arg Val Gln Pro
    210                 215                 220
ggt agt aga aaa agg cgg gtt atc ggg att gat gcg tcc gcg cgg ccg       720
Gly Ser Arg Lys Arg Arg Val Ile Gly Ile Asp Ala Ser Ala Arg Pro
225                 230                 235                 240
gcg gag acg agg gcg caa gtg atg cgg att gcg agg agt aca gct gcg       768
Ala Glu Thr Arg Ala Gln Val Met Arg Ile Ala Arg Ser Thr Ala Ala
                245                 250                 255
aag att ggt ttg aag gac gag gat atc tcc gag gag gat gtg gtt ctg       816
Lys Ile Gly Leu Lys Asp Glu Asp Ile Ser Glu Glu Asp Val Val Leu
            260                 265                 270
aat gag aat tac cat gag ggg gtt tac ggg gta cct ggc gag ggg acc       864
Asn Glu Asn Tyr His Glu Gly Val Tyr Gly Val Pro Gly Glu Gly Thr
        275                 280                 285
atc aag gct atg gag tat gcc gcc agc aaa gat gcg ttc att acg gac       912
Ile Lys Ala Met Glu Tyr Ala Ala Ser Lys Asp Ala Phe Ile Thr Asp
    290                 295                 300
cct gtg tac gaa ggg aag agc ttc gcg ggg ttg atc gat ttg gcg aag       960
Pro Val Tyr Glu Gly Lys Ser Phe Ala Gly Leu Ile Asp Leu Ala Lys
305                 310                 315                 320
aag ggc gag ttt gcg ggg aag acg gtg ctt tac gcc cat ctt ggg ggt      1008
Lys Gly Glu Phe Ala Gly Lys Thr Val Leu Tyr Ala His Leu Gly Gly
                325                 330                 335
cag ccg gct ttg aat gcg tat agc gag att ggt cgg gcg aag tag          1053
Gln Pro Ala Leu Asn Ala Tyr Ser Glu Ile Gly Arg Ala Lys
            340                 345                 350

<210> 63
<211> 350
<212> PRT
<213> Aspergillus fumigatus Af293

<400> 63
Met Thr Leu Glu Ile Pro Leu Pro Glu Pro Phe Ala Ser Ile Pro Arg
1               5                  10                  15
Tyr Thr Leu Thr Leu Gly Pro Ser Pro Ile His Leu Leu Pro Asn Thr
            20                  25                  30
Ser Ala Asp Leu His Thr Thr Ile Tyr Ala Lys Arg Glu Asp Leu Asn
        35                  40                  45
Ser Ala Leu Ala Tyr Gly Gly Asn Lys Thr Arg Lys Leu Glu Tyr Leu
```

```
    50                  55                  60
Leu Ala Asp Ala Leu Ala Gln Asn Ala Thr Thr Leu Leu Ser Ile Gly
65                  70                  75                  80
Gly Val Gln Ser Asn His Thr Arg Gln Val Ala Ala Ala Ala Ala His
                85                  90                  95
Ala Gly Leu Thr Ala Arg Leu Val Gln Glu His Trp Val Asp Trp Asn
            100                 105                 110

Asp Ala His Tyr Asp Gln Val Gly Asn Ile Gln Leu Ser Arg Leu Met
        115                 120                 125
Gly Ala Asp Val Arg Leu His Pro Ala Gly Phe Gly Ile Glu His Lys
    130                 135                 140
Glu Ser Leu Arg Gln Leu Leu Gly Glu Cys Glu Ala Arg Gly Glu Arg
145                 150                 155                 160
Ala Tyr Tyr Ile Pro Ala Gly Ala Ser Asp His Pro Leu Gly Gly Leu
                165                 170                 175
Gly Phe Ala Arg Trp Ala Phe Glu Val Ala Met Gln Glu Arg Glu Met
            180                 185                 190
Gly Val Phe Phe Asp Val Val Val Val Cys Ala Val Thr Gly Ser Thr
        195                 200                 205
Phe Ala Gly Met Ile Ala Gly Phe Lys Leu Leu Glu Arg Val Gln Pro
    210                 215                 220
Gly Ser Arg Lys Arg Arg Val Ile Gly Ile Asp Ala Ser Ala Arg Pro
225                 230                 235                 240
Ala Glu Thr Arg Ala Gln Val Met Arg Ile Ala Arg Ser Thr Ala Ala
                245                 250                 255
Lys Ile Gly Leu Lys Asp Glu Asp Ile Ser Glu Glu Asp Val Val Leu
            260                 265                 270
Asn Glu Asn Tyr His Glu Gly Val Tyr Gly Val Pro Gly Glu Gly Thr
        275                 280                 285
Ile Lys Ala Met Glu Tyr Ala Ala Ser Lys Asp Ala Phe Ile Thr Asp
    290                 295                 300
Pro Val Tyr Glu Gly Lys Ser Phe Ala Gly Leu Ile Asp Leu Ala Lys
305                 310                 315                 320
Lys Gly Glu Phe Ala Gly Lys Thr Val Leu Tyr Ala His Leu Gly Gly
                325                 330                 335
Gln Pro Ala Leu Asn Ala Tyr Ser Glu Ile Gly Arg Ala Lys
            340                 345                 350
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<210> 64
<211> 1248
<212> DNA
<213> Strongylocentrotus purpuratus

<220>
<221> CDS
<222> (1)..(1248)

<400> 64

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atg gca aac gat ggt ctg ttt ctt tcc aat gaa aat gaa gtg gct cta       48
Met Ala Asn Asp Gly Leu Phe Leu Ser Asn Glu Asn Glu Val Ala Leu
1               5                   10                  15
aca atc caa gtc ttc aga aac cat gct att aca ttt ttg gct aac ctg       96
Thr Ile Gln Val Phe Arg Asn His Ala Ile Thr Phe Leu Ala Asn Leu
            20                  25                  30
aac acc cct atc cac aaa tgg cgt ctt cca cgg aca cct gat gac ttt      144
Asn Thr Pro Ile His Lys Trp Arg Leu Pro Arg Thr Pro Asp Asp Phe
        35                  40                  45
gag gtc ttt gtc aag agg gat gac atg aca gga agt gtt ctc tca ggc      192
Glu Val Phe Val Lys Arg Asp Asp Met Thr Gly Ser Val Leu Ser Gly
    50                  55                  60
```

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

```
gga gtg atg tca tcc gcc atc gat ggc aag agc tct gca gaa aac aag        1200
Gly Val Met Ser Ser Ala Ile Asp Gly Lys Ser Ser Ala Glu Asn Lys
385                 390                 395                 400
gtc tat gat tgg atg gaa atg act gac aaa ttg cca ttc aac caa            1245
Val Tyr Asp Trp Met Glu Met Thr Asp Lys Leu Pro Phe Asn Gln
                405                 410                 415
tag                                                                   1248
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<210> 65
<211> 415
<212> PRT
<213> Strongylocentrotus purpuratus

<400> 65

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

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

```
Tyr His Thr Met Lys Leu Met Arg Glu Asn Pro Asp Arg Phe Ile Gly
        355                 360                 365
Lys Lys Ile Leu Phe Ile His Thr Gly Gly Trp Phe Asp Leu Phe Ser
    370                 375                 380
Gly Val Met Ser Ser Ala Ile Asp Gly Lys Ser Ser Ala Glu Asn Lys
385                 390                 395                 400
Val Tyr Asp Trp Met Glu Met Thr Asp Lys Leu Pro Phe Asn Gln
                405                 410                 415
```

<210> 66
<211> 1137
<212> DNA
<213> Strongylocentrotus purpuratus

<220>
<221> CDS
<222> (1)..(1137)

<400> 66

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

145                 150                 155                 160
tat cta aga gat tct cta gga aag aaa gcc tac cca atc cca ata ggt      528
Tyr Leu Arg Asp Ser Leu Gly Lys Lys Ala Tyr Pro Ile Pro Ile Gly
                165                 170                 175
gga tct aac tca gta gga gtc ttt gga tac ctg gaa tgc ttc aga gaa      576
Gly Ser Asn Ser Val Gly Val Phe Gly Tyr Leu Glu Cys Phe Arg Glu
            180                 185                 190
ctc ctc cag cag aat gtt cag gag agg ttc agc gat att gtc ata aca      624
Leu Leu Gln Gln Asn Val Gln Glu Arg Phe Ser Asp Ile Val Ile Thr
        195                 200                 205
tca ggc agt agt gga tca cta gct ggt ctt gca att ggc aac tat ctg      672
Ser Gly Ser Ser Gly Ser Leu Ala Gly Leu Ala Ile Gly Asn Tyr Leu
```

```
    210                 215                 220
aca gga agc aaa ctc agg att cat gga atg gca ata tgt gat gac gca       720
Thr Gly Ser Lys Leu Arg Ile His Gly Met Ala Ile Cys Asp Asp Ala
225                 230                 235                 240
aaa tat ttt cat gga gaa atc aac aag gtt tta cgt gaa ctt ggc atg       768
Lys Tyr Phe His Gly Glu Ile Asn Lys Val Leu Arg Glu Leu Gly Met
                245                 250                 255
cag gaa ggt caa ggg tca tca ggg gtc agg tca gag gac att gta gat       816
Gln Glu Gly Gln Gly Ser Ser Gly Val Arg Ser Glu Asp Ile Val Asp
            260                 265                 270
gtc gtg gaa ggg gtc aga ggg ctc ggg tat ggt tta tct cag cct gaa       864
Val Val Glu Gly Val Arg Gly Leu Gly Tyr Gly Leu Ser Gln Pro Glu
        275                 280                 285
gaa ctt gaa tgc att aac caa gta gcc agg acc act ggt atc ttt gtt       912
Glu Leu Glu Cys Ile Asn Gln Val Ala Arg Thr Thr Gly Ile Phe Val
    290                 295                 300
gac cca gtc tat act ggt aag gca acc ttt cac ctc atg cgt ctg atg       960
Asp Pro Val Tyr Thr Gly Lys Ala Thr Phe His Leu Met Arg Leu Met
305                 310                 315                 320
aag gag gaa cca gac aga ttc caa gga tcc aag att ctc ttc att cat      1008
Lys Glu Glu Pro Asp Arg Phe Gln Gly Ser Lys Ile Leu Phe Ile His
                325                 330                 335
aca gga gga gtg ttt gat ctg ttc agt ggt gcc atg ggt tct atg gct      1056
Thr Gly Gly Val Phe Asp Leu Phe Ser Gly Ala Met Gly Ser Met Ala
            340                 345                 350
gat aaa agg act tca tca gag aag aag gtt tat gat tgg atg gaa atg      1104
Asp Lys Arg Thr Ser Ser Glu Lys Lys Val Tyr Asp Trp Met Glu Met
        355                 360                 365
act gaa aaa aca ccc ctc tgc caa tca gga tga                         1137
Thr Glu Lys Thr Pro Leu Cys Gln Ser Gly
    370                 375
```

<210> 67
<211> 378
<212> PRT
<213> Strongylocentrotus purpuratus

<400> 67

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

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

<210> 68
<211> 1155
<212> DNA
<213> Strongylocentrotus purpuratus

<220>
<221> CDS
<222> (1)..(1155)

<400> 68
atg ggt cac gtg ttg gag cca aat aac gat tac ccc ctc ttg cca tac      48
Met Gly His Val Leu Glu Pro Asn Asn Asp Tyr Pro Leu Leu Pro Tyr
1               5                   10                  15
gat gct ccc gag tgg aca tcc cga ctc gcc gtc atc ccc aag tat cga      96
Asp Ala Pro Glu Trp Thr Ser Arg Leu Ala Val Ile Pro Lys Tyr Arg
            20                  25                  30
gtt cag ttg ggg tct cta ggc acc cct atc cag cgc tgg cgt ctc cca     144
Val Gln Leu Gly Ser Leu Gly Thr Pro Ile Gln Arg Trp Arg Leu Pro
        35                  40                  45
ggc atg cct gag gac ttc caa gtc cac atc aaa cga gac gat atg aca     192
Gly Met Pro Glu Asp Phe Gln Val His Ile Lys Arg Asp Asp Met Thr
    50                  55                  60
ggc agc gta ctc tct gga aac aag gtg agg aag cta gag ttt ttg atg     240
Gly Ser Val Leu Ser Gly Asn Lys Val Arg Lys Leu Glu Phe Leu Met
65                  70                  75                  80
gct gac tgc ttg gat cag ggt tgt gaa tcc atc ata acc tgt ggt ggt     288
Ala Asp Cys Leu Asp Gln Gly Cys Glu Ser Ile Ile Thr Cys Gly Gly
                85                  90                  95
gtg ttc tca aac tcc tgc cgg gcc gga gcc att gct gcc cgc caa atg     336
Val Phe Ser Asn Ser Cys Arg Ala Gly Ala Ile Ala Ala Arg Gln Met
            100                 105                 110
gga ctg gac agc cat ctc ttc ctc tgg tca gaa tcc acg gat ctg ccg     384
Gly Leu Asp Ser His Leu Phe Leu Trp Ser Glu Ser Thr Asp Leu Pro
        115                 120                 125
ttc acg ggg aat gct ttg ctg gac cgc ctg gtg ggc tgt aac ttc tac     432
```

```
Phe Thr Gly Asn Ala Leu Leu Asp Arg Leu Val Gly Cys Asn Phe Tyr
    130                 135                 140
ctc atg ccg tta gac tgc cct ctg gag acg caa gta tac cct cgc atg      480
Leu Met Pro Leu Asp Cys Pro Leu Glu Thr Gln Val Tyr Pro Arg Met
145                 150                 155                 160
aag cta ctt caa gac cac atc cag aaa acg acc aat aag aag gct tac      528
Lys Leu Leu Gln Asp His Ile Gln Lys Thr Thr Asn Lys Lys Ala Tyr
                165                 170                 175

aga ctg cct ttt gga gga tcc aat gag gtt gga gta tgg ggc tac atc      576
Arg Leu Pro Phe Gly Gly Ser Asn Glu Val Gly Val Trp Gly Tyr Ile
            180                 185                 190
gag tgc ttc cgt gaa cta atg ggc cag gga ctc ctg gac aga ttc acc      624
Glu Cys Phe Arg Glu Leu Met Gly Gln Gly Leu Leu Asp Arg Phe Thr
        195                 200                 205
gac att gta atc gca gcc ggt agc agc ggg tct gtg acc ggc ctt gcc      672
Asp Ile Val Ile Ala Ala Gly Ser Ser Gly Ser Val Thr Gly Leu Ala
    210                 215                 220
att gca aac tac ctc acc ggt agc aaa cta aag ata cac ggc ttt gca      720
Ile Ala Asn Tyr Leu Thr Gly Ser Lys Leu Lys Ile His Gly Phe Ala
225                 230                 235                 240
gca tgc aag gac caa atg ttt ttc tac gac ctc ggc gac aag aca ctc      768
Ala Cys Lys Asp Gln Met Phe Phe Tyr Asp Leu Gly Asp Lys Thr Leu
                245                 250                 255
caa tcc ctc ggg cta cag gac gct gat ggc gca ggg gtc aaa gcg gtc      816
Gln Ser Leu Gly Leu Gln Asp Ala Asp Gly Ala Gly Val Lys Ala Val
            260                 265                 270
gac atc atg cac att cgt gac gaa gtg gtt ggc atc ggg tat gcc gtc      864
Asp Ile Met His Ile Arg Asp Glu Val Val Gly Ile Gly Tyr Ala Val
        275                 280                 285
aac act tca gaa gaa tta gaa tgc atc gag cag gtg gcg atg aac acc      912
Asn Thr Ser Glu Glu Leu Glu Cys Ile Glu Gln Val Ala Met Asn Thr
    290                 295                 300
ggg att ctt gtg gac cct gtc tac tcc ggc aag gcc acc tat cat cta      960
Gly Ile Leu Val Asp Pro Val Tyr Ser Gly Lys Ala Thr Tyr His Leu
305                 310                 315                 320
ctc aaa ctc atg aac gag aaa cca gga acg ttc aag gga aag cag atc     1008
Leu Lys Leu Met Asn Glu Lys Pro Gly Thr Phe Lys Gly Lys Gln Ile
                325                 330                 335
ctc ttc ata cat aca ggt ggt gtc ttt gac ctg ttc agc ggt gcc gtt     1056
Leu Phe Ile His Thr Gly Gly Val Phe Asp Leu Phe Ser Gly Ala Val
            340                 345                 350
ggt tct cgg ctc aca aag aaa ggc cat aaa gaa aac aaa gtc tac gac     1104
Gly Ser Arg Leu Thr Lys Lys Gly His Lys Glu Asn Lys Val Tyr Asp
        355                 360                 365
tgg atg gac ctc tcc gac aaa gtc cca gac aag gtc tca gct gca tcc     1152
Trp Met Asp Leu Ser Asp Lys Val Pro Asp Lys Val Ser Ala Ala Ser
    370                 375                 380
tag                                                                1155
```

<210> 69
<211> 384
<212> PRT
<213> Strongylocentrotus purpuratus

<400> 69

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Met Gly His Val Leu Glu Pro Asn Asn Asp Tyr Pro Leu Leu Pro Tyr
1               5                   10                  15
Asp Ala Pro Glu Trp Thr Ser Arg Leu Ala Val Ile Pro Lys Tyr Arg
```

```
            20                  25                  30
Val Gln Leu Gly Ser Leu Gly Thr Pro Ile Gln Arg Trp Arg Leu Pro
        35                  40                  45
Gly Met Pro Glu Asp Phe Gln Val His Ile Lys Arg Asp Asp Met Thr
    50                  55                  60
Gly Ser Val Leu Ser Gly Asn Lys Val Arg Lys Leu Glu Phe Leu Met
65                  70                  75                  80
Ala Asp Cys Leu Asp Gln Gly Cys Glu Ser Ile Ile Thr Cys Gly Gly
                85                  90                  95
Val Phe Ser Asn Ser Cys Arg Ala Gly Ala Ile Ala Ala Arg Gln Met
            100                 105                 110
Gly Leu Asp Ser His Leu Phe Leu Trp Ser Glu Ser Thr Asp Leu Pro
        115                 120                 125
Phe Thr Gly Asn Ala Leu Leu Asp Arg Leu Val Gly Cys Asn Phe Tyr
    130                 135                 140
Leu Met Pro Leu Asp Cys Pro Leu Glu Thr Gln Val Tyr Pro Arg Met
145                 150                 155                 160
Lys Leu Leu Gln Asp His Ile Gln Lys Thr Thr Asn Lys Lys Ala Tyr
                165                 170                 175
Arg Leu Pro Phe Gly Gly Ser Asn Glu Val Gly Val Trp Gly Tyr Ile
            180                 185                 190
Glu Cys Phe Arg Glu Leu Met Gly Gln Gly Leu Leu Asp Arg Phe Thr
        195                 200                 205
Asp Ile Val Ile Ala Ala Gly Ser Ser Gly Ser Val Thr Gly Leu Ala
    210                 215                 220
Ile Ala Asn Tyr Leu Thr Gly Ser Lys Leu Lys Ile His Gly Phe Ala
225                 230                 235                 240
Ala Cys Lys Asp Gln Met Phe Phe Tyr Asp Leu Gly Asp Lys Thr Leu
                245                 250                 255
Gln Ser Leu Gly Leu Gln Asp Ala Asp Gly Ala Gly Val Lys Ala Val
            260                 265                 270
Asp Ile Met His Ile Arg Asp Glu Val Val Gly Ile Gly Tyr Ala Val
        275                 280                 285
Asn Thr Ser Glu Glu Leu Glu Cys Ile Glu Gln Val Ala Met Asn Thr
    290                 295                 300
Gly Ile Leu Val Asp Pro Val Tyr Ser Gly Lys Ala Thr Tyr His Leu
305                 310                 315                 320
Leu Lys Leu Met Asn Glu Lys Pro Gly Thr Phe Lys Gly Lys Gln Ile
                325                 330                 335
Leu Phe Ile His Thr Gly Gly Val Phe Asp Leu Phe Ser Gly Ala Val
            340                 345                 350
Gly Ser Arg Leu Thr Lys Lys Gly His Lys Glu Asn Lys Val Tyr Asp
        355                 360                 365
Trp Met Asp Leu Ser Asp Lys Val Pro Asp Lys Val Ser Ala Ala Ser
    370                 375                 380
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<210> 70
<211> 1155
<212> DNA
<213> Strongylocentrotus purpuratus

<220>
<221> CDS
<222> (1)..(1155)

<400> 70

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atg ggt cac gtg ttg gag cca aat aac gat tac ccc ctc ttg cca tac      48
Met Gly His Val Leu Glu Pro Asn Asn Asp Tyr Pro Leu Leu Pro Tyr
1               5                   10                  15
gat gct ccc gag tgg aca tcc cga ctc gct gtc atc ccc aag tat cga      96
Asp Ala Pro Glu Trp Thr Ser Arg Leu Ala Val Ile Pro Lys Tyr Arg
```

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

```
ggt tct cgg ctc aca aag aaa ggc cat aaa gaa aac aaa gtc tac gac      1104
Gly Ser Arg Leu Thr Lys Lys Gly His Lys Glu Asn Lys Val Tyr Asp
        355                 360                 365
tgg atg gac ctc tcc gac aaa gtc cca gac aag gtc tca gct gca tcc      1152
Trp Met Asp Leu Ser Asp Lys Val Pro Asp Lys Val Ser Ala Ala Ser
    370                 375                 380
tag                                                                 1155
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<210> 71
<211> 384
<212> PRT
<213> Strongylocentrotus purpuratus

<400> 71

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

```
Gly Ser Arg Leu Thr Lys Lys Gly His Lys Glu Asn Lys Val Tyr Asp
        355                 360                 365
Trp Met Asp Leu Ser Asp Lys Val Pro Asp Lys Val Ser Ala Ala Ser
    370                 375                 380

<210> 72
<211> 1017
<212> DNA
<213> Neurospora crassa N150

<220>
<221> CDS
<222> (1)..(1017)

<400> 72
atg gcc gac tta cta ctc ccc gaa ccg ttc gcc agc atc cct cgg gag      48
Met Ala Asp Leu Leu Leu Pro Glu Pro Phe Ala Ser Ile Pro Arg Glu
1               5                   10                  15
ccg cta acc ttt gga cct tct ccg atc cag cct ctc ccc cgc atc tcc      96
Pro Leu Thr Phe Gly Pro Ser Pro Ile Gln Pro Leu Pro Arg Ile Ser
            20                  25                  30
caa gcc ctc ggt gga aag gtc aac gtc ttt gct aaa cgc gag gac ctc     144
Gln Ala Leu Gly Gly Lys Val Asn Val Phe Ala Lys Arg Glu Asp Leu
        35                  40                  45
aac tcc ggt ctt gcc ttt gga ggc aac aag acc aga aag cta gag tat     192
Asn Ser Gly Leu Ala Phe Gly Gly Asn Lys Thr Arg Lys Leu Glu Tyr
    50                  55                  60
atc cca cca ccc gcc ctc gcc gcc gcc gcc tcc aag ctc ggc ctg cac     240
Ile Pro Pro Pro Ala Leu Ala Ala Ala Ala Ser Lys Leu Gly Leu His
65                  70                  75                  80
gcc gct ctc gtc caa gaa cac tgg gtc ccc gac tgg acc gat ccc ggc     288
Ala Ala Leu Val Gln Glu His Trp Val Pro Asp Trp Thr Asp Pro Gly
                85                  90                  95
tac gac aaa gtc ggc aac atc cag ctc tcc cgg ctg atg ggg gcc gac     336
Tyr Asp Lys Val Gly Asn Ile Gln Leu Ser Arg Leu Met Gly Ala Asp
            100                 105                 110
gtc cgt ctt gaa ccg cta gcc ggg ttc ggg atc gag cac aag cag acg     384
Val Arg Leu Glu Pro Leu Ala Gly Phe Gly Ile Glu His Lys Gln Thr
        115                 120                 125
ctg gcg aaa ctc aaa gat gat ctg gag aag gag ggg aga aag ccg tat     432
Leu Ala Lys Leu Lys Asp Asp Leu Glu Lys Glu Gly Arg Lys Pro Tyr
    130                 135                 140
tat atc ccg gct ggg gcg tcg gat cac cct ctt gga ggg ctg ggg ttc     480
Tyr Ile Pro Ala Gly Ala Ser Asp His Pro Leu Gly Gly Leu Gly Phe
145                 150                 155                 160
gcg agg tgg gcg ttt gag gtg gtg gcg cag gag gag gag ttg ggg att     528
Ala Arg Trp Ala Phe Glu Val Val Ala Gln Glu Glu Glu Leu Gly Ile
                165                 170                 175
cat ttc gac acg gtg gtg gtc tgt gcg gtg aca ggg tcg acg atg gcg     576
His Phe Asp Thr Val Val Val Cys Ala Val Thr Gly Ser Thr Met Ala
            180                 185                 190
ggc atg gtg gcc ggg ttt aag ttg gtt gag atg ttg gaa cgc cac tcg     624
Gly Met Val Ala Gly Phe Lys Leu Val Glu Met Leu Glu Arg His Ser
        195                 200                 205
gaa agg ctg ggc aag gtg aat aag agg agg gtg att ggg att gat gcg     672
Glu Arg Leu Gly Lys Val Asn Lys Arg Arg Val Ile Gly Ile Asp Ala
    210                 215                 220
tcc gcc aag gtt gag cag acg aga gcg cag gtg ctg agg att gcg aaa     720
Ser Ala Lys Val Glu Gln Thr Arg Ala Gln Val Leu Arg Ile Ala Lys
225                 230                 235                 240
cag aca gcg gcc aag att ggg ttg aag gag gag gat atc acg gag tcg     768
```

```
Gln Thr Ala Ala Lys Ile Gly Leu Lys Glu Glu Asp Ile Thr Glu Ser
                245                 250                 255
gat atc gtg ctg gat gat cgg tac cat gcg ggg gtt tat ggc gtg ccg        816
Asp Ile Val Leu Asp Asp Arg Tyr His Ala Gly Val Tyr Gly Val Pro
            260                 265                 270
gac gag aaa acg att gag gct atc aag ttt ggg gcg cgg acg gag gcg        864
Asp Glu Lys Thr Ile Glu Ala Ile Lys Phe Gly Ala Arg Thr Glu Ala
        275                 280                 285
ttc att acc gat ccc gtg tat gag ggc aaa agt ctg gcg ggc atg atg        912
Phe Ile Thr Asp Pro Val Tyr Glu Gly Lys Ser Leu Ala Gly Met Met
    290                 295                 300
gac atg att aag aat ggg gag att gag gcg gga agc aat gtg ctg tat        960
Asp Met Ile Lys Asn Gly Glu Ile Glu Ala Gly Ser Asn Val Leu Tyr
305                 310                 315                 320
gcg cac ctt gga ggg caa ttg gca ctg aat gcg tac tcc gct ttg ggg       1008
Ala His Leu Gly Gly Gln Leu Ala Leu Asn Ala Tyr Ser Ala Leu Gly
                325                 330                 335
ttg gaa taa                                                          1017
Leu Glu
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<210> 73
<211> 338
<212> PRT
<213> Neurospora crassa N150

<400> 73

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

```
Asp Glu Lys Thr Ile Glu Ala Ile Lys Phe Gly Ala Arg Thr Glu Ala
        275                 280                 285
Phe Ile Thr Asp Pro Val Tyr Glu Gly Lys Ser Leu Ala Gly Met Met
    290                 295                 300
Asp Met Ile Lys Asn Gly Glu Ile Glu Ala Gly Ser Asn Val Leu Tyr
305                 310                 315                 320
Ala His Leu Gly Gly Gln Leu Ala Leu Asn Ala Tyr Ser Ala Leu Gly
                325                 330                 335
Leu Glu
```

<210> 74
<211> 999
<212> DNA
<213> Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough

<220>
<221> CDS
<222> (1)..(999)
<223> transl_table=11

<400> 74

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

```
aac aac gcc aac atc cct gtc tcc ggc atc aac gtg agc cgc acc aag       672
Asn Asn Ala Asn Ile Pro Val Ser Gly Ile Asn Val Ser Arg Thr Lys
    210                 215                 220
gcc gac cag gag gca ctg gtg cgc aag ctg gcc cgc gag acg gcg cag       720
Ala Asp Gln Glu Ala Leu Val Arg Lys Leu Ala Arg Glu Thr Ala Gln
225                 230                 235                 240
cgc gtg ggc atg agt ggc gag ttc ccc gat gaa gcg gtg acc tgc ttt       768
Arg Val Gly Met Ser Gly Glu Phe Pro Asp Glu Ala Val Thr Cys Phe
                245                 250                 255
gac ggt tat gtg ggc ccc ggc tat tcg ctg ccc acc gag agc atg gtc       816
Asp Gly Tyr Val Gly Pro Gly Tyr Ser Leu Pro Thr Glu Ser Met Val
            260                 265                 270
gaa gcc gtg cgt ctt ctg gcc cag acc gaa ggc ata ctg ctc gac ccg       864
Glu Ala Val Arg Leu Leu Ala Gln Thr Glu Gly Ile Leu Leu Asp Pro
        275                 280                 285
gtg tac tcg ggc aag gcc atg gcc ggt ctt gtg gac ctc gtg cgt agc       912
Val Tyr Ser Gly Lys Ala Met Ala Gly Leu Val Asp Leu Val Arg Ser
    290                 295                 300
ggc tac ttt gcc gaa ggt tcg aat gtg ctt ttc ctg cac acc ggt gga       960
Gly Tyr Phe Ala Glu Gly Ser Asn Val Leu Phe Leu His Thr Gly Gly
305                 310                 315                 320
tcg cca gcg ctt tac gcc tac ctc gat acg ttc aag taa                   999
Ser Pro Ala Leu Tyr Ala Tyr Leu Asp Thr Phe Lys
                325                 330
```

<210> 75
<211> 332
<212> PRT
<213> Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough

<400> 75

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

```
Arg Val Gly Met Ser Gly Glu Phe Pro Asp Glu Ala Val Thr Cys Phe
                245                 250                 255
Asp Gly Tyr Val Gly Pro Gly Tyr Ser Leu Pro Thr Glu Ser Met Val
            260                 265                 270
Glu Ala Val Arg Leu Leu Ala Gln Thr Glu Gly Ile Leu Leu Asp Pro
        275                 280                 285
Val Tyr Ser Gly Lys Ala Met Ala Gly Leu Val Asp Leu Val Arg Ser
    290                 295                 300
Gly Tyr Phe Ala Glu Gly Ser Asn Val Leu Phe Leu His Thr Gly Gly
305                 310                 315                 320
Ser Pro Ala Leu Tyr Ala Tyr Leu Asp Thr Phe Lys
                325                 330

<210> 76
<211> 996
<212> DNA
<213> Bacillus thuringiensis serovar konkukian str. 97-27

<220>
<221> CDS
<222> (1)..(996)
<223> transl_table=11

<400> 76
atg aat tta gct aaa ttc ccg aga aaa aaa tat aca gag tca tat aca       48
Met Asn Leu Ala Lys Phe Pro Arg Lys Lys Tyr Thr Glu Ser Tyr Thr
1               5                   10                  15
cca att gaa aaa tta aac aat ttt tct gag gca ctt ggt ggg ccg act       96
Pro Ile Glu Lys Leu Asn Asn Phe Ser Glu Ala Leu Gly Gly Pro Thr
            20                  25                  30
att tat ttt aaa cga gat gat tta ctt ggt tta aca gca ggc ggt aat      144
Ile Tyr Phe Lys Arg Asp Asp Leu Leu Gly Leu Thr Ala Gly Gly Asn
        35                  40                  45
aag acg aga aag tta gag ttt cta gtt gcg gat gca cag gca aaa ggt      192
Lys Thr Arg Lys Leu Glu Phe Leu Val Ala Asp Ala Gln Ala Lys Gly
    50                  55                  60
gcg gat acg tta att aca gct ggt ggc att cag tcc aat cat tgc cgt      240
Ala Asp Thr Leu Ile Thr Ala Gly Gly Ile Gln Ser Asn His Cys Arg
65                  70                  75                  80
cta aca ctg gca gcg gcg gta aaa gaa aaa atg aaa tgt att ctt gta      288
Leu Thr Leu Ala Ala Ala Val Lys Glu Lys Met Lys Cys Ile Leu Val
                85                  90                  95
tta gaa gaa ggg ctt gag cca gaa gag aag cga gac ttt aac gga aac      336
Leu Glu Glu Gly Leu Glu Pro Glu Glu Lys Arg Asp Phe Asn Gly Asn
            100                 105                 110
tat ttc tta tat cat tta cta ggt gct gaa aat gta att gtt gta cca      384
Tyr Phe Leu Tyr His Leu Leu Gly Ala Glu Asn Val Ile Val Val Pro
        115                 120                 125
aac gga gca gat ctt atg gaa gag atg cat aaa gta gca aaa gaa gtt      432
Asn Gly Ala Asp Leu Met Glu Glu Met His Lys Val Ala Lys Glu Val
    130                 135                 140
agt gaa aaa ggg aat aca cca tat gta ata cca gtt ggt gga tcg aat      480
Ser Glu Lys Gly Asn Thr Pro Tyr Val Ile Pro Val Gly Gly Ser Asn
145                 150                 155                 160
cct act ggt gca atg gga tac gtt gct tgt gcg caa gaa att atg gcg      528
Pro Thr Gly Ala Met Gly Tyr Val Ala Cys Ala Gln Glu Ile Met Ala
                165                 170                 175
caa tca ttt gac caa gga att gat ttc agt tca gtc gtt tgc gta agt      576
Gln Ser Phe Asp Gln Gly Ile Asp Phe Ser Ser Val Val Cys Val Ser
            180                 185                 190
ggt agc ggc ggt atg cac gct ggt tta att aca ggt ttt gct gga aca      624
```

```
Gly Ser Gly Gly Met His Ala Gly Leu Ile Thr Gly Phe Ala Gly Thr
        195                 200                 205
caa agt aac atc ccc gta atc gga att aac gta agt aga gga aaa gca       672
Gln Ser Asn Ile Pro Val Ile Gly Ile Asn Val Ser Arg Gly Lys Ala
    210                 215                 220
gag caa gaa gag aaa gta gca aaa ctt gta gat gaa acg tca gct cat       720
Glu Gln Glu Glu Lys Val Ala Lys Leu Val Asp Glu Thr Ser Ala His
225                 230                 235                 240
gtt ggt att cca aac ttt atc ccg cgc gaa gcg gtt aca tgc ttt gat       768
Val Gly Ile Pro Asn Phe Ile Pro Arg Glu Ala Val Thr Cys Phe Asp
                245                 250                 255
gaa tat gta gga cca ggt tac gcg tta cca acg cca gaa atg gtg gaa       816
Glu Tyr Val Gly Pro Gly Tyr Ala Leu Pro Thr Pro Glu Met Val Glu

            260                 265                 270
gca gtg cag ctg tta gcg aaa aca gaa ggt att tta ctt gat cca gta       864
Ala Val Gln Leu Leu Ala Lys Thr Glu Gly Ile Leu Leu Asp Pro Val
        275                 280                 285
tat aca ggt aaa gca gta gcg gga tta atc gac tta att aga aaa ggt       912
Tyr Thr Gly Lys Ala Val Ala Gly Leu Ile Asp Leu Ile Arg Lys Gly
    290                 295                 300
aca ttt aat aaa gag gac aac att tta ttc gta cat tca ggt ggt tca       960
Thr Phe Asn Lys Glu Asp Asn Ile Leu Phe Val His Ser Gly Gly Ser
305                 310                 315                 320
cca gct tta tat gcg aat aca tct tta ttt gcg taa                       996
Pro Ala Leu Tyr Ala Asn Thr Ser Leu Phe Ala
                325                 330
```

<210> 77
<211> 331
<212> PRT
<213> Bacillus thuringiensis serovar konkukian str. 97-27

<400> 77

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

```
    210                 215                 220
Glu Gln Glu Glu Lys Val Ala Lys Leu Val Asp Glu Thr Ser Ala His
225                 230                 235                 240
Val Gly Ile Pro Asn Phe Ile Pro Arg Glu Ala Val Thr Cys Phe Asp
                245                 250                 255
Glu Tyr Val Gly Pro Gly Tyr Ala Leu Pro Thr Pro Glu Met Val Glu
            260                 265                 270
Ala Val Gln Leu Leu Ala Lys Thr Glu Gly Ile Leu Leu Asp Pro Val
        275                 280                 285
Tyr Thr Gly Lys Ala Val Ala Gly Leu Ile Asp Leu Ile Arg Lys Gly
    290                 295                 300
Thr Phe Asn Lys Glu Asp Asn Ile Leu Phe Val His Ser Gly Gly Ser
305                 310                 315                 320
Pro Ala Leu Tyr Ala Asn Thr Ser Leu Phe Ala
                325                 330
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<210> 78
<211> 885
<212> DNA
<213> Acinetobacter sp. ADP1

<220>
<221> CDS
<222> (1)..(885)
<223> transl_table=11

<400> 78

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

```
Thr Leu Ala Gly Leu Ile Glu Ala Ser His His Gly Gln Tyr Val Ile
            180                 185                 190
ggt ttc tcc gca ctc aaa gga gac ttt ctt cac aat gat gtc cag cgc       624
Gly Phe Ser Ala Leu Lys Gly Asp Phe Leu His Asn Asp Val Gln Arg
        195                 200                 205
cat acc aat aaa acc aac tgg cat att ctg gat gat tat tgc ttt ggg       672
His Thr Asn Lys Thr Asn Trp His Ile Leu Asp Asp Tyr Cys Phe Gly
    210                 215                 220
gga tac gca aaa aca tct tct gaa ctg ttc gac ttt ata gct ggg ttt       720
Gly Tyr Ala Lys Thr Ser Ser Glu Leu Phe Asp Phe Ile Ala Gly Phe
225                 230                 235                 240
gaa caa aaa tat cag att cca ctc gaa cag gta tat acc gcc aaa atg       768
Glu Gln Lys Tyr Gln Ile Pro Leu Glu Gln Val Tyr Thr Ala Lys Met
                245                 250                 255
cta tat gga ctg ctc gac ctg att cag aaa aat gat ttt gat caa ggt       816
Leu Tyr Gly Leu Leu Asp Leu Ile Gln Lys Asn Asp Phe Asp Gln Gly
            260                 265                 270
aca cgc atc ctt gct ctg cat aca ggc ggt tta caa gga cgt cgc cat       864
Thr Arg Ile Leu Ala Leu His Thr Gly Gly Leu Gln Gly Arg Arg His
        275                 280                 285
gac att ggc gtt aca gaa taa                                          885
Asp Ile Gly Val Thr Glu
    290
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<210> 79
<211> 294
<212> PRT
<213> Acinetobacter sp. ADP1

<400> 79

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

```
                245                 250                 255
Leu Tyr Gly Leu Leu Asp Leu Ile Gln Lys Asn Asp Phe Asp Gln Gly
            260                 265                 270
Thr Arg Ile Leu Ala Leu His Thr Gly Gly Leu Gln Gly Arg Arg His
        275                 280                 285
Asp Ile Gly Val Thr Glu
    290

<210> 80
<211> 1014
<212> DNA
<213> Erwinia carotovora subsp. atroseptica SCRI1043

<220>
<221> CDS
<222> (1)..(1014)
<223> transl_table=11

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

```
gca aag cag gag gag aat gtt tac gcg tta gcg cag cgc acc tgg caa       720
Ala Lys Gln Glu Glu Asn Val Tyr Ala Leu Ala Gln Arg Thr Trp Gln
225                 230                 235                 240
ctg ctg ggc att ccg ggc gaa ctg ccg cgc agc gcc gta cgg gtg aac       768
Leu Leu Gly Ile Pro Gly Glu Leu Pro Arg Ser Ala Val Arg Val Asn
                245                 250                 255
agc gac tac gtt ggc aaa ggc tat ggc att ccc act gaa gga acg tta       816
Ser Asp Tyr Val Gly Lys Gly Tyr Gly Ile Pro Thr Glu Gly Thr Leu
            260                 265                 270
gaa gcg ctc agg ctg ttg gcg cag ttg gaa ggg att ttg ctc gat ccg       864
Glu Ala Leu Arg Leu Leu Ala Gln Leu Glu Gly Ile Leu Leu Asp Pro
        275                 280                 285
gtc tat tca gga aaa ggg atg gcg gga ctg atc gat tta atc cgt cag       912
Val Tyr Ser Gly Lys Gly Met Ala Gly Leu Ile Asp Leu Ile Arg Gln
    290                 295                 300
ggg cat ttt cgc gcc gat gaa aac atc gtc ttt att cat acc ggt ggc       960
Gly His Phe Arg Ala Asp Glu Asn Ile Val Phe Ile His Thr Gly Gly
305                 310                 315                 320
tca gcg ggg ctg ttt ggc tac cgc caa ctg ttc gaa caa acg gca gca      1008
Ser Ala Gly Leu Phe Gly Tyr Arg Gln Leu Phe Glu Gln Thr Ala Ala
                325                 330                 335
caa tga                                                             1014
Gln
```

<210> 81
<211> 337
<212> PRT
<213> Erwinia carotovora subsp. atroseptica SCRI1043

<400> 81

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

```
225                 230                 235                 240
Leu Leu Gly Ile Pro Gly Glu Leu Pro Arg Ser Ala Val Arg Val Asn
                245                 250                 255
Ser Asp Tyr Val Gly Lys Gly Tyr Gly Ile Pro Thr Glu Gly Thr Leu
            260                 265                 270
Glu Ala Leu Arg Leu Leu Ala Gln Leu Glu Gly Ile Leu Leu Asp Pro
        275                 280                 285
Val Tyr Ser Gly Lys Gly Met Ala Gly Leu Ile Asp Leu Ile Arg Gln
    290                 295                 300
Gly His Phe Arg Ala Asp Glu Asn Ile Val Phe Ile His Thr Gly Gly
305                 310                 315                 320
Ser Ala Gly Leu Phe Gly Tyr Arg Gln Leu Phe Glu Gln Thr Ala Ala
                325                 330                 335
Gln
```

<210> 82
<211> 999
<212> DNA
<213> Desulfotalea psychrophila LSv54

<220>
<221> CDS
<222> (1)..(999)
<223> transl_table=11

<400> 82

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

```
Gln Gln Leu Phe Gln Gln Asn Ile Asn Ile Thr Asp Ile Val Val Pro
            180                 185                 190
agt ggt agc gcc ggt acc cat gca ggt gtc gcc gtc ggt atg tac gga       624
Ser Gly Ser Ala Gly Thr His Ala Gly Val Ala Val Gly Met Tyr Gly
        195                 200                 205
att aat tcc ggt att agg gta agc ggt atc aat gta agt aag cct aag       672
Ile Asn Ser Gly Ile Arg Val Ser Gly Ile Asn Val Ser Lys Pro Lys
    210                 215                 220
gat gtc cag gaa gag aat gtt tat aag ttg gca tac gaa act gca aaa       720
Asp Val Gln Glu Glu Asn Val Tyr Lys Leu Ala Tyr Glu Thr Ala Lys
225                 230                 235                 240
gca gta ggt gtg tgc gga gag ctt cca cgc ggt gag ata acc tgt ttt       768
Ala Val Gly Val Cys Gly Glu Leu Pro Arg Gly Glu Ile Thr Cys Phe
                245                 250                 255
gat ggc tat gta ggt gca ggt tat tct ctg ccc acc gat tca atg gtt       816
Asp Gly Tyr Val Gly Ala Gly Tyr Ser Leu Pro Thr Asp Ser Met Val
            260                 265                 270
gag gca gta aag ctt ctt gct cga act gag gca atc ctg ctt gat cct       864
Glu Ala Val Lys Leu Leu Ala Arg Thr Glu Ala Ile Leu Leu Asp Pro
        275                 280                 285
gtt tat tcc ggc aag gtt atg gct ggt atg atc gac ctt att cga aac       912
Val Tyr Ser Gly Lys Val Met Ala Gly Met Ile Asp Leu Ile Arg Asn
    290                 295                 300
gat tat ttc gct cca gga aca aat gtt tta ttt ctg cat acc ggt gga       960
Asp Tyr Phe Ala Pro Gly Thr Asn Val Leu Phe Leu His Thr Gly Gly
305                 310                 315                 320
tct ccc gcc ctc tat gca tat acc gat acg ttt aaa tag                   999
Ser Pro Ala Leu Tyr Ala Tyr Thr Asp Thr Phe Lys
                325                 330
```

<210> 83
<211> 332
<212> PRT
<213> Desulfotalea psychrophila LSv54

<400> 83

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

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

<210> 84
<211> 1035
<212> DNA
<213> Desulfotalea psychrophila LSv54

<220>
<221> CDS
<222> (1)..(1035)
<223> transl_table=11

<400> 84

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

```
                165                 170                 175
gca acc ggt tat gtt gcc tgt gcc cag gaa att cag caa cag ctt ttt       576
Ala Thr Gly Tyr Val Ala Cys Ala Gln Glu Ile Gln Gln Gln Leu Phe
            180                 185                 190
gag caa aac att aat ata act gat ata gtt gtc ccg agt ggt agt gcc       624
Glu Gln Asn Ile Asn Ile Thr Asp Ile Val Val Pro Ser Gly Ser Ala
        195                 200                 205
ggt acc cat gct ggt gtt gcc gtt ggt atg tac gga att aat tcg ggt       672
Gly Thr His Ala Gly Val Ala Val Gly Met Tyr Gly Ile Asn Ser Gly
    210                 215                 220
att aca gta agt ggt atc aat gta agt aag cct aag gct gtc cag gaa       720
Ile Thr Val Ser Gly Ile Asn Val Ser Lys Pro Lys Ala Val Gln Glu
225                 230                 235                 240
gag aat gtt tat aaa ttg gcc aag gaa act gca aaa aga gta ggt gtc       768
Glu Asn Val Tyr Lys Leu Ala Lys Glu Thr Ala Lys Arg Val Gly Val
                245                 250                 255
cgc gga gag ttt cca cgc gat gag ata acc tgt ttt gat ggc tat gtc       816
Arg Gly Glu Phe Pro Arg Asp Glu Ile Thr Cys Phe Asp Gly Tyr Val
            260                 265                 270
ggt gca ggg tat tcg ttg ccc acc gat tca atg gtt gag gct gta aag       864
Gly Ala Gly Tyr Ser Leu Pro Thr Asp Ser Met Val Glu Ala Val Lys
        275                 280                 285
ctt ctt gct cga act gag gca atc ctg ctt gat cct gtt tat tcc ggc       912
Leu Leu Ala Arg Thr Glu Ala Ile Leu Leu Asp Pro Val Tyr Ser Gly
    290                 295                 300
aag gtt atg gct ggt atg atc gac ctt att cga aac gat tat ttt gcc       960
Lys Val Met Ala Gly Met Ile Asp Leu Ile Arg Asn Asp Tyr Phe Ala
305                 310                 315                 320
ccg ggg gca aat gtt tta ttt ctg cat acc ggt gga tct ccc gcc ctc      1008
Pro Gly Ala Asn Val Leu Phe Leu His Thr Gly Gly Ser Pro Ala Leu
                325                 330                 335
tat gca tat acc gac acg ttt aag taa                                 1035
Tyr Ala Tyr Thr Asp Thr Phe Lys
            340
```

<210> 85
<211> 344
<212> PRT
<213> Desulfotalea psychrophila LSv54

<400> 85

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

```
Gly Lys Lys Pro Tyr Ile Ile Pro Gly Gly Ala Ser Asn Ala Ile Gly
                165                 170                 175
Ala Thr Gly Tyr Val Ala Cys Ala Gln Glu Ile Gln Gln Leu Phe
            180                 185                 190
Glu Gln Asn Ile Asn Ile Thr Asp Ile Val Val Pro Ser Gly Ser Ala
        195                 200                 205
Gly Thr His Ala Gly Val Ala Val Gly Met Tyr Gly Ile Asn Ser Gly
    210                 215                 220
Ile Thr Val Ser Gly Ile Asn Val Ser Lys Pro Lys Ala Val Gln Glu
225                 230                 235                 240
Glu Asn Val Tyr Lys Leu Ala Lys Glu Thr Ala Lys Arg Val Gly Val
                245                 250                 255
Arg Gly Glu Phe Pro Arg Asp Glu Ile Thr Cys Phe Asp Gly Tyr Val
            260                 265                 270
Gly Ala Gly Tyr Ser Leu Pro Thr Asp Ser Met Val Glu Ala Val Lys
        275                 280                 285
Leu Leu Ala Arg Thr Glu Ala Ile Leu Leu Asp Pro Val Tyr Ser Gly
    290                 295                 300
Lys Val Met Ala Gly Met Ile Asp Leu Ile Arg Asn Asp Tyr Phe Ala
305                 310                 315                 320
Pro Gly Ala Asn Val Leu Phe Leu His Thr Gly Gly Ser Pro Ala Leu
                325                 330                 335
Tyr Ala Tyr Thr Asp Thr Phe Lys
            340
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<210> 86
<211> 993
<212> DNA
<213> Yersinia pseudotuberculosis IP 32953

<220>
<221> CDS
<222> (1)..(993)
<223> transl_table=11

<400> 86

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gtg acg ctt caa cac aaa ctg acg caa ttc ccg cgt ctc gat ctg gtc       48
Met Thr Leu Gln His Lys Leu Thr Gln Phe Pro Arg Leu Asp Leu Val
1               5                   10                  15
ggt aat gcg acg cca tta gaa aag ctg tct cgt cta tct gat tat ctg       96
Gly Asn Ala Thr Pro Leu Glu Lys Leu Ser Arg Leu Ser Asp Tyr Leu
            20                  25                  30
gga cgt gaa att tac att aaa cgt gat gat gtc acg cct gtg gcg ctt      144
Gly Arg Glu Ile Tyr Ile Lys Arg Asp Asp Val Thr Pro Val Ala Leu
        35                  40                  45
ggc ggg aat aaa ctg cgc aag cta gaa ttc tta gcc gca gat gcc ttg      192
Gly Gly Asn Lys Leu Arg Lys Leu Glu Phe Leu Ala Ala Asp Ala Leu
    50                  55                  60
aga cag gga gcc gat acg ctg gtt acg gct ggt gct att caa tct aat      240
Arg Gln Gly Ala Asp Thr Leu Val Thr Ala Gly Ala Ile Gln Ser Asn
65                  70                  75                  80
cat gtc cgc caa acc gcc gcc gtg gcc gcg aaa ctg ggg ctg cat tgc      288
His Val Arg Gln Thr Ala Ala Val Ala Ala Lys Leu Gly Leu His Cys
                85                  90                  95
gtt gcg ctg ttg gaa aac ccc att ggt act gag cag gca aac tat ctg      336
Val Ala Leu Leu Glu Asn Pro Ile Gly Thr Glu Gln Ala Asn Tyr Leu
            100                 105                 110
acc aat ggg aac cgg ctg tta ctg gac cta ttc aat gtt gat gtt gtg      384
Thr Asn Gly Asn Arg Leu Leu Leu Asp Leu Phe Asn Val Asp Val Val
        115                 120                 125
atg tgt gag gca ttg aac gat cca aat cag caa tta gca gaa ttg gct      432
```

```
Met Cys Glu Ala Leu Asn Asp Pro Asn Gln Gln Leu Ala Glu Leu Ala
    130                 135                 140
acc cgc gtg gaa gcg cag ggt ttc cgc cca tat gtg gta ccg att ggc       480
Thr Arg Val Glu Ala Gln Gly Phe Arg Pro Tyr Val Val Pro Ile Gly
145                 150                 155                 160
ggt tct aat gcc ttg ggc gcg ctg ggt tat gtg cag tgc tca ctg gaa       528
Gly Ser Asn Ala Leu Gly Ala Leu Gly Tyr Val Gln Cys Ser Leu Glu
                165                 170                 175
att gct gct caa gcc gcg ggc aat gtt gcg ttt agt tcg gtc gtc gtg       576
Ile Ala Ala Gln Ala Ala Gly Asn Val Ala Phe Ser Ser Val Val Val
            180                 185                 190
gcc tct ggc agt gcg gga aca cat gca gga ttg gcg gtt ggt cta cag       624
Ala Ser Gly Ser Ala Gly Thr His Ala Gly Leu Ala Val Gly Leu Gln
        195                 200                 205
cag ttg tta ccc gat gcg gaa tta atc ggt gtg acg gta tca cgt agt       672

Gln Leu Leu Pro Asp Ala Glu Leu Ile Gly Val Thr Val Ser Arg Ser
    210                 215                 220
gcc gat gaa cag cgg cct aaa gtg gca cag att caa caa gcg ttg gcg       720
Ala Asp Glu Gln Arg Pro Lys Val Ala Gln Ile Gln Gln Ala Leu Ala
225                 230                 235                 240
aca tca tta ggg atg acg gac cca ttg gca aaa atc acc ttg tgg gat       768
Thr Ser Leu Gly Met Thr Asp Pro Leu Ala Lys Ile Thr Leu Trp Asp
                245                 250                 255
agt tat ttt gcc ccg caa tat ggg atg cca aac gaa gag ggg ata gcg       816
Ser Tyr Phe Ala Pro Gln Tyr Gly Met Pro Asn Glu Glu Gly Ile Ala
            260                 265                 270
gct att aag ctc ttg gca aga ctg gaa gga ata ttg ttg gac cct gtg       864
Ala Ile Lys Leu Leu Ala Arg Leu Glu Gly Ile Leu Leu Asp Pro Val
        275                 280                 285
tat acc ggt aag gcg atg gcg ggc tta ctt gat ggt att gaa cag caa       912
Tyr Thr Gly Lys Ala Met Ala Gly Leu Leu Asp Gly Ile Glu Gln Gln
    290                 295                 300
aaa ttc tgc gac aaa ggg cca att tta ttt atc cac act ggc ggg gca       960
Lys Phe Cys Asp Lys Gly Pro Ile Leu Phe Ile His Thr Gly Gly Ala
305                 310                 315                 320
cct gcg ctg ttt gct tat cat ccg cag gtg tag                           993
Pro Ala Leu Phe Ala Tyr His Pro Gln Val
                325                 330

<210> 87

<211> 330
<212> PRT
<213> Yersinia pseudotuberculosis IP 32953

<400> 87
Met Thr Leu Gln His Lys Leu Thr Gln Phe Pro Arg Leu Asp Leu Val
1               5                   10                  15
Gly Asn Ala Thr Pro Leu Glu Lys Leu Ser Arg Leu Ser Asp Tyr Leu
            20                  25                  30
Gly Arg Glu Ile Tyr Ile Lys Arg Asp Asp Val Thr Pro Val Ala Leu
        35                  40                  45
Gly Gly Asn Lys Leu Arg Lys Leu Glu Phe Leu Ala Ala Asp Ala Leu
    50                  55                  60
Arg Gln Gly Ala Asp Thr Leu Val Thr Ala Gly Ala Ile Gln Ser Asn
65                  70                  75                  80
His Val Arg Gln Thr Ala Ala Val Ala Ala Lys Leu Gly Leu His Cys
                85                  90                  95
Val Ala Leu Leu Glu Asn Pro Ile Gly Thr Glu Gln Ala Asn Tyr Leu
            100                 105                 110
```

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

<210> 88
<211> 996
<212> DNA
<213> Bacillus cereus E33L

<220>
<221> CDS
<222> (1)..(996)
<223> transl_table=11

<400> 88

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atg aat tta gct aaa ttc ccg aga aaa aaa tat aca gag tca tat aca       48
Met Asn Leu Ala Lys Phe Pro Arg Lys Lys Tyr Thr Glu Ser Tyr Thr
1               5                   10                  15
cca att gaa aaa tta aac aat ttt tca gaa gca ctt ggt ggg ccg act       96
Pro Ile Glu Lys Leu Asn Asn Phe Ser Glu Ala Leu Gly Gly Pro Thr
            20                  25                  30
att tat ttt aaa cga gat gat tta ctt ggt tta aca gct ggt ggt aat      144
Ile Tyr Phe Lys Arg Asp Asp Leu Leu Gly Leu Thr Ala Gly Gly Asn
        35                  40                  45
aag acg aga aag tta gag ttt tta gtt gcg gat gca cag gca aag ggt      192
Lys Thr Arg Lys Leu Glu Phe Leu Val Ala Asp Ala Gln Ala Lys Gly
    50                  55                  60
gca gat acg tta att aca gct ggt ggt att cag tca aat cat tgc cgc      240
Ala Asp Thr Leu Ile Thr Ala Gly Gly Ile Gln Ser Asn His Cys Arg
65                  70                  75                  80
cta aca ctt gca gcg gcg gta aaa gaa aaa atg aaa tgt atc ctt gta      288
Leu Thr Leu Ala Ala Ala Val Lys Glu Lys Met Lys Cys Ile Leu Val
                85                  90                  95
tta gaa gaa ggg ctt gag cca gaa gag aag cca gac ttt aat gga aac      336
Leu Glu Glu Gly Leu Glu Pro Glu Glu Lys Pro Asp Phe Asn Gly Asn
            100                 105                 110
```

```
tat ttc tta tat cat tta cta ggt gct gaa aat gta att gtt gta cga       384
Tyr Phe Leu Tyr His Leu Leu Gly Ala Glu Asn Val Ile Val Val Arg
        115                 120                 125
aac gga gca gat ctt atg gaa gag atg cat aaa gtc gcg aaa gaa gtt       432
Asn Gly Ala Asp Leu Met Glu Glu Met His Lys Val Ala Lys Glu Val
    130                 135                 140
agt gaa aaa ggg aat aca cca tat gtc att ccg gtc ggt gga tcg aat       480
Ser Glu Lys Gly Asn Thr Pro Tyr Val Ile Pro Val Gly Gly Ser Asn
145                 150                 155                 160
cct act ggc gca atg gga tac gtt gct tgt gcg caa gaa att atg gtg       528
Pro Thr Gly Ala Met Gly Tyr Val Ala Cys Ala Gln Glu Ile Met Val
                165                 170                 175
caa tca ttt gac caa gga att gat ttc agt tca gtc gtt tgc gta agt       576
Gln Ser Phe Asp Gln Gly Ile Asp Phe Ser Ser Val Val Cys Val Ser
            180                 185                 190
ggt agt ggc ggt atg cac gct ggt tta att aca ggt ttt gct gga aca       624
Gly Ser Gly Gly Met His Ala Gly Leu Ile Thr Gly Phe Ala Gly Thr
        195                 200                 205
caa agt aac atc ccc gta atc gga att aac gta agt aga gga aaa gca       672
Gln Ser Asn Ile Pro Val Ile Gly Ile Asn Val Ser Arg Gly Lys Ala
    210                 215                 220
gag caa gaa gag aaa gta gca aaa ctt gta gat gaa acg tca gct cat       720
Glu Gln Glu Glu Lys Val Ala Lys Leu Val Asp Glu Thr Ser Ala His
225                 230                 235                 240
gtt ggt att cca aac ttt atc ccg cgc gaa gcg gtt aca tgc ttt gat       768
Val Gly Ile Pro Asn Phe Ile Pro Arg Glu Ala Val Thr Cys Phe Asp
                245                 250                 255
gaa tat gta gga cca ggt tac gcg tta cca acg cca gaa atg gtg gaa       816
Glu Tyr Val Gly Pro Gly Tyr Ala Leu Pro Thr Pro Glu Met Val Glu
            260                 265                 270
gca gtg cag ctg tta gca aaa aca gaa ggt att tta ctt gat cca gta       864
Ala Val Gln Leu Leu Ala Lys Thr Glu Gly Ile Leu Leu Asp Pro Val
        275                 280                 285
tat aca ggt aaa gca gta gcg gga tta atc gac tta att aga aaa ggt       912
Tyr Thr Gly Lys Ala Val Ala Gly Leu Ile Asp Leu Ile Arg Lys Gly
    290                 295                 300
aca ttt aat aaa gag gac aac att tta ttc gta cat tca ggt ggt tca       960
Thr Phe Asn Lys Glu Asp Asn Ile Leu Phe Val His Ser Gly Gly Ser
305                 310                 315                 320
cca gct tta tat gcg aat aca tct tta ttt gcg taa                       996
Pro Ala Leu Tyr Ala Asn Thr Ser Leu Phe Ala
                325                 330
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<210> 89
<211> 331
<212> PRT
<213> Bacillus cereus E33L

<400> 89

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

```
Leu Glu Glu Gly Leu Glu Pro Glu Glu Lys Pro Asp Phe Asn Gly Asn
            100                 105                 110
Tyr Phe Leu Tyr His Leu Leu Gly Ala Glu Asn Val Ile Val Val Arg
        115                 120                 125
Asn Gly Ala Asp Leu Met Glu Glu Met His Lys Val Ala Lys Glu Val
    130                 135                 140
Ser Glu Lys Gly Asn Thr Pro Tyr Val Ile Pro Val Gly Gly Ser Asn
145                 150                 155                 160
Pro Thr Gly Ala Met Gly Tyr Val Ala Cys Ala Gln Glu Ile Met Val
                165                 170                 175
Gln Ser Phe Asp Gln Gly Ile Asp Phe Ser Ser Val Val Cys Val Ser
            180                 185                 190
Gly Ser Gly Gly Met His Ala Gly Leu Ile Thr Gly Phe Ala Gly Thr
        195                 200                 205
Gln Ser Asn Ile Pro Val Ile Gly Ile Asn Val Ser Arg Gly Lys Ala
    210                 215                 220
Glu Gln Glu Glu Lys Val Ala Lys Leu Val Asp Glu Thr Ser Ala His
225                 230                 235                 240
Val Gly Ile Pro Asn Phe Ile Pro Arg Glu Ala Val Thr Cys Phe Asp
                245                 250                 255
Glu Tyr Val Gly Pro Gly Tyr Ala Leu Pro Thr Pro Glu Met Val Glu
            260                 265                 270
Ala Val Gln Leu Leu Ala Lys Thr Glu Gly Ile Leu Leu Asp Pro Val
        275                 280                 285
Tyr Thr Gly Lys Ala Val Ala Gly Leu Ile Asp Leu Ile Arg Lys Gly
    290                 295                 300
Thr Phe Asn Lys Glu Asp Asn Ile Leu Phe Val His Ser Gly Gly Ser
305                 310                 315                 320
Pro Ala Leu Tyr Ala Asn Thr Ser Leu Phe Ala
                325                 330
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<210> 90
<211> 1020
<212> DNA
<213> Burkholderia mallei ATCC 23344

<220>
<221> CDS
<222> (1)..(1020)
<223> transl_table=11

<400> 90

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atg aac acg acg acg ctc tcg acg aaa ctg aac gcc ttc gcc cgc ctg       48
Met Asn Thr Thr Thr Leu Ser Thr Lys Leu Asn Ala Phe Ala Arg Leu
1               5                   10                  15
aac ctg atc gac gcg ccg acg ccg ctg cag tac ttg ccg cgc ctg tcc       96
Asn Leu Ile Asp Ala Pro Thr Pro Leu Gln Tyr Leu Pro Arg Leu Ser
            20                  25                  30
gcg cac gtc ggc cgc gac atc cac gtg aag cgc gac gac tgc acg ccg      144
Ala His Val Gly Arg Asp Ile His Val Lys Arg Asp Asp Cys Thr Pro
        35                  40                  45
ctc gcg atg ggc ggc aac aag ctg cgc aag ctc gaa ttc ctc gcc gcg      192
Leu Ala Met Gly Gly Asn Lys Leu Arg Lys Leu Glu Phe Leu Ala Ala
    50                  55                  60
gac gcg ctc ggc caa aac gcg gac gtg ctg gtg acc gcg ggc gcg atc      240
Asp Ala Leu Gly Gln Asn Ala Asp Val Leu Val Thr Ala Gly Ala Ile
65                  70                  75                  80
cag tcg aat cac gtc cgg cag acg gcc gcg ctc gtc gcg cag ctc ggc      288
Gln Ser Asn His Val Arg Gln Thr Ala Ala Leu Val Ala Gln Leu Gly
                85                  90                  95
ctc ggc tgt gtc gcg ctg ctc gaa aac ccg atc gca gcc gcg cgc gac      336
```

```
Leu Gly Cys Val Ala Leu Leu Glu Asn Pro Ile Ala Ala Ala Arg Asp
            100                 105                 110
gat tat ctg caa agc ggc aac cgg ctg ctg ctc gat ctg ttc gac gtg       384
Asp Tyr Leu Gln Ser Gly Asn Arg Leu Leu Leu Asp Leu Phe Asp Val
        115                 120                 125
cgc gcg cac gtc gtc gac ggg ctc gac gac gtc gac cgg caa ctc gaa       432
Arg Ala His Val Val Asp Gly Leu Asp Asp Val Asp Arg Gln Leu Glu
    130                 135                 140
gcc gcc gcg cgg cgg ctg cgc gac gaa ggg cgg cgc ccg tac gtg atc       480
Ala Ala Ala Arg Arg Leu Arg Asp Glu Gly Arg Arg Pro Tyr Val Ile
145                 150                 155                 160
ccg atc ggc gga tcg aat ccg ctc ggc gcg ctc ggc tac gtg cgc gcg       528
Pro Ile Gly Gly Ser Asn Pro Leu Gly Ala Leu Gly Tyr Val Arg Ala
                165                 170                 175
ggc ctc gag ctc gcg cag cag atc cgc gcg gcc gag cgc gat ttc gcg       576
Gly Leu Glu Leu Ala Gln Gln Ile Arg Ala Ala Glu Arg Asp Phe Ala
            180                 185                 190
gct gtc gtg ctc gcg tcc ggc agc gcc ggc acg cac gcg ggc ctc gcg       624
Ala Val Val Leu Ala Ser Gly Ser Ala Gly Thr His Ala Gly Leu Ala
        195                 200                 205
ttc gcg ctc gcg cac gcg ttg ccc ggg ctg ccg gtg atc ggc gtg acg       672
Phe Ala Leu Ala His Ala Leu Pro Gly Leu Pro Val Ile Gly Val Thr
    210                 215                 220
gta tcg cgc acc gac gcg cag cag cgc ccg aag gtg cgg cat ctg ctc       720
Val Ser Arg Thr Asp Ala Gln Gln Arg Pro Lys Val Arg His Leu Leu
225                 230                 235                 240
gac ggc atg agc ggg ctg ctc gac gtc gcg ttg ccg gcg ggc gcg cgc       768
Asp Gly Met Ser Gly Leu Leu Asp Val Ala Leu Pro Ala Gly Ala Arg
                245                 250                 255
atc gat ctg tgg gac gac tac ttc gcg ccg cgc tac ggc gag ccc aat       816
Ile Asp Leu Trp Asp Asp Tyr Phe Ala Pro Arg Tyr Gly Glu Pro Asn
            260                 265                 270
cgc gcg ggc atc gac gcg ctg cgg ctg ctc gcg cga acc gag ggg ctg       864
Arg Ala Gly Ile Asp Ala Leu Arg Leu Leu Ala Arg Thr Glu Gly Leu
        275                 280                 285
ctg ctc gat ccg gtg tac acg ggc aag gcg atg gcg ggt ctc atc gac       912
Leu Leu Asp Pro Val Tyr Thr Gly Lys Ala Met Ala Gly Leu Ile Asp
    290                 295                 300
ggc gtc gcg cgc ggc cgc ttc gac gga aac ggc ccg gtg ctg ttc gtg       960
Gly Val Ala Arg Gly Arg Phe Asp Gly Asn Gly Pro Val Leu Phe Val
305                 310                 315                 320
cat acg ggc ggc gcg ccc gcg ctg ttc gcg tat cag gac acg tgc cgc      1008
His Thr Gly Gly Ala Pro Ala Leu Phe Ala Tyr Gln Asp Thr Cys Arg
                325                 330                 335
gcg agc cga tga                                                     1020
Ala Ser Arg
```

<210> 91
<211> 339
<212> PRT
<213> Burkholderia mallei ATCC 23344

<400> 91

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Met Asn Thr Thr Thr Leu Ser Thr Lys Leu Asn Ala Phe Ala Arg Leu
1               5                   10                  15
Asn Leu Ile Asp Ala Pro Thr Pro Leu Gln Tyr Leu Pro Arg Leu Ser
            20                  25                  30
Ala His Val Gly Arg Asp Ile His Val Lys Arg Asp Asp Cys Thr Pro
        35                  40                  45
Leu Ala Met Gly Gly Asn Lys Leu Arg Lys Leu Glu Phe Leu Ala Ala
```

```
    50                  55                  60
Asp Ala Leu Gly Gln Asn Ala Asp Val Leu Val Thr Ala Gly Ala Ile
65                  70                  75                  80
Gln Ser Asn His Val Arg Gln Thr Ala Ala Leu Val Ala Gln Leu Gly
                85                  90                  95
Leu Gly Cys Val Ala Leu Leu Glu Asn Pro Ile Ala Ala Ala Arg Asp
            100                 105                 110
Asp Tyr Leu Gln Ser Gly Asn Arg Leu Leu Leu Asp Leu Phe Asp Val
        115                 120                 125
Arg Ala His Val Val Asp Gly Leu Asp Asp Val Asp Arg Gln Leu Glu
    130                 135                 140
Ala Ala Ala Arg Arg Leu Arg Asp Glu Gly Arg Arg Pro Tyr Val Ile
145                 150                 155                 160
Pro Ile Gly Gly Ser Asn Pro Leu Gly Ala Leu Gly Tyr Val Arg Ala
                165                 170                 175
Gly Leu Glu Leu Ala Gln Gln Ile Arg Ala Ala Glu Arg Asp Phe Ala
            180                 185                 190
Ala Val Val Leu Ala Ser Gly Ser Ala Gly Thr His Ala Gly Leu Ala
        195                 200                 205
Phe Ala Leu Ala His Ala Leu Pro Gly Leu Pro Val Ile Gly Val Thr
    210                 215                 220
Val Ser Arg Thr Asp Ala Gln Gln Arg Pro Lys Val Arg His Leu Leu
225                 230                 235                 240
Asp Gly Met Ser Gly Leu Leu Asp Val Ala Leu Pro Ala Gly Ala Arg
                245                 250                 255
Ile Asp Leu Trp Asp Asp Tyr Phe Ala Pro Arg Tyr Gly Glu Pro Asn
            260                 265                 270
Arg Ala Gly Ile Asp Ala Leu Arg Leu Leu Ala Arg Thr Glu Gly Leu
        275                 280                 285
Leu Leu Asp Pro Val Tyr Thr Gly Lys Ala Met Ala Gly Leu Ile Asp
    290                 295                 300
Gly Val Ala Arg Gly Arg Phe Asp Gly Asn Gly Pro Val Leu Phe Val
305                 310                 315                 320
His Thr Gly Gly Ala Pro Ala Leu Phe Ala Tyr Gln Asp Thr Cys Arg
                325                 330                 335
Ala Ser Arg
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<210> 92
<211> 1020
<212> DNA
<213> Burkholderia pseudomallei K96243

<220>
<221> CDS
<222> (1)..(1020)
<223> transl_table=11

<400> 92

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atg aac acg acg acg ctc tcg acg aaa ctg aac gcc ttc gcc cgc ctg       48
Met Asn Thr Thr Thr Leu Ser Thr Lys Leu Asn Ala Phe Ala Arg Leu
1               5                   10                  15
aac ctg atc gac gcg ccg acg ccg ctg cag tac ttg ccg cgc ctg tcc       96
Asn Leu Ile Asp Ala Pro Thr Pro Leu Gln Tyr Leu Pro Arg Leu Ser
            20                  25                  30
gcg cac gtc ggc cgc gac atc cac gtg aag cgc gac gac tgc acg ccg      144
Ala His Val Gly Arg Asp Ile His Val Lys Arg Asp Asp Cys Thr Pro
        35                  40                  45
ctc gcg atg ggc ggt aac aag ctg cgc aag ctc gaa ttc ctc gcc gcg      192
Leu Ala Met Gly Gly Asn Lys Leu Arg Lys Leu Glu Phe Leu Ala Ala
    50                  55                  60
```

```
gac gcg ctc ggc caa aac gcg gac gtg ctg gtg acc gcg ggc gcg atc       240
Asp Ala Leu Gly Gln Asn Ala Asp Val Leu Val Thr Ala Gly Ala Ile
65                  70                  75                  80
cag tcg aat cac gtc cgg cag acg gcc gcg ctc gcc gcg cag ctc ggc       288
Gln Ser Asn His Val Arg Gln Thr Ala Ala Leu Ala Ala Gln Leu Gly
                85                  90                  95
ctc ggc tgt gtc gcg ctg ctc gaa aac ccg atc gca gcc gcg cgc gac       336
Leu Gly Cys Val Ala Leu Leu Glu Asn Pro Ile Ala Ala Ala Arg Asp
            100                 105                 110
gat tat ctg caa agc ggc aac cgg ctg ctg ctc gat ctg ttc gac gtg       384
Asp Tyr Leu Gln Ser Gly Asn Arg Leu Leu Leu Asp Leu Phe Asp Val
        115                 120                 125
cgc gcg cac gtc gtc gac ggg ctc gac gac gtc gac cgg caa ctc gaa       432
Arg Ala His Val Val Asp Gly Leu Asp Asp Val Asp Arg Gln Leu Glu
    130                 135                 140
gcc gcc gcg cgg cgg ctg cgc gac gaa ggg cgg cgc ccg tac gtg atc       480
Ala Ala Ala Arg Arg Leu Arg Asp Glu Gly Arg Arg Pro Tyr Val Ile
145                 150                 155                 160
ccg atc ggc gga tcg aat ccg ctc ggc gcg ctc ggc tac gtg cgc gcg       528
Pro Ile Gly Gly Ser Asn Pro Leu Gly Ala Leu Gly Tyr Val Arg Ala
                165                 170                 175
ggc ctc gag ctc gcg cag cag atc cgc gcg gcc gag cgc gat ttc gcg       576
Gly Leu Glu Leu Ala Gln Gln Ile Arg Ala Ala Glu Arg Asp Phe Ala
            180                 185                 190
gct gtc gtg ctc gcg tcc ggc agc gcc ggc acg cac gcg ggc ctc gcg       624
Ala Val Val Leu Ala Ser Gly Ser Ala Gly Thr His Ala Gly Leu Ala
        195                 200                 205
ttc gcg ctc gcg cac gcg ttg ccc ggg ctg ccg gtg atc ggc gtg acg       672
Phe Ala Leu Ala His Ala Leu Pro Gly Leu Pro Val Ile Gly Val Thr
    210                 215                 220
gta tcg cgc acc gac gcg cag cag cgc ccg aag gtg cgg cat ctg ctc       720
Val Ser Arg Thr Asp Ala Gln Gln Arg Pro Lys Val Arg His Leu Leu
225                 230                 235                 240
gac ggc atg agc ggg ctg ctc gac gtc gcg ttg ccg gcg ggc gca cgc       768
Asp Gly Met Ser Gly Leu Leu Asp Val Ala Leu Pro Ala Gly Ala Arg
                245                 250                 255
atc gat ctg tgg gac gac tac ttc gcg ccg cgc tac ggc gag ccc aat       816
Ile Asp Leu Trp Asp Asp Tyr Phe Ala Pro Arg Tyr Gly Glu Pro Asn
            260                 265                 270
cgc gcg ggc atc gac gcg ctg cgg ctg ctc gcg cga acc gag ggg ttg       864
Arg Ala Gly Ile Asp Ala Leu Arg Leu Leu Ala Arg Thr Glu Gly Leu
        275                 280                 285
ctg ctc gat ccg gtg tac acg ggc aag gcg atg gcg ggt ctc atc gac       912
Leu Leu Asp Pro Val Tyr Thr Gly Lys Ala Met Ala Gly Leu Ile Asp
    290                 295                 300
ggc gtc gcg cgc ggc cgc ttc gac gga aac ggc ccg gtg ctg ttc gtg       960
Gly Val Ala Arg Gly Arg Phe Asp Gly Asn Gly Pro Val Leu Phe Val
305                 310                 315                 320
cat acg ggc ggc gcg ccc gcg ctg ttc gcg tat cag gac gcg tgc cgc      1008
His Thr Gly Gly Ala Pro Ala Leu Phe Ala Tyr Gln Asp Ala Cys Arg
                325                 330                 335
gcg agc cga tga                                                     1020
Ala Ser Arg
```

<210> 93
<211> 339
<212> PRT
<213> Burkholderia pseudomallei K96243

<400> 93

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Met Asn Thr Thr Thr Leu Ser Thr Lys Leu Asn Ala Phe Ala Arg Leu
1               5                  10                  15
Asn Leu Ile Asp Ala Pro Thr Pro Leu Gln Tyr Leu Pro Arg Leu Ser
            20                  25                  30
Ala His Val Gly Arg Asp Ile His Val Lys Arg Asp Asp Cys Thr Pro
        35                  40                  45
Leu Ala Met Gly Gly Asn Lys Leu Arg Lys Leu Glu Phe Leu Ala Ala
    50                  55                  60
Asp Ala Leu Gly Gln Asn Ala Asp Val Leu Val Thr Ala Gly Ala Ile
65                  70                  75                  80
Gln Ser Asn His Val Arg Gln Thr Ala Ala Leu Ala Ala Gln Leu Gly
                85                  90                  95
Leu Gly Cys Val Ala Leu Leu Glu Asn Pro Ile Ala Ala Ala Arg Asp
            100                 105                 110
Asp Tyr Leu Gln Ser Gly Asn Arg Leu Leu Leu Asp Leu Phe Asp Val
        115                 120                 125
Arg Ala His Val Val Asp Gly Leu Asp Asp Val Asp Arg Gln Leu Glu
    130                 135                 140
Ala Ala Ala Arg Arg Leu Arg Asp Glu Gly Arg Arg Pro Tyr Val Ile
145                 150                 155                 160
Pro Ile Gly Gly Ser Asn Pro Leu Gly Ala Leu Gly Tyr Val Arg Ala
                165                 170                 175
Gly Leu Glu Leu Ala Gln Gln Ile Arg Ala Ala Glu Arg Asp Phe Ala
            180                 185                 190
Ala Val Val Leu Ala Ser Gly Ser Ala Gly Thr His Ala Gly Leu Ala
        195                 200                 205
Phe Ala Leu Ala His Ala Leu Pro Gly Leu Pro Val Ile Gly Val Thr
    210                 215                 220
Val Ser Arg Thr Asp Ala Gln Gln Arg Pro Lys Val Arg His Leu Leu
225                 230                 235                 240
Asp Gly Met Ser Gly Leu Leu Asp Val Ala Leu Pro Ala Gly Ala Arg
                245                 250                 255
Ile Asp Leu Trp Asp Asp Tyr Phe Ala Pro Arg Tyr Gly Glu Pro Asn
            260                 265                 270
Arg Ala Gly Ile Asp Ala Leu Arg Leu Leu Ala Arg Thr Glu Gly Leu
        275                 280                 285
Leu Leu Asp Pro Val Tyr Thr Gly Lys Ala Met Ala Gly Leu Ile Asp
    290                 295                 300
Gly Val Ala Arg Gly Arg Phe Asp Gly Asn Gly Pro Val Leu Phe Val
305                 310                 315                 320
His Thr Gly Gly Ala Pro Ala Leu Phe Ala Tyr Gln Asp Ala Cys Arg
                325                 330                 335
Ala Ser Arg
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<210> 94
<211> 987
<212> DNA
<213> Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC

<220>
<221> CDS
<222> (1)..(987)
<223> transl_table=11

<400> 94

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Met Pro Leu His His Leu Thr Arg Phe Pro Arg Leu Glu Leu Ile Gly
1               5                  10                  15
gcg ccg acc ccg ctc gaa tac ctg ccg cga ttg tct gat tat cct ggc       96
Ala Pro Thr Pro Leu Glu Tyr Leu Pro Arg Leu Ser Asp Tyr Pro Gly
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            20                  25                  30
cgt gag att tac att aag cgc gat gac gtt acg ccc att gca atg ggc      144
Arg Glu Ile Tyr Ile Lys Arg Asp Asp Val Thr Pro Ile Ala Met Gly
        35                  40                  45
ggt aat aaa ctg cgt aag ctg gag ttt ctg gtg gcc gac gcg ctg cga      192
Gly Asn Lys Leu Arg Lys Leu Glu Phe Leu Val Ala Asp Ala Leu Arg
    50                  55                  60
gaa ggg gcg gat acg ctg ata acc gca ggg gcg att cag tcg aac cat      240
Glu Gly Ala Asp Thr Leu Ile Thr Ala Gly Ala Ile Gln Ser Asn His
65                  70                  75                  80
gtc cgt cag acg gcg gca gtc gcg gcc aaa ttg gga ctg cat tgc gtc      288
Val Arg Gln Thr Ala Ala Val Ala Ala Lys Leu Gly Leu His Cys Val
                85                  90                  95
gcc ttg ctg gaa aat cca atc ggt acc acc gcg gaa aat tac ctg acg      336
Ala Leu Leu Glu Asn Pro Ile Gly Thr Thr Ala Glu Asn Tyr Leu Thr
            100                 105                 110
aat ggt aat cgc ctg tta ctg gat tta ttt aat acg caa att gag atg      384
Asn Gly Asn Arg Leu Leu Leu Asp Leu Phe Asn Thr Gln Ile Glu Met
        115                 120                 125
tgc gat gtg cta acc gat ccg gat gcg cag ctg caa acg ctg gcg acg      432
Cys Asp Val Leu Thr Asp Pro Asp Ala Gln Leu Gln Thr Leu Ala Thr
    130                 135                 140
cgc att gaa gcg caa ggg ttc agg ccc tat gtg att ccg gtc ggc ggc      480
Arg Ile Glu Ala Gln Gly Phe Arg Pro Tyr Val Ile Pro Val Gly Gly
145                 150                 155                 160
tcc agc gcg ctg ggc gca atg gga tac gta gag agc gcc ctg gaa atc      528
Ser Ser Ala Leu Gly Ala Met Gly Tyr Val Glu Ser Ala Leu Glu Ile
                165                 170                 175
gcc cag cag tgt gaa gaa gtc gtc ggg ctc tct tcg gtg gtg gtg gcc      576
Ala Gln Gln Cys Glu Glu Val Val Gly Leu Ser Ser Val Val Val Ala
            180                 185                 190
tcc ggc agc gcc gga acg cac gcc ggg tta gct gtc ggg ctg gaa cat      624
Ser Gly Ser Ala Gly Thr His Ala Gly Leu Ala Val Gly Leu Glu His
        195                 200                 205
ctg atg cct gac gtc gaa ctg att ggc gtg acc gtt tca cgt tct gtc      672
Leu Met Pro Asp Val Glu Leu Ile Gly Val Thr Val Ser Arg Ser Val
    210                 215                 220
gcc gag cag aaa ccc aaa gtg att gcc ttg cag cag gct att gcc ggt      720
Ala Glu Gln Lys Pro Lys Val Ile Ala Leu Gln Gln Ala Ile Ala Gly
225                 230                 235                 240
cag ctg gcg ctg acg gcg acg gcg gat att cat tta tgg gat gac tat      768
Gln Leu Ala Leu Thr Ala Thr Ala Asp Ile His Leu Trp Asp Asp Tyr
                245                 250                 255
ttt gcc ccg ggt tac ggc gtg cca aat gac gcg ggg atg gag gcg gtg      816
Phe Ala Pro Gly Tyr Gly Val Pro Asn Asp Ala Gly Met Glu Ala Val
            260                 265                 270
aaa ctg ctg gcg agc ctg gag ggg gtg ttg ctg gat ccg gta tat acc      864
Lys Leu Leu Ala Ser Leu Glu Gly Val Leu Leu Asp Pro Val Tyr Thr
        275                 280                 285
ggc aaa gcg atg gcg ggt ctg ata gac ggc atc agc cag aaa cgc ttt      912
Gly Lys Ala Met Ala Gly Leu Ile Asp Gly Ile Ser Gln Lys Arg Phe
    290                 295                 300
aac gat gac ggg ccg att ctc ttt att cac acc ggt ggg gcg cct gcg      960
Asn Asp Asp Gly Pro Ile Leu Phe Ile His Thr Gly Gly Ala Pro Ala
305                 310                 315                 320
ctg ttt gcc tac cat cct cat gta taa                                 987
Leu Phe Ala Tyr His Pro His Val
                325
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<210> 95
<211> 328

<212> PRT
<213> Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC

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

<210> 96
<211> 1020
<212> DNA
<213> Silicibacter pomeroyi DSS-3

<220>
<221> CDS
<222> (1)..(1020)
<223> transl_table=11

<400> 96
atg cat ctt gcc cgc tat ccc cgc cgc ttc atc gcc cat ctg ccg acg 48
Met His Leu Ala Arg Tyr Pro Arg Arg Phe Ile Ala His Leu Pro Thr
1 5 10 15

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ccg ctg gaa cgg ctg gac cgg ctg acc gcc gaa ctg ggc ggg ccc gag        96
Pro Leu Glu Arg Leu Asp Arg Leu Thr Ala Glu Leu Gly Gly Pro Glu
            20                  25                  30
atc tgg atc aag cgc gac gac tgc acc ggc ctg tcc acc ggc ggc aac       144
Ile Trp Ile Lys Arg Asp Asp Cys Thr Gly Leu Ser Thr Gly Gly Asn
        35                  40                  45
aag acc cgc aag ctg gaa ttc ctg atg gcc gag gcc gag ctg caa ggc       192
Lys Thr Arg Lys Leu Glu Phe Leu Met Ala Glu Ala Glu Leu Gln Gly
    50                  55                  60
gct gac atg gtg atg acg cag ggc gcg acc cag tcc aac cat gcc cgc       240
Ala Asp Met Val Met Thr Gln Gly Ala Thr Gln Ser Asn His Ala Arg
65                  70                  75                  80
cag acc gcc gca ttc gcc gcc aag ctg ggc atg gat tgc cat atc ctg       288
Gln Thr Ala Ala Phe Ala Ala Lys Leu Gly Met Asp Cys His Ile Leu
                85                  90                  95
ctc gag gac cgg acc ggc tcg aac aac gcc aac tac aac aac aac ggc       336
Leu Glu Asp Arg Thr Gly Ser Asn Asn Ala Asn Tyr Asn Asn Asn Gly
            100                 105                 110
aac gtt ctg ctc gac cat ctg cat ggc gcc acc act gaa aag cgc ccc       384
Asn Val Leu Leu Asp His Leu His Gly Ala Thr Thr Glu Lys Arg Pro
        115                 120                 125
ggc agc ggt ctg gac atg aat gcc gag atg gaa aag gtg gcc gag aag       432
Gly Ser Gly Leu Asp Met Asn Ala Glu Met Glu Lys Val Ala Glu Lys
    130                 135                 140
ttc cgc gcc gac ggg cgc aag gtc tat acc atc ccc ggc ggc ggc tcg       480
Phe Arg Ala Asp Gly Arg Lys Val Tyr Thr Ile Pro Gly Gly Gly Ser
145                 150                 155                 160
aac ccg acc ggc gcg ctg gga tat gtc aac tgc gct ttc gag atg ctg       528
Asn Pro Thr Gly Ala Leu Gly Tyr Val Asn Cys Ala Phe Glu Met Leu
                165                 170                 175
aac cag ttc aat gag cgc ggg ctg aag gtg gac cat atc gtg cat gcc       576
Asn Gln Phe Asn Glu Arg Gly Leu Lys Val Asp His Ile Val His Ala
            180                 185                 190
acc ggc agc gcg ggc acc cag gca ggg ctg atc acc ggg ctt cag gcg       624
Thr Gly Ser Ala Gly Thr Gln Ala Gly Leu Ile Thr Gly Leu Gln Ala
        195                 200                 205
atg aac gct cag atc ccg ctc ttg ggc atc ggc gtg cgt gcg ccc aag       672
Met Asn Ala Gln Ile Pro Leu Leu Gly Ile Gly Val Arg Ala Pro Lys
    210                 215                 220
ccc aag cag gaa gag aat gtc tat aac ctg gcc tgc gcc acc gcc gag       720
Pro Lys Gln Glu Glu Asn Val Tyr Asn Leu Ala Cys Ala Thr Ala Glu
225                 230                 235                 240
aag ctg ggt tgc ccc ggt gtc gtc gcg cgc gag gac gtg gtg gcc aat       768
Lys Leu Gly Cys Pro Gly Val Val Ala Arg Glu Asp Val Val Ala Asn
                245                 250                 255
acc gac tat gtc ggc gaa ggc tat ggc atc ccg acc gaa agc ggg ctg       816
Thr Asp Tyr Val Gly Glu Gly Tyr Gly Ile Pro Thr Glu Ser Gly Leu
            260                 265                 270
gag gcg atc cgc atg ttc gcc gag ctt gag gcg atc ctg ctt gac ccg       864
Glu Ala Ile Arg Met Phe Ala Glu Leu Glu Ala Ile Leu Leu Asp Pro
        275                 280                 285
gtc tat tcg gcc aag ggc gcg gct ggc ttc atc gac ctg atc cgc aag       912
Val Tyr Ser Ala Lys Gly Ala Ala Gly Phe Ile Asp Leu Ile Arg Lys
    290                 295                 300
ggt cat ttc aaa aag ggc gag cgg gtg gtg ttc ctg cat acc ggc ggc       960
Gly His Phe Lys Lys Gly Glu Arg Val Val Phe Leu His Thr Gly Gly
305                 310                 315                 320
gct gtg gcg ctg ttc ggc tat gac aac gcc ttt gac tat tcg gga cgc      1008
Ala Val Ala Leu Phe Gly Tyr Asp Asn Ala Phe Asp Tyr Ser Gly Arg
                325                 330                 335
tgg gtg gcc taa                                                     1020
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Trp Val Ala

<210> 97
<211> 339
<212> PRT
<213> Silicibacter pomeroyi DSS-3

<400> 97
Met His Leu Ala Arg Tyr Pro Arg Arg Phe Ile Ala His Leu Pro Thr
1 5 10 15
Pro Leu Glu Arg Leu Asp Arg Leu Thr Ala Glu Leu Gly Gly Pro Glu
20 25 30
Ile Trp Ile Lys Arg Asp Asp Cys Thr Gly Leu Ser Thr Gly Gly Asn
35 40 45
Lys Thr Arg Lys Leu Glu Phe Leu Met Ala Glu Ala Glu Leu Gln Gly
50 55 60
Ala Asp Met Val Met Thr Gln Gly Ala Thr Gln Ser Asn His Ala Arg
65 70 75 80
Gln Thr Ala Ala Phe Ala Ala Lys Leu Gly Met Asp Cys His Ile Leu
85 90 95
Leu Glu Asp Arg Thr Gly Ser Asn Asn Ala Asn Tyr Asn Asn Asn Gly
100 105 110
Asn Val Leu Leu Asp His Leu His Gly Ala Thr Thr Glu Lys Arg Pro
115 120 125
Gly Ser Gly Leu Asp Met Asn Ala Glu Met Glu Lys Val Ala Glu Lys
130 135 140
Phe Arg Ala Asp Gly Arg Lys Val Tyr Thr Ile Pro Gly Gly Gly Ser
145 150 155 160
Asn Pro Thr Gly Ala Leu Gly Tyr Val Asn Cys Ala Phe Glu Met Leu
165 170 175
Asn Gln Phe Asn Glu Arg Gly Leu Lys Val Asp His Ile Val His Ala
180 185 190
Thr Gly Ser Ala Gly Thr Gln Ala Gly Leu Ile Thr Gly Leu Gln Ala
195 200 205
Met Asn Ala Gln Ile Pro Leu Leu Gly Ile Gly Val Arg Ala Pro Lys
210 215 220
Pro Lys Gln Glu Glu Asn Val Tyr Asn Leu Ala Cys Ala Thr Ala Glu
225 230 235 240
Lys Leu Gly Cys Pro Gly Val Val Ala Arg Glu Asp Val Val Ala Asn
245 250 255
Thr Asp Tyr Val Gly Glu Gly Tyr Gly Ile Pro Thr Glu Ser Gly Leu
260 265 270
Glu Ala Ile Arg Met Phe Ala Glu Leu Glu Ala Ile Leu Leu Asp Pro
275 280 285
Val Tyr Ser Ala Lys Gly Ala Ala Gly Phe Ile Asp Leu Ile Arg Lys
290 295 300
Gly His Phe Lys Lys Gly Glu Arg Val Val Phe Leu His Thr Gly Gly
305 310 315 320
Ala Val Ala Leu Phe Gly Tyr Asp Asn Ala Phe Asp Tyr Ser Gly Arg
325 330 335
Trp Val Ala

<210> 98
<211> 1158
<212> DNA
<213> Silicibacter pomeroyi DSS-3

<220>
<221> CDS

<222> (1)..(1158)
<223> transl_table=11

<400> 98

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1               5                  10                  15
acc ctg aga aaa aat atg cca atc cag ggg ggc atc gtg aag acg ttt       96
Thr Leu Arg Lys Asn Met Pro Ile Gln Gly Gly Ile Val Lys Thr Phe
            20                  25                  30
gtg gat gcg ccc gtt tca ggg gcg gtg gac gat cag gca ttg ctg cgc       144
Val Asp Ala Pro Val Ser Gly Ala Val Asp Asp Gln Ala Leu Leu Arg
        35                  40                  45
cgc gca ttg gag cgg ttc gcg cgt atc cgc ctg ggg cat ctg ccg agt       192
Arg Ala Leu Glu Arg Phe Ala Arg Ile Arg Leu Gly His Leu Pro Ser
    50                  55                  60
ccg ctg gaa ccg ctg gac cgg ctg agc gag gcg ctt ggc ggt ccg cgc       240
Pro Leu Glu Pro Leu Asp Arg Leu Ser Glu Ala Leu Gly Gly Pro Arg
65                  70                  75                  80
atc tgg gtc aag cgc gac gac tgc acc ggc ctg tcc agc ggc ggc aac       288
Ile Trp Val Lys Arg Asp Asp Cys Thr Gly Leu Ser Ser Gly Gly Asn

                85                  90                  95
aag acc cgc aag ctg gaa ttc ctg atg gca agc gcg tgc gag gcc ggc       336
Lys Thr Arg Lys Leu Glu Phe Leu Met Ala Ser Ala Cys Glu Ala Gly
            100                 105                 110
gcc gac acg atc atc acc cag ggc gcg atc cag tcc aac cat gcc cgc       384
Ala Asp Thr Ile Ile Thr Gln Gly Ala Ile Gln Ser Asn His Ala Arg
        115                 120                 125
cag acc gcc gcc gcc gcg gcg cgg ctg ggc ctg cat tgc cac ctg ttg       432
Gln Thr Ala Ala Ala Ala Ala Arg Leu Gly Leu His Cys His Leu Leu
    130                 135                 140
ctg gaa gac cgg acc ggc gcc gcg gac ctg gcc tat acc ctg aac ggc       480
Leu Glu Asp Arg Thr Gly Ala Ala Asp Leu Ala Tyr Thr Leu Asn Gly
145                 150                 155                 160
aat gtg ctg ctt gac cgg ttg cac ggc gcc acg atc tcg cga cgg gcc       528
Asn Val Leu Leu Asp Arg Leu His Gly Ala Thr Ile Ser Arg Arg Ala
                165                 170                 175
ggc ggg tcg gac atg gcg gcc gag atg gag cgg ctg gcc gcg acg ttg       576
Gly Gly Ser Asp Met Ala Ala Glu Met Glu Arg Leu Ala Ala Thr Leu
            180                 185                 190
agg ggc aag ggc aag cgc ccc tat gtc att ccc ggc ggc gga tcg aac       624
Arg Gly Lys Gly Lys Arg Pro Tyr Val Ile Pro Gly Gly Gly Ser Asn
        195                 200                 205
cgg gtg ggt gcc ctt ggc tat gtc aat tgc gcg ctg gaa ctg agc gaa       672
Arg Val Gly Ala Leu Gly Tyr Val Asn Cys Ala Leu Glu Leu Ser Glu
    210                 215                 220
cag gcc ctg agc atg ggc ctg gac atc gac gcg ctg atc cat gcg acg       720
Gln Ala Leu Ser Met Gly Leu Asp Ile Asp Ala Leu Ile His Ala Thr
225                 230                 235                 240
ggc agt tgc ggc acg cag gcc ggc ctg gtc gcg ggc ctg gcc ggc ctg       768
Gly Ser Cys Gly Thr Gln Ala Gly Leu Val Ala Gly Leu Ala Gly Leu
                245                 250                 255
tcc tgg aac acc cat ctg ctg ggg atc ggc gtg cgc gcg ccg cag gag       816
Ser Trp Asn Thr His Leu Leu Gly Ile Gly Val Arg Ala Pro Gln Glu
            260                 265                 270
cgg caa gag gcc atg gtc ttt gat ctg gcc tgc gag acc atg gat tac       864
Arg Gln Glu Ala Met Val Phe Asp Leu Ala Cys Glu Thr Met Asp Tyr
        275                 280                 285
ctt ggc atg gga ata ccg atc gtg cgc tcg ggc gtg cgg gcc aat tgc       912
Leu Gly Met Gly Ile Pro Ile Val Arg Ser Gly Val Arg Ala Asn Cys
```

```
    290                 295                 300
gac cat gtc ggg ccg ggc tat ggc ctg ccg acc gag gcc atg tgc gag       960
Asp His Val Gly Pro Gly Tyr Gly Leu Pro Thr Glu Ala Met Cys Glu
305                 310                 315                 320
gcg gtc agg atg ctg gcg cgg ctc gag ggt ctg ctg ctt gac ccg gtc      1008
Ala Val Arg Met Leu Ala Arg Leu Glu Gly Leu Leu Leu Asp Pro Val
                325                 330                 335
tat acc ggc aag gcc atg gcg ggc ctg atc gac ctg aca cgg cag gga      1056
Tyr Thr Gly Lys Ala Met Ala Gly Leu Ile Asp Leu Thr Arg Gln Gly
            340                 345                 350
tat ttc gac ggg atg gcg aat atc gtc ttc ctg cat acc ggc ggc agt      1104
Tyr Phe Asp Gly Met Ala Asn Ile Val Phe Leu His Thr Gly Gly Ser
        355                 360                 365
gcg gcg ctt ttc ggg tat ccg gaa atc ttc gga ctg ccg gga tac caa      1152
Ala Ala Leu Phe Gly Tyr Pro Glu Ile Phe Gly Leu Pro Gly Tyr Gln
    370                 375                 380
cca taa                                                             1158
Pro
385

<210> 99

<211> 385
<212> PRT
<213> Silicibacter pomeroyi DSS-3

<400> 99
Met Gly Ser Met Gln Ile Arg His Tyr Ser Asn Arg Phe Leu Leu Ser
1               5                   10                  15
Thr Leu Arg Lys Asn Met Pro Ile Gln Gly Gly Ile Val Lys Thr Phe
            20                  25                  30
Val Asp Ala Pro Val Ser Gly Ala Val Asp Asp Gln Ala Leu Leu Arg
        35                  40                  45
Arg Ala Leu Glu Arg Phe Ala Arg Ile Arg Leu Gly His Leu Pro Ser
    50                  55                  60
Pro Leu Glu Pro Leu Asp Arg Leu Ser Glu Ala Leu Gly Gly Pro Arg
65                  70                  75                  80
Ile Trp Val Lys Arg Asp Asp Cys Thr Gly Leu Ser Ser Gly Gly Asn
                85                  90                  95
Lys Thr Arg Lys Leu Glu Phe Leu Met Ala Ser Ala Cys Glu Ala Gly
            100                 105                 110
Ala Asp Thr Ile Ile Thr Gln Gly Ala Ile Gln Ser Asn His Ala Arg
        115                 120                 125
Gln Thr Ala Ala Ala Ala Ala Arg Leu Gly Leu His Cys His Leu Leu
    130                 135                 140
Leu Glu Asp Arg Thr Gly Ala Ala Asp Leu Ala Tyr Thr Leu Asn Gly
145                 150                 155                 160
Asn Val Leu Leu Asp Arg Leu His Gly Ala Thr Ile Ser Arg Arg Ala
                165                 170                 175
Gly Gly Ser Asp Met Ala Ala Glu Met Glu Arg Leu Ala Ala Thr Leu
            180                 185                 190
Arg Gly Lys Gly Lys Arg Pro Tyr Val Ile Pro Gly Gly Gly Ser Asn
        195                 200                 205
Arg Val Gly Ala Leu Gly Tyr Val Asn Cys Ala Leu Glu Leu Ser Glu
    210                 215                 220
Gln Ala Leu Ser Met Gly Leu Asp Ile Asp Ala Leu Ile His Ala Thr
225                 230                 235                 240
Gly Ser Cys Gly Thr Gln Ala Gly Leu Val Ala Gly Leu Ala Gly Leu
                245                 250                 255
Ser Trp Asn Thr His Leu Leu Gly Ile Gly Val Arg Ala Pro Gln Glu
            260                 265                 270
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```
Arg Gln Glu Ala Met Val Phe Asp Leu Ala Cys Glu Thr Met Asp Tyr
        275                 280                 285
Leu Gly Met Gly Ile Pro Ile Val Arg Ser Gly Val Arg Ala Asn Cys
    290                 295                 300
Asp His Val Gly Pro Gly Tyr Gly Leu Pro Thr Glu Ala Met Cys Glu
305                 310                 315                 320
Ala Val Arg Met Leu Ala Arg Leu Glu Gly Leu Leu Leu Asp Pro Val
                325                 330                 335
Tyr Thr Gly Lys Ala Met Ala Gly Leu Ile Asp Leu Thr Arg Gln Gly
            340                 345                 350
Tyr Phe Asp Gly Met Ala Asn Ile Val Phe Leu His Thr Gly Gly Ser
        355                 360                 365
Ala Ala Leu Phe Gly Tyr Pro Glu Ile Phe Gly Leu Pro Gly Tyr Gln
    370                 375                 380
Pro
385
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<210> 100
<211> 987
<212> DNA
<213> Salmonella enterica subsp. enterica serovar Choleraesuis str

<220>
<221> CDS
<222> (1)..(987)
<223> transl_table=11

<400> 100

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

225                 230                 235                 240
cag ctg gcg ctg acg gcg acg gcg gat att cat tta tgg gat gac tat       768
Gln Leu Ala Leu Thr Ala Thr Ala Asp Ile His Leu Trp Asp Asp Tyr
                245                 250                 255
ttt gcc ccg ggt tac ggc gtg cca aat gac gcg ggg atg gag gcg gtg       816
Phe Ala Pro Gly Tyr Gly Val Pro Asn Asp Ala Gly Met Glu Ala Val
            260                 265                 270
aaa ctg ctg gcg agc ctg gag ggg gtg ttg ctg gat ccg gta tat acc       864
Lys Leu Leu Ala Ser Leu Glu Gly Val Leu Leu Asp Pro Val Tyr Thr
        275                 280                 285
ggc aaa gcg atg gcg ggt ctg ata gac ggc atc agc cag aaa cgc ttt       912
Gly Lys Ala Met Ala Gly Leu Ile Asp Gly Ile Ser Gln Lys Arg Phe
    290                 295                 300
aac gat gac ggg ccg att ctc ttt att cac acc ggt ggg gcg cct gcg       960
Asn Asp Asp Gly Pro Ile Leu Phe Ile His Thr Gly Gly Ala Pro Ala
305                 310                 315                 320
ctg ttt gcc tac cat cct cat gta taa                                  987
Leu Phe Ala Tyr His Pro His Val
                325
```

<210> 101
<211> 328
<212> PRT
<213> Salmonella enterica subsp. enterica serovar Choleraesuis str

<400> 101

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

```
            180                 185                 190
Ser Gly Ser Ala Gly Thr His Ala Gly Leu Ala Val Gly Leu Glu His
        195                 200                 205
Leu Met Pro Asp Val Glu Leu Ile Gly Val Thr Val Ser Arg Ser Val
    210                 215                 220
Ala Glu Gln Lys Pro Arg Val Ile Ser Leu Gln Gln Ala Ile Ala Gly
225                 230                 235                 240
Gln Leu Ala Leu Thr Ala Thr Ala Asp Ile His Leu Trp Asp Asp Tyr
                245                 250                 255
Phe Ala Pro Gly Tyr Gly Val Pro Asn Asp Ala Gly Met Glu Ala Val
            260                 265                 270
Lys Leu Leu Ala Ser Leu Glu Gly Val Leu Leu Asp Pro Val Tyr Thr
        275                 280                 285
Gly Lys Ala Met Ala Gly Leu Ile Asp Gly Ile Ser Gln Lys Arg Phe
    290                 295                 300
Asn Asp Asp Gly Pro Ile Leu Phe Ile His Thr Gly Gly Ala Pro Ala
305                 310                 315                 320
Leu Phe Ala Tyr His Pro His Val
                325
```

<210> 102
<211> 999
<212> DNA
<213> Pseudomonas syringae pv. syringae B728a

<220>
<221> CDS
<222> (1)..(999)
<223> transl_table=11

<400> 102

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

```
tca agc ccg gtg ggt gcg ctg ggt tat gtg cgc gcc ggg ctg gaa ctg       528
Ser Ser Pro Val Gly Ala Leu Gly Tyr Val Arg Ala Gly Leu Glu Leu
                165                 170                 175
gcc gag cag atc aag cag acc ggc atc gag ttt gcg gct gtc gtt ctg       576
Ala Glu Gln Ile Lys Gln Thr Gly Ile Glu Phe Ala Ala Val Val Leu
            180                 185                 190
gcc tcc ggc agt gcc ggc acg cac agc ggc ctg gcg ttg gca ctg gct       624
Ala Ser Gly Ser Ala Gly Thr His Ser Gly Leu Ala Leu Ala Leu Ala
        195                 200                 205
cac gag ctg ccg caa ttg ccg gtc atc ggt gtg acc gtg tcg cgc agt       672
His Glu Leu Pro Gln Leu Pro Val Ile Gly Val Thr Val Ser Arg Ser
    210                 215                 220
gaa gaa gca cag ctg ccc aag gtc cag ggc ctg gcc gag cgc acc gca       720
Glu Glu Ala Gln Leu Pro Lys Val Gln Gly Leu Ala Glu Arg Thr Ala
225                 230                 235                 240
gag ttg ctc ggc gtt gcg ctg cct gaa cac ttc aag gtc gaa ctg tgg       768
Glu Leu Leu Gly Val Ala Leu Pro Glu His Phe Lys Val Glu Leu Trp
                245                 250                 255
gat gag tat ttc gcc ccg cga tat ggt gaa ccg aac gcc ggt acg ctg       816
Asp Glu Tyr Phe Ala Pro Arg Tyr Gly Glu Pro Asn Ala Gly Thr Leu
            260                 265                 270
tca gcc atc aag ctg gtg gcc agc cac gaa gga ctg ttg ctt gac ccg       864
Ser Ala Ile Lys Leu Val Ala Ser His Glu Gly Leu Leu Leu Asp Pro
        275                 280                 285
gtc tac acc ggc aag gcc atg tcc ggt ctg ctc gat ggc atc ggc cgt       912
Val Tyr Thr Gly Lys Ala Met Ser Gly Leu Leu Asp Gly Ile Gly Arg
    290                 295                 300
caa cgc ttc aac gac ggc ccg ctg atc ttc ctg cac acc ggc ggt gcg       960
Gln Arg Phe Asn Asp Gly Pro Leu Ile Phe Leu His Thr Gly Gly Ala
305                 310                 315                 320
cca gcg ctg ttt gcc tat ccg gat gcg ttc gac cag tga                   999
Pro Ala Leu Phe Ala Tyr Pro Asp Ala Phe Asp Gln
                325                 330
```

<210> 103
<211> 332
<212> PRT
<213> Pseudomonas syringae pv. syringae B728a

<400> 103

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

```
                165                 170                 175
Ala Glu Gln Ile Lys Gln Thr Gly Ile Glu Phe Ala Ala Val Val Leu
            180                 185                 190
Ala Ser Gly Ser Ala Gly Thr His Ser Gly Leu Ala Leu Ala Leu Ala
        195                 200                 205
His Glu Leu Pro Gln Leu Pro Val Ile Gly Val Thr Val Ser Arg Ser
    210                 215                 220
Glu Glu Ala Gln Leu Pro Lys Val Gln Gly Leu Ala Glu Arg Thr Ala
225                 230                 235                 240
Glu Leu Leu Gly Val Ala Leu Pro Glu His Phe Lys Val Glu Leu Trp
                245                 250                 255
Asp Glu Tyr Phe Ala Pro Arg Tyr Gly Glu Pro Asn Ala Gly Thr Leu
            260                 265                 270
Ser Ala Ile Lys Leu Val Ala Ser His Glu Gly Leu Leu Leu Asp Pro
        275                 280                 285
Val Tyr Thr Gly Lys Ala Met Ser Gly Leu Leu Asp Gly Ile Gly Arg
    290                 295                 300
Gln Arg Phe Asn Asp Gly Pro Leu Ile Phe Leu His Thr Gly Gly Ala
305                 310                 315                 320
Pro Ala Leu Phe Ala Tyr Pro Asp Ala Phe Asp Gln
                325                 330
```

<210> 104
<211> 945
<212> DNA
<213> Pseudomonas syringae pv. syringae B728a

<220>
<221> CDS
<222> (1)..(945)
<223> transl_table=11

<400> 104

```
atg atg ctc gac gcc ctc ggc tgg caa ccc act gct ccc ctg gaa cgc        48

Met Met Leu Asp Ala Leu Gly Trp Gln Pro Thr Ala Pro Leu Glu Arg
1               5                   10                  15
ttg aac ctg ccc tgg ctg caa gac acc ggg gtc gag gtt gcg atc ctg        96
Leu Asn Leu Pro Trp Leu Gln Asp Thr Gly Val Glu Val Ala Ile Leu
            20                  25                  30
cgc ctg gac ctt atc gac gcg ctg atc agc ggt aac aaa tgg ttc aag       144
Arg Leu Asp Leu Ile Asp Ala Leu Ile Ser Gly Asn Lys Trp Phe Lys
        35                  40                  45
ctc agc gag cac ctc agt ctg gct gtt gat tcg ggt gcc gag ggg ttg       192
Leu Ser Glu His Leu Ser Leu Ala Val Asp Ser Gly Ala Glu Gly Leu
    50                  55                  60
atc agc ctc ggc ggc gca cat tcc aat cat ctg cat gcc ctg gcc gct       240
Ile Ser Leu Gly Gly Ala His Ser Asn His Leu His Ala Leu Ala Ala
65                  70                  75                  80
gca ggc aaa cgc ttc ggt ttc ccg acg gtc ggc ctg ttg cgc ggt cat       288
Ala Gly Lys Arg Phe Gly Phe Pro Thr Val Gly Leu Leu Arg Gly His
                85                  90                  95
acc cag cag acg cca acg gtg ctc gat ctg cag gct ttc ggc atg caa       336
Thr Gln Gln Thr Pro Thr Val Leu Asp Leu Gln Ala Phe Gly Met Gln
            100                 105                 110
ctg cac tgg ctg ggt tat gcc ggc tat cgt gag cgg cat gct gcg ggc       384
Leu His Trp Leu Gly Tyr Ala Gly Tyr Arg Glu Arg His Ala Ala Gly
        115                 120                 125
ttc tgg tcg ccg tgg cag gcc cgc tat ccc ggt ctt tat ccg att gcc       432
Phe Trp Ser Pro Trp Gln Ala Arg Tyr Pro Gly Leu Tyr Pro Ile Ala
    130                 135                 140
```

```
gaa ggc ggt ggc ggg ctt gcc ggt gca ttg ggt tgc ggt cgg ttg cgg       480
Glu Gly Gly Gly Gly Leu Ala Gly Ala Leu Gly Cys Gly Arg Leu Arg
145                 150                 155                 160
gca atg ctc gac gcg cag ctc ggg cac ctg ggc tgg gac gat tac cac       528
Ala Met Leu Asp Ala Gln Leu Gly His Leu Gly Trp Asp Asp Tyr His
                165                 170                 175
gga tgg tgg ttg gcg gca ggc acc ggc acc acg ctg gcc ggc ttg ctg       576
Gly Trp Trp Leu Ala Ala Gly Thr Gly Thr Thr Leu Ala Gly Leu Leu
            180                 185                 190
ttg gca gag gcg ggc gcc cgg ccg gtg tat ggg gcg atg gct gtg ccc       624
Leu Ala Glu Ala Gly Ala Arg Pro Val Tyr Gly Ala Met Ala Val Pro
        195                 200                 205
gag gat cac ggg gtc gcg caa aac atc atc gcg gtg ctg aat gag gcg       672
Glu Asp His Gly Val Ala Gln Asn Ile Ile Ala Val Leu Asn Glu Ala
    210                 215                 220
gcc ggt gcg caa acc gat gtc gcg ccg cgc ctg cca ccc act tgt att       720
Ala Gly Ala Gln Thr Asp Val Ala Pro Arg Leu Pro Pro Thr Cys Ile
225                 230                 235                 240
ctg ctc gat gcc agc cgc ggc ggt ttc gcc aga acc gac gcg gcg ctg       768
Leu Leu Asp Ala Ser Arg Gly Gly Phe Ala Arg Thr Asp Ala Ala Leu
                245                 250                 255
ctc ggt ttc att gcc gac agc gag gca cag agc ggt gta cct ctg gag       816
Leu Gly Phe Ile Ala Asp Ser Glu Ala Gln Ser Gly Val Pro Leu Glu
            260                 265                 270
ccg ctg tac acc ggc aag gcg ttg ctg gcc ctg cat gat gaa gtg ctg       864
Pro Leu Tyr Thr Gly Lys Ala Leu Leu Ala Leu His Asp Glu Val Leu
        275                 280                 285
gcc ggt cgt ttc gcg ccc ggc acc cgg ctg gtc ttc gtc cac acc ggc       912
Ala Gly Arg Phe Ala Pro Gly Thr Arg Leu Val Phe Val His Thr Gly
    290                 295                 300
ggc ctt cag ggg cgg cgt gcg atg ggc ctg taa                           945
Gly Leu Gln Gly Arg Arg Ala Met Gly Leu
305                 310
```

<210> 105
<211> 314
<212> PRT
<213> Pseudomonas syringae pv. syringae B728a

<400> 105

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

```
                165                 170                 175
Gly Trp Trp Leu Ala Ala Gly Thr Gly Thr Thr Leu Ala Gly Leu Leu
            180                 185                 190
Leu Ala Glu Ala Gly Ala Arg Pro Val Tyr Gly Ala Met Ala Val Pro
        195                 200                 205
Glu Asp His Gly Val Ala Gln Asn Ile Ile Ala Val Leu Asn Glu Ala
    210                 215                 220
Ala Gly Ala Gln Thr Asp Val Ala Pro Arg Leu Pro Pro Thr Cys Ile
225                 230                 235                 240
Leu Leu Asp Ala Ser Arg Gly Gly Phe Ala Arg Thr Asp Ala Ala Leu
                245                 250                 255
Leu Gly Phe Ile Ala Asp Ser Glu Ala Gln Ser Gly Val Pro Leu Glu
            260                 265                 270
Pro Leu Tyr Thr Gly Lys Ala Leu Leu Ala Leu His Asp Glu Val Leu
        275                 280                 285
Ala Gly Arg Phe Ala Pro Gly Thr Arg Leu Val Phe Val His Thr Gly
    290                 295                 300
Gly Leu Gln Gly Arg Arg Ala Met Gly Leu
305                 310
```

<210> 106
<211> 1017
<212> DNA
<213> Pseudomonas syringae pv. syringae B728a

<220>
<221> CDS
<222> (1)..(1017)
<223> transl_table=11

<400> 106

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

```
ggc tgc tcg gaa cac cct tat ggc ggc ctg ggg ttc gtg cgt ttt gcc       528
Gly Cys Ser Glu His Pro Tyr Gly Gly Leu Gly Phe Val Arg Phe Ala
                165                 170                 175
gat gaa gtg cgc cag cag gaa gaa gag ctg ggc ttc aaa ttc gac tac       576
Asp Glu Val Arg Gln Gln Glu Glu Glu Leu Gly Phe Lys Phe Asp Tyr
            180                 185                 190
att gtg gtc tgc tcg gtg acc ggc agc act cac gca ggc atg ctg gtg       624
Ile Val Val Cys Ser Val Thr Gly Ser Thr His Ala Gly Met Leu Val
        195                 200                 205
ggc ttc gct gcc gat ggc cgg gca caa cgt gtg atc ggt atc gac gcg       672
Gly Phe Ala Ala Asp Gly Arg Ala Gln Arg Val Ile Gly Ile Asp Ala
    210                 215                 220
tcg gcg aaa ccg gaa aag acc cgc gcg cag gtc ctg cgc atc gct cag       720
Ser Ala Lys Pro Glu Lys Thr Arg Ala Gln Val Leu Arg Ile Ala Gln
225                 230                 235                 240
aac act gca aaa ctg gtg gag ctg ggc cgc gaa ata acc gcc gaa gac       768
Asn Thr Ala Lys Leu Val Glu Leu Gly Arg Glu Ile Thr Ala Glu Asp
                245                 250                 255
gtg gtg ctc gac acc cgc tac gcc tac ccg gaa tac ggc ctg ccg aac       816
Val Val Leu Asp Thr Arg Tyr Ala Tyr Pro Glu Tyr Gly Leu Pro Asn
            260                 265                 270
gat ggc acc ctc gaa gcc atc cgc ctc tgc gcc cgc ctg gaa ggc gtg       864
Asp Gly Thr Leu Glu Ala Ile Arg Leu Cys Ala Arg Leu Glu Gly Val
        275                 280                 285
ctg acc gac ccg gtc tac gaa ggc aaa tcc atg cac ggc atg atc gac       912
Leu Thr Asp Pro Val Tyr Glu Gly Lys Ser Met His Gly Met Ile Asp
    290                 295                 300
atg gtg cgc aat ggc gaa ttc ccc gaa ggc tcg aaa gtg ctc tac gcc       960
Met Val Arg Asn Gly Glu Phe Pro Glu Gly Ser Lys Val Leu Tyr Ala
305                 310                 315                 320
cac ctg ggc ggc gtg ccg gcg ctg aat gcc tac agc ttt ctg ttc aag      1008
His Leu Gly Gly Val Pro Ala Leu Asn Ala Tyr Ser Phe Leu Phe Lys
                325                 330                 335
gac ggt tga                                                         1017
Asp Gly
```

<210> 107
<211> 338
<212> PRT
<213> Pseudomonas syringae pv. syringae B728a

<400> 107

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

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

<210> 108
<211> 996
<212> DNA
<213> Pseudomonas fluorescens Pf-5

<220>
<221> CDS
<222> (1)..(996)
<223> transl_table=11

<400> 108

```
atg atc aaa caa cag ctc gcc cgc ttt aac cgt ctc gac ctg ctc agg       48
Met Ile Lys Gln Gln Leu Ala Arg Phe Asn Arg Leu Asp Leu Leu Arg
1               5                   10                  15
tct acc acc gcc ctg gaa aaa ctc gaa cgc ctg tcg gcc tgg atc ggt       96
Ser Thr Thr Ala Leu Glu Lys Leu Glu Arg Leu Ser Ala Trp Ile Gly
            20                  25                  30
cgc gat gtc tac gtc aag cgt gac gac agc aca ccc ctg gcc atg ggc      144
Arg Asp Val Tyr Val Lys Arg Asp Asp Ser Thr Pro Leu Ala Met Gly
        35                  40                  45
ggc aac aag ctg cgc aag ctc gaa tac ctg gcc gcc gat gcc ctg gcc      192
Gly Asn Lys Leu Arg Lys Leu Glu Tyr Leu Ala Ala Asp Ala Leu Ala
    50                  55                  60
cag ggc gcc gac acc ctg atc acc gcc ggt gcc atc cag tcc aac cat      240
Gln Gly Ala Asp Thr Leu Ile Thr Ala Gly Ala Ile Gln Ser Asn His
65                  70                  75                  80
gtg cgc cag acc gca gcc ctg gct gcc aag ttg ggg ctg ggc tgc gtg      288
Val Arg Gln Thr Ala Ala Leu Ala Ala Lys Leu Gly Leu Gly Cys Val
                85                  90                  95
gcc ctg ctg gaa aac ccc acc ggc acc caa gac ccc aac tac ctg ggc      336
Ala Leu Leu Glu Asn Pro Thr Gly Thr Gln Asp Pro Asn Tyr Leu Gly
            100                 105                 110
aat ggc aac cgc ctg ctg ctg gac ctg ttc gac gcc aag gtg gag ctg      384
Asn Gly Asn Arg Leu Leu Leu Asp Leu Phe Asp Ala Lys Val Glu Leu
```

```
        115                 120                 125
gtg gaa aac ctc gac cag gcc gac gag caa ctg cac gcc ctg gcc gcg       432
Val Glu Asn Leu Asp Gln Ala Asp Glu Gln Leu His Ala Leu Ala Ala
    130                 135                 140
cgc ctg cgc agc aac ggc aag aaa ccc tac ctg gtg ccc atc ggc ggc       480
Arg Leu Arg Ser Asn Gly Lys Lys Pro Tyr Leu Val Pro Ile Gly Gly
145                 150                 155                 160
tcc aac gcc ctg ggg gcc ctg ggc tac gtg cgc gcc ggc ctg gag ctg       528
Ser Asn Ala Leu Gly Ala Leu Gly Tyr Val Arg Ala Gly Leu Glu Leu
                165                 170                 175
gcg cag cag atc gaa gac agc ggc ctg gaa ttt gcc gcc gtg gtc ctg       576
Ala Gln Gln Ile Glu Asp Ser Gly Leu Glu Phe Ala Ala Val Val Leu
            180                 185                 190
gcc tcc ggc agc gcc ggc acc cac agc ggc ctg gcc ctg gcc ttg agc       624
Ala Ser Gly Ser Ala Gly Thr His Ser Gly Leu Ala Leu Ala Leu Ser
        195                 200                 205
gaa gtg ctg ccg caa ctg ccg gtg atc ggg gtc acc gtg tcg cgc agc       672
Glu Val Leu Pro Gln Leu Pro Val Ile Gly Val Thr Val Ser Arg Ser
    210                 215                 220
gaa gaa gac cag cgg ccc aag gtc cag ggc ctg gcc gaa cgc acc gcc       720
Glu Glu Asp Gln Arg Pro Lys Val Gln Gly Leu Ala Glu Arg Thr Ala
225                 230                 235                 240
gag ttg ctg gga gtg aag ctg ccc gac gct ttc aac gtg cag ttg tgg       768
Glu Leu Leu Gly Val Lys Leu Pro Asp Ala Phe Asn Val Gln Leu Trp
                245                 250                 255
gac gag tac ttc gcc ccg cgc tac ggt gag ccc aat gcc ggg acg ctg       816
Asp Glu Tyr Phe Ala Pro Arg Tyr Gly Glu Pro Asn Ala Gly Thr Leu
            260                 265                 270
gcg gcg gtc aag ctg ctg gcc agc cag gaa ggc ctg ttg ctg gac ccg       864
Ala Ala Val Lys Leu Leu Ala Ser Gln Glu Gly Leu Leu Leu Asp Pro
        275                 280                 285
gtg tac acc ggc aag gcc atg gcc ggc ctg ctg gac ggg gtc ggt cgc       912
Val Tyr Thr Gly Lys Ala Met Ala Gly Leu Leu Asp Gly Val Gly Arg
    290                 295                 300
cag cgc ttc gac gat ggc ccg ctg att ttc ctg cac acc ggc ggc gcc       960
Gln Arg Phe Asp Asp Gly Pro Leu Ile Phe Leu His Thr Gly Gly Ala
305                 310                 315                 320
ccg gcc ctg ttc gcc tac gcc ggc gcc ttc tcg tag                       996
Pro Ala Leu Phe Ala Tyr Ala Gly Ala Phe Ser
                325                 330
```

<210> 109
<211> 331
<212> PRT
<213> Pseudomonas fluorescens Pf-5

<400> 109

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

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

<210> 110
<211> 1023
<212> DNA
<213> Psychrobacter arcticus 273-4

<220>
<221> CDS
<222> (1)..(1023)
<223> transl_table=11

<400> 110

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atg caa aat aaa tct ata cca agc ctg ccg agc atg aat cga caa cct        48
Met Gln Asn Lys Ser Ile Pro Ser Leu Pro Ser Met Asn Arg Gln Pro
1               5                   10                  15
tta gga ttt ttc cca acg ccg ttg att gag ctg acc aga tta agc aaa        96
Leu Gly Phe Phe Pro Thr Pro Leu Ile Glu Leu Thr Arg Leu Ser Lys
            20                  25                  30
gca ctt aat ggc cct aaa att tat atg aaa cga gat gac aat acg gga       144
Ala Leu Asn Gly Pro Lys Ile Tyr Met Lys Arg Asp Asp Asn Thr Gly
        35                  40                  45
ctg gca tta ggc ggt aat aaa acc aga aag ctt gag ttt att att ggg       192
Leu Ala Leu Gly Gly Asn Lys Thr Arg Lys Leu Glu Phe Ile Ile Gly
    50                  55                  60
gat gca ctt gct caa ggt gcg gat acg atc gtg aca gca ggt gct gcg       240
Asp Ala Leu Ala Gln Gly Ala Asp Thr Ile Val Thr Ala Gly Ala Ala
65                  70                  75                  80
cag tca aat cat tgt cgc cag acc gca gcc gcc gca gcc agt ttg gga       288
Gln Ser Asn His Cys Arg Gln Thr Ala Ala Ala Ala Ala Ser Leu Gly
                85                  90                  95
ctt gaa tgc cat tta gtt ttg ggc gga caa gag ccg gat cag ctc aat       336
Leu Glu Cys His Leu Val Leu Gly Gly Gln Glu Pro Asp Gln Leu Asn
            100                 105                 110
```

```
ggc aat ctt tta ctg gat aag att ttt ggc tgt cat att cac tgg gca       384
Gly Asn Leu Leu Leu Asp Lys Ile Phe Gly Cys His Ile His Trp Ala
        115                 120                 125
ggc aat aat cgt aaa gga gaa gac att cct gat att gta gag cag ctc       432
Gly Asn Asn Arg Lys Gly Glu Asp Ile Pro Asp Ile Val Glu Gln Leu
    130                 135                 140
gaa aat gca ggt aag aaa ccc tat gtt gtc cct tat ggg ggc tca agc       480
Glu Asn Ala Gly Lys Lys Pro Tyr Val Val Pro Tyr Gly Gly Ser Ser
145                 150                 155                 160
gag ctg ggg gct ttt gcc ttt atc gaa gct ttc aaa gag ctt gaa tcg       528
Glu Leu Gly Ala Phe Ala Phe Ile Glu Ala Phe Lys Glu Leu Glu Ser
                165                 170                 175
caa cgt caa gag atg gat atc tcg ttc act cat atc gtt ttt gcg tct       576
Gln Arg Gln Glu Met Asp Ile Ser Phe Thr His Ile Val Phe Ala Ser
            180                 185                 190
agc tcc ggt ggg aca caa gcg ggc tta atg ctt ggc aat aaa atc ttt       624
Ser Ser Gly Gly Thr Gln Ala Gly Leu Met Leu Gly Asn Lys Ile Phe
        195                 200                 205
aac tca cct tat caa ata gtg ggc atc aat att gat aaa ggt gaa acg       672
Asn Ser Pro Tyr Gln Ile Val Gly Ile Asn Ile Asp Lys Gly Glu Thr
    210                 215                 220
gat aaa gta cct ttt gat cag tat att gtc tcc ctt gcc aac agc aca       720
Asp Lys Val Pro Phe Asp Gln Tyr Ile Val Ser Leu Ala Asn Ser Thr
225                 230                 235                 240
gca gca ttg atc ggt gca gac tat agc ttt tca gag aca gat cta atg       768
Ala Ala Leu Ile Gly Ala Asp Tyr Ser Phe Ser Glu Thr Asp Leu Met
                245                 250                 255
ctt aat tct gat tat gtg gga gac ggt tat ggg gtt att ggc gca tta       816
Leu Asn Ser Asp Tyr Val Gly Asp Gly Tyr Gly Val Ile Gly Ala Leu
            260                 265                 270
gaa aat gaa gcc att gcc atg acc gcg caa acg gaa ggc ata tta tta       864
Glu Asn Glu Ala Ile Ala Met Thr Ala Gln Thr Glu Gly Ile Leu Leu
        275                 280                 285
gat cct gtt tat acg ggt cgt gcg atg ggc ggg ctc ata gat atg att       912
Asp Pro Val Tyr Thr Gly Arg Ala Met Gly Gly Leu Ile Asp Met Ile
    290                 295                 300
cgt acc ggt aaa atc aag aaa acg gac agt gtg tta ttt tgg cat act       960
Arg Thr Gly Lys Ile Lys Lys Thr Asp Ser Val Leu Phe Trp His Thr
305                 310                 315                 320
ggc ggc gcg ccc gct ttg ttc gct tat gcc agt gct tta gcg gtg tct      1008
Gly Gly Ala Pro Ala Leu Phe Ala Tyr Ala Ser Ala Leu Ala Val Ser
                325                 330                 335
caa agc gat agt tag                                              1023
Gln Ser Asp Ser
            340
```

<210> 111
<211> 340
<212> PRT
<213> Psychrobacter arcticus 273-4

<400> 111

```
Met Gln Asn Lys Ser Ile Pro Ser Leu Pro Ser Met Asn Arg Gln Pro
1               5                   10                  15
Leu Gly Phe Phe Pro Thr Pro Leu Ile Glu Leu Thr Arg Leu Ser Lys
            20                  25                  30
Ala Leu Asn Gly Pro Lys Ile Tyr Met Lys Arg Asp Asp Asn Thr Gly
        35                  40                  45
Leu Ala Leu Gly Gly Asn Lys Thr Arg Lys Leu Glu Phe Ile Ile Gly
    50                  55                  60
Asp Ala Leu Ala Gln Gly Ala Asp Thr Ile Val Thr Ala Gly Ala Ala
```

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

<210> 112
<211> 960
<212> DNA
<213> Colwellia psychrerythraea 34H

<220>
<221> CDS
<222> (1)..(960)
<223> transl_table=11

<400> 112

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atg cat aag cca ttg tcc aaa ata caa aaa tta gaa cac cct ctc ttt       48
Met His Lys Pro Leu Ser Lys Ile Gln Lys Leu Glu His Pro Leu Phe
1               5                   10                  15
gat aaa tac aac cta gat gtt cgc gtc aag cgt gat gat tta ctg cat       96
Asp Lys Tyr Asn Leu Asp Val Arg Val Lys Arg Asp Asp Leu Leu His
            20                  25                  30
aac atc ata tca ggc aat aaa tgg cgc aaa cta aag cac aac cta gag      144
Asn Ile Ile Ser Gly Asn Lys Trp Arg Lys Leu Lys His Asn Leu Glu
        35                  40                  45
caa ctt aaa act aat gat tac caa gga gca tta act ttt ggt ggt agt      192
Gln Leu Lys Thr Asn Asp Tyr Gln Gly Ala Leu Thr Phe Gly Gly Ser
    50                  55                  60
tac tca aac cat att cat gct ttt gct tac gca tgt aaa cag cat aac      240
```

```
Tyr Ser Asn His Ile His Ala Phe Ala Tyr Ala Cys Lys Gln His Asn
65                  70                  75                  80
atc ccc tgc atc ggt gtt att aga ggg gaa gct aac tat gcg aat aac      288
Ile Pro Cys Ile Gly Val Ile Arg Gly Glu Ala Asn Tyr Ala Asn Asn
                85                  90                  95
ttt aca ttg agt tgg gcg cgg cac tgg ggc atg caa tgt cac ttt gtc      336
Phe Thr Leu Ser Trp Ala Arg His Trp Gly Met Gln Cys His Phe Val
            100                 105                 110
gac aga aag acc tat cgt cgc cgt ttt gag aca aac ttt att gat gaa      384
Asp Arg Lys Thr Tyr Arg Arg Arg Phe Glu Thr Asn Phe Ile Asp Glu
        115                 120                 125
cta aaa aca cta tat cct aat tac ttt gtt att cct gaa ggt ggc agt      432
Leu Lys Thr Leu Tyr Pro Asn Tyr Phe Val Ile Pro Glu Gly Gly Ser
    130                 135                 140
aat tca ctt gct ata cca ggc gtt gcc gag gtg ttg act gaa ttg aat      480
Asn Ser Leu Ala Ile Pro Gly Val Ala Glu Val Leu Thr Glu Leu Asn
145                 150                 155                 160
agc caa gta gat ttc gat acc tta atc acc cca gta ggt agc gga ggt      528
Ser Gln Val Asp Phe Asp Thr Leu Ile Thr Pro Val Gly Ser Gly Gly
                165                 170                 175
acg tta gca ggt tta att tcg gga gat agt gtc gcc aat cag aaa caa      576
Thr Leu Ala Gly Leu Ile Ser Gly Asp Ser Val Ala Asn Gln Lys Gln
            180                 185                 190
cat aaa att ttg ggt att gct gta tta aaa caa gcg gaa tat tta gtt      624
His Lys Ile Leu Gly Ile Ala Val Leu Lys Gln Ala Glu Tyr Leu Val
        195                 200                 205
gat gac att aag cgc ttg ctt act gaa gaa gct aag aac cat gag aac      672
Asp Asp Ile Lys Arg Leu Leu Thr Glu Glu Ala Lys Asn His Glu Asn
    210                 215                 220
tgg aag tta tta acc aac ttt cat cgt ggt ggt tat ggc aag ttt agt      720
Trp Lys Leu Leu Thr Asn Phe His Arg Gly Gly Tyr Gly Lys Phe Ser
225                 230                 235                 240
gag gat gat gtc aaa cga ata ata aca ttc aac cag caa acc ggc gta      768
Glu Asp Asp Val Lys Arg Ile Ile Thr Phe Asn Gln Gln Thr Gly Val
                245                 250                 255
tgc ttt gaa ccg gta tat tca ggt aaa atg gta tta gct tta ctt gat      816
Cys Phe Glu Pro Val Tyr Ser Gly Lys Met Val Leu Ala Leu Leu Asp
            260                 265                 270
tta ata acg caa ggc tat ttt cag ccg caa gaa cgc att gtt tta ttg      864
Leu Ile Thr Gln Gly Tyr Phe Gln Pro Gln Glu Arg Ile Val Leu Leu
        275                 280                 285
cac act ggt gga tta caa gga ctg ggc ggc atg ata gaa caa ggt agg      912
His Thr Gly Gly Leu Gln Gly Leu Gly Gly Met Ile Glu Gln Gly Arg
    290                 295                 300
tta gat gcc aat gac tgg cca cca tta agc agc gtt gac aat gaa          957
Leu Asp Ala Asn Asp Trp Pro Pro Leu Ser Ser Val Asp Asn Glu
305                 310                 315
taa                                                                 960
```

<210> 113
<211> 319
<212> PRT
<213> Colwellia psychrerythraea 34H

<400> 113

```
Met His Lys Pro Leu Ser Lys Ile Gln Lys Leu Glu His Pro Leu Phe
1               5                   10                  15
Asp Lys Tyr Asn Leu Asp Val Arg Val Lys Arg Asp Asp Leu Leu His
            20                  25                  30
```

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

<210> 114
<211> 999
<212> DNA
<213> Pseudomonas syringae pv. phaseolicola 1448A

<220>
<221> CDS
<222> (1)..(999)
<223> transl_table=11

<400> 114

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atg atc aaa aat cag ctt gcc cgt ttc aat cgc ctg gac ttg atc agc       48
Met Ile Lys Asn Gln Leu Ala Arg Phe Asn Arg Leu Asp Leu Ile Ser
1               5                   10                  15
gcg ccg acg gct ctg gaa aag ctt gag cgc ctg tcg atc tgg gca gat       96
Ala Pro Thr Ala Leu Glu Lys Leu Glu Arg Leu Ser Ile Trp Ala Asp
            20                  25                  30
cgc gat atc tac atc aag cgt gat gac acc acc acc ctg gcg ctg ggc      144
Arg Asp Ile Tyr Ile Lys Arg Asp Asp Thr Thr Thr Leu Ala Leu Gly
        35                  40                  45
ggc aac aag gtt cgc aaa ctt gaa tac ctc gcc gca gac gcg ctg gcc      192
Gly Asn Lys Val Arg Lys Leu Glu Tyr Leu Ala Ala Asp Ala Leu Ala
    50                  55                  60
caa ggt gcc gac acg ctg atc act gcg ggc gct atc cag tcc aac cat      240
```

```
Gln Gly Ala Asp Thr Leu Ile Thr Ala Gly Ala Ile Gln Ser Asn His
65                  70                  75                  80
gtt cgc cag act gct gcc ctg gcg gcg cgc ctg ggc ttt ggc tgc gtg       288
Val Arg Gln Thr Ala Ala Leu Ala Ala Arg Leu Gly Phe Gly Cys Val
                85                  90                  95
gcg ctg ctg gaa aac ccc atc ggc act gaa gac ccg agt tac ctg aaa       336
Ala Leu Leu Glu Asn Pro Ile Gly Thr Glu Asp Pro Ser Tyr Leu Lys
            100                 105                 110
aac ggc aat cgc ctg ctg ctg gag ctg ttc gat gcc aag gtc gag ctg       384
Asn Gly Asn Arg Leu Leu Leu Glu Leu Phe Asp Ala Lys Val Glu Leu
        115                 120                 125
gtc gaa aac ctc gac aac gcc gac gaa caa ctg cac gcg ctg gct gcg       432
Val Glu Asn Leu Asp Asn Ala Asp Glu Gln Leu His Ala Leu Ala Ala
    130                 135                 140
cgt ctg cgc tcc agc ggc aag aag cct tat ctg gta ccc atc ggt ggc       480
Arg Leu Arg Ser Ser Gly Lys Lys Pro Tyr Leu Val Pro Ile Gly Gly
145                 150                 155                 160
tca agc ccg gtc ggt gcg ctg ggt tat gtt cgc gcc ggg ctg gaa ctg       528
Ser Ser Pro Val Gly Ala Leu Gly Tyr Val Arg Ala Gly Leu Glu Leu
                165                 170                 175
gct gag cag atc aag cag acc ggc atc gac ttt gcg gcg gtt gtt ctg       576
Ala Glu Gln Ile Lys Gln Thr Gly Ile Asp Phe Ala Ala Val Val Leu
            180                 185                 190
gcc tcc ggc agc gcg ggc acc cac agc ggc ctg gcg ttg gca ctg gct       624
Ala Ser Gly Ser Ala Gly Thr His Ser Gly Leu Ala Leu Ala Leu Ala
        195                 200                 205
cac gag ttg ccg caa ttg ccg gtt atc ggc gtg acc gtt tcg cgc agt       672
His Glu Leu Pro Gln Leu Pro Val Ile Gly Val Thr Val Ser Arg Ser
    210                 215                 220
gaa gaa gca caa ctg ccc aaa gtg cag ggc ttg gcc gag cgt acg gca       720
Glu Glu Ala Gln Leu Pro Lys Val Gln Gly Leu Ala Glu Arg Thr Ala
225                 230                 235                 240
gaa tta ctg gat atc gcc ctg ccg gag cac ttc aag gtt gaa ctg tgg       768
Glu Leu Leu Asp Ile Ala Leu Pro Glu His Phe Lys Val Glu Leu Trp
                245                 250                 255
gac gaa tat ttc gct ccg cgt tat ggc gaa ccg aac gcc ggt acg ctg       816
Asp Glu Tyr Phe Ala Pro Arg Tyr Gly Glu Pro Asn Ala Gly Thr Leu
            260                 265                 270
gcg gcg atc aag ctg gtg gcc agc cac gaa ggg ctg ttg ctg gac ccg       864
Ala Ala Ile Lys Leu Val Ala Ser His Glu Gly Leu Leu Leu Asp Pro
        275                 280                 285
gtt tat acc ggc aag gcc atg tcc ggc ttg ctg gat ggc att ggc cgt       912
Val Tyr Thr Gly Lys Ala Met Ser Gly Leu Leu Asp Gly Ile Gly Arg
    290                 295                 300
caa cgc ttc aac gac ggc ccg ctg atc ttt ctg cac act ggc ggt gct       960
Gln Arg Phe Asn Asp Gly Pro Leu Ile Phe Leu His Thr Gly Gly Ala
305                 310                 315                 320
ccg gcg ctg ttt gcc tac ccg gat gcg ttt gat cag taa                   999
Pro Ala Leu Phe Ala Tyr Pro Asp Ala Phe Asp Gln
                325                 330
```

<210> 115
<211> 332
<212> PRT
<213> Pseudomonas syringae pv. phaseolicola 1448A

<400> 115

```
Met Ile Lys Asn Gln Leu Ala Arg Phe Asn Arg Leu Asp Leu Ile Ser
1               5                   10                  15
Ala Pro Thr Ala Leu Glu Lys Leu Glu Arg Leu Ser Ile Trp Ala Asp
            20                  25                  30
```

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

<210> 116
<211> 945
<212> DNA
<213> Pseudomonas syringae pv. phaseolicola 1448A

<220>
<221> CDS
<222> (1)..(945)
<223> transl_table=11

<400> 116

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atg atc gtt gac gcc ctt gac tgg cag ccc act gct gcg ctg caa cgc       48
Met Ile Val Asp Ala Leu Asp Trp Gln Pro Thr Ala Ala Leu Gln Arg
1               5                   10                  15
ttg aac ctg ccc tgg ctg caa gat gcc ggg gtc gag gtg gcg atc ctg       96
Leu Asn Leu Pro Trp Leu Gln Asp Ala Gly Val Glu Val Ala Ile Leu
            20                  25                  30
cgt ctt gac ctt att gac tcg ctc atc agc ggc aac aaa tgg ttc aag      144
Arg Leu Asp Leu Ile Asp Ser Leu Ile Ser Gly Asn Lys Trp Phe Lys
        35                  40                  45
ctc agc gaa cac ctg acc cag gct gta gag gcg ggt gca gag gga ttg      192
Leu Ser Glu His Leu Thr Gln Ala Val Glu Ala Gly Ala Glu Gly Leu
```

```
    50                  55                  60
atc agc ctg ggc ggc gca tac tcc aat cat ctc cat gct ctg gca gca       240
Ile Ser Leu Gly Gly Ala Tyr Ser Asn His Leu His Ala Leu Ala Ala
65                  70                  75                  80
gcg ggc agg cgc ttc ggt ttc ccg acg gtg ggc ctg ttg cgt ggt cac       288
Ala Gly Arg Arg Phe Gly Phe Pro Thr Val Gly Leu Leu Arg Gly His
                85                  90                  95
gcc cag cag acg ccg acg gta ctg gac ctg caa gct ttt ggc atg caa       336
Ala Gln Gln Thr Pro Thr Val Leu Asp Leu Gln Ala Phe Gly Met Gln
            100                 105                 110
ttg cat tgg ttg ggt tat gcg ggt tat cga gca cga cat gct gcg gat       384
Leu His Trp Leu Gly Tyr Ala Gly Tyr Arg Ala Arg His Ala Ala Asp
        115                 120                 125
ttc tgg ctg ccc tgg cag gcg caa tat cct gag ctg tat ccg att gcc       432
Phe Trp Leu Pro Trp Gln Ala Gln Tyr Pro Glu Leu Tyr Pro Ile Ala
    130                 135                 140
gaa ggc ggt ggc ggg ctt gcc ggt gcg ctg ggc tgc gca agg ttg cgg       480
Glu Gly Gly Gly Gly Leu Ala Gly Ala Leu Gly Cys Ala Arg Leu Arg
145                 150                 155                 160
gag atg gtc gat agc cag ctc ggg cac ctt ggc tgg gac gat tat cac       528
Glu Met Val Asp Ser Gln Leu Gly His Leu Gly Trp Asp Asp Tyr His
                165                 170                 175
ggc tgg tgg ctg gca gtc ggc acc ggc aca acg ctt gcc ggt ttg ctg       576
Gly Trp Trp Leu Ala Val Gly Thr Gly Thr Thr Leu Ala Gly Leu Leu
            180                 185                 190
ttg gcc gag gcc ggc gcc cat ccg gta tat ggc gcg atg gcg gtg ccg       624
Leu Ala Glu Ala Gly Ala His Pro Val Tyr Gly Ala Met Ala Val Pro
        195                 200                 205
gac gat cat ggc gtt gct caa aac atc gtg gct gtg ttg aaa gaa gcc       672
Asp Asp His Gly Val Ala Gln Asn Ile Val Ala Val Leu Lys Glu Ala
    210                 215                 220
gca ggg tcg cag gtg aac gcc tcg ccg aac ctg ccc gct gcc tgt gtc       720
Ala Gly Ser Gln Val Asn Ala Ser Pro Asn Leu Pro Ala Ala Cys Val
225                 230                 235                 240
ctg ctg gag gcc agc cgg ggc ggt ttc gcc agg acc gat gcc gcg ctg       768
Leu Leu Glu Ala Ser Arg Gly Gly Phe Ala Arg Thr Asp Ala Ala Leu
                245                 250                 255
ctc gac ttc atc gcc agc agc gag gcg cat acc ggc gta cct ctg gag       816
Leu Asp Phe Ile Ala Ser Ser Glu Ala His Thr Gly Val Pro Leu Glu
            260                 265                 270
ccc ttg tac acc ggc aag gct ttg ctg gcc ctg cac gat gag gtg ctg       864
Pro Leu Tyr Thr Gly Lys Ala Leu Leu Ala Leu His Asp Glu Val Leu
        275                 280                 285
gcc ggt cgg ttc aag tca ggc agc cgt ctg gtc ttc gtc cat acc ggt       912
Ala Gly Arg Phe Lys Ser Gly Ser Arg Leu Val Phe Val His Thr Gly
    290                 295                 300
ggc ctg cag ggg cgg cgc gcg atg ggc ctg taa                           945
Gly Leu Gln Gly Arg Arg Ala Met Gly Leu
305                 310
```

<210> 117
<211> 314
<212> PRT
<213> Pseudomonas syringae pv. phaseolicola 1448A

<400> 117

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Met Ile Val Asp Ala Leu Asp Trp Gln Pro Thr Ala Ala Leu Gln Arg
1               5                   10                  15
Leu Asn Leu Pro Trp Leu Gln Asp Ala Gly Val Glu Val Ala Ile Leu
            20                  25                  30
Arg Leu Asp Leu Ile Asp Ser Leu Ile Ser Gly Asn Lys Trp Phe Lys
```

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

<210> 118
<211> 1017
<212> DNA
<213> Pseudomonas syringae pv. phaseolicola 1448A

<220>
<221> CDS
<222> (1)..(1017)
<223> transl_table=11

<400> 118

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atg aac ctg agc aag ttc aag cgc tac cct ctg acc ttc ggc ccc tcg       48
Met Asn Leu Ser Lys Phe Lys Arg Tyr Pro Leu Thr Phe Gly Pro Ser
1               5                   10                  15
ccc atc acc cct ctg aaa cgc ttg agc gag cat ctg ggt ggc aag gtc       96
Pro Ile Thr Pro Leu Lys Arg Leu Ser Glu His Leu Gly Gly Lys Val
            20                  25                  30
gag ttg tat gcc aag cgc gag gat tgc aac agc ggt ctg gct ttt ggc      144
Glu Leu Tyr Ala Lys Arg Glu Asp Cys Asn Ser Gly Leu Ala Phe Gly
        35                  40                  45
ggt aac aag acc cgc aaa ctg gaa tac ctg gtg ccg gaa gcc atc gac      192
Gly Asn Lys Thr Arg Lys Leu Glu Tyr Leu Val Pro Glu Ala Ile Asp
    50                  55                  60
ggc ggc tac gac aca ctg gtg tcg atc ggc ggc atc cag tcc aac cag      240
Gly Gly Tyr Asp Thr Leu Val Ser Ile Gly Gly Ile Gln Ser Asn Gln
```

```
65                  70                  75                  80
acc cgt cag gtg gca gca gtc gcg gcg cat ctg ggt atg aaa tgc gtg       288
Thr Arg Gln Val Ala Ala Val Ala Ala His Leu Gly Met Lys Cys Val
                85                  90                  95
ctg gtt cag gaa aac tgg gtc aac tat tca gac gcc ctg tac gac cga       336
Leu Val Gln Glu Asn Trp Val Asn Tyr Ser Asp Ala Leu Tyr Asp Arg
            100                 105                 110
gtg ggc aat atc gag atg tca cgc atc atg ggg gcc gat gtg cgc ctg       384
Val Gly Asn Ile Glu Met Ser Arg Ile Met Gly Ala Asp Val Arg Leu
        115                 120                 125
gac tcg gca ggc ttc gat atc ggc att cgg ccg agc tgg gaa aag gcc       432
Asp Ser Ala Gly Phe Asp Ile Gly Ile Arg Pro Ser Trp Glu Lys Ala
    130                 135                 140
atg tcc gac gtc gag gaa agc ggt ggc aag ccg ttc ccg att cct gcg       480
Met Ser Asp Val Glu Glu Ser Gly Gly Lys Pro Phe Pro Ile Pro Ala
145                 150                 155                 160
ggc tgc tcg gaa cac cct tat ggc ggc ctg gga ttc gtg cgt ttt gcc       528
Gly Cys Ser Glu His Pro Tyr Gly Gly Leu Gly Phe Val Arg Phe Ala
                165                 170                 175
gat gag gta cgc cag cag gaa gaa gaa ctc ggc ttc aaa ttc gac tac       576
Asp Glu Val Arg Gln Gln Glu Glu Glu Leu Gly Phe Lys Phe Asp Tyr
            180                 185                 190
atc gtg gtc tgc tcg gtg acc ggc agc act cac gca ggc atg ctc gtc       624
Ile Val Val Cys Ser Val Thr Gly Ser Thr His Ala Gly Met Leu Val
        195                 200                 205
ggc ttc gcg gcc gat ggc cgg gca cag cgt gtg atc ggt atc gat gcg       672
Gly Phe Ala Ala Asp Gly Arg Ala Gln Arg Val Ile Gly Ile Asp Ala
    210                 215                 220
tcg gcc aaa ccg gaa aag acc cgc gca caa gtc ctg cgc atc gct cag       720
Ser Ala Lys Pro Glu Lys Thr Arg Ala Gln Val Leu Arg Ile Ala Gln
225                 230                 235                 240
aac acc gca aaa ctg gtg gaa ctg ggc cgc gaa atc acc gcc gaa gac       768
Asn Thr Ala Lys Leu Val Glu Leu Gly Arg Glu Ile Thr Ala Glu Asp
                245                 250                 255
gtg gtg ctc gac acc cgc tac gcc tac ccc gaa tac ggc ctg ccg aac       816
Val Val Leu Asp Thr Arg Tyr Ala Tyr Pro Glu Tyr Gly Leu Pro Asn
            260                 265                 270
gag ggc acc ctt gaa gcc att cgc ctt tgc gcg cgc ctt gaa ggc gta       864
Glu Gly Thr Leu Glu Ala Ile Arg Leu Cys Ala Arg Leu Glu Gly Val
        275                 280                 285
ttg acc gac ccg gtc tac gaa ggc aaa tcc atg cac ggc atg atc gac       912
Leu Thr Asp Pro Val Tyr Glu Gly Lys Ser Met His Gly Met Ile Asp
    290                 295                 300
atg gtg cgc aat ggt gaa ttc ccc gag ggc tca aaa gtg ctc tac gca       960
Met Val Arg Asn Gly Glu Phe Pro Glu Gly Ser Lys Val Leu Tyr Ala
305                 310                 315                 320
cat ttg ggc ggc gta ccg gcg ttg aat gcc tac agt ttt ctg ttc aag      1008
His Leu Gly Gly Val Pro Ala Leu Asn Ala Tyr Ser Phe Leu Phe Lys
                325                 330                 335
gac ggt taa                                                         1017
Asp Gly
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<210> 119
<211> 338
<212> PRT
<213> Pseudomonas syringae pv. phaseolicola 1448A

<400> 119

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

<210> 120
<211> 1017
<212> DNA
<213> Ralstonia eutropha JMP134

<220>
<221> CDS
<222> (1)..(1017)
<223> transl_table=11

<400> 120

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atg aaa aaa atc tcg gat cgc att gct tca ttt tcc cgc ctt caa ctg       48
Met Lys Lys Ile Ser Asp Arg Ile Ala Ser Phe Ser Arg Leu Gln Leu
1               5                   10                  15
gtc ggc gcg gtc acc ccc ctg gag aaa ctc gat cgc ttg tct cgt atg       96
Val Gly Ala Val Thr Pro Leu Glu Lys Leu Asp Arg Leu Ser Arg Met
            20                  25                  30
ctc ggt cgc gat gtc tac atc aag cgc gat gac acc acg cca ctc gcc      144
```

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

atg cgc aag cgc ttt gcg ggt gag ggt ccg ctg ctg ttc ctg cat acc      960
Met Arg Lys Arg Phe Ala Gly Glu Gly Pro Leu Leu Phe Leu His Thr
305                 310                 315                 320
ggc ggc gca ccg gcg cta ttt gcc tat cgc gac gcg ctc ccg gca gtc     1008
Gly Gly Ala Pro Ala Leu Phe Ala Tyr Arg Asp Ala Leu Pro Ala Val
                325                 330                 335
ctc att taa                                                       1017
Leu Ile
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<210> 121
<211> 338
<212> PRT
<213> Ralstonia eutropha JMP134

<400> 121
Met Lys Lys Ile Ser Asp Arg Ile Ala Ser Phe Ser Arg Leu Gln Leu
1 5 10 15
Val Gly Ala Val Thr Pro Leu Glu Lys Leu Asp Arg Leu Ser Arg Met
20 25 30
Leu Gly Arg Asp Val Tyr Ile Lys Arg Asp Asp Thr Thr Pro Leu Ala
35 40 45
Phe Gly Gly Asn Lys Leu Arg Lys Leu Glu Phe Leu Ala Ala Asp Ala
50 55 60
Leu Ser Lys Gly Ala Asp Thr Leu Val Thr Ala Gly Ala Ile Gln Ser
65 70 75 80
Asn His Val Arg Gln Thr Ala Ala Val Ala Ala Arg Leu Gly Leu Arg
85 90 95
Cys His Ala Leu Leu Glu Asn Pro Ile Asn Thr Thr Asp Val Asp Tyr
100 105 110
Leu Arg Ser Gly Asn Arg Leu Leu Leu Asp Leu Phe Asp Ala His Gly
115 120 125
Glu Pro Val Ala Thr Leu Asp Asn Ala Asp Ala Gln Leu Gln Ala Leu
130 135 140
Ala Glu Arg Leu Arg Gly Asp Gly Tyr Gln Pro Tyr Ile Ile Pro Ile
145 150 155 160
Gly Gly Ser Asn Pro Leu Gly Ala Leu Gly Tyr Val His Ala Gly Leu
165 170 175
Glu Met Ala Gln Gln Ala Asp Ala Met Gly Val Ser Phe Ala Ala Val
180 185 190
Val Leu Ala Ser Gly Ser Ala Gly Thr His Gly Gly Leu Ala Leu Ala
195 200 205
Leu Ala His Ala Met Pro Asp Ala Gln Val Val Gly Ile Thr Val Ser
210 215 220
Arg Pro Val Glu Ala Gln Ala Pro Lys Val Ala Gly Leu Ile Asp Gly
225 230 235 240
Thr Ala Glu Leu Leu Asp Ile Glu Val Pro Ala Glu Leu Arg Leu Glu
245 250 255
Leu Trp Asp Glu Tyr Phe Leu Pro Arg Tyr Gly Glu Pro Asn Arg Ala
260 265 270
Ala Leu Asp Ala Ile Arg Leu Leu Ala Arg Thr Glu Gly Val Leu Leu
275 280 285
Asp Pro Val Tyr Thr Gly Lys Ala Met Ala Gly Leu Leu Asp Gly Val
290 295 300
Met Arg Lys Arg Phe Ala Gly Glu Gly Pro Leu Leu Phe Leu His Thr
305 310 315 320
Gly Gly Ala Pro Ala Leu Phe Ala Tyr Arg Asp Ala Leu Pro Ala Val
325 330 335
Leu Ile

<210> 122
<211> 987
<212> DNA
<213> Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305

<220>
<221> CDS
<222> (1)..(987)
<223> transl_table=11

<400> 122

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atg tta cat aat aaa tta gat att gcc aat tta aat aca cca att caa       48
Met Leu His Asn Lys Leu Asp Ile Ala Asn Leu Asn Thr Pro Ile Gln
1               5                  10                  15
aaa tta gat cag tta agt gat gca tta gga aaa aat att tat att aag       96
Lys Leu Asp Gln Leu Ser Asp Ala Leu Gly Lys Asn Ile Tyr Ile Lys
            20                  25                  30
aga gat gat tac act gga tca gaa ata tca ggt aat aag gtg cgt aaa      144
Arg Asp Asp Tyr Thr Gly Ser Glu Ile Ser Gly Asn Lys Val Arg Lys
        35                  40                  45
ctc gag tat aca atg caa tat gta tta gat cat gga tat gac act att      192
Leu Glu Tyr Thr Met Gln Tyr Val Leu Asp His Gly Tyr Asp Thr Ile
    50                  55                  60
ata aca acc ggg gca att aca tcg aat cac gca cgt gct aca gct gcc      240
Ile Thr Thr Gly Ala Ile Thr Ser Asn His Ala Arg Ala Thr Ala Ala
65                  70                  75                  80
ttg tgt gct aag tgt aat gta tca tat ctt gtt cta aga gga gag atg      288
Leu Cys Ala Lys Cys Asn Val Ser Tyr Leu Val Leu Arg Gly Glu Met
                85                  90                  95
gca gaa tat gaa ggg aat cta ttt tta gat gca atg tta ggt gcg cat      336
Ala Glu Tyr Glu Gly Asn Leu Phe Leu Asp Ala Met Leu Gly Ala His
            100                 105                 110
ata cat atc atc gaa cca aca agt tct cgg gaa gat gcg atg gat aag      384
Ile His Ile Ile Glu Pro Thr Ser Ser Arg Glu Asp Ala Met Asp Lys
        115                 120                 125
cta tat aag aca ttt gaa gga caa ggg aaa act cca ttt tta att cca      432
Leu Tyr Lys Thr Phe Glu Gly Gln Gly Lys Thr Pro Phe Leu Ile Pro
    130                 135                 140

gtg ggt gct tcg gat tgg ata gga aca cat ggt tac gtt aat gcg tat      480
Val Gly Ala Ser Asp Trp Ile Gly Thr His Gly Tyr Val Asn Ala Tyr
145                 150                 155                 160
aat gaa atc ata aag caa cag gat gag ctg aaa gta cat ttt gat tca      528
Asn Glu Ile Ile Lys Gln Gln Asp Glu Leu Lys Val His Phe Asp Ser
                165                 170                 175
atc aat gtt gct gtt ggt tct ggt ggt acg tat gct ggt ctt tgg tat      576
Ile Asn Val Ala Val Gly Ser Gly Gly Thr Tyr Ala Gly Leu Trp Tyr
            180                 185                 190
ggg caa atg att aac tgt gaa act acg caa att ata ggt tat gca gta      624
Gly Gln Met Ile Asn Cys Glu Thr Thr Gln Ile Ile Gly Tyr Ala Val

        195                 200                 205
gac caa agt gca cat aca ttc aaa aat aaa gtg ata gag ata ata aag      672
Asp Gln Ser Ala His Thr Phe Lys Asn Lys Val Ile Glu Ile Ile Lys
    210                 215                 220
caa tta gat gaa aca att caa tca tac gag aca att acg ata aac gat      720
Gln Leu Asp Glu Thr Ile Gln Ser Tyr Glu Thr Ile Thr Ile Asn Asp
225                 230                 235                 240
gct tat att gga ctg gga tat ggt aaa gca act gac gaa gaa tta caa      768
Ala Tyr Ile Gly Leu Gly Tyr Gly Lys Ala Thr Asp Glu Glu Leu Gln
                245                 250                 255
ttt tat atc gat att gca caa aaa gaa ggc att ata cta gat cca aca      816
Phe Tyr Ile Asp Ile Ala Gln Lys Glu Gly Ile Ile Leu Asp Pro Thr
            260                 265                 270
tat act gga aaa gct ttt aga ggt tta gtt cat gaa ata aaa tct ggt      864
Tyr Thr Gly Lys Ala Phe Arg Gly Leu Val His Glu Ile Lys Ser Gly
        275                 280                 285
gcg tat gat aat caa gac aac att cta ttt ata cat acg ggt gga cta      912
Ala Tyr Asp Asn Gln Asp Asn Ile Leu Phe Ile His Thr Gly Gly Leu
    290                 295                 300
caa ggc tat act caa gag aca cgt tta cgt ttg caa acg atg ttg cat      960
```

Gln Gly Tyr Thr Gln Glu Thr Arg Leu Arg Leu Gln Thr Met Leu His
305 310 315 320
aaa ata gat ctt tca tta tta aag taa 987
Lys Ile Asp Leu Ser Leu Leu Lys
325

<210> 123
<211> 328
<212> PRT
<213> Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305

<400> 123
Met Leu His Asn Lys Leu Asp Ile Ala Asn Leu Asn Thr Pro Ile Gln
1 5 10 15
Lys Leu Asp Gln Leu Ser Asp Ala Leu Gly Lys Asn Ile Tyr Ile Lys
20 25 30
Arg Asp Asp Tyr Thr Gly Ser Glu Ile Ser Gly Asn Lys Val Arg Lys
35 40 45
Leu Glu Tyr Thr Met Gln Tyr Val Leu Asp His Gly Tyr Asp Thr Ile
50 55 60
Ile Thr Thr Gly Ala Ile Thr Ser Asn His Ala Arg Ala Thr Ala Ala
65 70 75 80
Leu Cys Ala Lys Cys Asn Val Ser Tyr Leu Val Leu Arg Gly Glu Met
85 90 95
Ala Glu Tyr Glu Gly Asn Leu Phe Leu Asp Ala Met Leu Gly Ala His
100 105 110
Ile His Ile Ile Glu Pro Thr Ser Ser Arg Glu Asp Ala Met Asp Lys
115 120 125
Leu Tyr Lys Thr Phe Glu Gly Gln Gly Lys Thr Pro Phe Leu Ile Pro
130 135 140
Val Gly Ala Ser Asp Trp Ile Gly Thr His Gly Tyr Val Asn Ala Tyr
145 150 155 160
Asn Glu Ile Ile Lys Gln Gln Asp Glu Leu Lys Val His Phe Asp Ser
165 170 175
Ile Asn Val Ala Val Gly Ser Gly Gly Thr Tyr Ala Gly Leu Trp Tyr
180 185 190
Gly Gln Met Ile Asn Cys Glu Thr Thr Gln Ile Ile Gly Tyr Ala Val
195 200 205
Asp Gln Ser Ala His Thr Phe Lys Asn Lys Val Ile Glu Ile Ile Lys
210 215 220
Gln Leu Asp Glu Thr Ile Gln Ser Tyr Glu Thr Ile Thr Ile Asn Asp
225 230 235 240
Ala Tyr Ile Gly Leu Gly Tyr Gly Lys Ala Thr Asp Glu Glu Leu Gln
245 250 255
Phe Tyr Ile Asp Ile Ala Gln Lys Glu Gly Ile Ile Leu Asp Pro Thr
260 265 270
Tyr Thr Gly Lys Ala Phe Arg Gly Leu Val His Glu Ile Lys Ser Gly
275 280 285
Ala Tyr Asp Asn Gln Asp Asn Ile Leu Phe Ile His Thr Gly Gly Leu
290 295 300
Gln Gly Tyr Thr Gln Glu Thr Arg Leu Arg Leu Gln Thr Met Leu His
305 310 315 320
Lys Ile Asp Leu Ser Leu Leu Lys
325

<210> 124
<211> 987
<212> DNA
<213> Shigella sonnei Ss046

<220>

<221> CDS
<222> (1)..(987)
<223> transl_table=11

<400> 124

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atg cca ctg cat aat tta acc cgt ttt cca cgg ttg gag ttt atc ggc      48
Met Pro Leu His Asn Leu Thr Arg Phe Pro Arg Leu Glu Phe Ile Gly
1               5                  10                  15
gcg cca acg ccg ctc gaa tat ctg ccg cgc ttt tct gat tat cta gga      96
Ala Pro Thr Pro Leu Glu Tyr Leu Pro Arg Phe Ser Asp Tyr Leu Gly
            20                  25                  30
cgg gaa att ttc atc aaa cgg gat gac gtc acc ccc atg gca atg ggc     144
Arg Glu Ile Phe Ile Lys Arg Asp Asp Val Thr Pro Met Ala Met Gly
        35                  40                  45
ggc aat aaa tta cgt aag cta gaa ttt ctc gcg gca gat gct ctg cgc     192
Gly Asn Lys Leu Arg Lys Leu Glu Phe Leu Ala Ala Asp Ala Leu Arg
    50                  55                  60
gaa ggt gcc gat acg ctg att act gcc ggg gtg atc cag tct aac cat     240
Glu Gly Ala Asp Thr Leu Ile Thr Ala Gly Val Ile Gln Ser Asn His
65                  70                  75                  80
gtg cgg cag act gcc gca gtt gcg gcg aaa ctc ggt ctg cac tgt gtg     288
Val Arg Gln Thr Ala Ala Val Ala Ala Lys Leu Gly Leu His Cys Val
                85                  90                  95
gcg ctg ctg gaa aat cct att ggc aca acc gca gaa aac tat tta acc     336
Ala Leu Leu Glu Asn Pro Ile Gly Thr Thr Ala Glu Asn Tyr Leu Thr
            100                 105                 110
aac ggc aat cgc ttg ttg ctg gat ctg ttc aat acc cag att gaa atg     384
Asn Gly Asn Arg Leu Leu Leu Asp Leu Phe Asn Thr Gln Ile Glu Met
        115                 120                 125
tgc gaa gca ctg acc gat ccc aat gcc caa ctg gaa gag ctg gcg acg     432
Cys Glu Ala Leu Thr Asp Pro Asn Ala Gln Leu Glu Glu Leu Ala Thr
    130                 135                 140
cga gtc gaa gca caa ggc ttt cgc ccg tat gtc att ccg gtt ggc ggt     480
Arg Val Glu Ala Gln Gly Phe Arg Pro Tyr Val Ile Pro Val Gly Gly
145                 150                 155                 160
tct aat gct ctt ggc gcg cta ggt tat gtg gag agt gcg ctg gaa atc     528
Ser Asn Ala Leu Gly Ala Leu Gly Tyr Val Glu Ser Ala Leu Glu Ile
                165                 170                 175
gcg caa cag tgt gaa ggg gcg gtt aat att tcg tcg gtg gta gtc gca     576
Ala Gln Gln Cys Glu Gly Ala Val Asn Ile Ser Ser Val Val Val Ala
            180                 185                 190
tcg ggc agt gcc gga act cac gcc gga ctg gct gtt ggg ctg gaa cac     624
Ser Gly Ser Ala Gly Thr His Ala Gly Leu Ala Val Gly Leu Glu His
        195                 200                 205
ctg atg cct gaa agc gaa ctg att ggc gtg acc gtg tcg cgt tcc gtt     672
Leu Met Pro Glu Ser Glu Leu Ile Gly Val Thr Val Ser Arg Ser Val
    210                 215                 220
gcc gat cag ttg ccg aaa gtg gtt aac cta caa cag gcg att gcg aaa     720
Ala Asp Gln Leu Pro Lys Val Val Asn Leu Gln Gln Ala Ile Ala Lys
225                 230                 235                 240
gaa ctg gag ctg acc gca tca gcg gaa att ata ctc tgg gat gac tat     768
Glu Leu Glu Leu Thr Ala Ser Ala Glu Ile Ile Leu Trp Asp Asp Tyr
                245                 250                 255
ttt gca cct ggc tac ggc gtg ccg aac gac gaa ggc atg gaa gca gtg     816
Phe Ala Pro Gly Tyr Gly Val Pro Asn Asp Glu Gly Met Glu Ala Val
            260                 265                 270
aaa ttg ctg gcg cgg ctg gaa ggc att ctg ctt gat cct gtg tat acc     864
Lys Leu Leu Ala Arg Leu Glu Gly Ile Leu Leu Asp Pro Val Tyr Thr
        275                 280                 285
gga aaa gcg atg gcg ggg ctg att ggc tgt atc agt cag aaa cgc ttc     912
```

```
Gly Lys Ala Met Ala Gly Leu Ile Gly Cys Ile Ser Gln Lys Arg Phe
    290                 295                 300
aaa gat gaa ggg ccg att ctg ttt att cat acc ggc ggt gcg cct gcg       960
Lys Asp Glu Gly Pro Ile Leu Phe Ile His Thr Gly Gly Ala Pro Ala
305                 310                 315                 320
ctg ttc gcc tat cat ccc cac gtt tag                                   987
Leu Phe Ala Tyr His Pro His Val
                325
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<210> 125
<211> 328
<212> PRT
<213> Shigella sonnei Ss046

<400> 125

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

<210> 126
<211> 924
<212> DNA

<213> Anabaena variabilis ATCC 29413

<220>
<221> CDS
<222> (1)..(924)
<223> transl_table=11

<400> 126

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

```
        275                 280                 285
atc ttg atg att cac acc ggt ggc tta caa gga aat atc ggg atg agt       912
Ile Leu Met Ile His Thr Gly Gly Leu Gln Gly Asn Ile Gly Met Ser
    290                 295                 300
gaa cga ttg taa                                                    924
Glu Arg Leu
305
```

<210> 127
<211> 307
<212> PRT
<213> Anabaena variabilis ATCC 29413

<400> 127

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

<210> 128
<211> 1017
<212> DNA
<213> Burkholderia pseudomallei 1710b

<220>
<221> CDS
<222> (1)..(1017)
<223> transl_table=11

<400> 128

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atg aat ctc cag aaa ttt ccg cgt tat ccg ctg acc ttc ggc ccg acg       48
Met Asn Leu Gln Lys Phe Pro Arg Tyr Pro Leu Thr Phe Gly Pro Thr
1               5                  10                  15
ccg atc cag ccg ctc aag cgg ctt tcc gcg cat ctc ggc ggc aag gtc       96
Pro Ile Gln Pro Leu Lys Arg Leu Ser Ala His Leu Gly Gly Lys Val
            20                  25                  30
gag ctg tac gcg aag cgc gac gac tgc aac agc ggc ctc gcg ttc ggc      144
Glu Leu Tyr Ala Lys Arg Asp Asp Cys Asn Ser Gly Leu Ala Phe Gly
        35                  40                  45
ggc aac aag acg cgc aag ctc gaa tac ctg atc ccg gac gcg ctc gcg      192
Gly Asn Lys Thr Arg Lys Leu Glu Tyr Leu Ile Pro Asp Ala Leu Ala
    50                  55                  60
caa ggc tgc gac acg ctc gta tcg atc ggc ggc atc cag tcg aac cag      240
Gln Gly Cys Asp Thr Leu Val Ser Ile Gly Gly Ile Gln Ser Asn Gln
65                  70                  75                  80
acg cgc cag gtc gcg gcg gtg gcc gcg cat ctc ggc atg aag tgc gtg      288
Thr Arg Gln Val Ala Ala Val Ala Ala His Leu Gly Met Lys Cys Val
                85                  90                  95
ctc gtg cag gag aac tgg gtc aac tat cac gac gcc gtc tac gat cgc      336
Leu Val Gln Glu Asn Trp Val Asn Tyr His Asp Ala Val Tyr Asp Arg
            100                 105                 110
gtc ggc aac atc cag atg tcg cgc atg atg ggc gcc gac gtg cgc ctc      384
Val Gly Asn Ile Gln Met Ser Arg Met Met Gly Ala Asp Val Arg Leu
        115                 120                 125
gtg ccg gac ggc ttc gac atc ggc ttt cgc aag agc tgg gag gat gcg      432
Val Pro Asp Gly Phe Asp Ile Gly Phe Arg Lys Ser Trp Glu Asp Ala
    130                 135                 140
ctc gcc gat gtc cgc gcg agg ggc ggc aag ccg tat gcg att ccg gcc      480
Leu Ala Asp Val Arg Ala Arg Gly Gly Lys Pro Tyr Ala Ile Pro Ala
145                 150                 155                 160
ggc tgc tcc gac cat ccg ctc ggc ggc ctc ggc ttc gtc ggc ttt gcc      528
Gly Cys Ser Asp His Pro Leu Gly Gly Leu Gly Phe Val Gly Phe Ala
                165                 170                 175
gag gaa gtg cgc gcg cag gag gcc gag ctc ggt ttc caa ttc gat tac      576
Glu Glu Val Arg Ala Gln Glu Ala Glu Leu Gly Phe Gln Phe Asp Tyr
            180                 185                 190
gtc gtg gtg tgc tcg gtg acg ggc agc acg cag gcc ggg atg gtc gtc      624
Val Val Val Cys Ser Val Thr Gly Ser Thr Gln Ala Gly Met Val Val
        195                 200                 205
ggc ttc gcg gcg gac ggg cgc gcg gac cgc gtg atc ggc gtc gac gcg      672
Gly Phe Ala Ala Asp Gly Arg Ala Asp Arg Val Ile Gly Val Asp Ala
    210                 215                 220
tcg gcg aag ccc gcg cag acg cgc gag cag atc ctt cgg atc gcg aag      720
Ser Ala Lys Pro Ala Gln Thr Arg Glu Gln Ile Leu Arg Ile Ala Lys
225                 230                 235                 240
cat acc gcc gat cgc gtc gag ctg ggc cgc gac atc acg agc gcc gac      768
His Thr Ala Asp Arg Val Glu Leu Gly Arg Asp Ile Thr Ser Ala Asp
                245                 250                 255
gtc gtg ctc gac gag cgc ttc ggc ggc ccc gag tac ggg ctg ccg aac      816
Val Val Leu Asp Glu Arg Phe Gly Gly Pro Glu Tyr Gly Leu Pro Asn
            260                 265                 270
gag ggc acg ctc gag gcg atc cgg ctg tgc gcg aag ctc gaa ggc gtg      864
Glu Gly Thr Leu Glu Ala Ile Arg Leu Cys Ala Lys Leu Glu Gly Val
        275                 280                 285
ctg acc gat ccc gtc tac gaa ggc aag tcg atg cac ggg atg atc gag      912
```

```
Leu Thr Asp Pro Val Tyr Glu Gly Lys Ser Met His Gly Met Ile Glu
    290                 295                 300
aag gtg cgg ctc ggc gaa ttc ccg gcc ggc tcg aag gtg ctg tac gcg       960
Lys Val Arg Leu Gly Glu Phe Pro Ala Gly Ser Lys Val Leu Tyr Ala
305                 310                 315                 320
cat ctc ggc ggc gtg ccc gcg ctg aac gcg tac agc ttt ttg ttc cgc       1008
His Leu Gly Gly Val Pro Ala Leu Asn Ala Tyr Ser Phe Leu Phe Arg
                325                 330                 335
gac ggc tga                                                          1017
Asp Gly
```

<210> 129
<211> 338
<212> PRT
<213> Burkholderia pseudomallei 1710b

<400> 129

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

<210> 130
<211> 909
<212> DNA
<213> Pseudoalteromonas haloplanktis TAC125

<220>
<221> CDS
<222> (1)..(909)
<223> transl_table=11

<400> 130

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

```
cct att tat act ggt aaa atg atg cat gct ttg tgg caa tta att gcg       816
Pro Ile Tyr Thr Gly Lys Met Met His Ala Leu Trp Gln Leu Ile Ala
            260                 265                 270
cag gac tac ttt gcg cca ggc agt aaa att att gcg gtt cat acg ggt       864
Gln Asp Tyr Phe Ala Pro Gly Ser Lys Ile Ile Ala Val His Thr Gly
        275                 280                 285
ggg tta caa gga tta gat ggt tta aaa tac aga gga ctt att taa           909
Gly Leu Gln Gly Leu Asp Gly Leu Lys Tyr Arg Gly Leu Ile
    290                 295                 300
```

<210> 131
<211> 302
<212> PRT
<213> Pseudoalteromonas haloplanktis TAC125

<400> 131

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

<210> 132
<211> 1005
<212> DNA
<213> Pseudomonas fluorescens Pf0-1

<220>

<221> CDS
<222> (1)..(1005)
<223> transl_table=11

<400> 132

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atg tcc aca caa ccg atc aaa caa cag ctg caa cgc ttc aac cgc ctc      48
Met Ser Thr Gln Pro Ile Lys Gln Gln Leu Gln Arg Phe Asn Arg Leu
1               5                  10                  15
gac ctg ctc ggc caa ccg acc cca ctg gaa aag ctc gag cgt ctg tcc      96
Asp Leu Leu Gly Gln Pro Thr Pro Leu Glu Lys Leu Glu Arg Leu Ser
            20                  25                  30
acc tgg ctc ggc cgc gat gtc tac atc aaa cgc gat gac ctg acg cct     144
Thr Trp Leu Gly Arg Asp Val Tyr Ile Lys Arg Asp Asp Leu Thr Pro
        35                  40                  45
ttg gcc atg ggc ggc aac aag ctg cgc aag ctc gaa tac ctc gcc gcc     192
Leu Ala Met Gly Gly Asn Lys Leu Arg Lys Leu Glu Tyr Leu Ala Ala
    50                  55                  60
gat gcc atc gcc caa ggc gcg gat acc ctg atc acc gcc ggt gca ctg     240
Asp Ala Ile Ala Gln Gly Ala Asp Thr Leu Ile Thr Ala Gly Ala Leu
65                  70                  75                  80
caa tcg aac cac gtt cgc cag act gcc gcg ctg gcc gcc aaa ctg ggc     288
Gln Ser Asn His Val Arg Gln Thr Ala Ala Leu Ala Ala Lys Leu Gly
                85                  90                  95
ctg ggt tgc gta gcg ctg ctg gaa aac ccg ctg ggc acc gac gac agc     336
Leu Gly Cys Val Ala Leu Leu Glu Asn Pro Leu Gly Thr Asp Asp Ser
            100                 105                 110
aac tac acc ggc aac ggc aac cgc ctg ctg ctg gac ctg ttc gac acc     384
Asn Tyr Thr Gly Asn Gly Asn Arg Leu Leu Leu Asp Leu Phe Asp Thr
        115                 120                 125
aag gtc gag ctg gtc gac aac ctc gac aac gcc gac gaa caa ctg gcc     432
Lys Val Glu Leu Val Asp Asn Leu Asp Asn Ala Asp Glu Gln Leu Ala
    130                 135                 140
gcc ctc gcc gtg cgc ctg cgc agc aac ggc aag aag ccg tat ctg gtg     480
Ala Leu Ala Val Arg Leu Arg Ser Asn Gly Lys Lys Pro Tyr Leu Val
145                 150                 155                 160
ccg atc ggt ggc tcc aac gcc atc ggt gcg ctg ggt tat gtg cgc gcc     528
Pro Ile Gly Gly Ser Asn Ala Ile Gly Ala Leu Gly Tyr Val Arg Ala
                165                 170                 175
ggt ctg gag ctg gca gaa cag atc aag gac acc ggc ctg caa ttc tcc     576
Gly Leu Glu Leu Ala Glu Gln Ile Lys Asp Thr Gly Leu Gln Phe Ser
            180                 185                 190
gcc gtc gtt ttg gcc tct ggc agc gcc ggt act cac agc ggt ctg gcg     624
Ala Val Val Leu Ala Ser Gly Ser Ala Gly Thr His Ser Gly Leu Ala
        195                 200                 205
ctg gcc ctg agc gaa gcc ctg cca caa ctg ccg gtg att ggc gtg acg     672
Leu Ala Leu Ser Glu Ala Leu Pro Gln Leu Pro Val Ile Gly Val Thr
    210                 215                 220
gtg tcg cgc agc gaa gaa gat cag cgc ccg aaa gtc cag ggc ctc gcc     720
Val Ser Arg Ser Glu Glu Asp Gln Arg Pro Lys Val Gln Gly Leu Ala
225                 230                 235                 240
gaa cgc acc gcc gac ctg ctg ggt gtg gcg ctg ccg gac agc ttc aag     768
Glu Arg Thr Ala Asp Leu Leu Gly Val Ala Leu Pro Asp Ser Phe Lys
                245                 250                 255
gtc gag ttg tgg gac gaa tac ttc ggc ccg cgc tat ggt gag ccg aat     816
Val Glu Leu Trp Asp Glu Tyr Phe Gly Pro Arg Tyr Gly Glu Pro Asn
            260                 265                 270
gcc ggg acg ctg tcg gcg gtg aag ctg ctg gcc agc cag gac gcc gtg     864
Ala Gly Thr Leu Ser Ala Val Lys Leu Leu Ala Ser Gln Asp Ala Val
        275                 280                 285
ttg ctc gat ccg gtc tac acc ggc aag gcc atg gcc gga ctg ctc gac     912
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Leu Leu Asp Pro Val Tyr Thr Gly Lys Ala Met Ala Gly Leu Leu Asp
290 295 300
ggc atc ggt cgc ggg cgt ttc gac gac ggc ccg atc atc ttc ctg cac 960
Gly Ile Gly Arg Gly Arg Phe Asp Asp Gly Pro Ile Ile Phe Leu His
305 310 315 320
acc ggc ggc gcc ccg gcg ttg ttt gcg tac aag gat ttt ctc tga 1005
Thr Gly Gly Ala Pro Ala Leu Phe Ala Tyr Lys Asp Phe Leu
325 330

<210> 133
<211> 334
<212> PRT
<213> Pseudomonas fluorescens Pf0-1

<400> 133
Met Ser Thr Gln Pro Ile Lys Gln Gln Leu Gln Arg Phe Asn Arg Leu
1 5 10 15
Asp Leu Leu Gly Gln Pro Thr Pro Leu Glu Lys Leu Glu Arg Leu Ser
20 25 30
Thr Trp Leu Gly Arg Asp Val Tyr Ile Lys Arg Asp Asp Leu Thr Pro
35 40 45
Leu Ala Met Gly Gly Asn Lys Leu Arg Lys Leu Glu Tyr Leu Ala Ala
50 55 60
Asp Ala Ile Ala Gln Gly Ala Asp Thr Leu Ile Thr Ala Gly Ala Leu
65 70 75 80
Gln Ser Asn His Val Arg Gln Thr Ala Ala Leu Ala Ala Lys Leu Gly
85 90 95
Leu Gly Cys Val Ala Leu Leu Glu Asn Pro Leu Gly Thr Asp Asp Ser
100 105 110
Asn Tyr Thr Gly Asn Gly Asn Arg Leu Leu Leu Asp Leu Phe Asp Thr
115 120 125
Lys Val Glu Leu Val Asp Asn Leu Asp Asn Ala Asp Glu Gln Leu Ala
130 135 140
Ala Leu Ala Val Arg Leu Arg Ser Asn Gly Lys Lys Pro Tyr Leu Val
145 150 155 160
Pro Ile Gly Gly Ser Asn Ala Ile Gly Ala Leu Gly Tyr Val Arg Ala
165 170 175
Gly Leu Glu Leu Ala Glu Gln Ile Lys Asp Thr Gly Leu Gln Phe Ser
180 185 190
Ala Val Val Leu Ala Ser Gly Ser Ala Gly Thr His Ser Gly Leu Ala
195 200 205
Leu Ala Leu Ser Glu Ala Leu Pro Gln Leu Pro Val Ile Gly Val Thr
210 215 220
Val Ser Arg Ser Glu Glu Asp Gln Arg Pro Lys Val Gln Gly Leu Ala
225 230 235 240
Glu Arg Thr Ala Asp Leu Leu Gly Val Ala Leu Pro Asp Ser Phe Lys
245 250 255
Val Glu Leu Trp Asp Glu Tyr Phe Gly Pro Arg Tyr Gly Glu Pro Asn
260 265 270
Ala Gly Thr Leu Ser Ala Val Lys Leu Leu Ala Ser Gln Asp Ala Val
275 280 285
Leu Leu Asp Pro Val Tyr Thr Gly Lys Ala Met Ala Gly Leu Leu Asp
290 295 300
Gly Ile Gly Arg Gly Arg Phe Asp Asp Gly Pro Ile Ile Phe Leu His
305 310 315 320
Thr Gly Gly Ala Pro Ala Leu Phe Ala Tyr Lys Asp Phe Leu
325 330

<210> 134
<211> 1080
<212> DNA

<213> Burkholderia sp. 383

<220>
<221> CDS
<222> (1)..(1080)
<223> transl_table=11

<400> 134

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atg act ttc aac gcg cca acc tct ctc gcg tac cct gcg cga gcg aac       48
Met Thr Phe Asn Ala Pro Thr Ser Leu Ala Tyr Pro Ala Arg Ala Asn
1               5                  10                  15
ctc cag gga ttg ttc ggc ttc gat tca atc cgg gtg ccg cgt tac cgt       96
Leu Gln Gly Leu Phe Gly Phe Asp Ser Ile Arg Val Pro Arg Tyr Arg
            20                  25                  30
ctg ctc gat ggc gca acg ccg att cat ccc ctg ccg cgc ctg agt gcc      144
Leu Leu Asp Gly Ala Thr Pro Ile His Pro Leu Pro Arg Leu Ser Ala
        35                  40                  45
tat ctt ggc ggg gcg acc att cat gtc aag cgg gag gac gta gcg agc      192
Tyr Leu Gly Gly Ala Thr Ile His Val Lys Arg Glu Asp Val Ala Ser
    50                  55                  60
gtg ggc ggc ggc ggc aac aaa ttg cgg aaa ctg gag ctc ctg att ggc      240
Val Gly Gly Gly Gly Asn Lys Leu Arg Lys Leu Glu Leu Leu Ile Gly
65                  70                  75                  80
gag gca tta cag tca ggc gcc gac acg gtc atc acg gtt ggc gcg agg      288
Glu Ala Leu Gln Ser Gly Ala Asp Thr Val Ile Thr Val Gly Ala Arg
                85                  90                  95
caa tcg aat cac gca cgg ctg acc gcg gct gcc gca gcc cac gcg ggg      336

Gln Ser Asn His Ala Arg Leu Thr Ala Ala Ala Ala Ala His Ala Gly
            100                 105                 110
atg cga tgc gag gtt gtg ctc aca cgc tcc gtg ccg cgc gac gac gcc      384
Met Arg Cys Glu Val Val Leu Thr Arg Ser Val Pro Arg Asp Asp Ala
        115                 120                 125
gat tac atc gaa agc ggc aac gtc ctg ctc gat aac ctg ttc aac gct      432
Asp Tyr Ile Glu Ser Gly Asn Val Leu Leu Asp Asn Leu Phe Asn Ala
    130                 135                 140
cgt gtg cac gat ttg ccg gct tcg gcc gac gcg atg gca tac gcc atc      480
Arg Val His Asp Leu Pro Ala Ser Ala Asp Ala Met Ala Tyr Ala Ile
145                 150                 155                 160
gca cgt gca gac gaa ctg cgt gct gca ggc cac cgt gtc tat gtc tgc      528
Ala Arg Ala Asp Glu Leu Arg Ala Ala Gly His Arg Val Tyr Val Cys
                165                 170                 175
ccg ttc ggc gga tca agc ccg gtt ggc tgc ctc gcc tat gct gcg tgc      576
Pro Phe Gly Gly Ser Ser Pro Val Gly Cys Leu Ala Tyr Ala Ala Cys
            180                 185                 190
gca gcc gaa atc gtc cag cag tct cag gcg cta ggc act cgc ttc gat      624
Ala Ala Glu Ile Val Gln Gln Ser Gln Ala Leu Gly Thr Arg Phe Asp
        195                 200                 205
cgc atc atc gtg ccc aac gga agt ggc ggc aca cat gcc ggg ctg gtt      672
Arg Ile Ile Val Pro Asn Gly Ser Gly Gly Thr His Ala Gly Leu Val
    210                 215                 220
gcc ggc ttc gcg gca ctc ggg acc ggg acg gtc gaa gtc gat gcc tac      720
Ala Gly Phe Ala Ala Leu Gly Thr Gly Thr Val Glu Val Asp Ala Tyr
225                 230                 235                 240
acc gtc tat gcc cca gcc gcg gac gcg tat cgc gcc acg ctc gac aag      768
Thr Val Tyr Ala Pro Ala Ala Asp Ala Tyr Arg Ala Thr Leu Asp Lys
                245                 250                 255
gcg cag cag acg gcc aac atc atc cat cct gat acg gaa atc tcg ccc      816
Ala Gln Gln Thr Ala Asn Ile Ile His Pro Asp Thr Glu Ile Ser Pro
            260                 265                 270
gat gcc gtt cgc gtc gac gcg tcg caa ctc ggc ccc ggt tac ggt atc      864
```

Asp Ala Val Arg Val Asp Ala Ser Gln Leu Gly Pro Gly Tyr Gly Ile
275 280 285
ccc acg gac gcc atg cgc cgc gcc gtc cgg ctg ctg gcc tcg caa gaa 912
Pro Thr Asp Ala Met Arg Arg Ala Val Arg Leu Leu Ala Ser Gln Glu
290 295 300
ggg cta ttg ctc gat ccg gtc tat agc gga aag gcg ttt gcg ggg ctg 960
Gly Leu Leu Leu Asp Pro Val Tyr Ser Gly Lys Ala Phe Ala Gly Leu
305 310 315 320
atc gaa ggc gtt gcg tca ggt cgt tac gca tcc gac caa agc att ctc 1008
Ile Glu Gly Val Ala Ser Gly Arg Tyr Ala Ser Asp Gln Ser Ile Leu
325 330 335
ttc gtc atg acc ggg gga ttg cct ggc tta ttc gcg tac cgg cgc gag 1056
Phe Val Met Thr Gly Gly Leu Pro Gly Leu Phe Ala Tyr Arg Arg Glu
340 345 350
ttt cag atg gct cta gat ggc tga 1080
Phe Gln Met Ala Leu Asp Gly
355

<210> 135
<211> 359
<212> PRT
<213> Burkholderia sp. 383

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

```
    290                 295                 300
Gly Leu Leu Leu Asp Pro Val Tyr Ser Gly Lys Ala Phe Ala Gly Leu
305                 310                 315                 320
Ile Glu Gly Val Ala Ser Gly Arg Tyr Ala Ser Asp Gln Ser Ile Leu
                325                 330                 335
Phe Val Met Thr Gly Gly Leu Pro Gly Leu Phe Ala Tyr Arg Arg Glu
            340                 345                 350
Phe Gln Met Ala Leu Asp Gly
        355
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<210> 136
<211> 1017
<212> DNA
<213> Burkholderia sp. 383

<220>
<221> CDS
<222> (1)..(1017)
<223> transl_table=11

<400> 136

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

```
Gly Phe Ala Ala Asp Gly Arg Ala Asn Arg Val Ile Gly Ile Asp Ala
    210                 215                 220
tcg gcc acc ccc gag cgc acg cac gag cag atc acg cgc atc gcg cgg      720
Ser Ala Thr Pro Glu Arg Thr His Glu Gln Ile Thr Arg Ile Ala Arg
225                 230                 235                 240
cac acg gcc gag ctc gtc gat ctc ggc cgg ccg atc acc acg gcg gac      768
His Thr Ala Glu Leu Val Asp Leu Gly Arg Pro Ile Thr Thr Ala Asp
                245                 250                 255
gtc gtg ctc gac aca cgc tac gcc ggc ccc gaa tac ggg ctg ccg aac      816
Val Val Leu Asp Thr Arg Tyr Ala Gly Pro Glu Tyr Gly Leu Pro Asn
            260                 265                 270
gac ggc acg ctc gaa gcg att cgc ctg tgt gcg cgg ctc gaa ggc atg      864
Asp Gly Thr Leu Glu Ala Ile Arg Leu Cys Ala Arg Leu Glu Gly Met
        275                 280                 285
ctg acg gat ccg gtg tac gaa ggg aag tcg atg cac ggg atg atc gac      912
Leu Thr Asp Pro Val Tyr Glu Gly Lys Ser Met His Gly Met Ile Asp
    290                 295                 300
aag gta cag ctc ggg gaa ttc gaa ccg ggg tcg aag gtg ctg tat gcg      960
Lys Val Gln Leu Gly Glu Phe Glu Pro Gly Ser Lys Val Leu Tyr Ala
305                 310                 315                 320
cat ctc ggc ggc gtg ccg gcg ttg agt gcg tac cac gag act ttc cgg     1008
His Leu Gly Gly Val Pro Ala Leu Ser Ala Tyr His Glu Thr Phe Arg
                325                 330                 335
aac ggt tga                                                        1017
Asn Gly
```

<210> 137
<211> 338
<212> PRT
<213> Burkholderia sp. 383

<400> 137

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

```
Ser Ala Thr Pro Glu Arg Thr His Glu Gln Ile Thr Arg Ile Ala Arg
225                 230                 235                 240
His Thr Ala Glu Leu Val Asp Leu Gly Arg Pro Ile Thr Thr Ala Asp
                245                 250                 255
Val Val Leu Asp Thr Arg Tyr Ala Gly Pro Glu Tyr Gly Leu Pro Asn
            260                 265                 270
Asp Gly Thr Leu Glu Ala Ile Arg Leu Cys Ala Arg Leu Glu Gly Met
        275                 280                 285
Leu Thr Asp Pro Val Tyr Glu Gly Lys Ser Met His Gly Met Ile Asp
    290                 295                 300
Lys Val Gln Leu Gly Glu Phe Glu Pro Gly Ser Lys Val Leu Tyr Ala
305                 310                 315                 320
His Leu Gly Gly Val Pro Ala Leu Ser Ala Tyr His Glu Thr Phe Arg
                325                 330                 335
Asn Gly
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<210> 138
<211> 1002
<212> DNA
<213> Desulfovibrio desulfuricans G20

<220>
<221> CDS
<222> (1)..(1002)
<223> transl_table=11

<400> 138

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

```
cag cag ctt ttt gaa cag ggc atc aac atc gac cac atg gtg gtt ccc        576
Gln Gln Leu Phe Glu Gln Gly Ile Asn Ile Asp His Met Val Val Pro
            180                 185                 190
agt ggc agc gca ggc aca cat gca ggt att gtt gtg ggc atg gcc gcc        624
Ser Gly Ser Ala Gly Thr His Ala Gly Ile Val Val Gly Met Ala Ala
        195                 200                 205
acc aat tcc ggc att ccg gta agc ggc gtc aac gtg agc cgc acc aaa        672
Thr Asn Ser Gly Ile Pro Val Ser Gly Val Asn Val Ser Arg Thr Lys
    210                 215                 220
cct gtt cag gaa gag ctg gtg cat aag ctg gcc tgt gcc act gca gaa        720
Pro Val Gln Glu Glu Leu Val His Lys Leu Ala Cys Ala Thr Ala Glu
225                 230                 235                 240
cgt gtc ggc gta agc ggc ggc att gcc cgt gaa gaa gtg gta tgc ttt        768
Arg Val Gly Val Ser Gly Gly Ile Ala Arg Glu Glu Val Val Cys Phe
                245                 250                 255
gac ggt tac gtg ggc gca gga tac tct ctg ccc aca gat tcc atg gtc        816
Asp Gly Tyr Val Gly Ala Gly Tyr Ser Leu Pro Thr Asp Ser Met Val
            260                 265                 270
gag gct gtc aaa ctg ctt gct tcc acc gaa ggc att ctg ctc gac ccc        864
Glu Ala Val Lys Leu Leu Ala Ser Thr Glu Gly Ile Leu Leu Asp Pro
        275                 280                 285
gta tat tcc ggt aaa gcc atg gcc ggc ctt atc gac ctt gtg cgc aaa        912
Val Tyr Ser Gly Lys Ala Met Ala Gly Leu Ile Asp Leu Val Arg Lys
    290                 295                 300
ggt cat ttc ccc gaa ggt tcg aac gtg ctt ttc ctg cat acc ggc ggc        960
Gly His Phe Pro Glu Gly Ser Asn Val Leu Phe Leu His Thr Gly Gly
305                 310                 315                 320
tcg ccc gcg ctg tat gcg tac acc gat acc ttt atg gaa taa               1002
Ser Pro Ala Leu Tyr Ala Tyr Thr Asp Thr Phe Met Glu
                325                 330
```

<210> 139
<211> 333
<212> PRT

<213> Desulfovibrio desulfuricans G20

<400> 139

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

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

Gly His Phe Pro Glu Gly Ser Asn Val Leu Phe Leu His Thr Gly Gly
305                 310                 315                 320
Ser Pro Ala Leu Tyr Ala Tyr Thr Asp Thr Phe Met Glu
                325                 330
```

<210> 140
<211> 945
<212> DNA
<213> Thiomicrospira crunogena XCL-2

<220>
<221> CDS
<222> (1)..(945)
<223> transl_table=11

<400> 140

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

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145                 150                 155                 160
ttc gaa gaa ctc tcg cag caa ttg gcc atg caa tgc cct gat tgg agc       528
Phe Glu Glu Leu Ser Gln Gln Leu Ala Met Gln Cys Pro Asp Trp Ser
                165                 170                 175
cac ctt tac agc gcc gtg ggc acc ggc gga act tta gcg ggt tta atc       576
His Leu Tyr Ser Ala Val Gly Thr Gly Gly Thr Leu Ala Gly Leu Ile
            180                 185                 190
aag ttc agt gct ttt ttt tgt gat caa cca cgt ctt att tca ggc att       624
Lys Phe Ser Ala Phe Phe Cys Asp Gln Pro Arg Leu Ile Ser Gly Ile
        195                 200                 205
gcc acc tta aaa caa gcg agc tat tta atc cca aca ata gag cag ctc       672
Ala Thr Leu Lys Gln Ala Ser Tyr Leu Ile Pro Thr Ile Glu Gln Leu
    210                 215                 220
agt ggc gtt cat cac aat cag cgc ggc tta acc cag tgg caa cta ctg       720
Ser Gly Val His His Asn Gln Arg Gly Leu Thr Gln Trp Gln Leu Leu
225                 230                 235                 240
ttg gac tat tgc ggg caa ggc tac ggt aaa gaa gac agt gac att ctc       768
Leu Asp Tyr Cys Gly Gln Gly Tyr Gly Lys Glu Asp Ser Asp Ile Leu
                245                 250                 255
act gca cga aaa tgg ttt gaa gaa cag ttt gac att cca tta gac cct       816
Thr Ala Arg Lys Trp Phe Glu Glu Gln Phe Asp Ile Pro Leu Asp Pro
            260                 265                 270
gtg tac acc aat aag atg gtt tat ggc ttc ttg gaa gaa ctg gct gcg       864
Val Tyr Thr Asn Lys Met Val Tyr Gly Phe Leu Glu Glu Leu Ala Ala
        275                 280                 285
gat aag att cca gcc gga gcc aaa atc att tta tat cat tcc ggc gga       912
Asp Lys Ile Pro Ala Gly Ala Lys Ile Ile Leu Tyr His Ser Gly Gly
    290                 295                 300
ttg caa ggc cgc gct ctt gaa aaa aag gca taa                           945
Leu Gln Gly Arg Ala Leu Glu Lys Lys Ala
305                 310
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<210> 141
<211> 314
<212> PRT
<213> Thiomicrospira crunogena XCL-2

<400> 141

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

```
            180                 185                 190
Lys Phe Ser Ala Phe Phe Cys Asp Gln Pro Arg Leu Ile Ser Gly Ile
        195                 200                 205
Ala Thr Leu Lys Gln Ala Ser Tyr Leu Ile Pro Thr Ile Glu Gln Leu
    210                 215                 220
Ser Gly Val His His Asn Gln Arg Gly Leu Thr Gln Trp Gln Leu Leu
225                 230                 235                 240
Leu Asp Tyr Cys Gly Gln Gly Tyr Gly Lys Glu Asp Ser Asp Ile Leu
                245                 250                 255
Thr Ala Arg Lys Trp Phe Glu Glu Gln Phe Asp Ile Pro Leu Asp Pro

            260                 265                 270
Val Tyr Thr Asn Lys Met Val Tyr Gly Phe Leu Glu Glu Leu Ala Ala
        275                 280                 285
Asp Lys Ile Pro Ala Gly Ala Lys Ile Ile Leu Tyr His Ser Gly Gly
    290                 295                 300
Leu Gln Gly Arg Ala Leu Glu Lys Lys Ala
305                 310
```

<210> 142
<211> 1083
<212> DNA
<213> Shigella dysenteriae Sd197

<220>
<221> CDS
<222> (1)..(1083)
<223> transl_table=11

<400> 142

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atg aca aaa aag ggc gct ttc act agc gcc ttt ttt att tac gtg ttt      48
Met Thr Lys Lys Gly Ala Phe Thr Ser Ala Phe Phe Ile Tyr Val Phe
1               5                   10                  15
tca gcg tgc ata ata aga aaa tca caa caa cac aca tcg gag gct gtt      96
Ser Ala Cys Ile Ile Arg Lys Ser Gln Gln His Thr Ser Glu Ala Val
            20                  25                  30
atg cca ctg cat aat tta acc cgt ttt cca cgg ttg gag ttt atc ggc     144
Met Pro Leu His Asn Leu Thr Arg Phe Pro Arg Leu Glu Phe Ile Gly
        35                  40                  45
gcg cca acg ccg ctc gaa tat ctg ccg cgc ttt tct gat tat cta gga     192
Ala Pro Thr Pro Leu Glu Tyr Leu Pro Arg Phe Ser Asp Tyr Leu Gly
    50                  55                  60
cgg gaa att ttc atc aaa cgg gat gac gtc acc ccc atg gca atg ggc     240
Arg Glu Ile Phe Ile Lys Arg Asp Asp Val Thr Pro Met Ala Met Gly
65                  70                  75                  80
ggc aat aaa tta cgt aag cta gaa ttt ctc gcg gca gat gct ctg cgc     288
Gly Asn Lys Leu Arg Lys Leu Glu Phe Leu Ala Ala Asp Ala Leu Arg
                85                  90                  95
gaa ggt gcc gat acg ctg att act gcc ggg gcg atc cag tct aac cat     336
Glu Gly Ala Asp Thr Leu Ile Thr Ala Gly Ala Ile Gln Ser Asn His
            100                 105                 110
gtg cgc cag act gcc gca gtc gcg gcg aaa ctc gga ctg cac tgc gtg     384

Val Arg Gln Thr Ala Ala Val Ala Ala Lys Leu Gly Leu His Cys Val
        115                 120                 125
gcg ctg ctg gaa aat cct att ggc aca acc gca gaa aac tat tta acc     432
Ala Leu Leu Glu Asn Pro Ile Gly Thr Thr Ala Glu Asn Tyr Leu Thr
    130                 135                 140
aac ggc aat cgt ttg ttg ctg gat ctg ttc aat acc cag att gaa atg     480
Asn Gly Asn Arg Leu Leu Leu Asp Leu Phe Asn Thr Gln Ile Glu Met
145                 150                 155                 160
```

```
tgc gac gca ctg acc gat ccc aat gcc caa ctg gaa gag ttg gcg acg       528
Cys Asp Ala Leu Thr Asp Pro Asn Ala Gln Leu Glu Glu Leu Ala Thr
                165                 170                 175
cga gtc gaa gca caa ggc ttt cgc cca tat gtc att ccg gtt ggc ggt       576
Arg Val Glu Ala Gln Gly Phe Arg Pro Tyr Val Ile Pro Val Gly Gly
            180                 185                 190
tct aat gct ctg ggc gcg cta ggt tat gtg gag agt gcg ctg gaa atc       624
Ser Asn Ala Leu Gly Ala Leu Gly Tyr Val Glu Ser Ala Leu Glu Ile
        195                 200                 205
gcg caa cag tgt gaa ggg gcg gtt aat att tcg tcg gtg gtg gtc gca       672
Ala Gln Gln Cys Glu Gly Ala Val Asn Ile Ser Ser Val Val Val Ala
    210                 215                 220
tcg ggc agt gcc gga act cac gcc gga ctg gct gtt ggg ctg gaa cac       720
Ser Gly Ser Ala Gly Thr His Ala Gly Leu Ala Val Gly Leu Glu His
225                 230                 235                 240
ctg atg cct gaa agc gaa ctg att ggc gtg acc gtg tcg cgt tcc gtt       768
Leu Met Pro Glu Ser Glu Leu Ile Gly Val Thr Val Ser Arg Ser Val
                245                 250                 255
gcc gat caa ttg ccg aaa gtg gtt aac cta caa cag gcg att gcg aaa       816
Ala Asp Gln Leu Pro Lys Val Val Asn Leu Gln Gln Ala Ile Ala Lys
            260                 265                 270
gaa ctg gag ctg acc gca tca gcg gaa att tta ctc tgg gat gac tat       864
Glu Leu Glu Leu Thr Ala Ser Ala Glu Ile Leu Leu Trp Asp Asp Tyr
        275                 280                 285
ttt gca cct ggc tac ggc gtg ccg aac gac gaa ggc atg gaa gca gtg       912
Phe Ala Pro Gly Tyr Gly Val Pro Asn Asp Glu Gly Met Glu Ala Val
    290                 295                 300
aaa ttg ctg gcg cgg ctg gaa ggc att ctg ctt gat cct gtg tat acc       960
Lys Leu Leu Ala Arg Leu Glu Gly Ile Leu Leu Asp Pro Val Tyr Thr
305                 310                 315                 320
gga aaa gcg atg gcg ggt ctg att gac ggt atc agt cag aaa cgc ttc      1008
Gly Lys Ala Met Ala Gly Leu Ile Asp Gly Ile Ser Gln Lys Arg Phe
                325                 330                 335
aaa gat gaa ggg ccg att ctg ttt att cat acc agc ggt gcg cct gcg      1056
Lys Asp Glu Gly Pro Ile Leu Phe Ile His Thr Ser Gly Ala Pro Ala
            340                 345                 350
ctg ttc gcc tat cat cct cac gtt tag                                 1083

Leu Phe Ala Tyr His Pro His Val
        355                 360

<210> 143
<211> 360
<212> PRT
<213> Shigella dysenteriae Sd197

<400> 143
Met Thr Lys Lys Gly Ala Phe Thr Ser Ala Phe Phe Ile Tyr Val Phe
1               5                   10                  15
Ser Ala Cys Ile Ile Arg Lys Ser Gln Gln His Thr Ser Glu Ala Val
            20                  25                  30
Met Pro Leu His Asn Leu Thr Arg Phe Pro Arg Leu Glu Phe Ile Gly
        35                  40                  45
Ala Pro Thr Pro Leu Glu Tyr Leu Pro Arg Phe Ser Asp Tyr Leu Gly
    50                  55                  60
Arg Glu Ile Phe Ile Lys Arg Asp Asp Val Thr Pro Met Ala Met Gly
65                  70                  75                  80
Gly Asn Lys Leu Arg Lys Leu Glu Phe Leu Ala Ala Asp Ala Leu Arg
                85                  90                  95
Glu Gly Ala Asp Thr Leu Ile Thr Ala Gly Ala Ile Gln Ser Asn His
            100                 105                 110
```

```
Val Arg Gln Thr Ala Ala Val Ala Ala Lys Leu Gly Leu His Cys Val
        115                 120                 125
Ala Leu Leu Glu Asn Pro Ile Gly Thr Thr Ala Glu Asn Tyr Leu Thr
    130                 135                 140
Asn Gly Asn Arg Leu Leu Leu Asp Leu Phe Asn Thr Gln Ile Glu Met
145                 150                 155                 160
Cys Asp Ala Leu Thr Asp Pro Asn Ala Gln Leu Glu Glu Leu Ala Thr
                165                 170                 175
Arg Val Glu Ala Gln Gly Phe Arg Pro Tyr Val Ile Pro Val Gly Gly
            180                 185                 190
Ser Asn Ala Leu Gly Ala Leu Gly Tyr Val Glu Ser Ala Leu Glu Ile
        195                 200                 205
Ala Gln Gln Cys Glu Gly Ala Val Asn Ile Ser Ser Val Val Val Ala
    210                 215                 220
Ser Gly Ser Ala Gly Thr His Ala Gly Leu Ala Val Gly Leu Glu His
225                 230                 235                 240
Leu Met Pro Glu Ser Glu Leu Ile Gly Val Thr Val Ser Arg Ser Val
                245                 250                 255
Ala Asp Gln Leu Pro Lys Val Val Asn Leu Gln Gln Ala Ile Ala Lys
            260                 265                 270
Glu Leu Glu Leu Thr Ala Ser Ala Glu Ile Leu Leu Trp Asp Asp Tyr
        275                 280                 285
Phe Ala Pro Gly Tyr Gly Val Pro Asn Asp Glu Gly Met Glu Ala Val
    290                 295                 300
Lys Leu Leu Ala Arg Leu Glu Gly Ile Leu Leu Asp Pro Val Tyr Thr
305                 310                 315                 320
Gly Lys Ala Met Ala Gly Leu Ile Asp Gly Ile Ser Gln Lys Arg Phe
                325                 330                 335
Lys Asp Glu Gly Pro Ile Leu Phe Ile His Thr Ser Gly Ala Pro Ala
            340                 345                 350
Leu Phe Ala Tyr His Pro His Val
        355                 360
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<210> 144
<211> 1083
<212> DNA
<213> Shigella boydii Sb227

<220>
<221> CDS
<222> (1)..(1083)
<223> transl_table=11

<400> 144

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atg aca aaa aag ggc gct ttc act agc gcc ttt ttt att tac gcg ttt      48
Met Thr Lys Lys Gly Ala Phe Thr Ser Ala Phe Phe Ile Tyr Ala Phe
1               5                   10                  15
tca gcg tgc ata ata aga aaa tca caa caa cac aca tcg gag gct att      96
Ser Ala Cys Ile Ile Arg Lys Ser Gln Gln His Thr Ser Glu Ala Ile
            20                  25                  30
atg cca ctg cat aat tta acc cgt ttt cca cgg ctg gag ttt atc ggc     144
Met Pro Leu His Asn Leu Thr Arg Phe Pro Arg Leu Glu Phe Ile Gly
        35                  40                  45
gcg cca acg ccg ctc gaa tat ctg ccg cgc ttt tct gat tat ctt gga     192
Ala Pro Thr Pro Leu Glu Tyr Leu Pro Arg Phe Ser Asp Tyr Leu Gly
    50                  55                  60
cgg gaa att ttc atc aaa cgg gat gac gtc aca ccc atg gca atg ggc     240
Arg Glu Ile Phe Ile Lys Arg Asp Asp Val Thr Pro Met Ala Met Gly
65                  70                  75                  80
ggc aat aaa tta cgt aag ctg gaa ttt ctc gcg gca gat gcc ctg cgc     288
Gly Asn Lys Leu Arg Lys Leu Glu Phe Leu Ala Ala Asp Ala Leu Arg
```

```
                85                  90                  95
gaa ggt gcc gat acg ctg att act gcc ggc gcg atc cag tct aac cat       336
Glu Gly Ala Asp Thr Leu Ile Thr Ala Gly Ala Ile Gln Ser Asn His
            100                 105                 110
gtg cgg cag act gcc gca gtt gcg gcg aaa ctc ggc ctg cac tgc gtg       384
Val Arg Gln Thr Ala Ala Val Ala Ala Lys Leu Gly Leu His Cys Val
        115                 120                 125
gcg ctg ctg gaa aat cct att ggc aca acc gca gaa aac tat tta acc       432
Ala Leu Leu Glu Asn Pro Ile Gly Thr Thr Ala Glu Asn Tyr Leu Thr
    130                 135                 140
aac ggc aat cgt ttg ttg ctg aat ctg ttc aat acc cag att gaa atg       480
Asn Gly Asn Arg Leu Leu Leu Asn Leu Phe Asn Thr Gln Ile Glu Met
145                 150                 155                 160
tgc gac gca ctg acc gat ccc aat gcc caa ctg gaa gag ctg gcg acg       528
Cys Asp Ala Leu Thr Asp Pro Asn Ala Gln Leu Glu Glu Leu Ala Thr
                165                 170                 175
cga gtc gaa gca caa ggc ttt cgc ccg tat gtc att ccg gtt ggc ggt       576
Arg Val Glu Ala Gln Gly Phe Arg Pro Tyr Val Ile Pro Val Gly Gly
            180                 185                 190
tct aat gct ctg ggc gcg ctg ggt tat gtg gag agt gcg ctg gaa atc       624
Ser Asn Ala Leu Gly Ala Leu Gly Tyr Val Glu Ser Ala Leu Glu Ile
        195                 200                 205
gcg caa cag tgt gaa ggg gcg gtt aat att tcg tcg gtg gtg gtc gca       672
Ala Gln Gln Cys Glu Gly Ala Val Asn Ile Ser Ser Val Val Val Ala
    210                 215                 220
tcg ggc agt gcc gga act cac gcc gga ttg gct gtt ggg ctg gaa cac       720
Ser Gly Ser Ala Gly Thr His Ala Gly Leu Ala Val Gly Leu Glu His
225                 230                 235                 240
ctg atg cct gaa agc gaa ctg att ggc gtg acc gtg tcg cgt tcc gtt       768
Leu Met Pro Glu Ser Glu Leu Ile Gly Val Thr Val Ser Arg Ser Val
                245                 250                 255
gcc gat caa ttg ccg aaa gtg gtt aac cta caa cag gcg att gcg aaa       816
Ala Asp Gln Leu Pro Lys Val Val Asn Leu Gln Gln Ala Ile Ala Lys
            260                 265                 270
gaa ctg gag ctg acc gca tca gcg gaa att tta ctc tgg gat gac tat       864
Glu Leu Glu Leu Thr Ala Ser Ala Glu Ile Leu Leu Trp Asp Asp Tyr
        275                 280                 285
ttt gca cct ggc tac ggc gtg ccg aac gac gaa ggc atg gaa gca gtg       912
Phe Ala Pro Gly Tyr Gly Val Pro Asn Asp Glu Gly Met Glu Ala Val
    290                 295                 300
aaa ttg ctg gcg cgt ctg gaa ggc att ctg ctt gat cct gtg tat acc       960
Lys Leu Leu Ala Arg Leu Glu Gly Ile Leu Leu Asp Pro Val Tyr Thr
305                 310                 315                 320
gga aaa gcg atg gcg ggg ctg att gac ggt atc agt cag aaa cgc ttc      1008
Gly Lys Ala Met Ala Gly Leu Ile Asp Gly Ile Ser Gln Lys Arg Phe
                325                 330                 335
aaa gat gaa ggg ccg att ctg ttt att cat acc ggc ggc gcg cct gcg      1056
Lys Asp Glu Gly Pro Ile Leu Phe Ile His Thr Gly Gly Ala Pro Ala
            340                 345                 350
ctg ttc gcc tat cat ccc cac gtt tag                                 1083
Leu Phe Ala Tyr His Pro His Val
        355                 360
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<210> 145
<211> 360
<212> PRT
<213> Shigella boydii Sb227

<400> 145

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

Lys Asp Glu Gly Pro Ile Leu Phe Ile His Thr Gly Gly Ala Pro Ala
            340                 345                 350
Leu Phe Ala Tyr His Pro His Val
        355                 360

<210> 146
<211> 942
<212> DNA
<213> Hahella chejuensis KCTC 2396

<220>
<221> CDS
<222> (1)..(942)
<223> transl_table=11

<400> 146
gtg tcc tct ctg ctg tat caa ccc gat tgc gtc att caa ccg ctc agt      48
Met Ser Ser Leu Leu Tyr Gln Pro Asp Cys Val Ile Gln Pro Leu Ser
1               5                   10                  15
cac cct gtg gct gag cgc gct ggc gtg cgc ctg tgg atg gcg cgg ggt      96
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```
His Pro Val Ala Glu Arg Ala Gly Val Arg Leu Trp Met Ala Arg Gly
            20                  25                  30
gat ttg gtt cat gag tct gta tcc ggc aac aag tgg ttc aag ctc aaa      144
Asp Leu Val His Glu Ser Val Ser Gly Asn Lys Trp Phe Lys Leu Lys
        35                  40                  45
tac agc ctg ctg gag gcg gag cga aat caa gcg tcg gga ttg ttg agc      192
Tyr Ser Leu Leu Glu Ala Glu Arg Asn Gln Ala Ser Gly Leu Leu Ser
    50                  55                  60
ttc ggc ggc gcc tat tcc aac cac ttg cat gcg ctc gcc gca gcg ggc      240
Phe Gly Gly Ala Tyr Ser Asn His Leu His Ala Leu Ala Ala Ala Gly

65                  70                  75                  80
cgt atg ctg aat atc ccc acc ttt ggc gtg gtg cgc ggc gcc tgg cga      288
Arg Met Leu Asn Ile Pro Thr Phe Gly Val Val Arg Gly Ala Trp Arg
                85                  90                  95
cgt gag ctg acg cca act ctg cag gat gcc gag aag tgg ggg atg cgt      336
Arg Glu Leu Thr Pro Thr Leu Gln Asp Ala Glu Lys Trp Gly Met Arg
            100                 105                 110
ttg ctg ttc gtc agc aat gag gcg tat cgc tgc aaa gat gat cct gcc      384
Leu Leu Phe Val Ser Asn Glu Ala Tyr Arg Cys Lys Asp Asp Pro Ala
        115                 120                 125
tgg gtg gaa gga agc att gcg gac tgg ggg ctg tca gag ctg atc gat      432
Trp Val Glu Gly Ser Ile Ala Asp Trp Gly Leu Ser Glu Leu Ile Asp
    130                 135                 140
acg caa aag ctg atg atc atc ccc gag ggc ggt agc aat acg ctg gcg      480
Thr Gln Lys Leu Met Ile Ile Pro Glu Gly Gly Ser Asn Thr Leu Ala
145                 150                 155                 160
gtg aag ggt gta tct gag tgg gcg cag caa atc tat tcc tac ttt ccc      528
Val Lys Gly Val Ser Glu Trp Ala Gln Gln Ile Tyr Ser Tyr Phe Pro
                165                 170                 175
tcg act ccc gca tcc ata ttc ttg cct tgc ggc acc ggc ggt acg atg      576
Ser Thr Pro Ala Ser Ile Phe Leu Pro Cys Gly Thr Gly Gly Thr Met
            180                 185                 190
gcg ggg ttt gtc gcc gct cac tca cat cat gag gtg gtc ggt gtg cct      624
Ala Gly Phe Val Ala Ala His Ser His His Glu Val Val Gly Val Pro
        195                 200                 205
gtg ttg cgc gcc ggc gac tct att gca gct aag atc gat gag ttg ctg      672
Val Leu Arg Ala Gly Asp Ser Ile Ala Ala Lys Ile Asp Glu Leu Leu
    210                 215                 220
gct ttg aat aac cag caa cca gaa acc tgt ttt cgc ttt atg caa ggt      720
Ala Leu Asn Asn Gln Gln Pro Glu Thr Cys Phe Arg Phe Met Gln Gly
225                 230                 235                 240
tat gag ttt ggc ggt tac gcc aag acc agc ccc gag ctg atg gcc ttc      768
Tyr Glu Phe Gly Gly Tyr Ala Lys Thr Ser Pro Glu Leu Met Ala Phe
                245                 250                 255
act caa gca ttt tcc ggt cac acg ggc att ggt ttg gag cct gtc tac      816
Thr Gln Ala Phe Ser Gly His Thr Gly Ile Gly Leu Glu Pro Val Tyr
            260                 265                 270
acg gga aag atg gcg tat gca gcg ctg gag tgg ttg cgt cga ggc gag      864
Thr Gly Lys Met Ala Tyr Ala Ala Leu Glu Trp Leu Arg Arg Gly Glu
        275                 280                 285
gct cct aaa ggc tca gac gtt gtg ctt gtg cat act ggt ggt atg cag      912
Ala Pro Lys Gly Ser Asp Val Val Leu Val His Thr Gly Gly Met Gln
    290                 295                 300
ggc gcg cga ggt ttt ctt ggt aag cgt taa                              942
Gly Ala Arg Gly Phe Leu Gly Lys Arg
305                 310
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<210> 147
<211> 313
<212> PRT

<213> Hahella chejuensis KCTC 2396

<400> 147

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

<210> 148
<211> 1017
<212> DNA
<213> Burkholderia thailandensis E264

<220>
<221> CDS
<222> (1)..(1017)
<223> transl_table=11

<400> 148

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atg aat ctc cag aaa ttc ccg cgt tat ccg ctg acc ttc ggc ccg acg       48
Met Asn Leu Gln Lys Phe Pro Arg Tyr Pro Leu Thr Phe Gly Pro Thr
1               5                  10                  15
ccg atc cag ccg ctc aag cgg ctc tcc gcg cat ctc ggc ggc aag gtc       96
Pro Ile Gln Pro Leu Lys Arg Leu Ser Ala His Leu Gly Gly Lys Val
            20                  25                  30
```

```
gag ctg tac gcg aag cgc gac gac tgc aac agc ggc ctc gcg ttc ggc        144
Glu Leu Tyr Ala Lys Arg Asp Asp Cys Asn Ser Gly Leu Ala Phe Gly
        35                  40                  45
ggc aac aag acg cgc aag ctc gaa tac ctg atc ccg gat gcg ctc gcg        192
Gly Asn Lys Thr Arg Lys Leu Glu Tyr Leu Ile Pro Asp Ala Leu Ala
    50                  55                  60
caa ggc tgc gac acg ctc gtg tcg atc ggc ggc atc cag tcg aac cag        240
Gln Gly Cys Asp Thr Leu Val Ser Ile Gly Gly Ile Gln Ser Asn Gln
65                  70                  75                  80
acg cgc cag gtc gcg gcg gtg gcc gcg cat ctc ggc atg aag tgc gtg        288
Thr Arg Gln Val Ala Ala Val Ala Ala His Leu Gly Met Lys Cys Val
                85                  90                  95
ctc gtg cag gag aac tgg gtc aac tat cac gac gcc gtc tac gat cgc        336
Leu Val Gln Glu Asn Trp Val Asn Tyr His Asp Ala Val Tyr Asp Arg
            100                 105                 110
gtc ggc aac atc cag atg tcg cgg atg atg ggc gcc gac gtg cgc ctc        384
Val Gly Asn Ile Gln Met Ser Arg Met Met Gly Ala Asp Val Arg Leu
        115                 120                 125
gtg ccg gat ggc ttc gac atc ggc ttt cgc aag agc tgg gag gac gcg        432
Val Pro Asp Gly Phe Asp Ile Gly Phe Arg Lys Ser Trp Glu Asp Ala
    130                 135                 140
ctc gcc gat gtc cgc gcg agg ggc ggc aag ccg tat gcg att ccg gcc        480
Leu Ala Asp Val Arg Ala Arg Gly Gly Lys Pro Tyr Ala Ile Pro Ala
145                 150                 155                 160
ggc tgc tcc gat cat ccg ctc ggc ggc ctc ggc ttc gtc ggc ttc gcc        528
Gly Cys Ser Asp His Pro Leu Gly Gly Leu Gly Phe Val Gly Phe Ala
                165                 170                 175
gag gag gtg cgc gcg caa gag gcc gag ctc ggc ttc aag ttc gat tac        576

Glu Glu Val Arg Ala Gln Glu Ala Glu Leu Gly Phe Lys Phe Asp Tyr
            180                 185                 190
gtc gtc gtg tgc tcg gtg acg ggc agc acg cag gcc ggg atg gtc gtc        624
Val Val Val Cys Ser Val Thr Gly Ser Thr Gln Ala Gly Met Val Val
        195                 200                 205
ggg ttc gcg gcg gac ggg cgc gcg gat cgc gtg atc ggc atc gac gcg        672
Gly Phe Ala Ala Asp Gly Arg Ala Asp Arg Val Ile Gly Ile Asp Ala
    210                 215                 220
tcg gcg aag ccc gcg cag acg cgc gag cag atc ctt cgg atc gcg agg        720
Ser Ala Lys Pro Ala Gln Thr Arg Glu Gln Ile Leu Arg Ile Ala Arg
225                 230                 235                 240
aat acc gcc gat cgc gtc gag ctc ggc cgc gac atc gcg agc ggc gac        768
Asn Thr Ala Asp Arg Val Glu Leu Gly Arg Asp Ile Ala Ser Gly Asp
                245                 250                 255
gtc gtg ctc gac gag cgc ttc ggc ggc ccc gaa tac ggg ttg ccg aac        816
Val Val Leu Asp Glu Arg Phe Gly Gly Pro Glu Tyr Gly Leu Pro Asn
            260                 265                 270
gag ggc acg ctc gag gcg atc cgg ctg tgc gca aag ctc gaa ggc gtg        864
Glu Gly Thr Leu Glu Ala Ile Arg Leu Cys Ala Lys Leu Glu Gly Val
        275                 280                 285
ctg acc gat ccc gtc tac gaa ggc aag tcg atg cac ggg atg atc gag        912
Leu Thr Asp Pro Val Tyr Glu Gly Lys Ser Met His Gly Met Ile Glu
    290                 295                 300
aag gtg cgg ctc ggc gag ttt ccc gcc ggc tcg aag gtg ctg tac gcg        960
Lys Val Arg Leu Gly Glu Phe Pro Ala Gly Ser Lys Val Leu Tyr Ala
305                 310                 315                 320
cat ctc ggc ggc gtg ccc gcg ctg aac gcg tac agc ttc ctg ttt cgc       1008
His Leu Gly Gly Val Pro Ala Leu Asn Ala Tyr Ser Phe Leu Phe Arg
                325                 330                 335
gac ggc tga                                                           1017

Asp Gly
```

<210> 149
<211> 338
<212> PRT
<213> Burkholderia thailandensis E264

<400> 149
Met Asn Leu Gln Lys Phe Pro Arg Tyr Pro Leu Thr Phe Gly Pro Thr
1 5 10 15
Pro Ile Gln Pro Leu Lys Arg Leu Ser Ala His Leu Gly Gly Lys Val
20 25 30
Glu Leu Tyr Ala Lys Arg Asp Asp Cys Asn Ser Gly Leu Ala Phe Gly
35 40 45
Gly Asn Lys Thr Arg Lys Leu Glu Tyr Leu Ile Pro Asp Ala Leu Ala
50 55 60
Gln Gly Cys Asp Thr Leu Val Ser Ile Gly Gly Ile Gln Ser Asn Gln
65 70 75 80
Thr Arg Gln Val Ala Ala Val Ala Ala His Leu Gly Met Lys Cys Val
85 90 95
Leu Val Gln Glu Asn Trp Val Asn Tyr His Asp Ala Val Tyr Asp Arg
100 105 110
Val Gly Asn Ile Gln Met Ser Arg Met Met Gly Ala Asp Val Arg Leu
115 120 125
Val Pro Asp Gly Phe Asp Ile Gly Phe Arg Lys Ser Trp Glu Asp Ala
130 135 140
Leu Ala Asp Val Arg Ala Arg Gly Gly Lys Pro Tyr Ala Ile Pro Ala
145 150 155 160
Gly Cys Ser Asp His Pro Leu Gly Gly Leu Gly Phe Val Gly Phe Ala
165 170 175
Glu Glu Val Arg Ala Gln Glu Ala Glu Leu Gly Phe Lys Phe Asp Tyr
180 185 190
Val Val Val Cys Ser Val Thr Gly Ser Thr Gln Ala Gly Met Val Val
195 200 205
Gly Phe Ala Ala Asp Gly Arg Ala Asp Arg Val Ile Gly Ile Asp Ala
210 215 220
Ser Ala Lys Pro Ala Gln Thr Arg Glu Gln Ile Leu Arg Ile Ala Arg
225 230 235 240
Asn Thr Ala Asp Arg Val Glu Leu Gly Arg Asp Ile Ala Ser Gly Asp
245 250 255
Val Val Leu Asp Glu Arg Phe Gly Gly Pro Glu Tyr Gly Leu Pro Asn
260 265 270
Glu Gly Thr Leu Glu Ala Ile Arg Leu Cys Ala Lys Leu Glu Gly Val
275 280 285
Leu Thr Asp Pro Val Tyr Glu Gly Lys Ser Met His Gly Met Ile Glu
290 295 300
Lys Val Arg Leu Gly Glu Phe Pro Ala Gly Ser Lys Val Leu Tyr Ala
305 310 315 320
His Leu Gly Gly Val Pro Ala Leu Asn Ala Tyr Ser Phe Leu Phe Arg
325 330 335
Asp Gly

<210> 150
<211> 993
<212> DNA
<213> Sodalis glossinidius str. 'morsitans'

<220>
<221> CDS
<222> (1)..(993)

<223> transl_table=11

<400> 150

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atg agc gat ctt gcc caa cgg ttg gcc ggc gtt ccc cgg ctg gat att       48
Met Ser Asp Leu Ala Gln Arg Leu Ala Gly Val Pro Arg Leu Asp Ile
1               5                  10                  15
atc ggc ccg ccg acg ccg ctc gaa cat ctc ccc cgg ctg tcg gac ttt       96
Ile Gly Pro Pro Thr Pro Leu Glu His Leu Pro Arg Leu Ser Asp Phe
            20                  25                  30
ctg gcg cgg gat atc ttt atc aag cgc gac gat tta acc ccg ctg ggc      144
Leu Ala Arg Asp Ile Phe Ile Lys Arg Asp Asp Leu Thr Pro Leu Gly
        35                  40                  45
ctg ggc ggt aac aag ttg cgc aag ctg gag tac ctg gcc gct gac gcg      192
Leu Gly Gly Asn Lys Leu Arg Lys Leu Glu Tyr Leu Ala Ala Asp Ala
    50                  55                  60
ctg cgc cag ggt gcc gac acg ttg ctg acc gcc ggt gct atc cag tcg      240
Leu Arg Gln Gly Ala Asp Thr Leu Leu Thr Ala Gly Ala Ile Gln Ser
65                  70                  75                  80
aac cac gtg cgg caa acg gcg gcg ctg gcg gcc aaa ttg ggg ctg cat      288
Asn His Val Arg Gln Thr Ala Ala Leu Ala Ala Lys Leu Gly Leu His
                85                  90                  95
tgc gtc gcg ctg ttg gaa aag ccg atc gac aca ccc gcc ggt aac tac      336
Cys Val Ala Leu Leu Glu Lys Pro Ile Asp Thr Pro Ala Gly Asn Tyr
            100                 105                 110
ctg acc aac ggc aac cgt ctg ttg ctc gat ttg ttt cag tgc gag gtc      384
Leu Thr Asn Gly Asn Arg Leu Leu Leu Asp Leu Phe Gln Cys Glu Val
        115                 120                 125
atc gcg tgc gag gcc ctg act cag cct gct caa cag ctg gcc gat gcg      432
Ile Ala Cys Glu Ala Leu Thr Gln Pro Ala Gln Gln Leu Ala Asp Ala
    130                 135                 140
tcg ctg cgt ctg gag gca cag ggc ttt cgg ccc tat gtc ata cca gtg      480
Ser Leu Arg Leu Glu Ala Gln Gly Phe Arg Pro Tyr Val Ile Pro Val
145                 150                 155                 160
ggg gga tcc aac gcc ctg ggc tcg ctg ggt tac gtc ggt tgt gcg ctg      528
Gly Gly Ser Asn Ala Leu Gly Ser Leu Gly Tyr Val Gly Cys Ala Leu
                165                 170                 175
gag ata gcc cat cag tgt caa ggt gtg atc cag ccg ggc gcg gta gtg      576
Glu Ile Ala His Gln Cys Gln Gly Val Ile Gln Pro Gly Ala Val Val
            180                 185                 190
gtg tca tcg ggc agc ggc ggc acg cac gcg gga ctg gag gtc ggt ctg      624
Val Ser Ser Gly Ser Gly Gly Thr His Ala Gly Leu Glu Val Gly Leu
        195                 200                 205
gcc gcc gtg ctg ccg gaa acg gcg ttt atc ggc gtt acc gtt tcg cgt      672
Ala Ala Val Leu Pro Glu Thr Ala Phe Ile Gly Val Thr Val Ser Arg
    210                 215                 220
cgc tcg gaa cag cag cgg cct ctt atc gcc agt ctg gca gcg caa gtg      720
Arg Ser Glu Gln Gln Arg Pro Leu Ile Ala Ser Leu Ala Ala Gln Val
225                 230                 235                 240
agt gaa cag ttg tct ctc gcc gcg ccg gcc gcg gag ata acc ctg tgg      768
Ser Glu Gln Leu Ser Leu Ala Ala Pro Ala Ala Glu Ile Thr Leu Trp
                245                 250                 255
gat gag tat ttt gcc ccc ggt tat ggc cag ctc aat gac gag ggc cgc      816
Asp Glu Tyr Phe Ala Pro Gly Tyr Gly Gln Leu Asn Asp Glu Gly Arg
            260                 265                 270
gag gcg att gcg cta tta gcg cgt ctg gag ggc att gtg ctg gat ccg      864
Glu Ala Ile Ala Leu Leu Ala Arg Leu Glu Gly Ile Val Leu Asp Pro
        275                 280                 285
gtt tat gcc ggt aag gcc atg gca ggg ctg att gat ggc ctt gaa cgc      912
Val Tyr Ala Gly Lys Ala Met Ala Gly Leu Ile Asp Gly Leu Glu Arg
    290                 295                 300
gac cgt ttt cct gac ggg cca ctg gtg tgt tcg tgc ata ccg gcg gcg      960
```

```
Asp Arg Phe Pro Asp Gly Pro Leu Val Cys Ser Cys Ile Pro Ala Ala
305                 310                 315                 320
ctg ttt gct tat cat tat ctg gag acc cga tga                     993
Leu Phe Ala Tyr His Tyr Leu Glu Thr Arg
                325                 330
```

<210> 151
<211> 330
<212> PRT
<213> Sodalis glossinidius str. 'morsitans'

<400> 151

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

<210> 152
<211> 1023
<212> DNA
<213> Anaeromyxobacter dehalogenans 2CP-C

<220>

<221> CDS
<222> (1)..(1023)
<223> transl_table=11

<400> 152

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atg ccg gcc acc cgc gaa ccc gcc acc ctg aac ctg ccc ccg cgc gtg        48
Met Pro Ala Thr Arg Glu Pro Ala Thr Leu Asn Leu Pro Pro Arg Val
1               5                  10                  15
ccg ctc gcc cgg ctg ccc acg ccc atc gag ccg tcg ccg cgg ctc ggg        96
Pro Leu Ala Arg Leu Pro Thr Pro Ile Glu Pro Ser Pro Arg Leu Gly
            20                  25                  30
gcc gcg ctc ggg ctc gac ctc ctc tac aag cgc gac gac ctc acc ggc       144
Ala Ala Leu Gly Leu Asp Leu Leu Tyr Lys Arg Asp Asp Leu Thr Gly
        35                  40                  45
ctc gag ctg tcc ggc aac aag gcg cgg aag ctg gag tac ctg ctc gcc       192
Leu Glu Leu Ser Gly Asn Lys Ala Arg Lys Leu Glu Tyr Leu Leu Ala
    50                  55                  60
gag gcc gag gcg gcg ggg gcg gac acg gtg gtc acc tgc ggc ggc gtg       240
Glu Ala Glu Ala Ala Gly Ala Asp Thr Val Val Thr Cys Gly Gly Val
65                  70                  75                  80
cag tcc aac cac tgc cgc gcc acg gcg ttc gcg gcc gcg aag cgc ggg       288
Gln Ser Asn His Cys Arg Ala Thr Ala Phe Ala Ala Ala Lys Arg Gly
                85                  90                  95
ctg cgc gcg gtg ctc ctg ctg cgc gtg ccg gac ccg gcg cgg ccg ccc       336
Leu Arg Ala Val Leu Leu Leu Arg Val Pro Asp Pro Ala Arg Pro Pro
            100                 105                 110
gcg ccc gag gcg aac gtg ctg ctc gat ctc ctg gcc ggc gcg gag ctc       384
Ala Pro Glu Ala Asn Val Leu Leu Asp Leu Leu Ala Gly Ala Glu Leu
        115                 120                 125
cgc tgg gtc tcg cac gac gag tac cgg cgc cgc gcc gag cgc atg gac       432
Arg Trp Val Ser His Asp Glu Tyr Arg Arg Arg Ala Glu Arg Met Asp
    130                 135                 140
gcg gtg gcc tcg gag ctg cgc gcg gcc ggg cgg cgg gcc tac gtg atc       480
Ala Val Ala Ser Glu Leu Arg Ala Ala Gly Arg Arg Ala Tyr Val Ile
145                 150                 155                 160
ccg gag ggc ggc tcg tcg ccg ctg ggg agc ctg ggc tac ctg ctg gcc       528
Pro Glu Gly Gly Ser Ser Pro Leu Gly Ser Leu Gly Tyr Leu Leu Ala
                165                 170                 175
gtg gcg gag ctg cgg cgg cag ctc ccg gag gcg tgg cgg agc ggg ccg       576
Val Ala Glu Leu Arg Arg Gln Leu Pro Glu Ala Trp Arg Ser Gly Pro
            180                 185                 190
ctg acg ctc gcc tac gcc gcg ggc tcg ggc ggc acc ggc gcc ggg ctc       624
Leu Thr Leu Ala Tyr Ala Ala Gly Ser Gly Gly Thr Gly Ala Gly Leu
        195                 200                 205
gag ctc ggg gtg cgc gcg ctg ggg tgg aag gac gcg cga ccg gtg ggc       672
Glu Leu Gly Val Arg Ala Leu Gly Trp Lys Asp Ala Arg Pro Val Gly
    210                 215                 220
ttc gcg gtg tgc aac gac gcg gcg tac ttc cgc gcg acg atc gcg gcg       720
Phe Ala Val Cys Asn Asp Ala Ala Tyr Phe Arg Ala Thr Ile Ala Ala
225                 230                 235                 240
ctg tgc gcc gac gcg cgc cgg cgg tgg ccg gcg ctg ccc gag gtg ccc       768
Leu Cys Ala Asp Ala Arg Arg Arg Trp Pro Ala Leu Pro Glu Val Pro
                245                 250                 255
gcg gac gag atc cgg atc gac gac ggg ttc atc ggc ccg ggc tac gcc       816
Ala Asp Glu Ile Arg Ile Asp Asp Gly Phe Ile Gly Pro Gly Tyr Ala
            260                 265                 270
cag gcg acg ccg gag ggg ctg gag atc atc cgc cgc gcg gcg cgc gag       864
Gln Ala Thr Pro Glu Gly Leu Glu Ile Ile Arg Arg Ala Ala Arg Glu
        275                 280                 285
gac ggg gtg ctc ctc gat ccg gtc tac acc gga aag gcg atg ctc ggt       912
Asp Gly Val Leu Leu Asp Pro Val Tyr Thr Gly Lys Ala Met Leu Gly
```

```
    290                 295                 300
ctg gcc gcg cgg gcg cgc gag ccg ggt ggc ctg ccc gcg ccg cgc gtc       960
Leu Ala Ala Arg Ala Arg Glu Pro Gly Gly Leu Pro Ala Pro Arg Val
305                 310                 315                 320
gtg ttc ttc cac acc ggc ggc gcg ttc ggc ctc ttc ccg ttc gcg agc      1008
Val Phe Phe His Thr Gly Gly Ala Phe Gly Leu Phe Pro Phe Ala Ser
                325                 330                 335
gcg ctg acc ggc tga                                                  1023
Ala Leu Thr Gly
            340
```

<210> 153
<211> 340
<212> PRT
<213> Anaeromyxobacter dehalogenans 2CP-C

<400> 153

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

<210> 154
<211> 1029
<212> DNA
<213> Jannaschia sp. CCS1

<220>
<221> CDS
<222> (1)..(1029)
<223> transl_table=11

<400> 154

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

cgg gtc acg gac gcg gat atc atc aca tgg gac ggg gcc ttg tcg ccg      768
Arg Val Thr Asp Ala Asp Ile Ile Thr Trp Asp Gly Ala Leu Ser Pro
```

```
                245                 250                 255
gga tat ggc cag ttg gga cca gcc gcg cgg gac gcg atg gag atg atg      816
Gly Tyr Gly Gln Leu Gly Pro Ala Ala Arg Asp Ala Met Glu Met Met
            260                 265                 270
gcg cgc cat gag ggg ctg atg ctg gac ccg gtc tat acc gcc aag agt      864
Ala Arg His Glu Gly Leu Met Leu Asp Pro Val Tyr Thr Ala Lys Ser
        275                 280                 285
ttc gcc gcg atc ccg gcc ctt gtg gcc agc ggc gag atc ccc aag ggc      912
Phe Ala Ala Ile Pro Ala Leu Val Ala Ser Gly Glu Ile Pro Lys Gly
    290                 295                 300
agc cgg gtg tgt ttc gtg cat acc ggc ggg ctg gcg gct ttg ttt gcc      960
Ser Arg Val Cys Phe Val His Thr Gly Gly Leu Ala Ala Leu Phe Ala
305                 310                 315                 320
tat gag gcc gcg ctg aca gag ggg ctt gaa gcg cgg cct acg gat ctt     1008
Tyr Glu Ala Ala Leu Thr Glu Gly Leu Glu Ala Arg Pro Thr Asp Leu
                325                 330                 335
cca gac gcg gcg cgg cgc tga                                        1029
Pro Asp Ala Ala Arg Arg
            340
```

<210> 155
<211> 342
<212> PRT
<213> Jannaschia sp. CCS1

<400> 155

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

```
Ala Arg His Glu Gly Leu Met Leu Asp Pro Val Tyr Thr Ala Lys Ser
        275                 280                 285
Phe Ala Ala Ile Pro Ala Leu Val Ala Ser Gly Glu Ile Pro Lys Gly
    290                 295                 300
Ser Arg Val Cys Phe Val His Thr Gly Gly Leu Ala Ala Leu Phe Ala
305                 310                 315                 320
Tyr Glu Ala Ala Leu Thr Glu Gly Leu Glu Ala Arg Pro Thr Asp Leu
                325                 330                 335
Pro Asp Ala Ala Arg Arg
            340
```

<210> 156
<211> 1011
<212> DNA
<213> Saccharophagus degradans 2-40

<220>
<221> CDS
<222> (1)..(1011)
<223> transl_table=11

<400> 156

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

```
ttg ggg agt aaa gca aag gtt gtg ggt atg gct gtg tgc gac tca gag       672
Leu Gly Ser Lys Ala Lys Val Val Gly Met Ala Val Cys Asp Ser Glu
    210                 215                 220
gct tac ttt gag cgc aaa gct aaa caa gat ata acc ctg tgg cag caa       720
Ala Tyr Phe Glu Arg Lys Ala Lys Gln Asp Ile Thr Leu Trp Gln Gln
225                 230                 235                 240
aag tac ggg cag gca gct gga ata tct gct cag caa gct act cag gta       768
Lys Tyr Gly Gln Ala Ala Gly Ile Ser Ala Gln Gln Ala Thr Gln Val
                245                 250                 255
caa ata aat act atc gat aaa tat att ggc cca gga tat gca aaa gcc       816
Gln Ile Asn Thr Ile Asp Lys Tyr Ile Gly Pro Gly Tyr Ala Lys Ala
            260                 265                 270
tac cct gag ttg ctg gag cgt att cgc tgg ttg gca gcc acc gaa ggg       864
Tyr Pro Glu Leu Leu Glu Arg Ile Arg Trp Leu Ala Ala Thr Glu Gly
        275                 280                 285
gtg gtg cta gac ccc gtt tac aca ggc aaa gca ttt tat ggg ttg gtg       912
Val Val Leu Asp Pro Val Tyr Thr Gly Lys Ala Phe Tyr Gly Leu Val
    290                 295                 300
caa gaa att aaa tcg ggg cgc tgg gca aat atg aaa gac att gta ttt       960
Gln Glu Ile Lys Ser Gly Arg Trp Ala Asn Met Lys Asp Ile Val Phe
305                 310                 315                 320
gta cac act ggg ggg att ttt ggc ctt ttc ccc tat aga gat gaa ttt      1008
Val His Thr Gly Gly Ile Phe Gly Leu Phe Pro Tyr Arg Asp Glu Phe
                325                 330                 335
tag                                                                  1011
```

<210> 157
<211> 336
<212> PRT
<213> Saccharophagus degradans 2-40

<400> 157

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

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

<210> 158
<211> 978
<212> DNA
<213> Saccharophagus degradans 2-40

<220>
<221> CDS
<222> (1)..(978)
<223> transl_table=11

<400> 158

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

```
Cys Ser Glu Phe Leu Gln Arg Val Thr Pro Asn Glu Ser Asp Ala Tyr
            180                 185                 190
gtg gtg atg gct tgt ggc aca ggt aca acc ttt agc ggc gtt gtt aat      624
Val Val Met Ala Cys Gly Thr Gly Thr Thr Phe Ser Gly Val Val Asn
        195                 200                 205
ggc gtg ggg cct tct gtg cag gtg ttg ggc gtg cca gtg cta aag gtg      672
Gly Val Gly Pro Ser Val Gln Val Leu Gly Val Pro Val Leu Lys Val
    210                 215                 220
ggt ggc gaa tat aaa gcc gaa att gct gct gcc ata ggt gcg aat acc      720
Gly Gly Glu Tyr Lys Ala Glu Ile Ala Ala Ala Ile Gly Ala Asn Thr
225                 230                 235                 240
cgc tgg aag ctt tta gag gat ggg cat tgt ggt ggt tac gcc aag ttt      768
Arg Trp Lys Leu Leu Glu Asp Gly His Cys Gly Gly Tyr Ala Lys Phe
                245                 250                 255
cca gaa tac ctg cta aag ttt atg gta gaa aca gaa tta gaa gtt ggc      816
Pro Glu Tyr Leu Leu Lys Phe Met Val Glu Thr Glu Leu Glu Val Gly
            260                 265                 270
gtg caa tta gac cca gtg tat acg gcg aaa atg ctg tac agt ctg gca      864
Val Gln Leu Asp Pro Val Tyr Thr Ala Lys Met Leu Tyr Ser Leu Ala
        275                 280                 285
aca gcg att aag cag ggt aag ttt gca aga ggt agc cat att gtg gct      912
Thr Ala Ile Lys Gln Gly Lys Phe Ala Arg Gly Ser His Ile Val Ala
    290                 295                 300
att cac tct ggt ggc tta caa ggt agg cgc agt gtg gag aag caa tta      960
Ile His Ser Gly Gly Leu Gln Gly Arg Arg Ser Val Glu Lys Gln Leu
305                 310                 315                 320
atg gag ttg tat gta tga                                              978
Met Glu Leu Tyr Val
                325
```

<210> 159
<211> 325
<212> PRT
<213> Saccharophagus degradans 2-40

<400> 159

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

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

<210> 160
<211> 987
<212> DNA
<213> Escherichia coli UTI89

<220>
<221> CDS
<222> (1)..(987)
<223> transl_table=11

<400> 160

```
atg cca ctg cat aat tta acc cgt ttt cca cgg ctg gag ttt atc ggc       48

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

```
Ser Asn Ala Leu Gly Ala Leu Gly Tyr Val Glu Ser Ala Leu Glu Ile
                165                 170                 175
gcg caa cag tgt gaa ggg gca gtt aat att tcg tcg gtg gtg gtc gca       576
Ala Gln Gln Cys Glu Gly Ala Val Asn Ile Ser Ser Val Val Val Ala
            180                 185                 190
tcg ggc agt gcc gga act cac gcc gga ctg gct gtt ggg ctg gaa cac       624
Ser Gly Ser Ala Gly Thr His Ala Gly Leu Ala Val Gly Leu Glu His
        195                 200                 205
ctg atg cct gaa agc gaa ctg att ggc gtg act gtg tcg cgt tct gtt       672
Leu Met Pro Glu Ser Glu Leu Ile Gly Val Thr Val Ser Arg Ser Val
    210                 215                 220
gcc gat caa ttg ccg aaa gtg gtt aac ctc caa cag gcg att gcg aaa       720
Ala Asp Gln Leu Pro Lys Val Val Asn Leu Gln Gln Ala Ile Ala Lys
225                 230                 235                 240
gaa ctg gag ctg acc gca tca gcg gaa att tta ctc tgg gat gac tat       768
Glu Leu Glu Leu Thr Ala Ser Ala Glu Ile Leu Leu Trp Asp Asp Tyr
                245                 250                 255
ttt gca cct ggc tac ggc gtg ccg aac gac gaa ggc atg gaa gca gtg       816
Phe Ala Pro Gly Tyr Gly Val Pro Asn Asp Glu Gly Met Glu Ala Val
            260                 265                 270
aaa ttg ctg gcg cgg ctg gaa ggc att ctg ctt gat cct gtg tat acc       864
Lys Leu Leu Ala Arg Leu Glu Gly Ile Leu Leu Asp Pro Val Tyr Thr
        275                 280                 285
gga aaa gcg atg gcg ggg ctg att gac ggt atc agt cag aaa cgc ttc       912
Gly Lys Ala Met Ala Gly Leu Ile Asp Gly Ile Ser Gln Lys Arg Phe
    290                 295                 300
aaa gat gaa ggg ccg att ctg ttt att cat acc ggc ggt gcg cct gcg       960
Lys Asp Glu Gly Pro Ile Leu Phe Ile His Thr Gly Gly Ala Pro Ala
305                 310                 315                 320
ctg ttc gcc tat cat ccc cac gtt tag                                  987
Leu Phe Ala Tyr His Pro His Val
                325
```

<210> 161
<211> 328
<212> PRT
<213> Escherichia coli UTI89

```
<400> 161
Met Pro Leu His Asn Leu Thr Arg Phe Pro Arg Leu Glu Phe Ile Gly
1               5                   10                  15
Ala Pro Thr Pro Leu Glu Tyr Leu Pro Arg Phe Ser Asp Tyr Leu Gly
            20                  25                  30
Arg Glu Ile Phe Ile Lys Arg Asp Asp Val Thr Pro Met Ala Met Gly
        35                  40                  45
Gly Asn Lys Leu Arg Lys Leu Glu Phe Leu Ala Ala Asp Ala Leu Arg
    50                  55                  60
Glu Gly Ala Asp Thr Leu Ile Thr Ala Gly Ala Ile Gln Ser Asn His
65                  70                  75                  80
Val Arg Gln Thr Ala Ala Val Ala Ala Lys Leu Gly Leu His Cys Val
                85                  90                  95
Ala Leu Leu Glu Asn Pro Ile Gly Thr Thr Ala Glu Asn Tyr Leu Thr
            100                 105                 110
Asn Gly Asn Arg Leu Leu Leu Asp Leu Phe Asn Thr Gln Ile Glu Met
        115                 120                 125
Cys Asp Ala Leu Thr Asp Pro Asn Thr Gln Leu Glu Glu Leu Ala Thr
    130                 135                 140
Arg Val Glu Ala Gln Gly Phe Arg Pro Tyr Val Ile Pro Val Gly Gly
145                 150                 155                 160
Ser Asn Ala Leu Gly Ala Leu Gly Tyr Val Glu Ser Ala Leu Glu Ile
                165                 170                 175
```

```
Ala Gln Gln Cys Glu Gly Ala Val Asn Ile Ser Ser Val Val Val Ala
            180                 185                 190
Ser Gly Ser Ala Gly Thr His Ala Gly Leu Ala Val Gly Leu Glu His
        195                 200                 205
Leu Met Pro Glu Ser Glu Leu Ile Gly Val Thr Val Ser Arg Ser Val
    210                 215                 220
Ala Asp Gln Leu Pro Lys Val Val Asn Leu Gln Gln Ala Ile Ala Lys
225                 230                 235                 240
Glu Leu Glu Leu Thr Ala Ser Ala Glu Ile Leu Leu Trp Asp Asp Tyr
                245                 250                 255
Phe Ala Pro Gly Tyr Gly Val Pro Asn Asp Glu Gly Met Glu Ala Val
            260                 265                 270
Lys Leu Leu Ala Arg Leu Glu Gly Ile Leu Leu Asp Pro Val Tyr Thr
        275                 280                 285
Gly Lys Ala Met Ala Gly Leu Ile Asp Gly Ile Ser Gln Lys Arg Phe
    290                 295                 300
Lys Asp Glu Gly Pro Ile Leu Phe Ile His Thr Gly Gly Ala Pro Ala
305                 310                 315                 320
Leu Phe Ala Tyr His Pro His Val
                325
```

<210> 162
<211> 1038
<212> DNA
<213> Polaromonas sp. JS666

<220>
<221> CDS
<222> (1)..(1038)
<223> transl_table=11

<400> 162

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

```
145                 150                 155                 160
gtg ccg ggc ggt ggt tcc aac gcc att ggc ggt ctg ggt tat gtg gcc       528
Val Pro Gly Gly Gly Ser Asn Ala Ile Gly Gly Leu Gly Tyr Val Ala
                165                 170                 175
tgc gcg cag gag ctg cag cag cag ttt ttc gag cag ggc gtg cag atc       576
Cys Ala Gln Glu Leu Gln Gln Gln Phe Phe Glu Gln Gly Val Gln Ile
            180                 185                 190
gac aag atc gtc gtg ggc tcg ggc agc tcg ggc acg cac ggt ggc ctg       624
Asp Lys Ile Val Val Gly Ser Gly Ser Ser Gly Thr His Gly Gly Leu
        195                 200                 205
ctg gcc ggc ttc ctg ggc aac cac atc cat att ccc ctg atc ggc att       672
Leu Ala Gly Phe Leu Gly Asn His Ile His Ile Pro Leu Ile Gly Ile
    210                 215                 220
ggt gtg agc cgc gac ccg gtg gac cag gat ccc ctc gtg cac aag gag       720
Gly Val Ser Arg Asp Pro Val Asp Gln Asp Pro Leu Val His Lys Glu
225                 230                 235                 240
gcc cag gcc gtg gcc gac ctg ctg ggc ctg aat atg acc att ccg cgc       768
Ala Gln Ala Val Ala Asp Leu Leu Gly Leu Asn Met Thr Ile Pro Arg
                245                 250                 255
gaa gcg gtc gtg agc tat ggc gac tgg tgg agg ccc aag tat tcg gta       816
Glu Ala Val Val Ser Tyr Gly Asp Trp Trp Arg Pro Lys Tyr Ser Val
            260                 265                 270
ccc aac cag gcc atg gtc gaa gcc gtg cag atg ctg gcg cgc acc gag       864
Pro Asn Gln Ala Met Val Glu Ala Val Gln Met Leu Ala Arg Thr Glu
        275                 280                 285
gcc att ctg ctg gac ccg gtg tac acc ggc aag atc atg gcc ggg ctg       912
Ala Ile Leu Leu Asp Pro Val Tyr Thr Gly Lys Ile Met Ala Gly Leu
    290                 295                 300
atc gga ctg gcg cgc aaa ggc cat ttc cgc cgt gat gaa aac gtg ctg       960
Ile Gly Leu Ala Arg Lys Gly His Phe Arg Arg Asp Glu Asn Val Leu
305                 310                 315                 320
ttc att cac acc gga ggg gca ccg tcg ctg cat gcc tac gaa gcc gag      1008
Phe Ile His Thr Gly Gly Ala Pro Ser Leu His Ala Tyr Glu Ala Glu
                325                 330                 335
gtg ctg ggc ctg acc gag ctg ccg gcc tga                             1038
Val Leu Gly Leu Thr Glu Leu Pro Ala
            340                 345
```

<210> 163
<211> 345
<212> PRT
<213> Polaromonas sp. JS666

<400> 163

```
Met Asp Leu Ser Arg Phe Pro Arg Arg Arg Tyr Thr Gln Gly Pro Thr
1               5                   10                  15
Pro Leu Glu Phe Leu Pro His Phe Thr Glu Ala Leu Arg Ala Thr Cys
            20                  25                  30
Pro Glu Gly Ser Gly Pro Asn Ile Trp Ile Lys Arg Asp Asp Met Leu
        35                  40                  45
Gly Leu Thr Pro Gly Gly Asn Lys Thr Arg Lys Leu Glu Phe Leu Ala
    50                  55                  60
Ala Asp Ala Leu Ala Gln Gly Ala Asp Thr Leu Ile Thr Cys Gly Ala
65                  70                  75                  80
Pro Gln Ser Asn His Cys Arg Ala Thr Leu Cys Ala Ala Ile Lys Glu
                85                  90                  95
Gly Leu Lys Cys Arg Phe Val Ile Glu Glu Arg Val Pro Asn Ser Tyr
            100                 105                 110
Arg Glu Asn Ala Ser Gly Asn Asn Phe Leu Phe Arg Leu Leu Gly Val
        115                 120                 125
Glu Ala Ile Thr Val Val Pro Ala Gly Thr Asn Met Met Glu Ala Met
```

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

Ile Gly Leu Ala Arg Lys Gly His Phe Arg Arg Asp Glu Asn Val Leu
305                 310                 315                 320
Phe Ile His Thr Gly Gly Ala Pro Ser Leu His Ala Tyr Glu Ala Glu
                325                 330                 335
Val Leu Gly Leu Thr Glu Leu Pro Ala
            340                 345
```

<210> 164
<211> 1029
<212> DNA
<213> Polaromonas sp. JS666

<220>
<221> CDS
<222> (1)..(1029)
<223> transl_table=11

<400> 164

```
atg caa ctc acg ctc aac ctc aaa aag ttt ccc aga cat tcg ttg acc       48
Met Gln Leu Thr Leu Asn Leu Lys Lys Phe Pro Arg His Ser Leu Thr
1               5                   10                  15
ttc ggc ccc acg ccc atc cag ccg ctc agg cgc ctg agc gcc cac ctg       96
Phe Gly Pro Thr Pro Ile Gln Pro Leu Arg Arg Leu Ser Ala His Leu
            20                  25                  30
ggc ggc aag gtc gag ctg tac gcc aaa cgc gaa gac tgc aac agc ggc      144
Gly Gly Lys Val Glu Leu Tyr Ala Lys Arg Glu Asp Cys Asn Ser Gly
        35                  40                  45
ctg gcc ttt ggc ggc aac aaa acc cgc aag ctg gag tac ctg atc ccc      192
Leu Ala Phe Gly Gly Asn Lys Thr Arg Lys Leu Glu Tyr Leu Ile Pro
    50                  55                  60
gag gcg ctg gcg caa ggc tgc gac acg ctg gtc tcc atc ggc ggc atc      240
Glu Ala Leu Ala Gln Gly Cys Asp Thr Leu Val Ser Ile Gly Gly Ile
65                  70                  75                  80
cag tcc aac cag acg cgc cag gtg gcg gcc gtg gcc gcg cac ctg ggc      288
Gln Ser Asn Gln Thr Arg Gln Val Ala Ala Val Ala Ala His Leu Gly
                85                  90                  95
atg aag tgc gtg ctg gtg cag gag aac tgg gtg aac tat tcc gac gcc      336
Met Lys Cys Val Leu Val Gln Glu Asn Trp Val Asn Tyr Ser Asp Ala
            100                 105                 110
```

```
gtg tac gac cgc gtc ggc aat atc gag atg tcg cgc atc ctg ggc gcc       384
Val Tyr Asp Arg Val Gly Asn Ile Glu Met Ser Arg Ile Leu Gly Ala
        115                 120                 125
gac gtg cgc ctg gat gcg gcc ggt ttt gac atc ggc att cgc ccc agc       432
Asp Val Arg Leu Asp Ala Ala Gly Phe Asp Ile Gly Ile Arg Pro Ser
    130                 135                 140
tgg gag cag gcc atg gac gac gtg cgc aaa gcc ggt ggc aag ccc ttc       480
Trp Glu Gln Ala Met Asp Asp Val Arg Lys Ala Gly Gly Lys Pro Phe
145                 150                 155                 160
ccc att ccg gcc ggc tgc tcc gaa cat cct tat ggc ggc ctg ggc ttt       528
Pro Ile Pro Ala Gly Cys Ser Glu His Pro Tyr Gly Gly Leu Gly Phe
                165                 170                 175
gtc ggc ttt gcc gaa gaa gtg cgg gcg cag gaa gct gaa ctc ggc ttc       576
Val Gly Phe Ala Glu Glu Val Arg Ala Gln Glu Ala Glu Leu Gly Phe
            180                 185                 190
agg ttc gac tac atc gtt gtc tgc tcg gtc acc ggc agc acg cag gcc       624
Arg Phe Asp Tyr Ile Val Val Cys Ser Val Thr Gly Ser Thr Gln Ala
        195                 200                 205
ggc atg gtg gtt ggt ttt gcc gcc gac ggc cgt gcc gac cgc gtg atc       672
Gly Met Val Val Gly Phe Ala Ala Asp Gly Arg Ala Asp Arg Val Ile
    210                 215                 220
ggc ata gac gcc tct gcc aag cct gag aag acc aag gcg caa atc ctg       720
Gly Ile Asp Ala Ser Ala Lys Pro Glu Lys Thr Lys Ala Gln Ile Leu
225                 230                 235                 240
cgc atc gca aag aac acc gcc agg ctg gtc gag ctg gat cgc gac atc       768
Arg Ile Ala Lys Asn Thr Ala Arg Leu Val Glu Leu Asp Arg Asp Ile
                245                 250                 255
acc gcg aaa gac gtg gtg ctc gac acc cgc tac ggc ggg ccc gaa tac       816
Thr Ala Lys Asp Val Val Leu Asp Thr Arg Tyr Gly Gly Pro Glu Tyr
            260                 265                 270
ggc ctg ccg aac gaa ggc acg ctg gag gcc att cgc ctg tgc gcc cgg       864
Gly Leu Pro Asn Glu Gly Thr Leu Glu Ala Ile Arg Leu Cys Ala Arg
        275                 280                 285
cag gag ggc atg ctg acg gac ccg gtc tac gag ggc aag tcc atg cac       912
Gln Glu Gly Met Leu Thr Asp Pro Val Tyr Glu Gly Lys Ser Met His
    290                 295                 300
ggc atg atc gac atg gtg cgc cgc ggt gag ttc gcc gag ggg tcc aag       960
Gly Met Ile Asp Met Val Arg Arg Gly Glu Phe Ala Glu Gly Ser Lys
305                 310                 315                 320
gtg ctg tat gcc cac ctg ggt ggc gtg ccc gcg ctc aat gcg tac agc      1008
Val Leu Tyr Ala His Leu Gly Gly Val Pro Ala Leu Asn Ala Tyr Ser
                325                 330                 335
ttc ctg ttc cgc aac ggc tga                                         1029
Phe Leu Phe Arg Asn Gly
            340
```

<210> 165
<211> 342
<212> PRT
<213> Polaromonas sp. JS666

<400> 165

```
Met Gln Leu Thr Leu Asn Leu Lys Lys Phe Pro Arg His Ser Leu Thr
1               5                   10                  15
Phe Gly Pro Thr Pro Ile Gln Pro Leu Arg Arg Leu Ser Ala His Leu
            20                  25                  30
Gly Gly Lys Val Glu Leu Tyr Ala Lys Arg Glu Asp Cys Asn Ser Gly
        35                  40                  45
Leu Ala Phe Gly Gly Asn Lys Thr Arg Lys Leu Glu Tyr Leu Ile Pro
    50                  55                  60
Glu Ala Leu Ala Gln Gly Cys Asp Thr Leu Val Ser Ile Gly Gly Ile
```

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

<210> 166
<211> 1017
<212> DNA
<213> Burkholderia xenovorans LB400

<220>
<221> CDS
<222> (1)..(1017)
<223> transl_table=11

<400> 166

```
atg aat ctg caa cga ttt cct cgt tac ccg ctg act ttc ggg ccg acg       48
Met Asn Leu Gln Arg Phe Pro Arg Tyr Pro Leu Thr Phe Gly Pro Thr
1               5                   10                  15
ccg atc caa ccg cta gcg cgt ctg agc aag cat ctc ggc ggc aaa gtg       96
Pro Ile Gln Pro Leu Ala Arg Leu Ser Lys His Leu Gly Gly Lys Val
            20                  25                  30
cat ctg tat gcg aaa cgc gag gac tgc aac agc ggt ctt gcc ttc ggc      144
His Leu Tyr Ala Lys Arg Glu Asp Cys Asn Ser Gly Leu Ala Phe Gly
        35                  40                  45
ggc aac aag aca cgc aaa ctc gaa tat ctg atc cct gaa gtg ctt gcg      192
Gly Asn Lys Thr Arg Lys Leu Glu Tyr Leu Ile Pro Glu Val Leu Ala
    50                  55                  60
cag ggt tgc gac acg ctc gtg tcg atc ggc ggc atc cag tcg aac cag      240
Gln Gly Cys Asp Thr Leu Val Ser Ile Gly Gly Ile Gln Ser Asn Gln
```

```
65                  70                  75                  80
acg cgc cag gtg gcg gcc gtg gca gcg cat ctg ggc atg aaa tgc gtg       288
Thr Arg Gln Val Ala Ala Val Ala Ala His Leu Gly Met Lys Cys Val
                85                  90                  95
ctg gta cag gag aac tgg gtc aac tac tcg gac gcg gtc tac gac cgg       336
Leu Val Gln Glu Asn Trp Val Asn Tyr Ser Asp Ala Val Tyr Asp Arg
            100                 105                 110
gtc ggc aac atc cag atg tcg cgt att ctc ggc gcc gat gtg cgc ctc       384
Val Gly Asn Ile Gln Met Ser Arg Ile Leu Gly Ala Asp Val Arg Leu
        115                 120                 125
gtg ccc gac ggc ttc gac atc ggc ttt cgc aag agc tgg gag gag gcg       432
Val Pro Asp Gly Phe Asp Ile Gly Phe Arg Lys Ser Trp Glu Glu Ala
    130                 135                 140
ctc gaa agc gtg cgc gcc gcc ggc ggc aaa ccg tat gcg att ccg gcc       480
Leu Glu Ser Val Arg Ala Ala Gly Gly Lys Pro Tyr Ala Ile Pro Ala
145                 150                 155                 160
ggc tgc tcg gac cat ccg ctc ggc ggc ctc ggt ttc gtc ggc ttc gcg       528
Gly Cys Ser Asp His Pro Leu Gly Gly Leu Gly Phe Val Gly Phe Ala
                165                 170                 175
gaa gag gtg cgt cag cag gaa gcc gaa ttg ggc ttc aag ttc gac tac       576

Glu Glu Val Arg Gln Gln Glu Ala Glu Leu Gly Phe Lys Phe Asp Tyr
            180                 185                 190
gtc gtg gtg tgt tcc gta acc ggc agc acg caa gcc ggc atg gtg gtg       624
Val Val Val Cys Ser Val Thr Gly Ser Thr Gln Ala Gly Met Val Val
        195                 200                 205
ggt ttt gcc gcc gac ggc cgc gct gat cgc gtg atc ggc atc gac gca       672
Gly Phe Ala Ala Asp Gly Arg Ala Asp Arg Val Ile Gly Ile Asp Ala
    210                 215                 220
tcg gca aag ccc gcg cag acg cgc gag cag atc acg cga atc gcc cgg       720
Ser Ala Lys Pro Ala Gln Thr Arg Glu Gln Ile Thr Arg Ile Ala Arg
225                 230                 235                 240
caa acg gcg gaa aaa gtc ggc ctg ggc cgc gat atc acg agc gaa gac       768
Gln Thr Ala Glu Lys Val Gly Leu Gly Arg Asp Ile Thr Ser Glu Asp
                245                 250                 255
gtg gtg ctc gac gag cgc ttc gcc ggt ccg gaa tac ggc ctg ccg aat       816
Val Val Leu Asp Glu Arg Phe Ala Gly Pro Glu Tyr Gly Leu Pro Asn
            260                 265                 270
gac ggc acg ctg gaa gca atc cgc ttg tgc gcc cgc atg gag ggc gtg       864
Asp Gly Thr Leu Glu Ala Ile Arg Leu Cys Ala Arg Met Glu Gly Val
        275                 280                 285
ctg acc gat ccc gtc tac gaa ggc aaa tcc atg cac ggc atg atc gag       912
Leu Thr Asp Pro Val Tyr Glu Gly Lys Ser Met His Gly Met Ile Glu
    290                 295                 300
atg gtg cgc aac ggc gaa ttt ccg gaa ggt tcg cgc gtg ctg tat gcg       960
Met Val Arg Asn Gly Glu Phe Pro Glu Gly Ser Arg Val Leu Tyr Ala
305                 310                 315                 320
cac ctc ggc ggc gtg ccg gcg ttg aac ggc tac agc ttc att ttc cgc      1008
His Leu Gly Gly Val Pro Ala Leu Asn Gly Tyr Ser Phe Ile Phe Arg
                325                 330                 335
aac ggc taa                                                         1017

Asn Gly
```

<210> 167
<211> 338
<212> PRT
<213> Burkholderia xenovorans LB400

<400> 167

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

<210> 168
<211> 1023
<212> DNA
<213> Psychrobacter cryohalolentis K5

<220>
<221> CDS
<222> (1)..(1023)
<223> transl_table=11

<400> 168

```
atg caa aat aaa tct ata cca agc ctg ccg agt atg aat cgg caa cct      48
Met Gln Asn Lys Ser Ile Pro Ser Leu Pro Ser Met Asn Arg Gln Pro
1               5                  10                  15
tta ggg ttt ttc cca acg ccg ttg att gag ctg acc aga tta agc aaa      96
Leu Gly Phe Phe Pro Thr Pro Leu Ile Glu Leu Thr Arg Leu Ser Lys
```

```
            20                  25                  30
gca ctc gat ggt cct aaa att tat atg aaa cgc gat gac aat acg gga       144
Ala Leu Asp Gly Pro Lys Ile Tyr Met Lys Arg Asp Asp Asn Thr Gly
        35                  40                  45
ctg gca tta ggc ggt aat aaa acc aga aag ctt gaa ttt atc att ggg       192
Leu Ala Leu Gly Gly Asn Lys Thr Arg Lys Leu Glu Phe Ile Ile Gly
    50                  55                  60
gac gct ctt gct caa ggt gcg gat aca atc gtg aca gca ggt gcc gcg       240
Asp Ala Leu Ala Gln Gly Ala Asp Thr Ile Val Thr Ala Gly Ala Ala
65                  70                  75                  80
cag tca aac cat tgt cgc cag acc gca gct gcc gca gcc agt ttg gga       288
Gln Ser Asn His Cys Arg Gln Thr Ala Ala Ala Ala Ala Ser Leu Gly
                85                  90                  95
ctt gaa tgc cat tta gtt ttg ggt gga caa gaa cca gaa cag ttg caa       336
Leu Glu Cys His Leu Val Leu Gly Gly Gln Glu Pro Glu Gln Leu Gln
            100                 105                 110
ggc aat ctc tta ctg gat aag att ttt ggc tgt cat atc cac tgg gca       384
Gly Asn Leu Leu Leu Asp Lys Ile Phe Gly Cys His Ile His Trp Ala
        115                 120                 125
ggc agc aac cgt aaa ggg gaa gac ata cct gat atc gta gaa caa ctc       432
Gly Ser Asn Arg Lys Gly Glu Asp Ile Pro Asp Ile Val Glu Gln Leu
    130                 135                 140
aaa aaa gaa ggt aag aaa cct tac att gtt cct tat ggc ggc tca agc       480
Lys Lys Glu Gly Lys Lys Pro Tyr Ile Val Pro Tyr Gly Gly Ser Ser
145                 150                 155                 160
gag ctc ggt gct ttt gcc ttt gtt gaa gcg ttt aaa gag ctt gaa tta       528
Glu Leu Gly Ala Phe Ala Phe Val Glu Ala Phe Lys Glu Leu Glu Leu
                165                 170                 175
caa cgt caa gag atg gat atc tca ttc acg cat atc gtt ttt gcc tcc       576
Gln Arg Gln Glu Met Asp Ile Ser Phe Thr His Ile Val Phe Ala Ser
            180                 185                 190
agc tcc ggc ggg aca caa gcg ggc ttg atg ctg ggc aat aaa atc ttt       624
Ser Ser Gly Gly Thr Gln Ala Gly Leu Met Leu Gly Asn Lys Ile Phe
        195                 200                 205
aac tcg cct tat cag gta gtg ggc atc aat att gat aaa agt gaa acc       672
Asn Ser Pro Tyr Gln Val Val Gly Ile Asn Ile Asp Lys Ser Glu Thr
    210                 215                 220
gat aaa gtg ccg ttt gat cag tat atc atc tcc ctc acc aat agc acg       720
Asp Lys Val Pro Phe Asp Gln Tyr Ile Ile Ser Leu Thr Asn Ser Thr
225                 230                 235                 240
gcg gca ttg att ggg gca gat tac acc ttc tca gag gca gat tta gtg       768
Ala Ala Leu Ile Gly Ala Asp Tyr Thr Phe Ser Glu Ala Asp Leu Val
                245                 250                 255
ctt aac tct gat tat gtg gga gac ggt tat gga gtg att ggt gca cta       816
Leu Asn Ser Asp Tyr Val Gly Asp Gly Tyr Gly Val Ile Gly Ala Leu
            260                 265                 270
gaa aat gaa gcc att gcc atg acc gcg caa atg gaa ggg ata tta tta       864
Glu Asn Glu Ala Ile Ala Met Thr Ala Gln Met Glu Gly Ile Leu Leu
        275                 280                 285
gat cct gtt tat aca ggt cgt gcg atg ggc gga cta ctc gat atg att       912
Asp Pro Val Tyr Thr Gly Arg Ala Met Gly Gly Leu Leu Asp Met Ile
    290                 295                 300
cgt acc ggt aaa atc aaa aaa acg gac agt gtg ttg ttt tgg cat act       960
Arg Thr Gly Lys Ile Lys Lys Thr Asp Ser Val Leu Phe Trp His Thr
305                 310                 315                 320
ggc ggc gcg ccc gct tta ttt gct tat gct agt gat tta gca gta tct      1008
Gly Gly Ala Pro Ala Leu Phe Ala Tyr Ala Ser Asp Leu Ala Val Ser
                325                 330                 335
caa agc gat agt taa                                              1023
Gln Ser Asp Ser
            340
```

<210> 169
<211> 340
<212> PRT
<213> Psychrobacter cryohalolentis K5

<400> 169
Met Gln Asn Lys Ser Ile Pro Ser Leu Pro Ser Met Asn Arg Gln Pro
1 5 10 15
Leu Gly Phe Phe Pro Thr Pro Leu Ile Glu Leu Thr Arg Leu Ser Lys
20 25 30
Ala Leu Asp Gly Pro Lys Ile Tyr Met Lys Arg Asp Asp Asn Thr Gly
35 40 45
Leu Ala Leu Gly Gly Asn Lys Thr Arg Lys Leu Glu Phe Ile Ile Gly
50 55 60
Asp Ala Leu Ala Gln Gly Ala Asp Thr Ile Val Thr Ala Gly Ala Ala
65 70 75 80
Gln Ser Asn His Cys Arg Gln Thr Ala Ala Ala Ala Ala Ser Leu Gly
85 90 95
Leu Glu Cys His Leu Val Leu Gly Gly Gln Glu Pro Glu Gln Leu Gln
100 105 110
Gly Asn Leu Leu Leu Asp Lys Ile Phe Gly Cys His Ile His Trp Ala
115 120 125
Gly Ser Asn Arg Lys Gly Glu Asp Ile Pro Asp Ile Val Glu Gln Leu
130 135 140
Lys Lys Glu Gly Lys Lys Pro Tyr Ile Val Pro Tyr Gly Gly Ser Ser
145 150 155 160
Glu Leu Gly Ala Phe Ala Phe Val Glu Ala Phe Lys Glu Leu Glu Leu
165 170 175
Gln Arg Gln Glu Met Asp Ile Ser Phe Thr His Ile Val Phe Ala Ser
180 185 190
Ser Ser Gly Gly Thr Gln Ala Gly Leu Met Leu Gly Asn Lys Ile Phe
195 200 205
Asn Ser Pro Tyr Gln Val Val Gly Ile Asn Ile Asp Lys Ser Glu Thr
210 215 220
Asp Lys Val Pro Phe Asp Gln Tyr Ile Ile Ser Leu Thr Asn Ser Thr
225 230 235 240
Ala Ala Leu Ile Gly Ala Asp Tyr Thr Phe Ser Glu Ala Asp Leu Val
245 250 255
Leu Asn Ser Asp Tyr Val Gly Asp Gly Tyr Gly Val Ile Gly Ala Leu
260 265 270
Glu Asn Glu Ala Ile Ala Met Thr Ala Gln Met Glu Gly Ile Leu Leu
275 280 285
Asp Pro Val Tyr Thr Gly Arg Ala Met Gly Gly Leu Leu Asp Met Ile
290 295 300
Arg Thr Gly Lys Ile Lys Lys Thr Asp Ser Val Leu Phe Trp His Thr
305 310 315 320
Gly Gly Ala Pro Ala Leu Phe Ala Tyr Ala Ser Asp Leu Ala Val Ser
325 330 335
Gln Ser Asp Ser
340

<210> 170
<211> 975
<212> DNA
<213> Nostoc punctiforme PCC 73102

<220>
<221> CDS
<222> (1)..(975)

<400> 170

```
atg tct gta ata ttt ttt cca cct ccc ata caa caa atc aac agc gaa        48
Met Ser Val Ile Phe Phe Pro Pro Pro Ile Gln Gln Ile Asn Ser Glu
1               5                  10                  15
atc atc cgt agc gct ggt gtt gat ctg tat gta cta cgc ctg gat ctc        96
Ile Ile Arg Ser Ala Gly Val Asp Leu Tyr Val Leu Arg Leu Asp Leu
            20                  25                  30
atg cac ccg tgg gtt aac ggc aat aag tgg ttc aag ctg aaa tac aat       144
Met His Pro Trp Val Asn Gly Asn Lys Trp Phe Lys Leu Lys Tyr Asn
        35                  40                  45
ctt ttg gag gcc aag gag aaa aat ttc aca acg ctg ctt act ttt ggc       192
Leu Leu Glu Ala Lys Glu Lys Asn Phe Thr Thr Leu Leu Thr Phe Gly
    50                  55                  60
ggc gct tat tcc aat cac atc tat gca act gcg gcg gct ggt aat ctt       240
Gly Ala Tyr Ser Asn His Ile Tyr Ala Thr Ala Ala Ala Gly Asn Leu
65                  70                  75                  80
ttc ggt ttt cgt acc atc ggc gta att cgt ggg gag gag aga cta cca       288
Phe Gly Phe Arg Thr Ile Gly Val Ile Arg Gly Glu Glu Arg Leu Pro
                85                  90                  95
tta aac ccg acg ctg aat ttt gct gta caa cag ggt atg cag ctt gtg       336
Leu Asn Pro Thr Leu Asn Phe Ala Val Gln Gln Gly Met Gln Leu Val
            100                 105                 110
tat acg aac cgc gaa atg tat cga cag cgc aac aca cca gtg gta gag       384
Tyr Thr Asn Arg Glu Met Tyr Arg Gln Arg Asn Thr Pro Val Val Glu
        115                 120                 125
gaa tat ctg caa caa cgc ttc ggt gaa gtg ttt atc att ccc gaa ggc       432
Glu Tyr Leu Gln Gln Arg Phe Gly Glu Val Phe Ile Ile Pro Glu Gly
    130                 135                 140
ggg agt aat tta aat ggt gtg cgc ggc tgt atg gag atc att ggt gat       480
Gly Ser Asn Leu Asn Gly Val Arg Gly Cys Met Glu Ile Ile Gly Asp
145                 150                 155                 160
gcg atg tct acg gcg gtc act gaa cgc agt cga agt gct ggc tac gcc       528
Ala Met Ser Thr Ala Val Thr Glu Arg Ser Arg Ser Ala Gly Tyr Ala
                165                 170                 175
tac gca ttt gat cgt ata tgc gta gcc tgc ggt aca gct acc aca ctt       576
Tyr Ala Phe Asp Arg Ile Cys Val Ala Cys Gly Thr Ala Thr Thr Leu
            180                 185                 190
act ggg att gcg ctt tca ttg cat caa gga caa aga gcg atc gct ttt       624
Thr Gly Ile Ala Leu Ser Leu His Gln Gly Gln Arg Ala Ile Ala Phe
        195                 200                 205
ccc gtt ctg aaa aat ggc tca ttt ctt gca caa gaa atc gaa agt ctg       672
Pro Val Leu Lys Asn Gly Ser Phe Leu Ala Gln Glu Ile Glu Ser Leu
    210                 215                 220
ctg aca aat tac ctc gcc tct gat tta ccc aca cca tct aac tcc cct       720
Leu Thr Asn Tyr Leu Ala Ser Asp Leu Pro Thr Pro Ser Asn Ser Pro
225                 230                 235                 240
gct ttt tgg gaa ttg gta tgt gat tac cac ttt ggc ggc tat gca aag       768
Ala Phe Trp Glu Leu Val Cys Asp Tyr His Phe Gly Gly Tyr Ala Lys
                245                 250                 255
gtg aac aag gag tta tta ttg ttc agc caa cag ttc agg gag gaa cat       816
Val Asn Lys Glu Leu Leu Leu Phe Ser Gln Gln Phe Arg Glu Glu His
            260                 265                 270
ggc ata cct ctt gat tac gta tat acc gcc aaa atg ttt tac ggt gtg       864
Gly Ile Pro Leu Asp Tyr Val Tyr Thr Ala Lys Met Phe Tyr Gly Val
        275                 280                 285
atg gat tta cta aaa cag gga ttt ttt agt aaa ggc gat tcg ttg ctg       912
Met Asp Leu Leu Lys Gln Gly Phe Phe Ser Lys Gly Asp Ser Leu Leu
    290                 295                 300
ctg gta cac aca gga ggc tta cag ggc aat gtc ggc atg gaa gaa agg       960
Leu Val His Thr Gly Gly Leu Gln Gly Asn Val Gly Met Glu Glu Arg
305                 310                 315                 320
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ttt caa aga atg tag 975
Phe Gln Arg Met

<210> 171
<211> 324
<212> PRT
<213> Nostoc punctiforme PCC 73102

<400> 171
Met Ser Val Ile Phe Phe Pro Pro Pro Ile Gln Gln Ile Asn Ser Glu
1 5 10 15
Ile Ile Arg Ser Ala Gly Val Asp Leu Tyr Val Leu Arg Leu Asp Leu
20 25 30
Met His Pro Trp Val Asn Gly Asn Lys Trp Phe Lys Leu Lys Tyr Asn
35 40 45
Leu Leu Glu Ala Lys Glu Lys Asn Phe Thr Thr Leu Leu Thr Phe Gly
50 55 60
Gly Ala Tyr Ser Asn His Ile Tyr Ala Thr Ala Ala Ala Gly Asn Leu
65 70 75 80
Phe Gly Phe Arg Thr Ile Gly Val Ile Arg Gly Glu Glu Arg Leu Pro
85 90 95
Leu Asn Pro Thr Leu Asn Phe Ala Val Gln Gln Gly Met Gln Leu Val
100 105 110
Tyr Thr Asn Arg Glu Met Tyr Arg Gln Arg Asn Thr Pro Val Val Glu
115 120 125
Glu Tyr Leu Gln Gln Arg Phe Gly Glu Val Phe Ile Ile Pro Glu Gly
130 135 140
Gly Ser Asn Leu Asn Gly Val Arg Gly Cys Met Glu Ile Ile Gly Asp
145 150 155 160
Ala Met Ser Thr Ala Val Thr Glu Arg Ser Arg Ser Ala Gly Tyr Ala
165 170 175
Tyr Ala Phe Asp Arg Ile Cys Val Ala Cys Gly Thr Ala Thr Thr Leu
180 185 190
Thr Gly Ile Ala Leu Ser Leu His Gln Gly Gln Arg Ala Ile Ala Phe
195 200 205
Pro Val Leu Lys Asn Gly Ser Phe Leu Ala Gln Glu Ile Glu Ser Leu
210 215 220
Leu Thr Asn Tyr Leu Ala Ser Asp Leu Pro Thr Pro Ser Asn Ser Pro
225 230 235 240
Ala Phe Trp Glu Leu Val Cys Asp Tyr His Phe Gly Gly Tyr Ala Lys
245 250 255
Val Asn Lys Glu Leu Leu Leu Phe Ser Gln Gln Phe Arg Glu Glu His
260 265 270
Gly Ile Pro Leu Asp Tyr Val Tyr Thr Ala Lys Met Phe Tyr Gly Val
275 280 285
Met Asp Leu Leu Lys Gln Gly Phe Phe Ser Lys Gly Asp Ser Leu Leu
290 295 300
Leu Val His Thr Gly Gly Leu Gln Gly Asn Val Gly Met Glu Glu Arg
305 310 315 320
Phe Gln Arg Met

<210> 172
<211> 900
<212> DNA
<213> Pseudomonas aeruginosa UCBPP-PA14

<220>
<221> CDS
<222> (1)..(900)

<400> 172

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

Ala Glu Ala Gly Trp Ala Asp Thr Gly Tyr Arg Leu Leu Asp Ala Ser
    210                 215                 220
cgt ggc ggt ttc gcc tgt ctc gat ggg agg ttg gcg cgg ttc atc gtc       720
Arg Gly Gly Phe Ala Cys Leu Asp Gly Arg Leu Ala Arg Phe Ile Val
225                 230                 235                 240
gag ttc gag acg gcc agc ggc gtc gcc ctc gaa ccg ctg tac acc ggc       768
Glu Phe Glu Thr Ala Ser Gly Val Ala Leu Glu Pro Leu Tyr Thr Gly
                245                 250                 255
aaa ctg ctg ctc gcc ctg cgc gag gcc gtg gag agc ggc gcg gtg gct       816
Lys Leu Leu Leu Ala Leu Arg Glu Ala Val Glu Ser Gly Ala Val Ala
            260                 265                 270
cgc ggc agc cgg ctg gtg gcg ctg cac agc gga ggc ctg cag ggc cgc       864
Arg Gly Ser Arg Leu Val Ala Leu His Ser Gly Gly Leu Gln Gly Arg
        275                 280                 285
cgg gca ttg cag gag cgt ttg ctg gcg ttg ctc tga                       900
Arg Ala Leu Gln Glu Arg Leu Leu Ala Leu Leu
    290                 295
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<210> 173
<211> 299
<212> PRT
<213> Pseudomonas aeruginosa UCBPP-PA14

<400> 173
Met Gln Arg Leu Glu Leu Asp Trp Leu Gln Arg Ala Gly Val Glu Leu
1 5 10 15
Ala Leu Leu Arg Leu Asp Gln Ala Asp Pro Leu Ile Ser Gly Asn Lys
20 25 30
Gly Phe Lys Leu Ala Pro His Leu Ala Leu Ala Arg Glu Gln Gly Leu
35 40 45
Asp Gly Leu Ile Ser Leu Gly Gly Ala His Ser Asn His Leu His Ala
50 55 60
Leu Ala Gly Ala Gly Ala Arg Phe Asp Phe Arg Cys Val Gly Leu Leu
65 70 75 80
Arg Gly His Glu Val Asp Thr Pro Thr Val Arg Asp Leu Arg Ser Leu
85 90 95
Gly Met Glu Leu His Trp Leu Gly Tyr Gly Gly Tyr Arg Gln Arg His
100 105 110
Ala Ala Gly Phe Trp Leu Pro Trp Arg Glu Arg Tyr Pro Gly Leu Leu
115 120 125
Pro Val Ala Glu Gly Gly Gly Gly Leu Leu Gly Ala Arg Gly Cys Ile
130 135 140
Gly Leu Val Glu Arg Ile Ala Thr Gln Leu Pro Thr Leu Gly Trp Asp
145 150 155 160
Asp Tyr Asp Ala Ile Trp Val Ala Ala Gly Thr Gly Thr Thr Leu Ala
165 170 175
Gly Leu Val Leu Gly Glu Ala Gly Arg His Pro Val Val Gly Ala Leu
180 185 190
Ala Val Pro Glu Asp His Gly Val Ala Ala Gln Val Ala Ala Thr Leu
195 200 205
Ala Glu Ala Gly Trp Ala Asp Thr Gly Tyr Arg Leu Leu Asp Ala Ser
210 215 220
Arg Gly Gly Phe Ala Cys Leu Asp Gly Arg Leu Ala Arg Phe Ile Val
225 230 235 240
Glu Phe Glu Thr Ala Ser Gly Val Ala Leu Glu Pro Leu Tyr Thr Gly
245 250 255
Lys Leu Leu Leu Ala Leu Arg Glu Ala Val Glu Ser Gly Ala Val Ala
260 265 270
Arg Gly Ser Arg Leu Val Ala Leu His Ser Gly Gly Leu Gln Gly Arg
275 280 285
Arg Ala Leu Gln Glu Arg Leu Leu Ala Leu Leu
290 295

<210> 174
<211> 996
<212> DNA
<213> Bacillus cereus G9241

<220>
<221> CDS
<222> (1)..(996)
<223> transl_table=11

<400> 174
atg aat tta gct aaa ttc ccg aga aaa aaa tat aca gag tca tat aca 48
Met Asn Leu Ala Lys Phe Pro Arg Lys Lys Tyr Thr Glu Ser Tyr Thr
1 5 10 15
cca att gaa aaa tta aac aat ttt tct gaa gca ctt ggt gga ccg act 96
Pro Ile Glu Lys Leu Asn Asn Phe Ser Glu Ala Leu Gly Gly Pro Thr

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            20                  25                  30
att tat ttt aaa cga gat gat tta ctt ggt tta aca gct ggt ggt aat       144
Ile Tyr Phe Lys Arg Asp Asp Leu Leu Gly Leu Thr Ala Gly Gly Asn
        35                  40                  45
aag acg aga aag tta gag ttt cta gtt gcg gat gca cag gca aag ggt       192
Lys Thr Arg Lys Leu Glu Phe Leu Val Ala Asp Ala Gln Ala Lys Gly
    50                  55                  60
gca gat acg tta att acg gct ggt ggt att cag tca aat cat tgc cgc       240
Ala Asp Thr Leu Ile Thr Ala Gly Gly Ile Gln Ser Asn His Cys Arg
65                  70                  75                  80
ctg aca ctg gca gct gcg gtg aaa gag aaa atg aaa tgt att ctt gta       288
Leu Thr Leu Ala Ala Ala Val Lys Glu Lys Met Lys Cys Ile Leu Val
                85                  90                  95
tta gaa gaa ggg ctt gag cca gaa gag aag cca gat ttt aac gga aac       336
Leu Glu Glu Gly Leu Glu Pro Glu Glu Lys Pro Asp Phe Asn Gly Asn
            100                 105                 110
tat ttc tta tat cat tta tta ggt gct gaa aat gta att gtt gta cga       384
Tyr Phe Leu Tyr His Leu Leu Gly Ala Glu Asn Val Ile Val Val Arg
        115                 120                 125
aat gga gca gat ctt atg gaa gag atg cat aaa gta gcg aaa gaa gtt       432
Asn Gly Ala Asp Leu Met Glu Glu Met His Lys Val Ala Lys Glu Val
    130                 135                 140
agt gaa aaa ggg aat aca cca tat gtc att cca gtt ggt gga tca aat       480
Ser Glu Lys Gly Asn Thr Pro Tyr Val Ile Pro Val Gly Gly Ser Asn
145                 150                 155                 160
cct act ggc gca atg gga tac att gct tgt gcg caa gaa att atg gcg       528
Pro Thr Gly Ala Met Gly Tyr Ile Ala Cys Ala Gln Glu Ile Met Ala
                165                 170                 175
caa tca ttt gac caa gga att gat ttc agt tca gtc gtt tgc gta agc       576
Gln Ser Phe Asp Gln Gly Ile Asp Phe Ser Ser Val Val Cys Val Ser
            180                 185                 190
ggt agc ggc ggt atg cac gcc ggt tta att aca ggt ttt gct gga aca       624
Gly Ser Gly Gly Met His Ala Gly Leu Ile Thr Gly Phe Ala Gly Thr
        195                 200                 205
caa agt cac atc cca gta atc gga att aac gta agt aga gga aaa gca       672
Gln Ser His Ile Pro Val Ile Gly Ile Asn Val Ser Arg Gly Lys Ala
    210                 215                 220
gag caa gaa gag aaa gta gca aaa ctt gta gat gaa act tca gct cac       720
Glu Gln Glu Glu Lys Val Ala Lys Leu Val Asp Glu Thr Ser Ala His
225                 230                 235                 240
gtt ggt att cca aac ttt atc ccg cgc gaa gct gtt aca tgc ttt gat       768
Val Gly Ile Pro Asn Phe Ile Pro Arg Glu Ala Val Thr Cys Phe Asp
                245                 250                 255
gaa tat gta gga cca ggt tac gcg tta cca acg cca gaa atg gtg gaa       816
Glu Tyr Val Gly Pro Gly Tyr Ala Leu Pro Thr Pro Glu Met Val Glu
            260                 265                 270
gca gtg cag ctg tta gca aaa aca gaa ggt att tta ctg gat cca gtg       864
Ala Val Gln Leu Leu Ala Lys Thr Glu Gly Ile Leu Leu Asp Pro Val
        275                 280                 285
tat acg ggt aaa gcg gta gcg gga cta atc gat tta att aaa aaa ggt       912
Tyr Thr Gly Lys Ala Val Ala Gly Leu Ile Asp Leu Ile Lys Lys Gly
    290                 295                 300
aca ttt aaa aaa gaa gac aac att tta ttc gta cat tca ggt ggt tca       960
Thr Phe Lys Lys Glu Asp Asn Ile Leu Phe Val His Ser Gly Gly Ser
305                 310                 315                 320
cca gct tta tat gcg aat acg tct tta ttt gcg taa                       996
Pro Ala Leu Tyr Ala Asn Thr Ser Leu Phe Ala
                325                 330
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<210> 175
<211> 331

<212> PRT
<213> Bacillus cereus G9241

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

<210> 176
<211> 1017
<212> DNA
<213> Rubrivivax gelatinosus PM1

<220>
<221> CDS
<222> (1)..(1017)

<400> 176
atg aac ctc cag cgc ttc cct cgc cat ccg ctc acc ttc ggg ccc acg 48
Met Asn Leu Gln Arg Phe Pro Arg His Pro Leu Thr Phe Gly Pro Thr
1 5 10 15
ccc atc cag ccg ctc aag cgc ctg agt gcg cac ctc ggc ggc cag gtc 96

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Pro Ile Gln Pro Leu Lys Arg Leu Ser Ala His Leu Gly Gly Gln Val
            20                  25                  30
gag ctc tac gcc aag cgc gag gac tgc aac agc ggc ctc gcc ttc ggc      144
Glu Leu Tyr Ala Lys Arg Glu Asp Cys Asn Ser Gly Leu Ala Phe Gly
        35                  40                  45
ggc aac aag acc cgc aag ctc gag tac ctg atc ccc gag gcg ctg gcg      192
Gly Asn Lys Thr Arg Lys Leu Glu Tyr Leu Ile Pro Glu Ala Leu Ala
    50                  55                  60
cag ggc tgc gac acg ctg gtg tcg atc ggc ggc atc cag tcc aac cag      240
Gln Gly Cys Asp Thr Leu Val Ser Ile Gly Gly Ile Gln Ser Asn Gln
65                  70                  75                  80
acg cgc cag gtc gcc gcg gtg gcg gcc cac ctc ggc atg aag tgc gtg      288
Thr Arg Gln Val Ala Ala Val Ala Ala His Leu Gly Met Lys Cys Val
                85                  90                  95
ctg gtg cag gag aac tgg gtc aac tac tcc gac gcg gtg tac gac cgc      336
Leu Val Gln Glu Asn Trp Val Asn Tyr Ser Asp Ala Val Tyr Asp Arg
            100                 105                 110
gtc ggc aac atc gag atg tcg cgc atc ctc ggc gcc gac gtg cgg ctc      384
Val Gly Asn Ile Glu Met Ser Arg Ile Leu Gly Ala Asp Val Arg Leu
        115                 120                 125
gac gcc gct ggc ttc gac atc ggc atc cgc ccg agc tgg gag cag gcg      432
Asp Ala Ala Gly Phe Asp Ile Gly Ile Arg Pro Ser Trp Glu Gln Ala
    130                 135                 140
atg gcc gac gtg cgg gcc gcc ggc ggc aag ccc ttc ccc att ccc gcc      480
Met Ala Asp Val Arg Ala Ala Gly Gly Lys Pro Phe Pro Ile Pro Ala
145                 150                 155                 160
ggc tgc tcc gag cac cgg ctc ggc ggc ctg ggc ttc gtc ggc ttc gcc      528
Gly Cys Ser Glu His Arg Leu Gly Gly Leu Gly Phe Val Gly Phe Ala
                165                 170                 175
gag gag gtg cgc gcg cag gag gcc gag ctc ggc ttc aag ttc gac tac      576
Glu Glu Val Arg Ala Gln Glu Ala Glu Leu Gly Phe Lys Phe Asp Tyr
            180                 185                 190
atc gtg gtc tgc tcg gtg acc ggc agc acg cag gcc ggc atg gtg gtg      624
Ile Val Val Cys Ser Val Thr Gly Ser Thr Gln Ala Gly Met Val Val
        195                 200                 205
ggc ttc gcg gcc gac ggc cgg gcc gag cgc gtg atc ggc atc gac gcc      672
Gly Phe Ala Ala Asp Gly Arg Ala Glu Arg Val Ile Gly Ile Asp Ala
    210                 215                 220
tcg gcc aag ccc gag cag acc cac gcg cag atc ctg cgc atc gcg cag      720
Ser Ala Lys Pro Glu Gln Thr His Ala Gln Ile Leu Arg Ile Ala Gln
225                 230                 235                 240
aac acg gcc gag ctg gtg ggc ctg ggc cgc gag atc acc gcg cag gac      768
Asn Thr Ala Glu Leu Val Gly Leu Gly Arg Glu Ile Thr Ala Gln Asp
                245                 250                 255
gtg gtg ctc gac acc cgc tac ggc ggc ccc gag tac ggc ctg ccg agc      816
Val Val Leu Asp Thr Arg Tyr Gly Gly Pro Glu Tyr Gly Leu Pro Ser
            260                 265                 270
gag ggc acg ctg gag gcc atc cgc ctg tgc gcg cgc cag gaa ggc atg      864
Glu Gly Thr Leu Glu Ala Ile Arg Leu Cys Ala Arg Gln Glu Gly Met
        275                 280                 285
ctc acc gac ccg gtg tac gag ggc aag tcg atg cac ggc atg atc gac      912
Leu Thr Asp Pro Val Tyr Glu Gly Lys Ser Met His Gly Met Ile Asp
    290                 295                 300
aag gtg aag cgc ggc gag ttc ccc gcc ggc tcc agg gtg ttg tac gcc      960
Lys Val Lys Arg Gly Glu Phe Pro Ala Gly Ser Arg Val Leu Tyr Ala
305                 310                 315                 320
cac ctc ggc ggc gtg ccg gcg ctc aac gcc tac agc ttc ctg ttc cgc     1008
His Leu Gly Gly Val Pro Ala Leu Asn Ala Tyr Ser Phe Leu Phe Arg
                325                 330                 335
aac ggc tga                                                        1017
Asn Gly
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PCT/US06/27117

<210> 177
<211> 338
<212> PRT
<213> Rubrivivax gelatinosus PM1

<400> 177
Met Asn Leu Gln Arg Phe Pro Arg His Pro Leu Thr Phe Gly Pro Thr
1 5 10 15
Pro Ile Gln Pro Leu Lys Arg Leu Ser Ala His Leu Gly Gly Gln Val
20 25 30
Glu Leu Tyr Ala Lys Arg Glu Asp Cys Asn Ser Gly Leu Ala Phe Gly
35 40 45
Gly Asn Lys Thr Arg Lys Leu Glu Tyr Leu Ile Pro Glu Ala Leu Ala
50 55 60
Gln Gly Cys Asp Thr Leu Val Ser Ile Gly Gly Ile Gln Ser Asn Gln
65 70 75 80
Thr Arg Gln Val Ala Ala Val Ala Ala His Leu Gly Met Lys Cys Val
85 90 95
Leu Val Gln Glu Asn Trp Val Asn Tyr Ser Asp Ala Val Tyr Asp Arg
100 105 110
Val Gly Asn Ile Glu Met Ser Arg Ile Leu Gly Ala Asp Val Arg Leu
115 120 125
Asp Ala Ala Gly Phe Asp Ile Gly Ile Arg Pro Ser Trp Glu Gln Ala
130 135 140
Met Ala Asp Val Arg Ala Ala Gly Gly Lys Pro Phe Pro Ile Pro Ala
145 150 155 160
Gly Cys Ser Glu His Arg Leu Gly Gly Leu Gly Phe Val Gly Phe Ala
165 170 175
Glu Glu Val Arg Ala Gln Glu Ala Glu Leu Gly Phe Lys Phe Asp Tyr
180 185 190
Ile Val Val Cys Ser Val Thr Gly Ser Thr Gln Ala Gly Met Val Val
195 200 205
Gly Phe Ala Ala Asp Gly Arg Ala Glu Arg Val Ile Gly Ile Asp Ala
210 215 220
Ser Ala Lys Pro Glu Gln Thr His Ala Gln Ile Leu Arg Ile Ala Gln
225 230 235 240
Asn Thr Ala Glu Leu Val Gly Leu Gly Arg Glu Ile Thr Ala Gln Asp
245 250 255
Val Val Leu Asp Thr Arg Tyr Gly Gly Pro Glu Tyr Gly Leu Pro Ser
260 265 270
Glu Gly Thr Leu Glu Ala Ile Arg Leu Cys Ala Arg Gln Glu Gly Met
275 280 285
Leu Thr Asp Pro Val Tyr Glu Gly Lys Ser Met His Gly Met Ile Asp
290 295 300
Lys Val Lys Arg Gly Glu Phe Pro Ala Gly Ser Arg Val Leu Tyr Ala
305 310 315 320
His Leu Gly Gly Val Pro Ala Leu Asn Ala Tyr Ser Phe Leu Phe Arg
325 330 335
Asn Gly

<210> 178
<211> 909
<212> DNA
<213> Cytophaga hutchinsonii

<220>
<221> CDS
<222> (1)..(909)

<400> 178

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atg cat caa agt cca ctt caa cct atc att tta cca caa aca gaa aag        48
Met His Gln Ser Pro Leu Gln Pro Ile Ile Leu Pro Gln Thr Glu Lys
1               5                  10                  15
gct ggt gta caa ttg tat ctg aag cgc gac gat ctc att cat ccc tta        96
Ala Gly Val Gln Leu Tyr Leu Lys Arg Asp Asp Leu Ile His Pro Leu
            20                  25                  30
tat ggc ggt aat aag atc cgg aag tta aag tac aat gtg cag caa tgt       144
Tyr Gly Gly Asn Lys Ile Arg Lys Leu Lys Tyr Asn Val Gln Gln Cys
        35                  40                  45
ttg cgt gaa ggt aaa ata ggt ttg ctc acc tgc ggc ggc gcc tac tcc       192
Leu Arg Glu Gly Lys Ile Gly Leu Leu Thr Cys Gly Gly Ala Tyr Ser
    50                  55                  60
aac cac att att gca acg gca gcg tat gga aaa gag cat ggt ttg aaa       240
Asn His Ile Ile Ala Thr Ala Ala Tyr Gly Lys Glu His Gly Leu Lys
65                  70                  75                  80
acc aag gca atc att cgc gga gaa gag ctg ctg att gat aac cct acg       288
Thr Lys Ala Ile Ile Arg Gly Glu Glu Leu Leu Ile Asp Asn Pro Thr
                85                  90                  95
ctt aaa gat gcg gca gca ctt ggg atg gaa ttt gtt ttt gtt tca aga       336
Leu Lys Asp Ala Ala Ala Leu Gly Met Glu Phe Val Phe Val Ser Arg
            100                 105                 110
gaa aca tac cga agc att cgt gaa caa aat gcg ttg gct ttt gat tta       384
Glu Thr Tyr Arg Ser Ile Arg Glu Gln Asn Ala Leu Ala Phe Asp Leu
        115                 120                 125
agt aaa tcg aat tat aac gaa tgg tat ttt att ccc gaa ggc ggc acc       432
Ser Lys Ser Asn Tyr Asn Glu Trp Tyr Phe Ile Pro Glu Gly Gly Thr
    130                 135                 140
aat gct ttt gct gtt gaa ggt att gca gaa ctg gta gct gaa att gaa       480
Asn Ala Phe Ala Val Glu Gly Ile Ala Glu Leu Val Ala Glu Ile Glu
145                 150                 155                 160
atc ccg ttt gat tat atc gct aca ccc tgc ggt acg ggt ggt act ttt       528
Ile Pro Phe Asp Tyr Ile Ala Thr Pro Cys Gly Thr Gly Gly Thr Phe
                165                 170                 175
gcc ggt ttg atg aaa ggc att aaa gtt tat tcg ccg tgg cga acg aaa       576
Ala Gly Leu Met Lys Gly Ile Lys Val Tyr Ser Pro Trp Arg Thr Lys
            180                 185                 190
ctg ctt gtt ttt tcg gcg ttg aaa aac ggt aat tat att att gat gaa       624
Leu Leu Val Phe Ser Ala Leu Lys Asn Gly Asn Tyr Ile Ile Asp Glu
        195                 200                 205
gtg gct gaa ttg ctg aaa gca gat ttt gac aga aca acg tta gag ttg       672
Val Ala Glu Leu Leu Lys Ala Asp Phe Asp Arg Thr Thr Leu Glu Leu
    210                 215                 220
ttt act tca gag tac gtg ttt ggc ggc tat gga aag gtg aaa cct gaa       720
Phe Thr Ser Glu Tyr Val Phe Gly Gly Tyr Gly Lys Val Lys Pro Glu
225                 230                 235                 240
ctg att gct ttt gta aaa tcg ttt gag cat cag aca gga att tta tta       768
Leu Ile Ala Phe Val Lys Ser Phe Glu His Gln Thr Gly Ile Leu Leu
                245                 250                 255
gat cct att tat aac ggg aaa atg atg ttt ggt ctg ttg ggt aaa att       816
Asp Pro Ile Tyr Asn Gly Lys Met Met Phe Gly Leu Leu Gly Lys Ile
            260                 265                 270
gaa agt ggc tat ttt aaa aag ggt tca gtg att gtt gct att cac act       864
Glu Ser Gly Tyr Phe Lys Lys Gly Ser Val Ile Val Ala Ile His Thr
        275                 280                 285
gga gga atc caa gcc tgg aga ggg ttt aac aat aat ttt act taa           909
Gly Gly Ile Gln Ala Trp Arg Gly Phe Asn Asn Asn Phe Thr
    290                 295                 300
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<210> 179

<211> 302
<212> PRT
<213> Cytophaga hutchinsonii

<400> 179
Met His Gln Ser Pro Leu Gln Pro Ile Ile Leu Pro Gln Thr Glu Lys
1 5 10 15
Ala Gly Val Gln Leu Tyr Leu Lys Arg Asp Asp Leu Ile His Pro Leu
20 25 30
Tyr Gly Gly Asn Lys Ile Arg Lys Leu Lys Tyr Asn Val Gln Gln Cys
35 40 45
Leu Arg Glu Gly Lys Ile Gly Leu Leu Thr Cys Gly Gly Ala Tyr Ser
50 55 60
Asn His Ile Ile Ala Thr Ala Ala Tyr Gly Lys Glu His Gly Leu Lys
65 70 75 80
Thr Lys Ala Ile Ile Arg Gly Glu Glu Leu Leu Ile Asp Asn Pro Thr
85 90 95
Leu Lys Asp Ala Ala Ala Leu Gly Met Glu Phe Val Phe Val Ser Arg
100 105 110
Glu Thr Tyr Arg Ser Ile Arg Glu Gln Asn Ala Leu Ala Phe Asp Leu
115 120 125
Ser Lys Ser Asn Tyr Asn Glu Trp Tyr Phe Ile Pro Glu Gly Gly Thr
130 135 140
Asn Ala Phe Ala Val Glu Gly Ile Ala Glu Leu Val Ala Glu Ile Glu
145 150 155 160
Ile Pro Phe Asp Tyr Ile Ala Thr Pro Cys Gly Thr Gly Gly Thr Phe
165 170 175
Ala Gly Leu Met Lys Gly Ile Lys Val Tyr Ser Pro Trp Arg Thr Lys
180 185 190
Leu Leu Val Phe Ser Ala Leu Lys Asn Gly Asn Tyr Ile Ile Asp Glu
195 200 205
Val Ala Glu Leu Leu Lys Ala Asp Phe Asp Arg Thr Thr Leu Glu Leu
210 215 220
Phe Thr Ser Glu Tyr Val Phe Gly Gly Tyr Gly Lys Val Lys Pro Glu
225 230 235 240
Leu Ile Ala Phe Val Lys Ser Phe Glu His Gln Thr Gly Ile Leu Leu
245 250 255
Asp Pro Ile Tyr Asn Gly Lys Met Met Phe Gly Leu Leu Gly Lys Ile
260 265 270
Glu Ser Gly Tyr Phe Lys Lys Gly Ser Val Ile Val Ala Ile His Thr
275 280 285
Gly Gly Ile Gln Ala Trp Arg Gly Phe Asn Asn Asn Phe Thr
290 295 300

<210> 180
<211> 1026
<212> DNA
<213> Brevibacterium linens BL2

<220>
<221> CDS
<222> (1)..(1026)

<400> 180
atg gtc gac ctg aac aca ctg ccc cgc cgc cgc tac acc aag ggg ccc 48
Met Val Asp Leu Asn Thr Leu Pro Arg Arg Arg Tyr Thr Lys Gly Pro
1 5 10 15
acc ccg ctt gag cac ctc gga gcc ttg agt gcg aag ctg ggc ggg ccg 96
Thr Pro Leu Glu His Leu Gly Ala Leu Ser Ala Lys Leu Gly Gly Pro
20 25 30
cag atc tgg atc aaa cgc gat gac caa ctg ggc ctg acc cag ggt ggg 144

```
Gln Ile Trp Ile Lys Arg Asp Asp Gln Leu Gly Leu Thr Gln Gly Gly
        35                  40                  45
aat aag acc cgc aaa ctc gag ttc ctc atc gcc gat gct ctg gta cag       192
Asn Lys Thr Arg Lys Leu Glu Phe Leu Ile Ala Asp Ala Leu Val Gln
    50                  55                  60
ggg gct gac act ctc gtc acc gca ggc ggc gtg cag tcc aat cac tgc       240
Gly Ala Asp Thr Leu Val Thr Ala Gly Gly Val Gln Ser Asn His Cys
65                  70                  75                  80
cgg ctc aca ctc tcg gcg gct cgg cgt gaa gga ctc gac tgc cac ctc       288
Arg Leu Thr Leu Ser Ala Ala Arg Arg Glu Gly Leu Asp Cys His Leu
                85                  90                  95
gtg ctc gag gag gac ctc ggc ccc gat ggc aag ccg gtc cca gcg gaa       336
Val Leu Glu Glu Asp Leu Gly Pro Asp Gly Lys Pro Val Pro Ala Glu
            100                 105                 110
gcc ggt ggc aat cct gcc gag cac acg ggc aat ttc ctg ctc ttc gac       384
Ala Gly Gly Asn Pro Ala Glu His Thr Gly Asn Phe Leu Leu Phe Asp
        115                 120                 125
ctc ctc ggc gcg gat tcg gtt gag gtc cac ccc aat ggc agc gag ctc       432
Leu Leu Gly Ala Asp Ser Val Glu Val His Pro Asn Gly Ser Glu Leu
    130                 135                 140
atc gcc cgc gcc gac gag ctc gct gcc gaa ctc aag gga cag ggg aag       480
Ile Ala Arg Ala Asp Glu Leu Ala Ala Glu Leu Lys Gly Gln Gly Lys
145                 150                 155                 160
agc ccc tac gtc atc ccc gtc ggc ggc tcg aat atc acc ggg gct ctg       528
Ser Pro Tyr Val Ile Pro Val Gly Gly Ser Asn Ile Thr Gly Ala Leu
                165                 170                 175
ggg tat gtc gat tgc gcg caa gaa ctg ctc acc cag ttc gcc gag gtt       576
Gly Tyr Val Asp Cys Ala Gln Glu Leu Leu Thr Gln Phe Ala Glu Val
            180                 185                 190
ggg ctg gac gtc tcg tcg ctc gtc acc ccg agc ggg tct gcc ggg atg       624
Gly Leu Asp Val Ser Ser Leu Val Thr Pro Ser Gly Ser Ala Gly Met
        195                 200                 205
cag gcc gga ctc atc gct ggt ctc cac gcc gcg ggc agt cag atc ccg       672
Gln Ala Gly Leu Ile Ala Gly Leu His Ala Ala Gly Ser Gln Ile Pro
    210                 215                 220
gtc gtc ggg atc aac gtc agc cgc aca cag gag gac cag gaa caa aag       720
Val Val Gly Ile Asn Val Ser Arg Thr Gln Glu Asp Gln Glu Gln Lys
225                 230                 235                 240
atc gtg agc ctc gtt gat gag gtg gca tcg ttc ctc gag ctg ccg ccg       768
Ile Val Ser Leu Val Asp Glu Val Ala Ser Phe Leu Glu Leu Pro Pro
                245                 250                 255
gtc ccc cgc gat cgc agt gtc ggc ctg ggc ggc tac ttc ggc acc ggc       816
Val Pro Arg Asp Arg Ser Val Gly Leu Gly Gly Tyr Phe Gly Thr Gly
            260                 265                 270
tat gca ctg ccc aca ccc gga atg gcc gag gcg gtg cgt ctc ttc gcc       864
Tyr Ala Leu Pro Thr Pro Gly Met Ala Glu Ala Val Arg Leu Phe Ala
        275                 280                 285
gag acc gag ggc atc ctg ctc gat ccc gtc tat acg ggg aag gcc gcg       912
Glu Thr Glu Gly Ile Leu Leu Asp Pro Val Tyr Thr Gly Lys Ala Ala
    290                 295                 300
gcc ggg ctc atc gat ctg gtc cgc cag ggg cgg ttc gag ccc gac gac       960
Ala Gly Leu Ile Asp Leu Val Arg Gln Gly Arg Phe Glu Pro Asp Asp
305                 310                 315                 320
aac gtg gtc ttc atc cat tcg ggt gga gtg ccc gga ctc tat gct cgc      1008
Asn Val Val Phe Ile His Ser Gly Gly Val Pro Gly Leu Tyr Ala Arg
                325                 330                 335
gcc gga gca ttc gca tag                                           1026
Ala Gly Ala Phe Ala
            340
```

<210> 181

<211> 341
<212> PRT
<213> Brevibacterium linens BL2

<400> 181

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Met Val Asp Leu Asn Thr Leu Pro Arg Arg Arg Tyr Thr Lys Gly Pro
1               5                  10                  15
Thr Pro Leu Glu His Leu Gly Ala Leu Ser Ala Lys Leu Gly Gly Pro
            20                  25                  30
Gln Ile Trp Ile Lys Arg Asp Asp Gln Leu Gly Leu Thr Gln Gly Gly
        35                  40                  45
Asn Lys Thr Arg Lys Leu Glu Phe Leu Ile Ala Asp Ala Leu Val Gln
    50                  55                  60
Gly Ala Asp Thr Leu Val Thr Ala Gly Gly Val Gln Ser Asn His Cys
65                  70                  75                  80
Arg Leu Thr Leu Ser Ala Ala Arg Arg Glu Gly Leu Asp Cys His Leu
                85                  90                  95
Val Leu Glu Glu Asp Leu Gly Pro Asp Gly Lys Pro Val Pro Ala Glu
            100                 105                 110
Ala Gly Gly Asn Pro Ala Glu His Thr Gly Asn Phe Leu Leu Phe Asp
        115                 120                 125
Leu Leu Gly Ala Asp Ser Val Glu Val His Pro Asn Gly Ser Glu Leu
    130                 135                 140
Ile Ala Arg Ala Asp Glu Leu Ala Ala Glu Leu Lys Gly Gln Gly Lys
145                 150                 155                 160
Ser Pro Tyr Val Ile Pro Val Gly Gly Ser Asn Ile Thr Gly Ala Leu
                165                 170                 175
Gly Tyr Val Asp Cys Ala Gln Glu Leu Leu Thr Gln Phe Ala Glu Val
            180                 185                 190
Gly Leu Asp Val Ser Ser Leu Val Thr Pro Ser Gly Ser Ala Gly Met
        195                 200                 205
Gln Ala Gly Leu Ile Ala Gly Leu His Ala Ala Gly Ser Gln Ile Pro
    210                 215                 220
Val Val Gly Ile Asn Val Ser Arg Thr Gln Glu Asp Gln Glu Gln Lys
225                 230                 235                 240
Ile Val Ser Leu Val Asp Glu Val Ala Ser Phe Leu Glu Leu Pro Pro
                245                 250                 255
Val Pro Arg Asp Arg Ser Val Gly Leu Gly Gly Tyr Phe Gly Thr Gly
            260                 265                 270
Tyr Ala Leu Pro Thr Pro Gly Met Ala Glu Ala Val Arg Leu Phe Ala
        275                 280                 285
Glu Thr Glu Gly Ile Leu Leu Asp Pro Val Tyr Thr Gly Lys Ala Ala
    290                 295                 300
Ala Gly Leu Ile Asp Leu Val Arg Gln Gly Arg Phe Glu Pro Asp Asp
305                 310                 315                 320
Asn Val Val Phe Ile His Ser Gly Gly Val Pro Gly Leu Tyr Ala Arg
                325                 330                 335
Ala Gly Ala Phe Ala
            340
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<210> 182
<211> 1017
<212> DNA
<213> Brevibacterium linens BL2

<220>
<221> CDS
<222> (1)..(1017)

<400> 182

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atg gca atc acc gat ttc gaa cgt tac cca ttg acc ttc agg ccc agc        48
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Met Ala Ile Thr Asp Phe Glu Arg Tyr Pro Leu Thr Phe Arg Pro Ser
1               5                  10                  15
ccg gtc cac gag ctg aag cga ctc agt gac cgc ctc ggc ggg gcc cgg        96
Pro Val His Glu Leu Lys Arg Leu Ser Asp Arg Leu Gly Gly Ala Arg
            20                  25                  30
gta tgg gcc aag cgc gaa gac gtg aac tcc gga ctc gcg ttc ggc ggc       144
Val Trp Ala Lys Arg Glu Asp Val Asn Ser Gly Leu Ala Phe Gly Gly
        35                  40                  45
aac aag acc cgc aag ctc gaa tac atc gtt ccc gac atc ctc gcc tct       192
Asn Lys Thr Arg Lys Leu Glu Tyr Ile Val Pro Asp Ile Leu Ala Ser
    50                  55                  60
gac gcg gac acg ctc gtc tcg atc ggc ggc tac cag tcg aac cac acg       240
Asp Ala Asp Thr Leu Val Ser Ile Gly Gly Tyr Gln Ser Asn His Thr
65                  70                  75                  80
cgg cag gtc gcg gcc gtc gcg gca cac ctg gga ctg aag tcg cgg ctc       288
Arg Gln Val Ala Ala Val Ala Ala His Leu Gly Leu Lys Ser Arg Leu
                85                  90                  95
gtc cag gaa cgc tgg gtc gac tgg gac gat ccg gtc aac gac aaa gtc       336
Val Gln Glu Arg Trp Val Asp Trp Asp Asp Pro Val Asn Asp Lys Val
            100                 105                 110
ggc aac atc gaa ctc tcc cgc atc atg ggc gcc gat gtg cac ctc gac       384
Gly Asn Ile Glu Leu Ser Arg Ile Met Gly Ala Asp Val His Leu Asp
        115                 120                 125
tcc gct gga ttc gac atc ggc atc cgc tcg agc tgg gag aac gcc atc       432
Ser Ala Gly Phe Asp Ile Gly Ile Arg Ser Ser Trp Glu Asn Ala Ile

    130                 135                 140
gcc gag gtg gag gcc gca ggt ggc agg ccc tac ccc att ccg gcc ggt       480
Ala Glu Val Glu Ala Ala Gly Gly Arg Pro Tyr Pro Ile Pro Ala Gly
145                 150                 155                 160
gcc tcg gag cac aaa ttc ggt gca ctc ggc ttc gtc aac tgg gcc tac       528
Ala Ser Glu His Lys Phe Gly Ala Leu Gly Phe Val Asn Trp Ala Tyr
                165                 170                 175
gag gtc gca gaa cag gag agg gag ctc ggc gtc ttc ttc gac acg atc       576
Glu Val Ala Glu Gln Glu Arg Glu Leu Gly Val Phe Phe Asp Thr Ile
            180                 185                 190
atc gtc tgc acg gtc acc ggc tcc act cac gcg gga atg atc gca ggc       624
Ile Val Cys Thr Val Thr Gly Ser Thr His Ala Gly Met Ile Ala Gly
        195                 200                 205
ttc gcc gcg ctc gag gcg gcc gga ggt ccc aag cgc cag gtc atc ggc       672
Phe Ala Ala Leu Glu Ala Ala Gly Gly Pro Lys Arg Gln Val Ile Gly
    210                 215                 220
atc gac gcc tct gcg acc ctg gac aag acc cgt gac cag gtc aaa cgc       720
Ile Asp Ala Ser Ala Thr Leu Asp Lys Thr Arg Asp Gln Val Lys Arg
225                 230                 235                 240
atc gcg aac aat gcc gct gac ctc atc ggc ctc ggt cgg gag atc acc       768
Ile Ala Asn Asn Ala Ala Asp Leu Ile Gly Leu Gly Arg Glu Ile Thr
                245                 250                 255
gat gct gac gtc gac atc cgc tcc ggc tgg gaa ggc cct gcc tac ggc       816
Asp Ala Asp Val Asp Ile Arg Ser Gly Trp Glu Gly Pro Ala Tyr Gly
            260                 265                 270
gtc ccc gac gag acg acc gtc aac gcg atc cgc acc acc gcc gaa ctc       864
Val Pro Asp Glu Thr Thr Val Asn Ala Ile Arg Thr Thr Ala Glu Leu
        275                 280                 285
gaa ggc gtc atc ctc gac ccc gtc tac gag ggc aag tcg atg gcg ggg       912
Glu Gly Val Ile Leu Asp Pro Val Tyr Glu Gly Lys Ser Met Ala Gly
    290                 295                 300
ctg ctc gac ctc gtc gga agc ggc acg gtg gcg aag gat tcg acg gtc       960
Leu Leu Asp Leu Val Gly Ser Gly Thr Val Ala Lys Asp Ser Thr Val
305                 310                 315                 320
ctc tac gcc cac ctc ggc gga cag ctg gcg ctc aac gcc tac agc tcc      1008
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Leu Tyr Ala His Leu Gly Gly Gln Leu Ala Leu Asn Ala Tyr Ser Ser
325 330 335
atc ttc tga 1017
Ile Phe

<210> 183
<211> 338
<212> PRT
<213> Brevibacterium linens BL2

<400> 183
Met Ala Ile Thr Asp Phe Glu Arg Tyr Pro Leu Thr Phe Arg Pro Ser
1 5 10 15
Pro Val His Glu Leu Lys Arg Leu Ser Asp Arg Leu Gly Gly Ala Arg
20 25 30
Val Trp Ala Lys Arg Glu Asp Val Asn Ser Gly Leu Ala Phe Gly Gly
35 40 45
Asn Lys Thr Arg Lys Leu Glu Tyr Ile Val Pro Asp Ile Leu Ala Ser
50 55 60
Asp Ala Asp Thr Leu Val Ser Ile Gly Gly Tyr Gln Ser Asn His Thr
65 70 75 80
Arg Gln Val Ala Ala Val Ala Ala His Leu Gly Leu Lys Ser Arg Leu
85 90 95
Val Gln Glu Arg Trp Val Asp Trp Asp Asp Pro Val Asn Asp Lys Val
100 105 110
Gly Asn Ile Glu Leu Ser Arg Ile Met Gly Ala Asp Val His Leu Asp
115 120 125
Ser Ala Gly Phe Asp Ile Gly Ile Arg Ser Ser Trp Glu Asn Ala Ile
130 135 140
Ala Glu Val Glu Ala Ala Gly Gly Arg Pro Tyr Pro Ile Pro Ala Gly
145 150 155 160
Ala Ser Glu His Lys Phe Gly Ala Leu Gly Phe Val Asn Trp Ala Tyr
165 170 175
Glu Val Ala Glu Gln Glu Arg Glu Leu Gly Val Phe Phe Asp Thr Ile
180 185 190
Ile Val Cys Thr Val Thr Gly Ser Thr His Ala Gly Met Ile Ala Gly
195 200 205
Phe Ala Ala Leu Glu Ala Ala Gly Gly Pro Lys Arg Gln Val Ile Gly
210 215 220
Ile Asp Ala Ser Ala Thr Leu Asp Lys Thr Arg Asp Gln Val Lys Arg
225 230 235 240
Ile Ala Asn Asn Ala Ala Asp Leu Ile Gly Leu Gly Arg Glu Ile Thr
245 250 255
Asp Ala Asp Val Asp Ile Arg Ser Gly Trp Glu Gly Pro Ala Tyr Gly
260 265 270
Val Pro Asp Glu Thr Thr Val Asn Ala Ile Arg Thr Thr Ala Glu Leu
275 280 285
Glu Gly Val Ile Leu Asp Pro Val Tyr Glu Gly Lys Ser Met Ala Gly
290 295 300
Leu Leu Asp Leu Val Gly Ser Gly Thr Val Ala Lys Asp Ser Thr Val
305 310 315 320
Leu Tyr Ala His Leu Gly Gly Gln Leu Ala Leu Asn Ala Tyr Ser Ser
325 330 335
Ile Phe

<210> 184
<211> 1017
<212> DNA
<213> Burkholderia vietnamiensis G4

<220>
<221> CDS
<222> (1)..(1017)
<223> transl_table=11

<400> 184

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

```
ttg acg gac ccc gtc tac gaa ggc aaa tcg atg cac ggg atg atc gac      912
Leu Thr Asp Pro Val Tyr Glu Gly Lys Ser Met His Gly Met Ile Asp
    290                 295                 300
atg gtg cgt cgc ggg gaa ttc gag ccg gga tcg aag gtg ctg tat gcg      960
Met Val Arg Arg Gly Glu Phe Glu Pro Gly Ser Lys Val Leu Tyr Ala
305                 310                 315                 320
cat ctc ggc gga gtg cct gcg ctg agc gcc tac gcg gag atc ttt cgc     1008
His Leu Gly Gly Val Pro Ala Leu Ser Ala Tyr Ala Glu Ile Phe Arg
                325                 330                 335
gac ggc tga                                                        1017
Asp Gly
```

<210> 185
<211> 338
<212> PRT
<213> Burkholderia vietnamiensis G4

<400> 185

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

<210> 186
<211> 1017
<212> DNA
<213> Burkholderia cenocepacia AU 1054

<220>
<221> CDS
<222> (1)..(1017)
<223> transl_table=11

<400> 186
atg aat ctg caa cgc ttc ccc cgt tat ccg ctg acg ttc ggc ccg acg 48
Met Asn Leu Gln Arg Phe Pro Arg Tyr Pro Leu Thr Phe Gly Pro Thr
1 5 10 15
ccc atc cag ccg ctc aag cgc ctg agc gcg cat ctc ggc ggc aag gtc 96
Pro Ile Gln Pro Leu Lys Arg Leu Ser Ala His Leu Gly Gly Lys Val
20 25 30
gac ctg tat gcg aag cgc gag gac tgc aac agc ggc ctc gca ttc ggc 144
Asp Leu Tyr Ala Lys Arg Glu Asp Cys Asn Ser Gly Leu Ala Phe Gly
35 40 45
ggc aac aag acg cgc aag ctc gaa tat ctc gtt ccc gac gcg ctc gcg 192
Gly Asn Lys Thr Arg Lys Leu Glu Tyr Leu Val Pro Asp Ala Leu Ala
50 55 60
cag ggc gcc gac acg ctc gtg tcg atc ggc ggc gtg cag tcg aac cag 240
Gln Gly Ala Asp Thr Leu Val Ser Ile Gly Gly Val Gln Ser Asn Gln
65 70 75 80
acc cgc cag gtc gcg gcc gtc gcc gcg cat ctc gga atg aaa tgc gtg 288
Thr Arg Gln Val Ala Ala Val Ala Ala His Leu Gly Met Lys Cys Val
85 90 95
ctc gtg cag gag cac tgg gtc aac tat gaa gat ccg gtg tac gac cgg 336
Leu Val Gln Glu His Trp Val Asn Tyr Glu Asp Pro Val Tyr Asp Arg
100 105 110
gtc ggc aac atc cag ttg tcg cgg atg atg ggc gcc gac gtg cgg ctc 384
Val Gly Asn Ile Gln Leu Ser Arg Met Met Gly Ala Asp Val Arg Leu
115 120 125
gtc tcc gac ggt ttc gac atc ggc att cgc cgc agt tgg gaa gaa gcg 432
Val Ser Asp Gly Phe Asp Ile Gly Ile Arg Arg Ser Trp Glu Glu Ala
130 135 140

atg gag agc gtg cga cag gcg ggg ggc aag ccg tat ccg att ccg gcc 480
Met Glu Ser Val Arg Gln Ala Gly Gly Lys Pro Tyr Pro Ile Pro Ala
145 150 155 160
ggc tgc tcc gag cat ccg ctc ggc ggg ctc ggg ttc gtc ggc ttc gcg 528
Gly Cys Ser Glu His Pro Leu Gly Gly Leu Gly Phe Val Gly Phe Ala
165 170 175
gaa gaa gtg cgg gcg cag gaa gcg cag ctc ggc ttc aag ttc gac tac 576
Glu Glu Val Arg Ala Gln Glu Ala Gln Leu Gly Phe Lys Phe Asp Tyr
180 185 190
gtc gtc gtc tgc tcg gtg acg ggc agc acg cag gcg gga atg gtc gtg 624
Val Val Val Cys Ser Val Thr Gly Ser Thr Gln Ala Gly Met Val Val
195 200 205
ggc ttc gcg gcc gac gga cgc gcg gac cgc gtg atc ggc atc gac gca 672
Gly Phe Ala Ala Asp Gly Arg Ala Asp Arg Val Ile Gly Ile Asp Ala
210 215 220
tcg gcg aag ccg gaa cag aca cgc gaa cag atc acg cgc atc gcg cgg 720
Ser Ala Lys Pro Glu Gln Thr Arg Glu Gln Ile Thr Arg Ile Ala Arg
225 230 235 240

```
cat acg gcc gag ctg gtc gag ctg ggc cgc gat atc gtc gaa cag gac        768
His Thr Ala Glu Leu Val Glu Leu Gly Arg Asp Ile Val Glu Gln Asp
                245                 250                 255
gtc gtg ctc gac acg cgt tac ggc gga ccc gaa tat ggt ctg ccg agc        816
Val Val Leu Asp Thr Arg Tyr Gly Gly Pro Glu Tyr Gly Leu Pro Ser
            260                 265                 270
gac ggc acg ctg gaa gcg att cgg ctg tgc gca cgg ctg gaa ggc atg        864
Asp Gly Thr Leu Glu Ala Ile Arg Leu Cys Ala Arg Leu Glu Gly Met
        275                 280                 285
ctg acc gat ccc gtt tat gaa ggg aaa tcg atg cac ggg atg atc gac        912
Leu Thr Asp Pro Val Tyr Glu Gly Lys Ser Met His Gly Met Ile Asp
    290                 295                 300
aag gtg cgg ctc ggg gaa ttc gag ccg ggg tcg aag gtg ctg tat gcg        960
Lys Val Arg Leu Gly Glu Phe Glu Pro Gly Ser Lys Val Leu Tyr Ala
305                 310                 315                 320
cat ctc ggc ggg gcg ccg gcg ttg agt gcg tat aac ggg att ttt cgc       1008
His Leu Gly Gly Ala Pro Ala Leu Ser Ala Tyr Asn Gly Ile Phe Arg
                325                 330                 335
aac ggg tga                                                          1017
Asn Gly
```

<210> 187
<211> 338
<212> PRT
<213> Burkholderia cenocepacia AU 1054

<400> 187

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

```
Val Val Leu Asp Thr Arg Tyr Gly Gly Pro Glu Tyr Gly Leu Pro Ser
            260                 265                 270
Asp Gly Thr Leu Glu Ala Ile Arg Leu Cys Ala Arg Leu Glu Gly Met
        275                 280                 285
Leu Thr Asp Pro Val Tyr Glu Gly Lys Ser Met His Gly Met Ile Asp
    290                 295                 300
Lys Val Arg Leu Gly Glu Phe Glu Pro Gly Ser Lys Val Leu Tyr Ala
305                 310                 315                 320
His Leu Gly Gly Ala Pro Ala Leu Ser Ala Tyr Asn Gly Ile Phe Arg
                325                 330                 335
Asn Gly
```

<210> 188
<211> 969
<212> DNA
<213> Kineococcus radiotolerans SRS30216

<220>
<221> CDS
<222> (1)..(969)
<223> transl_table=11

<400> 188

```
gtg gca ccg cga gac gac cgc acc gtc ctg ggc acc tgg ccg acg ccg        48
Met Ala Pro Arg Asp Asp Arg Thr Val Leu Gly Thr Trp Pro Thr Pro
1               5                   10                  15
gtg gag gcc gcg ccc cgc ctg gcc gcg gcg atc ggc ctc gga ccc ggc        96
Val Glu Ala Ala Pro Arg Leu Ala Ala Ala Ile Gly Leu Gly Pro Gly
            20                  25                  30
gac ctg ctg gtc aag cgc gac gac ctc gtc ggc ctg gcc ggc ggg ggc       144
Asp Leu Leu Val Lys Arg Asp Asp Leu Val Gly Leu Ala Gly Gly Gly
        35                  40                  45
aac gag gtc cgc gag ctg gag cgc acc ctc ggc gcg gcc ctg gcg gag       192
Asn Glu Val Arg Glu Leu Glu Arg Thr Leu Gly Ala Ala Leu Ala Glu
    50                  55                  60
ggg gcg cgg acg gtg gtc acc agc ggc gcg ccg cag agc aac cac gcc       240
Gly Ala Arg Thr Val Val Thr Ser Gly Ala Pro Gln Ser Asn His Ala
65                  70                  75                  80
cgc ctc acc gcc gcc gcc ggt gcg cgc ctc ggc ctg gac gtc gtg ctc       288
Arg Leu Thr Ala Ala Ala Gly Ala Arg Leu Gly Leu Asp Val Val Leu
                85                  90                  95
gtg ctg gag ggg tcg ccc ccc gcg gcc ccg ggc ggg aac ctg ctg ctc       336
Val Leu Glu Gly Ser Pro Pro Ala Ala Pro Gly Gly Asn Leu Leu Leu
            100                 105                 110
gac gcg ctg ctg ggc gcc cgg atc gtc tgg gcc ggc gac gtc agc ccc       384
Asp Ala Leu Leu Gly Ala Arg Ile Val Trp Ala Gly Asp Val Ser Pro
        115                 120                 125
ggc gag ctg gcg gcc cgg gtc gag gcg gag gcc gag gac ctg cgg gcc       432
Gly Glu Leu Ala Ala Arg Val Glu Ala Glu Ala Glu Asp Leu Arg Ala
    130                 135                 140
ggc gac ggc gcg ggt ggg gtc gcg gtc gtg ccc ttc ggc ggt tcc agc       480
Gly Asp Gly Ala Gly Gly Val Ala Val Val Pro Phe Gly Gly Ser Ser
145                 150                 155                 160
gtg ctc ggg gcc cgc ggc tac gtc gac gcg ggg gcc gag ctg ctg gag       528
Val Leu Gly Ala Arg Gly Tyr Val Asp Ala Gly Ala Glu Leu Leu Glu
                165                 170                 175
cag gtc ccc gac ctc gac gtg gtc gtg gtc gcc gtc ggt tcc ggg ggg       576
Gln Val Pro Asp Leu Asp Val Val Val Val Ala Val Gly Ser Gly Gly
            180                 185                 190
acc atg gcc ggg ctc gtg cac gcc ctc ggc gcg cac cgc gtc ctc ggg       624
```

```
Thr Met Ala Gly Leu Val His Ala Leu Gly Ala His Arg Val Leu Gly
        195                 200                 205
gtc gac acc ggc gcg gtg gac gac ccc gag cag cgg gtg cgc ggg ttc       672
Val Asp Thr Gly Ala Val Asp Asp Pro Glu Gln Arg Val Arg Gly Phe
    210                 215                 220
gcc gcc ggt ctg gcc gcg cag gac ggg acc ccc gcg ccc ggg gcc ctg       720
Ala Ala Gly Leu Ala Ala Gln Asp Gly Thr Pro Ala Pro Gly Ala Leu
225                 230                 235                 240
cgg ttg cgc cgc gac gag gtc ggc gcc ggc tac ggc gtg ctc acc gcg       768
Arg Leu Arg Arg Asp Glu Val Gly Ala Gly Tyr Gly Val Leu Thr Ala
                245                 250                 255
cgg gtg cgg cag gcg ctg acg ctg gtc gcg cgc acc gag ggg atc gtc       816
Arg Val Arg Gln Ala Leu Thr Leu Val Ala Arg Thr Glu Gly Ile Val
            260                 265                 270
ctg gac ccc gtc tac acc ggc cgc gcc gcc gcg ggg ctg ctg acc gcg       864
Leu Asp Pro Val Tyr Thr Gly Arg Ala Ala Ala Gly Leu Leu Thr Ala
        275                 280                 285
gtg gag cag ggc gag atc cgt ccc ggg cag cgc acg gtc ctg ctg cac       912
Val Glu Gln Gly Glu Ile Arg Pro Gly Gln Arg Thr Val Leu Leu His
    290                 295                 300
agc ggc ggg ctg ccg ggg ttg ttc ggc cac ccc gac gcc gcg agc ctc       960
Ser Gly Gly Leu Pro Gly Leu Phe Gly His Pro Asp Ala Ala Ser Leu
305                 310                 315                 320
acg ggc tga                                                           969
Thr Gly
```

<210> 189
<211> 322
<212> PRT
<213> Kineococcus radiotolerans SRS30216

<400> 189

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

```
Ala Ala Gly Leu Ala Ala Gln Asp Gly Thr Pro Ala Pro Gly Ala Leu
225                 230                 235                 240
Arg Leu Arg Arg Asp Glu Val Gly Ala Gly Tyr Gly Val Leu Thr Ala
                245                 250                 255
Arg Val Arg Gln Ala Leu Thr Leu Val Ala Arg Thr Glu Gly Ile Val
            260                 265                 270
Leu Asp Pro Val Tyr Thr Gly Arg Ala Ala Ala Gly Leu Leu Thr Ala
        275                 280                 285
Val Glu Gln Gly Glu Ile Arg Pro Gly Gln Arg Thr Val Leu Leu His
    290                 295                 300
Ser Gly Gly Leu Pro Gly Leu Phe Gly His Pro Asp Ala Ala Ser Leu
305                 310                 315                 320
Thr Gly
```

<210> 190
<211> 969
<212> DNA
<213> Nocardioides sp. JS614

<220>
<221> CDS
<222> (1)..(969)
<223> transl_table=11

<400> 190

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

```
            180                 185                 190
caa gct gga ctc gtc gcc gga gcc cag tgg tcc ggc tgg gag atc gat       624
Gln Ala Gly Leu Val Ala Gly Ala Gln Trp Ser Gly Trp Glu Ile Asp
        195                 200                 205
gtc atc ggg atc acg acg agc cga tct ccc gag gag gcg gcg tcc cgg       672
Val Ile Gly Ile Thr Thr Ser Arg Ser Pro Glu Glu Ala Ala Ser Arg
    210                 215                 220
gtg cga gac ctg gcc tca gcg acg ctc gac ttg atc gga gtc ggc gac       720
Val Arg Asp Leu Ala Ser Ala Thr Leu Asp Leu Ile Gly Val Gly Asp
225                 230                 235                 240
acc tcc att gca gca ccc cag gtg cgc gga ggg tat ctc ggt gag ggc       768
Thr Ser Ile Ala Ala Pro Gln Val Arg Gly Gly Tyr Leu Gly Glu Gly
                245                 250                 255
tat ggc aag gcc tcc ccg gcg gga gct gct gca gcc cag ctc gtc gct       816
Tyr Gly Lys Ala Ser Pro Ala Gly Ala Ala Ala Ala Gln Leu Val Ala
            260                 265                 270
cag acc gaa ggc gtc ttc ctc gac cca gcc ttc gga gca aaa gcg atg       864
Gln Thr Glu Gly Val Phe Leu Asp Pro Ala Phe Gly Ala Lys Ala Met
        275                 280                 285
gca gcc ctg atc gat gca gcc cgt gat ggc acc gtt gag ggt ccg gtg       912
Ala Ala Leu Ile Asp Ala Ala Arg Asp Gly Thr Val Glu Gly Pro Val
    290                 295                 300
gtg ttc ctc gtc acc gga ggg gcc ccg acc ctc ttc act ccc gga gct       960
Val Phe Leu Val Thr Gly Gly Ala Pro Thr Leu Phe Thr Pro Gly Ala
305                 310                 315                 320
caa ctg tga                                                           969
Gln Leu
```

<210> 191
<211> 322
<212> PRT
<213> Nocardioides sp. JS614

<400> 191

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

```
Val Ile Gly Ile Thr Thr Ser Arg Ser Pro Glu Glu Ala Ala Ser Arg
    210                 215                 220
Val Arg Asp Leu Ala Ser Ala Thr Leu Asp Leu Ile Gly Val Gly Asp
225                 230                 235                 240
Thr Ser Ile Ala Ala Pro Gln Val Arg Gly Gly Tyr Leu Gly Glu Gly
                245                 250                 255
Tyr Gly Lys Ala Ser Pro Ala Gly Ala Ala Ala Ala Gln Leu Val Ala
            260                 265                 270
Gln Thr Glu Gly Val Phe Leu Asp Pro Ala Phe Gly Ala Lys Ala Met
        275                 280                 285
Ala Ala Leu Ile Asp Ala Ala Arg Asp Gly Thr Val Glu Gly Pro Val
    290                 295                 300
Val Phe Leu Val Thr Gly Gly Ala Pro Thr Leu Phe Thr Pro Gly Ala
305                 310                 315                 320
Gln Leu
```

<210> 192
<211> 969
<212> DNA
<213> Nocardioides sp. JS614

<220>
<221> CDS
<222> (1)..(969)
<223> transl_table=11

<400> 192

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

```
ggt gtc gac ccc gca acg ctc tgg gtg ccg acc gga tcc ggc ggc acc        576
Gly Val Asp Pro Ala Thr Leu Trp Val Pro Thr Gly Ser Gly Gly Thr
            180                 185                 190
cag gca gga ctt ctc gcc ggg gcg cac tgg ttg gga tgg gac gtt gcg        624
Gln Ala Gly Leu Leu Ala Gly Ala His Trp Leu Gly Trp Asp Val Ala
        195                 200                 205
gtg gtc ggg gtc gcc acc agc cgg act cct gaa gag gcc cag gtc cgc        672
Val Val Gly Val Ala Thr Ser Arg Thr Pro Glu Glu Ala Gln Val Arg
    210                 215                 220
gtt ggc gag ctc gcc tcg gcc act ctc gag ctg ctc gac gcc gat gac        720
Val Gly Glu Leu Ala Ser Ala Thr Leu Glu Leu Leu Asp Ala Asp Asp
225                 230                 235                 240
acg gct cga gca gcg ccg cac gtc ctc ggc ggg ttc ctc ggc gac ggc        768
Thr Ala Arg Ala Ala Pro His Val Leu Gly Gly Phe Leu Gly Asp Gly
                245                 250                 255
tat ggc gaa gtc tcg cca gcg ggt acc gcg gcg gcc gag ctc gtc gcg        816
Tyr Gly Glu Val Ser Pro Ala Gly Thr Ala Ala Ala Glu Leu Val Ala
            260                 265                 270
cgg acc gag ggc atc ttc ctc gac ccg gtg ttc ggc gcc aag gcg atg        864
Arg Thr Glu Gly Ile Phe Leu Asp Pro Val Phe Gly Ala Lys Ala Met
        275                 280                 285
gcg gct ctc ttg gct gaa gtc cgg cat gga acc gtc cga ggg ccg gtg        912
Ala Ala Leu Leu Ala Glu Val Arg His Gly Thr Val Arg Gly Pro Val
    290                 295                 300
atc ttc ctg gtc acc gga ggc gca ccc acc ctc ttc atg aag ggc acg        960
Ile Phe Leu Val Thr Gly Gly Ala Pro Thr Leu Phe Met Lys Gly Thr
305                 310                 315                 320
gaa ctg tga                                                           969
Glu Leu
```

<210> 193
<211> 322
<212> PRT
<213> Nocardioides sp. JS614

<400> 193

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

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

<210> 194
<211> 999
<212> DNA
<213> Syntrophobacter fumaroxidans MPOB

<220>
<221> CDS
<222> (1)..(999)
<223> transl_table=11

<400> 194

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

```
Met Gly Phe Val Ala Ala Val Arg Glu Leu Lys Gln Gln Leu Ala Ser
                165                 170                 175
cgg aac gaa aag atc gac acc gtg atc att ccg tcg agt tcc ggc ggg      576
Arg Asn Glu Lys Ile Asp Thr Val Ile Ile Pro Ser Ser Ser Gly Gly
            180                 185                 190
acc cac gcg ggt ctc acc gtg gga atc gat gcg ttc gat ttt ccg gca      624
Thr His Ala Gly Leu Thr Val Gly Ile Asp Ala Phe Asp Phe Pro Ala
        195                 200                 205
cag gtg atc ggc atc ggg atc gac aaa ggg gtg tcg ggc ggg ggt tca      672
Gln Val Ile Gly Ile Gly Ile Asp Lys Gly Val Ser Gly Gly Gly Ser
    210                 215                 220
tac gaa tcc gaa ctg gcg gtc ctg gcc aac cgg att gcc ggg acg ctc      720
Tyr Glu Ser Glu Leu Ala Val Leu Ala Asn Arg Ile Ala Gly Thr Leu
225                 230                 235                 240
ggg ctg cag gcg aac tac gac gcc gac cgg ttc cgg atg cgc tat gaa      768
Gly Leu Gln Ala Asn Tyr Asp Ala Asp Arg Phe Arg Met Arg Tyr Glu
                245                 250                 255
tac ctg ggt gcc gga tac ggg gtg gtg ggc gac ctc gag cgc gag gcg      816
Tyr Leu Gly Ala Gly Tyr Gly Val Val Gly Asp Leu Glu Arg Glu Ala
            260                 265                 270
atc cgc ctg ctg gcg cga tgc gaa ggg atc ctg gcc gat ccg gtc tac      864
Ile Arg Leu Leu Ala Arg Cys Glu Gly Ile Leu Ala Asp Pro Val Tyr
        275                 280                 285
acg ggg aga gcg ctg ggc ggc atg atc gac atg atc cgc ggg aag gaa      912
Thr Gly Arg Ala Leu Gly Gly Met Ile Asp Met Ile Arg Gly Lys Glu
    290                 295                 300
ttc gcg ccc ggc gat acg gtg ctg ttc tgg cac acg ggg ggc gtg ccg      960
Phe Ala Pro Gly Asp Thr Val Leu Phe Trp His Thr Gly Gly Val Pro
305                 310                 315                 320
gcg ctc ttc gag tat gcg ggc gag ctc cat gcc ggg tga                  999
Ala Leu Phe Glu Tyr Ala Gly Glu Leu His Ala Gly
                325                 330
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<210> 195
<211> 332
<212> PRT
<213> Syntrophobacter fumaroxidans MPOB

<400> 195

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

```
Arg Asn Glu Lys Ile Asp Thr Val Ile Ile Pro Ser Ser Ser Gly Gly
            180                 185                 190
Thr His Ala Gly Leu Thr Val Gly Ile Asp Ala Phe Asp Phe Pro Ala
        195                 200                 205
Gln Val Ile Gly Ile Gly Ile Asp Lys Gly Val Ser Gly Gly Gly Ser
    210                 215                 220
Tyr Glu Ser Glu Leu Ala Val Leu Ala Asn Arg Ile Ala Gly Thr Leu
225                 230                 235                 240
Gly Leu Gln Ala Asn Tyr Asp Ala Asp Arg Phe Arg Met Arg Tyr Glu
                245                 250                 255
Tyr Leu Gly Ala Gly Tyr Gly Val Val Gly Asp Leu Glu Arg Glu Ala
            260                 265                 270
Ile Arg Leu Leu Ala Arg Cys Glu Gly Ile Leu Ala Asp Pro Val Tyr
        275                 280                 285
Thr Gly Arg Ala Leu Gly Gly Met Ile Asp Met Ile Arg Gly Lys Glu
    290                 295                 300
Phe Ala Pro Gly Asp Thr Val Leu Phe Trp His Thr Gly Gly Val Pro
305                 310                 315                 320
Ala Leu Phe Glu Tyr Ala Gly Glu Leu His Ala Gly
                325                 330
```

<210> 196
<211> 1017
<212> DNA
<213> Burkholderia ambifaria AMMD

<220>
<221> CDS
<222> (1)..(1017)
<223> transl_table=11

<400> 196

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

```
145                 150                 155                 160
ggg tgt tcc gag cat ccg ctc ggc ggt ctc ggc ttc gtc ggc ttc gcg      528
Gly Cys Ser Glu His Pro Leu Gly Gly Leu Gly Phe Val Gly Phe Ala
                165                 170                 175
gaa gaa gtg cgc gag cag gaa gca cag ctc ggg ttc aag ttc gac tat      576
Glu Glu Val Arg Glu Gln Glu Ala Gln Leu Gly Phe Lys Phe Asp Tyr
            180                 185                 190
gtc gtg gtc tgc tcg gtg acg ggc agc act cag gcg ggg atg gtc gtc      624
Val Val Val Cys Ser Val Thr Gly Ser Thr Gln Ala Gly Met Val Val
        195                 200                 205
ggc ttc gcg gcc gac gga cgc gcg gat cgc gtg atc ggc atc gac gcg      672
Gly Phe Ala Ala Asp Gly Arg Ala Asp Arg Val Ile Gly Ile Asp Ala
    210                 215                 220
tcg gcg acg ccc gag cgc acg cac gaa cag atc acg cgc att gcg cgg      720
Ser Ala Thr Pro Glu Arg Thr His Glu Gln Ile Thr Arg Ile Ala Arg
225                 230                 235                 240
cat acg gcc gaa ctg gtc gat ctc ggc cgg ccg atc acc gag gcg gac      768
His Thr Ala Glu Leu Val Asp Leu Gly Arg Pro Ile Thr Glu Ala Asp
                245                 250                 255
gtc gtg ctc gac acg cgc tat gcc ggc ccg gaa tac gga ttg ccg aac      816
Val Val Leu Asp Thr Arg Tyr Ala Gly Pro Glu Tyr Gly Leu Pro Asn
            260                 265                 270
gat ggc acg ctg gag gcg att cgc ttg tgt gca cgg ctc gag ggg atg      864
Asp Gly Thr Leu Glu Ala Ile Arg Leu Cys Ala Arg Leu Glu Gly Met
        275                 280                 285
ctg acc gat ccc gtc tac gaa ggg aaa tcg atg cac ggg atg atc gac      912
Leu Thr Asp Pro Val Tyr Glu Gly Lys Ser Met His Gly Met Ile Asp
    290                 295                 300
aag gtg cgt cgc ggg gaa ttc gag ccg ggg tcg aag gtg ctg tat gcg      960
Lys Val Arg Arg Gly Glu Phe Glu Pro Gly Ser Lys Val Leu Tyr Ala
305                 310                 315                 320
cat ctc ggc ggg gtg ccg gcg ctg agc gcg tac gcg gag atc ttc cgc     1008
His Leu Gly Gly Val Pro Ala Leu Ser Ala Tyr Ala Glu Ile Phe Arg
                325                 330                 335
aac ggg tga                                                        1017
Asn Gly
```

<210> 197
<211> 338
<212> PRT
<213> Burkholderia ambifaria AMMD

<400> 197

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Met Asn Leu Gln Arg Phe Ser Arg Tyr Pro Leu Thr Phe Gly Pro Thr
1               5                   10                  15
Pro Ile Gln Pro Leu Lys Arg Leu Ser Gln His Leu Gly Gly Lys Val
            20                  25                  30
Glu Leu Tyr Ala Lys Arg Glu Asp Cys Asn Ser Gly Leu Ala Phe Gly
        35                  40                  45
Gly Asn Lys Thr Arg Lys Leu Glu Tyr Leu Val Pro Asp Ala Leu Ala
    50                  55                  60
Gln Gly Ala Asp Thr Leu Val Ser Ile Gly Gly Val Gln Ser Asn Gln
65                  70                  75                  80
Thr Arg Gln Val Ala Ala Val Ala Ala His Leu Gly Met Lys Cys Val
                85                  90                  95
Leu Val Gln Glu His Trp Val Asn Tyr Glu Asp Pro Val Tyr Asp Arg
            100                 105                 110
Val Gly Asn Ile Gln Leu Ser Arg Met Met Gly Ala Asp Val Arg Leu
        115                 120                 125
Val Ala Asp Gly Phe Asp Ile Gly Ile Arg Arg Ser Trp Glu Glu Ala
```

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

<210> 198
<211> 987
<212> DNA
<213> Shigella boydii BS512

<220>
<221> CDS
<222> (1)..(987)

<400> 198

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atg cca ctg cat aat tta acc cgt ttt cca cgg ctg gag ttt atc ggc        48
Met Pro Leu His Asn Leu Thr Arg Phe Pro Arg Leu Glu Phe Ile Gly
1               5                   10                  15
gcg cca acg ccg ctc gaa tat ctg ccg cgc ttt tct gat tat ctt gga        96
Ala Pro Thr Pro Leu Glu Tyr Leu Pro Arg Phe Ser Asp Tyr Leu Gly
            20                  25                  30
cgg gaa att ttc atc aaa cgg gat gac gtc aca ccc atg gca atg ggc       144
Arg Glu Ile Phe Ile Lys Arg Asp Asp Val Thr Pro Met Ala Met Gly
        35                  40                  45
ggc aat aaa tta cgt aag ctg gaa ttt ctc gcg gca gat gcc ctg cgc       192
Gly Asn Lys Leu Arg Lys Leu Glu Phe Leu Ala Ala Asp Ala Leu Arg
    50                  55                  60
gaa ggt gcc gat acg ctg att act gcc ggc gcg atc cag tct aac cat       240
Glu Gly Ala Asp Thr Leu Ile Thr Ala Gly Ala Ile Gln Ser Asn His
65                  70                  75                  80
gtg cgg cag act gcc gca gtt gcg gcg aaa ctc ggc ctg cac tgc gtg       288
Val Arg Gln Thr Ala Ala Val Ala Ala Lys Leu Gly Leu His Cys Val
                85                  90                  95
gcg ctg ctg gaa aat cct att ggc aca acc gca gaa aac tat tta acc       336
Ala Leu Leu Glu Asn Pro Ile Gly Thr Thr Ala Glu Asn Tyr Leu Thr
            100                 105                 110
aac ggc aat cgt ttg ttg ctg aat ctg ttc aat acc cag att gaa atg       384
Asn Gly Asn Arg Leu Leu Leu Asn Leu Phe Asn Thr Gln Ile Glu Met
```

```
        115                 120                 125
tgc gac gca ctg acc gat ccc aat gcc caa ctg gaa gag ctg gcg acg       432
Cys Asp Ala Leu Thr Asp Pro Asn Ala Gln Leu Glu Glu Leu Ala Thr
    130                 135                 140
cga gtc gaa gca caa ggc ttt cgc ccg tat gtc att ccg gtt ggc ggt       480
Arg Val Glu Ala Gln Gly Phe Arg Pro Tyr Val Ile Pro Val Gly Gly
145                 150                 155                 160
tct aat gct ctg ggc gcg ctg ggt tat gtg gag agt gcg ctg gaa atc       528
Ser Asn Ala Leu Gly Ala Leu Gly Tyr Val Glu Ser Ala Leu Glu Ile
                165                 170                 175
gcg caa cag tgt gaa ggg gcg gtt aat att tcg tcg gtg gtg gtc gca       576
Ala Gln Gln Cys Glu Gly Ala Val Asn Ile Ser Ser Val Val Val Ala
            180                 185                 190
tcg ggc agt gcc gga act cac gcc gga ttg gct gtt ggg ctg gaa cac       624
Ser Gly Ser Ala Gly Thr His Ala Gly Leu Ala Val Gly Leu Glu His
        195                 200                 205
ctg atg cct gaa agc gaa ctg att ggc gtg acc gtg tcg cgt tcc gtt       672
Leu Met Pro Glu Ser Glu Leu Ile Gly Val Thr Val Ser Arg Ser Val
    210                 215                 220
gcc gat caa ttg ccg aaa gtg gtt aac cta caa cag gcg att gcg aaa       720
Ala Asp Gln Leu Pro Lys Val Val Asn Leu Gln Gln Ala Ile Ala Lys

225                 230                 235                 240
gaa ctg gag ctg acc gca tca gcg gaa att tta ctc tgg gat gac tat       768
Glu Leu Glu Leu Thr Ala Ser Ala Glu Ile Leu Leu Trp Asp Asp Tyr
                245                 250                 255
ttt gca cct ggc tac ggc gtg ccg aac gac gaa ggc atg gaa gca gtg       816
Phe Ala Pro Gly Tyr Gly Val Pro Asn Asp Glu Gly Met Glu Ala Val
            260                 265                 270
aaa ttg ctg gcg cgt ctg gaa ggc att ctg ctt gat cct gtg tat acc       864
Lys Leu Leu Ala Arg Leu Glu Gly Ile Leu Leu Asp Pro Val Tyr Thr
        275                 280                 285
gga aaa gcg atg gcg ggg ctg att gac ggt atc agt cag aaa cgc ttc       912
Gly Lys Ala Met Ala Gly Leu Ile Asp Gly Ile Ser Gln Lys Arg Phe
    290                 295                 300
aaa gat gaa ggg ccg att ctg ttt att cat acc ggc ggc gcg cct gcg       960
Lys Asp Glu Gly Pro Ile Leu Phe Ile His Thr Gly Gly Ala Pro Ala
305                 310                 315                 320
ctg ttc gcc tat cat ccc cac gtt tag                                  987
Leu Phe Ala Tyr His Pro His Val
                325
```

<210> 199
<211> 328
<212> PRT
<213> Shigella boydii BS512

<400> 199

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

```
            100                 105                 110
Asn Gly Asn Arg Leu Leu Leu Asn Leu Phe Asn Thr Gln Ile Glu Met
        115                 120                 125
Cys Asp Ala Leu Thr Asp Pro Asn Ala Gln Leu Glu Glu Leu Ala Thr
    130                 135                 140
Arg Val Glu Ala Gln Gly Phe Arg Pro Tyr Val Ile Pro Val Gly Gly
145                 150                 155                 160
Ser Asn Ala Leu Gly Ala Leu Gly Tyr Val Glu Ser Ala Leu Glu Ile
                165                 170                 175
Ala Gln Gln Cys Glu Gly Ala Val Asn Ile Ser Ser Val Val Val Ala
            180                 185                 190
Ser Gly Ser Ala Gly Thr His Ala Gly Leu Ala Val Gly Leu Glu His
        195                 200                 205
Leu Met Pro Glu Ser Glu Leu Ile Gly Val Thr Val Ser Arg Ser Val
    210                 215                 220
Ala Asp Gln Leu Pro Lys Val Val Asn Leu Gln Gln Ala Ile Ala Lys
225                 230                 235                 240
Glu Leu Glu Leu Thr Ala Ser Ala Glu Ile Leu Leu Trp Asp Asp Tyr
                245                 250                 255
Phe Ala Pro Gly Tyr Gly Val Pro Asn Asp Glu Gly Met Glu Ala Val
            260                 265                 270
Lys Leu Leu Ala Arg Leu Glu Gly Ile Leu Leu Asp Pro Val Tyr Thr
        275                 280                 285
Gly Lys Ala Met Ala Gly Leu Ile Asp Gly Ile Ser Gln Lys Arg Phe
    290                 295                 300
Lys Asp Glu Gly Pro Ile Leu Phe Ile His Thr Gly Gly Ala Pro Ala
305                 310                 315                 320
Leu Phe Ala Tyr His Pro His Val
                325
```

<210> 200
<211> 1029
<212> DNA
<213> Escherichia coli E24377A

<220>
<221> CDS
<222> (1)..(1029)

<400> 200

```
atg cca ctg cat aat tta acc cgt ttt cca cgg ttg gag ttt atc ggc        48
Met Pro Leu His Asn Leu Thr Arg Phe Pro Arg Leu Glu Phe Ile Gly
1               5                   10                  15
gcg cca acg ccg ctc gaa tat ctg ccg cgc ttt tct gat tat ctt gga        96
Ala Pro Thr Pro Leu Glu Tyr Leu Pro Arg Phe Ser Asp Tyr Leu Gly
            20                  25                  30
cgg gaa att ttc atc aaa cgg gat gac gtc acc ccc atg gca atg ggc       144
Arg Glu Ile Phe Ile Lys Arg Asp Asp Val Thr Pro Met Ala Met Gly
        35                  40                  45
ggc aat aaa tta cgt aag ctg gaa ttt ctc gca gca gat gct ctg cgc       192
Gly Asn Lys Leu Arg Lys Leu Glu Phe Leu Ala Ala Asp Ala Leu Arg
    50                  55                  60
gaa ggt gcc gat acg ctg att act gcc ggc gcg atc cag tct aac cat       240
Glu Gly Ala Asp Thr Leu Ile Thr Ala Gly Ala Ile Gln Ser Asn His
65                  70                  75                  80
gtg cgc cag act gcc gca gtt gcg gcg aaa ctc ggt ctg cac tgc gtg       288
Val Arg Gln Thr Ala Ala Val Ala Ala Lys Leu Gly Leu His Cys Val
                85                  90                  95
gcg ctg ctg gaa aat cct att ggc aca acc gca gaa aac tat tta acc       336
Ala Leu Leu Glu Asn Pro Ile Gly Thr Thr Ala Glu Asn Tyr Leu Thr
            100                 105                 110
```

```
aac ggc aat cgc ttg ttg ctg gat ctg ttc aat acc cag att gaa atg        384
Asn Gly Asn Arg Leu Leu Leu Asp Leu Phe Asn Thr Gln Ile Glu Met
        115                 120                 125
tgc gac gca ctg acc gat ccc aat gcc caa ctg gaa gag ctg gcg acg        432
Cys Asp Ala Leu Thr Asp Pro Asn Ala Gln Leu Glu Glu Leu Ala Thr
    130                 135                 140
cga gtc gaa gca caa ggc ttt cgc ccg tat gtc att ccg gtt ggc ggt        480
Arg Val Glu Ala Gln Gly Phe Arg Pro Tyr Val Ile Pro Val Gly Gly
145                 150                 155                 160
tct aat gct ctg ggc gcg ctg ggt tat gtg gag agt gcg ctg gaa atc        528
Ser Asn Ala Leu Gly Ala Leu Gly Tyr Val Glu Ser Ala Leu Glu Ile
                165                 170                 175
gcg caa cag tgt gaa ggg gcg gtt aat att tcg tcg gtg gtg gtc gca        576
Ala Gln Gln Cys Glu Gly Ala Val Asn Ile Ser Ser Val Val Val Ala
            180                 185                 190
tcg ggc agt gcc gga act cac gcc gga ttg gct gtt ggg ctg gaa cac        624
Ser Gly Ser Ala Gly Thr His Ala Gly Leu Ala Val Gly Leu Glu His
        195                 200                 205
ctg atg cct gaa agc gaa ctg att ggc gtg acc gtg tcg cgt tcc gtt        672
Leu Met Pro Glu Ser Glu Leu Ile Gly Val Thr Val Ser Arg Ser Val
    210                 215                 220
gcc gat caa ttg ccg aaa gtg gtt aac cta caa cag gcg att gcg aaa        720
Ala Asp Gln Leu Pro Lys Val Val Asn Leu Gln Gln Ala Ile Ala Lys
225                 230                 235                 240
gaa ctg gag ctg acc gca tca gcg gaa att tta ctc tgg gat gac tat        768
Glu Leu Glu Leu Thr Ala Ser Ala Glu Ile Leu Leu Trp Asp Asp Tyr
                245                 250                 255
ttt gca cct ggc tac ggc gtg ccg aac gac gaa ggc atg gaa gca gtg        816
Phe Ala Pro Gly Tyr Gly Val Pro Asn Asp Glu Gly Met Glu Ala Val
            260                 265                 270
aaa ttg ctg gcg cgt ctg gaa ggc att ctg ctt gat cct gtg tat acc        864
Lys Leu Leu Ala Arg Leu Glu Gly Ile Leu Leu Asp Pro Val Tyr Thr
        275                 280                 285
gga aaa gcg atg gcg ggg ctg att gac ggt atc agt cag aaa cgc ttc        912
Gly Lys Ala Met Ala Gly Leu Ile Asp Gly Ile Ser Gln Lys Arg Phe
    290                 295                 300
aaa gat gaa ggg ccg att ctg ttt att cat acc ggc ggc gcg cct gcg        960
Lys Asp Glu Gly Pro Ile Leu Phe Ile His Thr Gly Gly Ala Pro Ala
305                 310                 315                 320
ctg ttc gcc tat cat ccc acg ttt agc tcc ggg aac gct cat gca aga       1008
Leu Phe Ala Tyr His Pro Thr Phe Ser Ser Gly Asn Ala His Ala Arg
                325                 330                 335
aag tat aca act ggt tat tga                                          1029
Lys Tyr Thr Thr Gly Tyr
            340
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<210> 201
<211> 342
<212> PRT
<213> Escherichia coli E24377A

<400> 201

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

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

<210> 202
<211> 987
<212> DNA
<213> Escherichia coli HS

<220>
<221> CDS
<222> (1)..(987)

<400> 202
atg cca ctg cat aat tta acc cgt ttt cca cgg ttg gag ttt atc ggc 48
Met Pro Leu His Asn Leu Thr Arg Phe Pro Arg Leu Glu Phe Ile Gly
1 5 10 15
gcg cca acg ccg ctc gaa tat ctg ccg cgc ttt tct gat tat ctt gga 96
Ala Pro Thr Pro Leu Glu Tyr Leu Pro Arg Phe Ser Asp Tyr Leu Gly
20 25 30
cgg gaa att ttc atc aaa cgg gat gac gtc acc ccc atg gca atg ggc 144
Arg Glu Ile Phe Ile Lys Arg Asp Asp Val Thr Pro Met Ala Met Gly
35 40 45
ggc aat aaa tta cgt aag ctg gaa ttt ctc gca gca gat gct ctg cgc 192
Gly Asn Lys Leu Arg Lys Leu Glu Phe Leu Ala Ala Asp Ala Leu Arg
50 55 60
gaa ggt gcc gat acg ctg att act gcc ggc gcg atc cag tct aac cat 240
Glu Gly Ala Asp Thr Leu Ile Thr Ala Gly Ala Ile Gln Ser Asn His
65 70 75 80

```
gtg cgc cag act gcc gca gtt gcg gcg aaa ctc ggt ctg cac tgc gtg      288
Val Arg Gln Thr Ala Ala Val Ala Ala Lys Leu Gly Leu His Cys Val
                85                  90                  95
gcg ctg ctg gaa aat cct att ggc aca acc gca gaa aac tat tta acc      336
Ala Leu Leu Glu Asn Pro Ile Gly Thr Thr Ala Glu Asn Tyr Leu Thr
            100                 105                 110
aac ggc aat cgc ttg ttg ctg gat ctg ttc aat acc cag att gaa atg      384
Asn Gly Asn Arg Leu Leu Leu Asp Leu Phe Asn Thr Gln Ile Glu Met
        115                 120                 125
tgc gac gca ctg acc gat ccc aat gcc caa ctg gaa gag ctg gcg acg      432
Cys Asp Ala Leu Thr Asp Pro Asn Ala Gln Leu Glu Glu Leu Ala Thr
    130                 135                 140
cga gtc gaa gca caa ggc ttt cgc ccg tat gtc att ccg gtt ggc ggt      480
Arg Val Glu Ala Gln Gly Phe Arg Pro Tyr Val Ile Pro Val Gly Gly
145                 150                 155                 160
tct aat gct ttg ggc gcg ctg ggt tat gtg gag agt gcg ctg gaa atc      528
Ser Asn Ala Leu Gly Ala Leu Gly Tyr Val Glu Ser Ala Leu Glu Ile
                165                 170                 175
gcg caa cag tgt gaa ggg gcg gtt aat att tcg tcg gtg gta gtc gca      576
Ala Gln Gln Cys Glu Gly Ala Val Asn Ile Ser Ser Val Val Val Ala
            180                 185                 190
tcg ggc agt gcc gga act cac gcc gga ctg gct gtt ggg ctg gaa cac      624
Ser Gly Ser Ala Gly Thr His Ala Gly Leu Ala Val Gly Leu Glu His
        195                 200                 205
ctg ctg cct gaa agc gaa ctg att ggc gtg acc gtg tcg cgt tcc gtt      672
Leu Leu Pro Glu Ser Glu Leu Ile Gly Val Thr Val Ser Arg Ser Val
    210                 215                 220
gcc gat caa ttg ccg aaa gtg gtt aac cta caa cag gcg att gcg aaa      720
Ala Asp Gln Leu Pro Lys Val Val Asn Leu Gln Gln Ala Ile Ala Lys
225                 230                 235                 240
gaa ctg gag ctg acc gca tca gcg gaa att tta ctc tgg gat gac tat      768
Glu Leu Glu Leu Thr Ala Ser Ala Glu Ile Leu Leu Trp Asp Asp Tyr
                245                 250                 255
ttt gca cct ggc tac ggc gtg ccg aac gac gaa ggc atg gaa gca gtg      816
Phe Ala Pro Gly Tyr Gly Val Pro Asn Asp Glu Gly Met Glu Ala Val
            260                 265                 270
aaa ttg ctg gcg cgg ttt gaa ggc att ctg ctt gat cct gtg tat acc      864
Lys Leu Leu Ala Arg Phe Glu Gly Ile Leu Leu Asp Pro Val Tyr Thr
        275                 280                 285
gga aaa gcg atg gcg ggt ctg att gac ggt atc agt cag aaa cgc ttc      912
Gly Lys Ala Met Ala Gly Leu Ile Asp Gly Ile Ser Gln Lys Arg Phe
    290                 295                 300
aaa gat gaa ggg ccg att ctg ttt att cat acc ggc ggc gcg cct gcg      960
Lys Asp Glu Gly Pro Ile Leu Phe Ile His Thr Gly Gly Ala Pro Ala
305                 310                 315                 320
ctg ttc gcc tat cat ccc cac gtt tag                                 987
Leu Phe Ala Tyr His Pro His Val
                325
```

<210> 203
<211> 328
<212> PRT
<213> Escherichia coli HS

<400> 203

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Met Pro Leu His Asn Leu Thr Arg Phe Pro Arg Leu Glu Phe Ile Gly
1               5                  10                  15
Ala Pro Thr Pro Leu Glu Tyr Leu Pro Arg Phe Ser Asp Tyr Leu Gly
            20                  25                  30
Arg Glu Ile Phe Ile Lys Arg Asp Asp Val Thr Pro Met Ala Met Gly
        35                  40                  45
```

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

<210> 204
<211> 987
<212> DNA
<213> Escherichia coli B7A

<220>
<221> CDS
<222> (1)..(987)

<400> 204

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atg cca ctg cat aat tta acc cgt ttt cca cgg ttg gag ttt atc ggc      48
Met Pro Leu His Asn Leu Thr Arg Phe Pro Arg Leu Glu Phe Ile Gly
1               5                   10                  15
gcg cca acg ccg ctc gaa tat ctg ccg cgc ttt tct gat tat ctt gga      96
Ala Pro Thr Pro Leu Glu Tyr Leu Pro Arg Phe Ser Asp Tyr Leu Gly
            20                  25                  30
cgg gaa att ttc atc aaa cgg gat gac gtc aca ccc atg gca atg ggc     144
Arg Glu Ile Phe Ile Lys Arg Asp Asp Val Thr Pro Met Ala Met Gly
        35                  40                  45
ggc aat aaa tta cgt aag ctg gaa ttt ctc gcg gca gat gcc ctg cgc     192
Gly Asn Lys Leu Arg Lys Leu Glu Phe Leu Ala Ala Asp Ala Leu Arg
    50                  55                  60
gaa ggt gcc gat acg ctg att act gcc ggc gcg atc cag tct aac cat     240
Glu Gly Ala Asp Thr Leu Ile Thr Ala Gly Ala Ile Gln Ser Asn His
```

```
65                  70                  75                  80
gtg cgc cag act gcc gca gtc gcg gcg aaa ctc ggt ctg cac tgc gtg      288
Val Arg Gln Thr Ala Ala Val Ala Ala Lys Leu Gly Leu His Cys Val
                85                  90                  95
gcg ctg ctg gaa aat cct att ggc aca acc gca gaa aac tat tta acc      336
Ala Leu Leu Glu Asn Pro Ile Gly Thr Thr Ala Glu Asn Tyr Leu Thr
            100                 105                 110
aac ggc aat cgt ttg ttg ctg gat ctg ttc aat acc cag att gaa atg      384
Asn Gly Asn Arg Leu Leu Leu Asp Leu Phe Asn Thr Gln Ile Glu Met
        115                 120                 125
tgc gat gca ctg acc gat ccc aat gcc caa ctg gaa gag ctg gcg acg      432
Cys Asp Ala Leu Thr Asp Pro Asn Ala Gln Leu Glu Glu Leu Ala Thr
    130                 135                 140
cga gtc gaa gca caa ggc ttt cgc ccg tat gtc att ccg gtt ggc ggt      480
Arg Val Glu Ala Gln Gly Phe Arg Pro Tyr Val Ile Pro Val Gly Gly
145                 150                 155                 160
tct aat gct ctt ggc gcg cta ggt tat gtg gag agt gcg ctg gaa atc      528
Ser Asn Ala Leu Gly Ala Leu Gly Tyr Val Glu Ser Ala Leu Glu Ile
                165                 170                 175
gcg caa cag tgt gaa ggg gcg gtt aat att tcg tcg gtg gta gtc gca      576
Ala Gln Gln Cys Glu Gly Ala Val Asn Ile Ser Ser Val Val Val Ala
            180                 185                 190
tcg ggc agt gcc gga act cac gcc gga ctg gct gtt ggg ctg gaa cac      624
Ser Gly Ser Ala Gly Thr His Ala Gly Leu Ala Val Gly Leu Glu His
        195                 200                 205
ctg atg cct gaa agc gaa ctg att ggc gtg acc gtg tcg cgt tcc gtt      672
Leu Met Pro Glu Ser Glu Leu Ile Gly Val Thr Val Ser Arg Ser Val
    210                 215                 220
gcc gat caa ttg ccg aaa gtg gtt aac cta caa cag gcg att gcg aaa      720
Ala Asp Gln Leu Pro Lys Val Val Asn Leu Gln Gln Ala Ile Ala Lys
225                 230                 235                 240
gaa ctg gag ctg acc gca tca gcg gaa att ttt ctc tgg gat gac tat      768
Glu Leu Glu Leu Thr Ala Ser Ala Glu Ile Phe Leu Trp Asp Asp Tyr
                245                 250                 255
ttt gca cct ggc tac ggc gtg ccg aac gac gaa ggc atg gaa gca gtg      816
Phe Ala Pro Gly Tyr Gly Val Pro Asn Asp Glu Gly Met Glu Ala Val
            260                 265                 270
aaa ttg ctg gcg cgg ctg gaa ggc att ctg ctt gat cct gtg tat acc      864
Lys Leu Leu Ala Arg Leu Glu Gly Ile Leu Leu Asp Pro Val Tyr Thr
        275                 280                 285
gga aaa gcg atg gcg ggg ctg att ggc ggt atc agt cag aaa cgc ttc      912
Gly Lys Ala Met Ala Gly Leu Ile Gly Gly Ile Ser Gln Lys Arg Phe
    290                 295                 300
aaa gat gaa ggg ccg att ctg ttt att cat acc ggc ggt gcg cct gcg      960
Lys Asp Glu Gly Pro Ile Leu Phe Ile His Thr Gly Gly Ala Pro Ala
305                 310                 315                 320
ctg ttc gcc tat cat ccc cac gtt tag                                 987
Leu Phe Ala Tyr His Pro His Val
                325
```

<210> 205
<211> 328
<212> PRT
<213> Escherichia coli B7A

<400> 205

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Met Pro Leu His Asn Leu Thr Arg Phe Pro Arg Leu Glu Phe Ile Gly
1               5                   10                  15
Ala Pro Thr Pro Leu Glu Tyr Leu Pro Arg Phe Ser Asp Tyr Leu Gly
            20                  25                  30
Arg Glu Ile Phe Ile Lys Arg Asp Asp Val Thr Pro Met Ala Met Gly
```

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

<210> 206
<211> 957
<212> DNA
<213> Pseudoalteromonas atlantica T6c

<220>
<221> CDS
<222> (1)..(957)
<223> transl_table=11

<400> 206

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gtg aac gac acc tta aac tta acg cct att ctt cag gac att tcc ctc        48
Met Asn Asp Thr Leu Asn Leu Thr Pro Ile Leu Gln Asp Ile Ser Leu
1               5                   10                  15
ccc tcc cct gcg cag cag ata ttc ccg gat tgg gag cat gct gat gaa        96
Pro Ser Pro Ala Gln Gln Ile Phe Pro Asp Trp Glu His Ala Asp Glu
            20                  25                  30
gta caa tta tgg gta aaa cgc gac gat cta att cac ccc ata gta tca       144
Val Gln Leu Trp Val Lys Arg Asp Asp Leu Ile His Pro Ile Val Ser
        35                  40                  45
ggg aat aaa tgg cgt aaa tta cgt tac aca ctt gag cga gct gtt ggc       192
Gly Asn Lys Trp Arg Lys Leu Arg Tyr Thr Leu Glu Arg Ala Val Gly
    50                  55                  60
```

```
act ggg gtt cgg cac atc gtc agc ttc ggc ggt gcg cat tcg aat cat       240
Thr Gly Val Arg His Ile Val Ser Phe Gly Gly Ala His Ser Asn His
65                  70                  75                  80
cta cat gca ctg ggt tat gct tgc aat agc cta aat ata aag cta aca       288
Leu His Ala Leu Gly Tyr Ala Cys Asn Ser Leu Asn Ile Lys Leu Thr
                85                  90                  95
gcg ata gta cgt ggt cac ttt cat aat aat ccg aca cct atg cta caa       336
Ala Ile Val Arg Gly His Phe His Asn Asn Pro Thr Pro Met Leu Gln
            100                 105                 110
gat tta gtg gca tgg caa gct gac gtg caa ttt gct gat cgt aag aca       384
Asp Leu Val Ala Trp Gln Ala Asp Val Gln Phe Ala Asp Arg Lys Thr
        115                 120                 125
tat caa ctg cgc aat gac gaa act tac ttg gcc tca tta gct cag caa       432
Tyr Gln Leu Arg Asn Asp Glu Thr Tyr Leu Ala Ser Leu Ala Gln Gln
    130                 135                 140
tat cct aat gct atg ttt atc cca gaa ggc ggc tct tct gag ttc gct       480
Tyr Pro Asn Ala Met Phe Ile Pro Glu Gly Gly Ser Ser Glu Phe Ala
145                 150                 155                 160
ctc gct ggc gtg gcg gac att gtt cgt gag ctc act caa cgt tat gac       528
Leu Ala Gly Val Ala Asp Ile Val Arg Glu Leu Thr Gln Arg Tyr Asp
                165                 170                 175
tac ttg tta acg cct gtt ggc agc ggg ggg aca tta gcc ggg ctt att       576
Tyr Leu Leu Thr Pro Val Gly Ser Gly Gly Thr Leu Ala Gly Leu Ile
            180                 185                 190
cat ggt gcg atg agt caa cct gtg cca tta cac acc aaa atc atc gga       624
His Gly Ala Met Ser Gln Pro Val Pro Leu His Thr Lys Ile Ile Gly
        195                 200                 205
atc gct gtg ctt aga ggt gag ggg tat ctc gaa gag ttg gtg agt aac       672
Ile Ala Val Leu Arg Gly Glu Gly Tyr Leu Glu Glu Leu Val Ser Asn
    210                 215                 220
tta ctg tca tcc cgg gct atg ttg cca tcg caa gct aac aca cgt gaa       720
Leu Leu Ser Ser Arg Ala Met Leu Pro Ser Gln Ala Asn Thr Arg Glu
225                 230                 235                 240
cct atc gct gat tgg cac att aac cac cag ttt cat ttt aat ggc tac       768
Pro Ile Ala Asp Trp His Ile Asn His Gln Phe His Phe Asn Gly Tyr
                245                 250                 255
gcg aag gct aca cct gaa ctg cat caa ttt tgt cag tcg ttc aat gag       816
Ala Lys Ala Thr Pro Glu Leu His Gln Phe Cys Gln Ser Phe Asn Glu
            260                 265                 270
aca ctg agc att cct att gag cct gtg tat agc ggc aag ctt ttt tgg       864
Thr Leu Ser Ile Pro Ile Glu Pro Val Tyr Ser Gly Lys Leu Phe Trp
        275                 280                 285
gcg gta aaa gaa ctc atg gct aaa aag gcg ttt aca ccc ggc agc aaa       912
Ala Val Lys Glu Leu Met Ala Lys Lys Ala Phe Thr Pro Gly Ser Lys
    290                 295                 300
att ttg cta ttg cat aca ggt gga cta caa ggc gct aga ggc taa           957
Ile Leu Leu Leu His Thr Gly Gly Leu Gln Gly Ala Arg Gly
305                 310                 315
```

<210> 207
<211> 318
<212> PRT
<213> Pseudoalteromonas atlantica T6c

<400> 207

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Met Asn Asp Thr Leu Asn Leu Thr Pro Ile Leu Gln Asp Ile Ser Leu
1               5                   10                  15
Pro Ser Pro Ala Gln Gln Ile Phe Pro Asp Trp Glu His Ala Asp Glu
            20                  25                  30
Val Gln Leu Trp Val Lys Arg Asp Asp Leu Ile His Pro Ile Val Ser
        35                  40                  45
```

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

<210> 208
<211> 993
<212> DNA
<213> Pseudoalteromonas atlantica T6c

<220>
<221> CDS
<222> (1)..(993)
<223> transl_table=11

<400> 208

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atg ata aac ttt gca ctt att cca cgg gta aca atc tcc cac aat cca      48
Met Ile Asn Phe Ala Leu Ile Pro Arg Val Thr Ile Ser His Asn Pro
1               5                   10                  15
aca ccc ctt gag agt tta ccc agg tta tct gaa aaa gtg gga tgc aag      96
Thr Pro Leu Glu Ser Leu Pro Arg Leu Ser Glu Lys Val Gly Cys Lys
            20                  25                  30
gtg tat atc aaa cgc gat gat tgc acc gga ctt gct ggt ggc ggc aat     144
Val Tyr Ile Lys Arg Asp Asp Cys Thr Gly Leu Ala Gly Gly Gly Asn
        35                  40                  45
aaa acc cgc aaa cta gag tat tta atc gcc gat gct cag caa cac ggg     192
Lys Thr Arg Lys Leu Glu Tyr Leu Ile Ala Asp Ala Gln Gln His Gly
    50                  55                  60
gcc gac act ctg gtg acg gtg gga ggc ttg caa tca aat cat gcg cgg     240
Ala Asp Thr Leu Val Thr Val Gly Gly Leu Gln Ser Asn His Ala Arg
65                  70                  75                  80
```

```
caa act gct gcc gcg gcc gct aaa ttt ggc tta ggt tgc gag ctt gtg       288
Gln Thr Ala Ala Ala Ala Lys Phe Gly Leu Gly Cys Glu Leu Val
                85                  90                  95
ctc gaa gat gtt aag ggc acg cct aaa gcg gat tat tat caa aac gga       336
Leu Glu Asp Val Lys Gly Thr Pro Lys Ala Asp Tyr Tyr Gln Asn Gly
            100                 105                 110
aat gtg tta ttg gac act cta ctg ggc gcc aat atc cat cgt tta ggc       384
Asn Val Leu Leu Asp Thr Leu Leu Gly Ala Asn Ile His Arg Leu Gly
        115                 120                 125
cta gaa caa gag gtt gaa gcg tat acc agt gcg ctg ctt gca aag cta       432
Leu Glu Gln Glu Val Glu Ala Tyr Thr Ser Ala Leu Leu Ala Lys Leu
    130                 135                 140
aaa att cag ggg cga aag ccg tat ttt att ccc atg ggc ggg tcg aat       480
Lys Ile Gln Gly Arg Lys Pro Tyr Phe Ile Pro Met Gly Gly Ser Asn
145                 150                 155                 160
gtg atg ggc agt tta ggc tat gtg cgc tgc gcc aaa gaa ata tta caa       528
Val Met Gly Ser Leu Gly Tyr Val Arg Cys Ala Lys Glu Ile Leu Gln
                165                 170                 175
caa ttg gca gat gat gat ctt cac atc gac caa att gtg ctc gcg acg       576
Gln Leu Ala Asp Asp Asp Leu His Ile Asp Gln Ile Val Leu Ala Thr

            180                 185                 190
ggc agt gca ggt acc caa gca ggc ttg ctt gca ggg ctg att gct gct       624
Gly Ser Ala Gly Thr Gln Ala Gly Leu Leu Ala Gly Leu Ile Ala Ala
        195                 200                 205
aac tca gac atc tcg gta ctg ggg gta gcg gtg agt cgc tcg aag gaa       672
Asn Ser Asp Ile Ser Val Leu Gly Val Ala Val Ser Arg Ser Lys Glu
    210                 215                 220
gcg caa gaa cag tta gtg gaa cag tta ctc aga gaa acg ctc act ttt       720
Ala Gln Glu Gln Leu Val Glu Gln Leu Leu Arg Glu Thr Leu Thr Phe
225                 230                 235                 240
tta gac att gat ccc aat cgg gcg aaa ggc aaa gtg gtt gcc aat ggc       768
Leu Asp Ile Asp Pro Asn Arg Ala Lys Gly Lys Val Val Ala Asn Gly
                245                 250                 255
aac tat ttt ggc gaa ggt tac ggt atg act acg cca tca atg gta acg       816
Asn Tyr Phe Gly Glu Gly Tyr Gly Met Thr Thr Pro Ser Met Val Thr
            260                 265                 270
gcc gtc aag cgc tgc gcc gaa cta gaa ggc gtg tta tta gat ccc gtc       864
Ala Val Lys Arg Cys Ala Glu Leu Glu Gly Val Leu Leu Asp Pro Val
        275                 280                 285
tat acg ggc aag gca atg gct ggc ttt atg gac ttg tgc gcc aca ggt       912
Tyr Thr Gly Lys Ala Met Ala Gly Phe Met Asp Leu Cys Ala Thr Gly
    290                 295                 300
gag att ggg gca aat agt cac cag cta ttt att cat act ggg ggc agt       960
Glu Ile Gly Ala Asn Ser His Gln Leu Phe Ile His Thr Gly Gly Ser
305                 310                 315                 320
cag ggg ctg ttt gct tac cgt gag gaa ttt taa                           993
Gln Gly Leu Phe Ala Tyr Arg Glu Glu Phe
                325                 330
```

<210> 209
<211> 330
<212> PRT
<213> Pseudoalteromonas atlantica T6c

<400> 209

```
Met Ile Asn Phe Ala Leu Ile Pro Arg Val Thr Ile Ser His Asn Pro
1               5                   10                  15
Thr Pro Leu Glu Ser Leu Pro Arg Leu Ser Glu Lys Val Gly Cys Lys
            20                  25                  30
Val Tyr Ile Lys Arg Asp Asp Cys Thr Gly Leu Ala Gly Gly Gly Asn
```

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

<210> 210
<211> 999
<212> DNA
<213> Pseudoalteromonas atlantica T6c

<220>
<221> CDS
<222> (1)..(999)
<223> transl_table=11

<400> 210

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atg ccc tta agc gcc ctt aaa aaa ata gaa ttg ggc gtt ttc cct acg      48
Met Pro Leu Ser Ala Leu Lys Lys Ile Glu Leu Gly Val Phe Pro Thr
1               5                   10                  15
ccc att cat aaa tta gcc cgt tta tca gct cat ctt gtt ggc ccg cag      96
Pro Ile His Lys Leu Ala Arg Leu Ser Ala His Leu Val Gly Pro Gln
            20                  25                  30
att tat atc aag cga gat gac ctt acc ggt tta gcg ctt ggg ggc aac     144
Ile Tyr Ile Lys Arg Asp Asp Leu Thr Gly Leu Ala Leu Gly Gly Asn
        35                  40                  45
aaa acc cgt aaa ctc gaa tac tta tta gct gat ggg cta gcc caa ggc     192
Lys Thr Arg Lys Leu Glu Tyr Leu Leu Ala Asp Gly Leu Ala Gln Gly
    50                  55                  60
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tgt gat tgt atc gtt act gca ggt gcg gct cag tca aat cat tgc agg        240
Cys Asp Cys Ile Val Thr Ala Gly Ala Ala Gln Ser Asn His Cys Arg
65                  70                  75                  80
cag act gcc gca gca gcc gct acc ttg ggg gta gaa tgc cat ttg atc        288
Gln Thr Ala Ala Ala Ala Ala Thr Leu Gly Val Glu Cys His Leu Ile
                85                  90                  95
ttg ggc ggg cag gcc cca att agc gcg aac gga aac cta ctt ctt gac        336
Leu Gly Gly Gln Ala Pro Ile Ser Ala Asn Gly Asn Leu Leu Leu Asp
            100                 105                 110
cag cta ttt gga gca cgt att cat tgg gct ggt cag aag cgc aaa ggt        384
Gln Leu Phe Gly Ala Arg Ile His Trp Ala Gly Gln Lys Arg Lys Gly
        115                 120                 125
gaa gat att cct gat att gtc agc acg ttg caa aag caa gga aag aga        432
Glu Asp Ile Pro Asp Ile Val Ser Thr Leu Gln Lys Gln Gly Lys Arg
    130                 135                 140
cct tat gtt gta ccg tat ggg ggc tct aat acc ata ggt tca gcc ggg        480
Pro Tyr Val Val Pro Tyr Gly Gly Ser Asn Thr Ile Gly Ser Ala Gly
145                 150                 155                 160
ttt atc gac gcc ttc aaa gag cta caa cag cag tgt cac gct agt agt        528
Phe Ile Asp Ala Phe Lys Glu Leu Gln Gln Gln Cys His Ala Ser Ser
                165                 170                 175
caa gta att gaa ttt tca gat att gtc ttc gcg tct agc tcg gga gca        576
Gln Val Ile Glu Phe Ser Asp Ile Val Phe Ala Ser Ser Ser Gly Ala
            180                 185                 190
acc cat tgc gga tta gtg ctt gga aaa gcg ctg tgt gat gcc gcc agt        624
Thr His Cys Gly Leu Val Leu Gly Lys Ala Leu Cys Asp Ala Ala Ser
        195                 200                 205
aat att att gga atc aat att gat aaa gat gag caa ggc aaa gat agc        672
Asn Ile Ile Gly Ile Asn Ile Asp Lys Asp Glu Gln Gly Lys Asp Ser
    210                 215                 220
ttt aaa tct cag ctg caa acg ctg atc gag gat acc gct cga aca ttc        720
Phe Lys Ser Gln Leu Gln Thr Leu Ile Glu Asp Thr Ala Arg Thr Phe
225                 230                 235                 240
tcg att aac tac gat ggt aca gtg gat gat gta cag tta atc gat gat        768
Ser Ile Asn Tyr Asp Gly Thr Val Asp Asp Val Gln Leu Ile Asp Asp
                245                 250                 255
tat atc ggc caa gga tat ggc gtg gtg ggc aat tta gag cgt gaa gcg        816
Tyr Ile Gly Gln Gly Tyr Gly Val Val Gly Asn Leu Glu Arg Glu Ala
            260                 265                 270
ata tct ttg tgc gcc caa ctt gaa ggg ata ttg tta gac cct gta tac        864
Ile Ser Leu Cys Ala Gln Leu Glu Gly Ile Leu Leu Asp Pro Val Tyr
        275                 280                 285
act gga cgg gcg atg ggc ggt tta att gac atg atc cgt caa ggt cgt        912
Thr Gly Arg Ala Met Gly Gly Leu Ile Asp Met Ile Arg Gln Gly Arg
    290                 295                 300
ttt gct tca aac agt aat gtg ctt ttt tgg cac act ggt ggg gcg cct        960
Phe Ala Ser Asn Ser Asn Val Leu Phe Trp His Thr Gly Gly Ala Pro
305                 310                 315                 320
gct atc ttt gca tat gcc gat gca tta caa cca agt tga                    999
Ala Ile Phe Ala Tyr Ala Asp Ala Leu Gln Pro Ser
                325                 330
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<210> 211
<211> 332
<212> PRT
<213> Pseudoalteromonas atlantica T6c

<400> 211
Met Pro Leu Ser Ala Leu Lys Lys Ile Glu Leu Gly Val Phe Pro Thr
1   5   10   15
Pro Ile His Lys Leu Ala Arg Leu Ser Ala His Leu Val Gly Pro Gln

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

Tyr Ile Gly Gln Gly Tyr Gly Val Val Gly Asn Leu Glu Arg Glu Ala
            260                 265                 270
Ile Ser Leu Cys Ala Gln Leu Glu Gly Ile Leu Leu Asp Pro Val Tyr
        275                 280                 285
Thr Gly Arg Ala Met Gly Gly Leu Ile Asp Met Ile Arg Gln Gly Arg
    290                 295                 300
Phe Ala Ser Asn Ser Asn Val Leu Phe Trp His Thr Gly Gly Ala Pro
305                 310                 315                 320
Ala Ile Phe Ala Tyr Ala Asp Ala Leu Gln Pro Ser
                325                 330
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<210> 212
<211> 1020
<212> DNA
<213> Yersinia pseudotuberculosis IP 31758

<220>
<221> CDS
<222> (1)..(1020)

<400> 212

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atg att cat caa ttc ctt ggg ggg cac gtg acg ctt caa cac aaa ctg       48
Met Ile His Gln Phe Leu Gly Gly His Val Thr Leu Gln His Lys Leu
1               5                   10                  15
acg caa ttc ccg cgt ctc gat ctg gtc ggt aat gcg acg cca tta gaa       96
Thr Gln Phe Pro Arg Leu Asp Leu Val Gly Asn Ala Thr Pro Leu Glu
            20                  25                  30
aag ctg tct cgt cta tct gat tat ctg gga cgt gaa att tac att aaa      144
Lys Leu Ser Arg Leu Ser Asp Tyr Leu Gly Arg Glu Ile Tyr Ile Lys
        35                  40                  45
cgt gat gat gtc acg cct gtg gcg ctt ggc ggg aat aaa ctg cgc aag      192
```

```
Arg Asp Asp Val Thr Pro Val Ala Leu Gly Gly Asn Lys Leu Arg Lys
    50                  55                  60
cta gaa ttc tta gcc gca gat gcc ttg aga cag gga gcc gat acg ctg      240
Leu Glu Phe Leu Ala Ala Asp Ala Leu Arg Gln Gly Ala Asp Thr Leu
65                  70                  75                  80
gtt acg gct ggt gct att caa tct aat cat gtc cgc caa acc gcc gcc      288
Val Thr Ala Gly Ala Ile Gln Ser Asn His Val Arg Gln Thr Ala Ala
                85                  90                  95
gtg gcc gcg aaa ctg ggg ctg cat tgc gtt gcg ctg ttg gaa aac ccc      336
Val Ala Ala Lys Leu Gly Leu His Cys Val Ala Leu Leu Glu Asn Pro
            100                 105                 110
att ggt act gag cag gca aac tat ctg acc aat ggg aac cgg ctg tta      384
Ile Gly Thr Glu Gln Ala Asn Tyr Leu Thr Asn Gly Asn Arg Leu Leu
        115                 120                 125
ctg gac cta ttc aat gtt gat gtt gtg atg tgt gag gca ttg aac gat      432
Leu Asp Leu Phe Asn Val Asp Val Val Met Cys Glu Ala Leu Asn Asp
    130                 135                 140
cca aat cag caa tta gca gaa ttg gct acc cgc gtg gaa gcg cag ggt      480
Pro Asn Gln Gln Leu Ala Glu Leu Ala Thr Arg Val Glu Ala Gln Gly
145                 150                 155                 160
ttc cgc cca tat gtg gta ccg att ggc ggt tct aat gcc ttg ggc gcg      528
Phe Arg Pro Tyr Val Val Pro Ile Gly Gly Ser Asn Ala Leu Gly Ala
                165                 170                 175
ctg ggt tat gtg cag tgc tca ctg gaa att gct gct caa gcc gcg ggc      576
Leu Gly Tyr Val Gln Cys Ser Leu Glu Ile Ala Ala Gln Ala Ala Gly
            180                 185                 190
aat gtt gcg ttt agt tcg gtc gtc gtg gcc tct ggc agt gcg gga aca      624
Asn Val Ala Phe Ser Ser Val Val Val Ala Ser Gly Ser Ala Gly Thr
        195                 200                 205
cat gca gga ttg gcg gtt ggt cta cag cag ttg tta ccc gat gcg gaa      672
His Ala Gly Leu Ala Val Gly Leu Gln Gln Leu Leu Pro Asp Ala Glu
    210                 215                 220
tta atc ggt gtg acg gta tca cgt agt gcc gat gaa cag cgg cct aaa      720
Leu Ile Gly Val Thr Val Ser Arg Ser Ala Asp Glu Gln Arg Pro Lys
225                 230                 235                 240
gtg gca cag att caa caa gcg ttg gcg aca tca tta ggg atg acg gac      768
Val Ala Gln Ile Gln Gln Ala Leu Ala Thr Ser Leu Gly Met Thr Asp
                245                 250                 255
cca ttg gca aaa atc acc ttg tgg gat agt tat ttt gcc ccg caa tat      816
Pro Leu Ala Lys Ile Thr Leu Trp Asp Ser Tyr Phe Ala Pro Gln Tyr
            260                 265                 270
ggg atg cca aac gaa gag ggg ata gcg gct att aag ctc ttg gca aga      864
Gly Met Pro Asn Glu Glu Gly Ile Ala Ala Ile Lys Leu Leu Ala Arg
        275                 280                 285
ctg gaa gga ata ttg ttg gac cct gtg tat acc ggt aag gcg atg gcg      912
Leu Glu Gly Ile Leu Leu Asp Pro Val Tyr Thr Gly Lys Ala Met Ala
    290                 295                 300
ggc tta ctt gat ggt att gaa cag caa aaa ttc tgc gac aaa ggg cca      960
Gly Leu Leu Asp Gly Ile Glu Gln Gln Lys Phe Cys Asp Lys Gly Pro
305                 310                 315                 320
att tta ttt atc cac act ggc ggg gca cct gcg ctg ttt gct tat cat     1008
Ile Leu Phe Ile His Thr Gly Gly Ala Pro Ala Leu Phe Ala Tyr His
                325                 330                 335
ccg cag gtg tag                                                    1020
Pro Gln Val
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<210> 213
<211> 339
<212> PRT
<213> Yersinia pseudotuberculosis IP 31758

<400> 213
Met Ile His Gln Phe Leu Gly Gly His Val Thr Leu Gln His Lys Leu
1 5 10 15
Thr Gln Phe Pro Arg Leu Asp Leu Val Gly Asn Ala Thr Pro Leu Glu
20 25 30
Lys Leu Ser Arg Leu Ser Asp Tyr Leu Gly Arg Glu Ile Tyr Ile Lys
35 40 45
Arg Asp Asp Val Thr Pro Val Ala Leu Gly Gly Asn Lys Leu Arg Lys
50 55 60
Leu Glu Phe Leu Ala Ala Asp Ala Leu Arg Gln Gly Ala Asp Thr Leu
65 70 75 80

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

<210> 214
<211> 984
<212> DNA
<213> Alkaliphilus metalliredigenes QYMF

<220>
<221> CDS
<222> (1)..(984)
<223> transl_table=11

<400> 214
atg aca ata cca aag tca ctt aaa ttg gca aac cta cct act aaa att 48
Met Thr Ile Pro Lys Ser Leu Lys Leu Ala Asn Leu Pro Thr Lys Ile

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1               5                   10                  15
gaa aag ctg gag aga ttg tct aaa agt ctg gga gac atc aat att tat      96
Glu Lys Leu Glu Arg Leu Ser Lys Ser Leu Gly Asp Ile Asn Ile Tyr
            20                  25                  30
atc aaa aga gat gat caa act ggg aca gaa gta tca gga aac aag gtg     144
Ile Lys Arg Asp Asp Gln Thr Gly Thr Glu Val Ser Gly Asn Lys Val
        35                  40                  45
aga aag ctg gaa ttt gca gta caa gag gcc ttg gac caa ggc tgt gat     192
Arg Lys Leu Glu Phe Ala Val Gln Glu Ala Leu Asp Gln Gly Cys Asp
    50                  55                  60
tat tta att aca tgt ggt ggg att caa tca aat cat gct aga gcc acg     240
Tyr Leu Ile Thr Cys Gly Gly Ile Gln Ser Asn His Ala Arg Ala Thr
65                  70                  75                  80
gcg gcg gtt gca gct aag ctg gac att aac tca tac cta gtg ttg aga     288
Ala Ala Val Ala Ala Lys Leu Asp Ile Asn Ser Tyr Leu Val Leu Arg
                85                  90                  95
agc aat ggg gac gat ccc gtt gaa ggg aat tat ttt cta aat aag att     336
Ser Asn Gly Asp Asp Pro Val Glu Gly Asn Tyr Phe Leu Asn Lys Ile
            100                 105                 110
ctt ggg gcg gaa att tgt ctc att acc cct gaa gag tat agg gat aat     384
Leu Gly Ala Glu Ile Cys Leu Ile Thr Pro Glu Glu Tyr Arg Asp Asn
        115                 120                 125
cgg atg aag gtg atg gaa gag ata caa aga gag cta gct ggt caa gga     432
Arg Met Lys Val Met Glu Glu Ile Gln Arg Glu Leu Ala Gly Gln Gly
    130                 135                 140
cat aag gct tat att tta ccc gaa gga gca tct aat ggg atc ggt aca     480
His Lys Ala Tyr Ile Leu Pro Glu Gly Ala Ser Asn Gly Ile Gly Thr
145                 150                 155                 160
ttt gga tac tat caa gcc atg gaa gaa att tta gag caa gaa gcg gag     528
Phe Gly Tyr Tyr Gln Ala Met Glu Glu Ile Leu Glu Gln Glu Ala Glu
                165                 170                 175
ttg gat gtc aag ttc gat gcc atc gtc aca gca gta gga tct ggg gga     576
Leu Asp Val Lys Phe Asp Ala Ile Val Thr Ala Val Gly Ser Gly Gly
            180                 185                 190
acc tac gca ggg tta ttt tac gct aat aaa ctc aga aag aat gag gcg     624
Thr Tyr Ala Gly Leu Phe Tyr Ala Asn Lys Leu Arg Lys Asn Glu Ala
        195                 200                 205
aaa att tat ggg atc aat gta tgt gat gat gca gat cat ttt aaa aat     672
Lys Ile Tyr Gly Ile Asn Val Cys Asp Asp Ala Asp His Phe Lys Asn
    210                 215                 220
aga gta caa gaa tta gtc cat gaa agc ata cag tat acc aaa aga ccc     720
Arg Val Gln Glu Leu Val His Glu Ser Ile Gln Tyr Thr Lys Arg Pro
225                 230                 235                 240
att cat ttc aaa aaa gaa gac att cat atg att gat ggg tat gta ggc     768
Ile His Phe Lys Lys Glu Asp Ile His Met Ile Asp Gly Tyr Val Gly
                245                 250                 255
gaa gga tat gct caa agt aga caa gaa gaa ctg aca ttt atc ctt gat     816
Glu Gly Tyr Ala Gln Ser Arg Gln Glu Glu Leu Thr Phe Ile Leu Asp
            260                 265                 270
ttt gca aag cta gag ggt att att ctg gat cct gtt tat aca ggt aag     864
Phe Ala Lys Leu Glu Gly Ile Ile Leu Asp Pro Val Tyr Thr Gly Lys
        275                 280                 285
gca atg tat ggt tta gtg gaa gaa att aaa aag gga agt ttt aat gga     912
Ala Met Tyr Gly Leu Val Glu Glu Ile Lys Lys Gly Ser Phe Asn Gly
    290                 295                 300
ttc aaa aac att ctc ttt atc cat acc ggt ggc ctt tac ggg ctg ttc     960
Phe Lys Asn Ile Leu Phe Ile His Thr Gly Gly Leu Tyr Gly Leu Phe
305                 310                 315                 320
ccc aag ggg aat cag ttg ttt taa                                    984
Pro Lys Gly Asn Gln Leu Phe
                325
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<210> 215
<211> 327
<212> PRT
<213> Alkaliphilus metalliredigenes QYMF

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

<210> 216
<211> 1053
<212> DNA
<213> Rhodopseudomonas palustris BisA53

<220>
<221> CDS
<222> (1)..(1053)
<223> transl_table=11

<400> 216

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atg gaa tcg atc gca cgg aat acg gta gtg cga gtg gag gag acg ttg       48
Met Glu Ser Ile Ala Arg Asn Thr Val Val Arg Val Glu Glu Thr Leu
1               5                   10                  15
gaa cca cag ttg cta tcg gct ttc ccc cgg gtg tcc atc gcc cat act       96
Glu Pro Gln Leu Leu Ser Ala Phe Pro Arg Val Ser Ile Ala His Thr
            20                  25                  30
ccg acg cca ttc gag ttc ttg gaa cga ctt tcc gcc cga ctc ggc gga      144
Pro Thr Pro Phe Glu Phe Leu Glu Arg Leu Ser Ala Arg Leu Gly Gly
        35                  40                  45
cca gcg atc tgg gtg aag cgc gat gac tgc acc ggg ctt gcc ggc ggt      192
Pro Ala Ile Trp Val Lys Arg Asp Asp Cys Thr Gly Leu Ala Gly Gly
    50                  55                  60
gga aac aag gtt cgt aag ctc gaa ttt ctg atc ggc gcc gca ctc gag      240
Gly Asn Lys Val Arg Lys Leu Glu Phe Leu Ile Gly Ala Ala Leu Glu
65                  70                  75                  80
tcc ggg gcc gat acc gtg att acc gcg ggc gct att cag tcc aat cac      288
Ser Gly Ala Asp Thr Val Ile Thr Ala Gly Ala Ile Gln Ser Asn His
                85                  90                  95
gcg cgc cag acg gcc gcg gcg gcc gcg cgc ctg aat ttg cgg tcc atc      336
Ala Arg Gln Thr Ala Ala Ala Ala Ala Arg Leu Asn Leu Arg Ser Ile
            100                 105                 110
ctg gtg ctc act gac acg gtc gga tgt cgc ggc ccc gcg tat cgc aat      384
Leu Val Leu Thr Asp Thr Val Gly Cys Arg Gly Pro Ala Tyr Arg Asn
        115                 120                 125
aac ggc aat ctg ctg atc gac agg ctt ctg ggc gcc gac atc cat ctg      432
Asn Gly Asn Leu Leu Ile Asp Arg Leu Leu Gly Ala Asp Ile His Leu
    130                 135                 140
gtc ggc ggc gat gtc gac act gag tct gtt ttg gaa agc atc gcc gat      480
Val Gly Gly Asp Val Asp Thr Glu Ser Val Leu Glu Ser Ile Ala Asp
145                 150                 155                 160
cga gaa cgc gaa agg ggc agg agc ccc ttc gtt att ccc gtc ggt ggc      528
Arg Glu Arg Glu Arg Gly Arg Ser Pro Phe Val Ile Pro Val Gly Gly
                165                 170                 175
tcg aat gca ccg gga gtg ctc ggt tat gtc gcc ggc ttc ttc gaa ctg      576
Ser Asn Ala Pro Gly Val Leu Gly Tyr Val Ala Gly Phe Phe Glu Leu
            180                 185                 190
cac gcg caa atc cag gaa caa gcc act gtt ttc gat gcc att gtg ctg      624
His Ala Gln Ile Gln Glu Gln Ala Thr Val Phe Asp Ala Ile Val Leu
        195                 200                 205
cca acc ggc agt gga ggc acc cag gcc gga ctg atc ctc ggt gct gcc      672
Pro Thr Gly Ser Gly Gly Thr Gln Ala Gly Leu Ile Leu Gly Ala Ala
    210                 215                 220
ttc tcc gga tgg tgc ggc gct atc atc gga atc agc gtc gga gcc tca      720
Phe Ser Gly Trp Cys Gly Ala Ile Ile Gly Ile Ser Val Gly Ala Ser
225                 230                 235                 240
gcc gaa cgc cag agg atg aaa atc gcg aag tcg ctg cga tcc gcc gcc      768
Ala Glu Arg Gln Arg Met Lys Ile Ala Lys Ser Leu Arg Ser Ala Ala
                245                 250                 255
gct ctg ctc gat att gaa gac tcc gac agc aac cgg gcg gac atc ctg      816
Ala Leu Leu Asp Ile Glu Asp Ser Asp Ser Asn Arg Ala Asp Ile Leu
            260                 265                 270
gtc gac gat cgc ttt gtc ggt ccc ggc tac ggc gaa cct gcc ccc gag      864
Val Asp Asp Arg Phe Val Gly Pro Gly Tyr Gly Glu Pro Ala Pro Glu
        275                 280                 285
acc ata gac gcg atc cgc atc gcg gcg gaa acc gag ggg ctt ttg ctg      912
Thr Ile Asp Ala Ile Arg Ile Ala Ala Glu Thr Glu Gly Leu Leu Leu
    290                 295                 300
gac cct gtc tac agc ggc aaa gcg atg gct ggg ctc ata gcg ctg ata      960
Asp Pro Val Tyr Ser Gly Lys Ala Met Ala Gly Leu Ile Ala Leu Ile
305                 310                 315                 320
```

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cgc gcg ggt cgg ttt cgg cgc gat cag aac gcg gtg ttt ctt cac acc       1008
Arg Ala Gly Arg Phe Arg Arg Asp Gln Asn Ala Val Phe Leu His Thr
                325                 330                 335
ggc ggt gcc cag gca ctc agc gcg tat cca gaa cac ttc ata taa           1053
Gly Gly Ala Gln Ala Leu Ser Ala Tyr Pro Glu His Phe Ile
            340                 345                 350
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<210> 217
<211> 350
<212> PRT
<213> Rhodopseudomonas palustris BisA53

<400> 217

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

<210> 218
<211> 1020
<212> DNA

<213> Bradyrhizobium sp. BTAi1

<220>
<221> CDS
<222> (1)..(1020)
<223> transl_table=11

<400> 218

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

```
Ser Ala Glu Thr Asn Glu Ala Ile Arg Leu Ala Ala Arg Thr Glu Ala
        275                 280                 285
atg atc acc gac ccg gtc tat gag ggc aag tcg atg cag ggc atg atc      912
Met Ile Thr Asp Pro Val Tyr Glu Gly Lys Ser Met Gln Gly Met Ile
    290                 295                 300
gac ctg gtc aag aag ggc tac ttc ccg gag ggc tcg aag gtg ctc tac      960
Asp Leu Val Lys Lys Gly Tyr Phe Pro Glu Gly Ser Lys Val Leu Tyr
305                 310                 315                 320
gcc cat ctc ggc ggc gcc ccc gcg atc aac ggc tac agc tac acg tac     1008
Ala His Leu Gly Gly Ala Pro Ala Ile Asn Gly Tyr Ser Tyr Thr Tyr

                325                 330                 335
cgc aac ggc tga                                                     1020
Arg Asn Gly
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<210> 219
<211> 339
<212> PRT
<213> Bradyrhizobium sp. BTAi1

<400> 219

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

```
305                 310                 315                 320
Ala His Leu Gly Gly Ala Pro Ala Ile Asn Gly Tyr Ser Tyr Thr Tyr
                325                 330                 335
Arg Asn Gly
```

<210> 220
<211> 987
<212> DNA
<213> Escherichia coli 101-1

<220>
<221> CDS
<222> (1)..(987)

<400> 220

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

```
gaa ctg gag ctg acc gca tca gcg gaa att tta ctc tgg gat gac tat       768
Glu Leu Glu Leu Thr Ala Ser Ala Glu Ile Leu Leu Trp Asp Asp Tyr
                245                 250                 255
ttt gca cct ggc tac ggc gtg ccg aac gac gaa ggc atg gaa gca gtg       816
Phe Ala Pro Gly Tyr Gly Val Pro Asn Asp Glu Gly Met Glu Ala Val
            260                 265                 270
aaa ttg ctg gcg cgg ctg gaa ggc att ctg ctt gat cct gtg tat acc       864
Lys Leu Leu Ala Arg Leu Glu Gly Ile Leu Leu Asp Pro Val Tyr Thr
        275                 280                 285
gga aaa gcg atg gcg ggg ctg att ggc ggt atc agt cag aaa cgc ttc       912
Gly Lys Ala Met Ala Gly Leu Ile Gly Gly Ile Ser Gln Lys Arg Phe
    290                 295                 300
aaa gat gaa ggg ccg att ctg ttt att cat acc ggc ggt gcg cct gcg       960
Lys Asp Glu Gly Pro Ile Leu Phe Ile His Thr Gly Gly Ala Pro Ala
305                 310                 315                 320
ctg ttc gcc tat cat ccc cac gtt tag                                  987
Leu Phe Ala Tyr His Pro His Val
                325
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<210> 221
<211> 328
<212> PRT
<213> Escherichia coli 101-1

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<400> 221
Met Pro Leu His Asn Leu Thr Arg Phe Pro Arg Leu Glu Phe Ile Gly
1               5                   10                  15
Ala Pro Thr Pro Leu Glu Tyr Leu Pro Arg Phe Ser Asp Tyr Leu Gly
            20                  25                  30
Arg Glu Ile Phe Ile Lys Arg Asp Asp Val Thr Pro Met Ala Met Gly
        35                  40                  45
Gly Asn Lys Leu Arg Lys Leu Glu Phe Leu Ala Ala Asp Ala Leu Arg
    50                  55                  60
Glu Gly Ala Asp Thr Leu Ile Thr Ala Gly Ala Ile Gln Ser Asn His
65                  70                  75                  80
Val Arg Gln Thr Ala Ala Val Ala Ala Lys Leu Gly Leu His Cys Val
                85                  90                  95
Ala Leu Leu Glu Asn Pro Ile Gly Thr Thr Ala Glu Asn Tyr Leu Thr
            100                 105                 110
Asn Gly Asn Arg Leu Leu Leu Asp Leu Phe Asn Thr Gln Ile Glu Met
        115                 120                 125
Cys Asp Ala Leu Thr Asp Pro Asn Ala Gln Leu Glu Glu Leu Ala Thr
    130                 135                 140
Arg Val Glu Ala Gln Gly Phe Arg Pro Tyr Val Ile Pro Val Gly Gly
145                 150                 155                 160
Ser Asn Ala Leu Gly Ala Leu Gly Tyr Val Glu Ser Ala Leu Glu Ile
                165                 170                 175
Ala Gln Gln Cys Glu Gly Ala Val Asn Ile Ser Ser Val Val Val Ala

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

```
       275                 280                 285
Gly Lys Ala Met Ala Gly Leu Ile Gly Gly Ile Ser Gln Lys Arg Phe
    290                 295                 300
Lys Asp Glu Gly Pro Ile Leu Phe Ile His Thr Gly Gly Ala Pro Ala
305                 310                 315                 320
Leu Phe Ala Tyr His Pro His Val
                325
```

<210> 222
<211> 1017
<212> DNA
<213> Ralstonia solanacearum UW551

<220>
<221> CDS
<222> (1)..(1017)
<223> transl_table=11

<400> 222

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

```
tcg gcc aag ccc ggg aag aca cgc gag cag atc ctg cgg atc gcc cgc        720
Ser Ala Lys Pro Gly Lys Thr Arg Glu Gln Ile Leu Arg Ile Ala Arg
225                 230                 235                 240
gac acc gcc agg ctg gtc gaa ctc ggc cgc gac atc gcg gaa gcc gac        768
Asp Thr Ala Arg Leu Val Glu Leu Gly Arg Asp Ile Ala Glu Ala Asp
                245                 250                 255
gtg gta ctc gat acg cgc tat ggc ggt ccc gaa tac ggc ctg ccg aac        816
Val Val Leu Asp Thr Arg Tyr Gly Gly Pro Glu Tyr Gly Leu Pro Asn
            260                 265                 270
gaa ggc acg ctg gag gcg atc cgg ctg tgc gcg cgc cag gaa ggc atg        864
Glu Gly Thr Leu Glu Ala Ile Arg Leu Cys Ala Arg Gln Glu Gly Met
        275                 280                 285
ctg acc gac ccg gtg tac gag ggc aag tcg atg cac ggc atg atc gac        912
Leu Thr Asp Pro Val Tyr Glu Gly Lys Ser Met His Gly Met Ile Asp
    290                 295                 300
cgg gtg cgc aac ggc gag ttt ccc gag ggc tcg cgc gtg ctg tat gcc        960
Arg Val Arg Asn Gly Glu Phe Pro Glu Gly Ser Arg Val Leu Tyr Ala
305                 310                 315                 320
cac ctg ggc ggc gtg ccg gcg ctc aat gcc tac agc ttt ctc ttc cgc       1008
His Leu Gly Gly Val Pro Ala Leu Asn Ala Tyr Ser Phe Leu Phe Arg
                325                 330                 335
aat ggc tga                                                          1017
Asn Gly
```

<210> 223
<211> 338
<212> PRT
<213> Ralstonia solanacearum UW551

<400> 223

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

```
Asp Thr Ala Arg Leu Val Glu Leu Gly Arg Asp Ile Ala Glu Ala Asp
                245                 250                 255
Val Val Leu Asp Thr Arg Tyr Gly Gly Pro Glu Tyr Gly Leu Pro Asn
            260                 265                 270
Glu Gly Thr Leu Glu Ala Ile Arg Leu Cys Ala Arg Gln Glu Gly Met
        275                 280                 285
Leu Thr Asp Pro Val Tyr Glu Gly Lys Ser Met His Gly Met Ile Asp
    290                 295                 300
Arg Val Arg Asn Gly Glu Phe Pro Glu Gly Ser Arg Val Leu Tyr Ala
305                 310                 315                 320
His Leu Gly Gly Val Pro Ala Leu Asn Ala Tyr Ser Phe Leu Phe Arg
                325                 330                 335
Asn Gly
```

<210> 224
<211> 1011
<212> DNA
<213> Roseovarius nubinhibens ISM

<220>
<221> CDS
<222> (1)..(1011)
<223> transl_table=11

<400> 224

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

```
            180                 185                 190
tat gtc gtg gcc tct ggc agc ggg gcg acc cat acc ggg ctc ttg gcc       624
Tyr Val Val Ala Ser Gly Ser Gly Ala Thr His Thr Gly Leu Leu Ala
        195                 200                 205
ggg ctg cgg ctg tgc ggg gca agc gct ccg gtg cat ggc atc tgt gtg       672
Gly Leu Arg Leu Cys Gly Ala Ser Ala Pro Val His Gly Ile Cys Val
    210                 215                 220
cgc cgt gac gcc gag gcc cag cgc gcc cgg atc ggg cgt ctc gcg gag       720
Arg Arg Asp Ala Glu Ala Gln Arg Ala Arg Ile Gly Arg Leu Ala Glu
225                 230                 235                 240
ctc ttg gca gag ctt ctg ggc gag gcg gtg ttc ggg gcg gcg gat atc       768
Leu Leu Ala Glu Leu Leu Gly Glu Ala Val Phe Gly Ala Ala Asp Ile
                245                 250                 255
gac atc tgg gat ggg gcg ctc gcc ccc ggc tat ggc cgg atg ggc gag       816
Asp Ile Trp Asp Gly Ala Leu Ala Pro Gly Tyr Gly Arg Met Gly Glu
            260                 265                 270
acc acg cgc cgg gcg ctc gat cag atg gca cgc tat gag ggg ctc ttc       864
Thr Thr Arg Arg Ala Leu Asp Gln Met Ala Arg Tyr Glu Gly Leu Phe
        275                 280                 285
ctc gat ccg gtc tat acc gcc aag agc ttt gcc ggg gtc gag ggg ctc       912
Leu Asp Pro Val Tyr Thr Ala Lys Ser Phe Ala Gly Val Glu Gly Leu
    290                 295                 300
ctg cag gag ggg gtg atc cag ccg ggc gca cgg gtc tgt ttc atc cat       960
Leu Gln Glu Gly Val Ile Gln Pro Gly Ala Arg Val Cys Phe Ile His
305                 310                 315                 320
agc ggc ggt ttg ccc gcg ctc ttt gcc tat ggc gag gat ctg ctc gca      1008
Ser Gly Gly Leu Pro Ala Leu Phe Ala Tyr Gly Glu Asp Leu Leu Ala
                325                 330                 335
tga                                                                  1011
```

<210> 225
<211> 336
<212> PRT
<213> Roseovarius nubinhibens ISM

<400> 225

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

```
            180                 185                 190
Tyr Val Val Ala Ser Gly Ser Gly Ala Thr His Thr Gly Leu Leu Ala
        195                 200                 205
Gly Leu Arg Leu Cys Gly Ala Ser Ala Pro Val His Gly Ile Cys Val
    210                 215                 220
Arg Arg Asp Ala Glu Ala Gln Arg Ala Arg Ile Gly Arg Leu Ala Glu
225                 230                 235                 240
Leu Leu Ala Glu Leu Leu Gly Glu Ala Val Phe Gly Ala Ala Asp Ile
                245                 250                 255
Asp Ile Trp Asp Gly Ala Leu Ala Pro Gly Tyr Gly Arg Met Gly Glu
            260                 265                 270
Thr Thr Arg Arg Ala Leu Asp Gln Met Ala Arg Tyr Glu Gly Leu Phe
        275                 280                 285
Leu Asp Pro Val Tyr Thr Ala Lys Ser Phe Ala Gly Val Glu Gly Leu
    290                 295                 300
Leu Gln Glu Gly Val Ile Gln Pro Gly Ala Arg Val Cys Phe Ile His
305                 310                 315                 320
Ser Gly Gly Leu Pro Ala Leu Phe Ala Tyr Gly Glu Asp Leu Leu Ala
                325                 330                 335
```

<210> 226
<211> 1017
<212> DNA
<213> Roseovarius nubinhibens ISM

<220>
<221> CDS
<222> (1)..(1017)
<223> transl_table=11

<400> 226

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

```
ccg acc ggc gcg ctc ggc tat gtc aac tgc gcc ttc gaa ctg ctg gcc        528
Pro Thr Gly Ala Leu Gly Tyr Val Asn Cys Ala Phe Glu Leu Leu Ala
                165                 170                 175
cag gcc aat gat ggc ggt ctc aag atc gac cat atc gtg cat gcc acc        576
Gln Ala Asn Asp Gly Gly Leu Lys Ile Asp His Ile Val His Ala Thr
            180                 185                 190
ggc agc gcc ggc acg cag gcc ggt ctg atc acc ggc ctc aag gcg atg        624
Gly Ser Ala Gly Thr Gln Ala Gly Leu Ile Thr Gly Leu Lys Ala Met
        195                 200                 205
aat gcg caa atc ccg ctg ctc ggc atc ggc gtg cgc gcc ccc aaa ccg        672
Asn Ala Gln Ile Pro Leu Leu Gly Ile Gly Val Arg Ala Pro Lys Pro
    210                 215                 220
aag cag gaa gaa aac gtc tac aac ctc gcc tgc gcc acg gct gaa aag        720
Lys Gln Glu Glu Asn Val Tyr Asn Leu Ala Cys Ala Thr Ala Glu Lys
225                 230                 235                 240
ctc ggc tgc ccc ggc gtc gtc gcc cgc gaa gat gtt gtc gcc aac acc        768
Leu Gly Cys Pro Gly Val Val Ala Arg Glu Asp Val Val Ala Asn Thr
                245                 250                 255
gat tac gtc ggc cag ggc tat ggc atc ccg acc gaa agc ggc atg gaa        816
Asp Tyr Val Gly Gln Gly Tyr Gly Ile Pro Thr Glu Ser Gly Met Glu
            260                 265                 270
gcg atc aag atg ttc gcc gag ctg gaa tcg atc ctg ctc gat ccg gtt        864
Ala Ile Lys Met Phe Ala Glu Leu Glu Ser Ile Leu Leu Asp Pro Val
        275                 280                 285
tat tcc gca aaa ggc gcg gca ggc ttt att gac ttg atc cgc aaa ggg        912
Tyr Ser Ala Lys Gly Ala Ala Gly Phe Ile Asp Leu Ile Arg Lys Gly
    290                 295                 300
cat ttc aag aag ggc gag cgc gtc gtg ttc ctc cac acc ggc ggg gcc        960
His Phe Lys Lys Gly Glu Arg Val Val Phe Leu His Thr Gly Gly Ala
305                 310                 315                 320
gca gcc ctg ttc ggc tat gat ggc gcg ttt gat ttc tcg tcc cgc tgg       1008
Ala Ala Leu Phe Gly Tyr Asp Gly Ala Phe Asp Phe Ser Ser Arg Trp
                325                 330                 335
gtc ggc tga                                                           1017
Val Gly
```

<210> 227
<211> 338
<212> PRT
<213> Roseovarius nubinhibens ISM

<400> 227

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

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

<210> 228
<211> 900
<212> DNA
<213> Pseudomonas aeruginosa C3719

<220>
<221> CDS
<222> (1)..(900)

<400> 228

```
ttg cag cgt ctc gaa ctc gac tgg ctg caa cgg gcc ggg gtc gaa ctg       48
Met Gln Arg Leu Glu Leu Asp Trp Leu Gln Arg Ala Gly Val Glu Leu
1               5                   10                  15
gcg ctg ctg cgc ctg gac cag gcc gat ccg ctg atc tcc ggc aac aag       96
Ala Leu Leu Arg Leu Asp Gln Ala Asp Pro Leu Ile Ser Gly Asn Lys
            20                  25                  30
ggg ttc aag ctc gcg cca cac ctg gcg ctg gcc cac gag cag ggg ctg      144
Gly Phe Lys Leu Ala Pro His Leu Ala Leu Ala His Glu Gln Gly Leu
        35                  40                  45
gac ggc ctg atc agc ctc ggc ggc gcc cat tcc aac cac ctg cac gcg      192
Asp Gly Leu Ile Ser Leu Gly Gly Ala His Ser Asn His Leu His Ala
    50                  55                  60
ctg gcc ggc gct ggc gcg cgt ttc ggt ttc cgt tgc gtc ggc ctg ttg      240
Leu Ala Gly Ala Gly Ala Arg Phe Gly Phe Arg Cys Val Gly Leu Leu
65                  70                  75                  80
cgc gga cac gaa gtc gat acg ccg acg gtg cgc gac ctg cgc agt ctc      288
Arg Gly His Glu Val Asp Thr Pro Thr Val Arg Asp Leu Arg Ser Leu
                85                  90                  95
ggc atg gaa ctg cac tgg ctc ggc tac ggc ggc tat cgc cag cgg cat      336
Gly Met Glu Leu His Trp Leu Gly Tyr Gly Gly Tyr Arg Gln Arg His
            100                 105                 110
gcc gcc ggc ttc tgg ctt ccc tgg cgg gaa cgt tac cca ggc ttg ctg      384
Ala Ala Gly Phe Trp Leu Pro Trp Arg Glu Arg Tyr Pro Gly Leu Leu
        115                 120                 125
```

```
ccg gtc gcc gag ggc ggt ggc ggg ctg ctg ggc gcg cgc ggt tgc atc        432
Pro Val Ala Glu Gly Gly Gly Gly Leu Leu Gly Ala Arg Gly Cys Ile
    130                 135                 140
ggg ctg gtg gag cgc atg gcg acc cag ttg ccg acg ctc ggc tgg gac        480
Gly Leu Val Glu Arg Met Ala Thr Gln Leu Pro Thr Leu Gly Trp Asp
145                 150                 155                 160
gat tac gac gcg atc tgg gtg gcc gcc ggt acc ggt acg aca ctg gcc        528
Asp Tyr Asp Ala Ile Trp Val Ala Ala Gly Thr Gly Thr Thr Leu Ala
                165                 170                 175
ggc ctg gtg ctc ggc gag gct ggg cgg cat ccc gtg gtg ggc gcg ctg        576
Gly Leu Val Leu Gly Glu Ala Gly Arg His Pro Val Val Gly Ala Leu
            180                 185                 190
gcg gtg ccg gag gac cac ggc gtc gcc gcc cag gtc gcg gcg acc ctt        624
Ala Val Pro Glu Asp His Gly Val Ala Ala Gln Val Ala Ala Thr Leu
        195                 200                 205
gcc gag gcg ggc tgg gcc gat acc ggc tat cgc ctg ctg gac gcc agc        672
Ala Glu Ala Gly Trp Ala Asp Thr Gly Tyr Arg Leu Leu Asp Ala Ser
    210                 215                 220
cgt ggc ggt ttc gcc tgt ctc gat ggg agg ttg gcg cgg ttc atc gtc        720
Arg Gly Gly Phe Ala Cys Leu Asp Gly Arg Leu Ala Arg Phe Ile Val
225                 230                 235                 240
gag ttc gag acg gcc agc ggc gtc gcc ctc gaa ccg ctg tac acc ggc        768
Glu Phe Glu Thr Ala Ser Gly Val Ala Leu Glu Pro Leu Tyr Thr Gly
                245                 250                 255
aaa ctg ctg ctc gcc ctg cgc gag gcc gtg gag agc ggc gcg gtg gct        816
Lys Leu Leu Leu Ala Leu Arg Glu Ala Val Glu Ser Gly Ala Val Ala
            260                 265                 270
cgc ggc agc cgg ctg gtg gcg ctg cac agc gga ggc ctg cag ggc cgc        864
Arg Gly Ser Arg Leu Val Ala Leu His Ser Gly Gly Leu Gln Gly Arg
        275                 280                 285
cgg gca ttg cag gag cgt ttg ctg gcg ttg ctc tga                        900
Arg Ala Leu Gln Glu Arg Leu Leu Ala Leu Leu
    290                 295
```

<210> 229
<211> 299
<212> PRT
<213> Pseudomonas aeruginosa C3719

<400> 229

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

```
                165                 170                 175
Gly Leu Val Leu Gly Glu Ala Gly Arg His Pro Val Val Gly Ala Leu
            180                 185                 190
Ala Val Pro Glu Asp His Gly Val Ala Ala Gln Val Ala Ala Thr Leu
        195                 200                 205
Ala Glu Ala Gly Trp Ala Asp Thr Gly Tyr Arg Leu Leu Asp Ala Ser
    210                 215                 220
Arg Gly Gly Phe Ala Cys Leu Asp Gly Arg Leu Ala Arg Phe Ile Val
225                 230                 235                 240
Glu Phe Glu Thr Ala Ser Gly Val Ala Leu Glu Pro Leu Tyr Thr Gly
                245                 250                 255
Lys Leu Leu Leu Ala Leu Arg Glu Ala Val Glu Ser Gly Ala Val Ala
            260                 265                 270
Arg Gly Ser Arg Leu Val Ala Leu His Ser Gly Gly Leu Gln Gly Arg
        275                 280                 285
Arg Ala Leu Gln Glu Arg Leu Leu Ala Leu Leu
    290                 295
```

<210> 230
<211> 900
<212> DNA
<213> Pseudomonas aeruginosa 2192

<220>
<221> CDS
<222> (1)..(900)

<400> 230

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

```
ggc ctg gtg ctc ggc gag gcc ggg cgg cat ccc gtg gtg ggc gcg ctg       576
Gly Leu Val Leu Gly Glu Ala Gly Arg His Pro Val Val Gly Ala Leu
            180                 185                 190
gcg gtg ccg gag gac cac ggc gtc gcc gcc cag gtc gcg gcg acc ctt       624
Ala Val Pro Glu Asp His Gly Val Ala Ala Gln Val Ala Ala Thr Leu
        195                 200                 205
gcc gag gcg ggc tgg gcc gat acc ggc tat cgc ctg ctg gac gcc agc       672
Ala Glu Ala Gly Trp Ala Asp Thr Gly Tyr Arg Leu Leu Asp Ala Ser
    210                 215                 220
cgt ggt ggt ttc gcc cgc ctc gat ggg cga ttg gcg cgg ttc atc gtc       720
Arg Gly Gly Phe Ala Arg Leu Asp Gly Arg Leu Ala Arg Phe Ile Val
225                 230                 235                 240
gag ttc gag acg gcc agc ggc gtc gcc ctc gaa ccg ctg tac acc ggc       768
Glu Phe Glu Thr Ala Ser Gly Val Ala Leu Glu Pro Leu Tyr Thr Gly
                245                 250                 255
aag ctg ctg ctc gcc ctg cgc gag gcc gtg gag agc ggc gcg gtg gct       816
Lys Leu Leu Leu Ala Leu Arg Glu Ala Val Glu Ser Gly Ala Val Ala
            260                 265                 270
cgc ggc agc cgg ttg gtg gcg ctg cac agc gga ggc ctg cag ggc cgc       864
Arg Gly Ser Arg Leu Val Ala Leu His Ser Gly Gly Leu Gln Gly Arg
        275                 280                 285
cgg gca ttg cag gag cgt ttg ctg gcg ttg ctc tga                       900
Arg Ala Leu Gln Glu Arg Leu Leu Ala Leu Leu
    290                 295
```

<210> 231
<211> 299
<212> PRT
<213> Pseudomonas aeruginosa 2192

<400> 231

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

```
Glu Phe Glu Thr Ala Ser Gly Val Ala Leu Glu Pro Leu Tyr Thr Gly
                245                 250                 255
Lys Leu Leu Leu Ala Leu Arg Glu Ala Val Glu Ser Gly Ala Val Ala
            260                 265                 270
Arg Gly Ser Arg Leu Val Ala Leu His Ser Gly Gly Leu Gln Gly Arg
        275                 280                 285
Arg Ala Leu Gln Glu Arg Leu Leu Ala Leu Leu
    290                 295

<210> 232
<211> 957
<212> DNA
<213> Burkholderia cenocepacia PC184

<220>
<221> CDS
<222> (1)..(957)

<400> 232
ttg ccg cgc ctc ggc aag gcg ctg ggt ggc aaa gtg cat ctc tat gca       48
Met Pro Arg Leu Gly Lys Ala Leu Gly Gly Lys Val His Leu Tyr Ala
1               5                   10                  15
aaa cgc gaa gac tgc aac agc ggc ctg gcg ttc ggc ggc aac aag acc       96
Lys Arg Glu Asp Cys Asn Ser Gly Leu Ala Phe Gly Gly Asn Lys Thr
            20                  25                  30
cgc aag ctc gag tac atc gtg ccg gac gtg ctg gcg agc ggc gcc gac      144
Arg Lys Leu Glu Tyr Ile Val Pro Asp Val Leu Ala Ser Gly Ala Asp
        35                  40                  45
acg ctt gta tcg att ggc ggc atc cag tcg aac cag acg cgt cag gtc      192
Thr Leu Val Ser Ile Gly Gly Ile Gln Ser Asn Gln Thr Arg Gln Val
    50                  55                  60
gcg gca gtc gcg gct cat ctt ggc ctg aaa tgc gtg ctg gtt caa gaa      240
Ala Ala Val Ala Ala His Leu Gly Leu Lys Cys Val Leu Val Gln Glu
65                  70                  75                  80
aac tgg gtc aac tac tcg gac gct gtg tat gac cgc gtt ggc aac att      288
Asn Trp Val Asn Tyr Ser Asp Ala Val Tyr Asp Arg Val Gly Asn Ile
                85                  90                  95
cag atg tcc cgc atg atg ggc gcc gac gtt cgg ctg gtc agc gac ggc      336
Gln Met Ser Arg Met Met Gly Ala Asp Val Arg Leu Val Ser Asp Gly
            100                 105                 110
ttc gac atc ggc att cgt ccg agc tgg gaa gag gcg ctg gag agt gtc      384
Phe Asp Ile Gly Ile Arg Pro Ser Trp Glu Glu Ala Leu Glu Ser Val
        115                 120                 125
cgc aac gcg ggc ggg aag ccg tat ccg atc ccc gcc ggt tgt tcc gag      432
Arg Asn Ala Gly Gly Lys Pro Tyr Pro Ile Pro Ala Gly Cys Ser Glu
    130                 135                 140
cat cgg ctt ggc ggc ctc ggg ttc gtc ggt ttc gcg gag gaa gtg cgc      480
His Arg Leu Gly Gly Leu Gly Phe Val Gly Phe Ala Glu Glu Val Arg
145                 150                 155                 160
gcc cag gaa gcc gaa ctc gga ttc aag ttc gac tac atc gtc gtg tgt      528
Ala Gln Glu Ala Glu Leu Gly Phe Lys Phe Asp Tyr Ile Val Val Cys
                165                 170                 175
tcg gtg acc gga agc acg cag gcc ggc atg gtc gtg ggg ttc gcg gcg      576
Ser Val Thr Gly Ser Thr Gln Ala Gly Met Val Val Gly Phe Ala Ala
            180                 185                 190
gac gga cgc gcg gat cgc gtg atc ggt atc gat gcg tcg gcc aaa ccc      624
Asp Gly Arg Ala Asp Arg Val Ile Gly Ile Asp Ala Ser Ala Lys Pro
        195                 200                 205
gag cag acg cgc gag cag att ctt cgc gtc gca cgc cag acc gcc gat      672
Glu Gln Thr Arg Glu Gln Ile Leu Arg Val Ala Arg Gln Thr Ala Asp
    210                 215                 220
```

```
ctc gtg gaa ctc gaa cgg ccg atc gag gac gcg gac gtg gtg ctc gat        720
Leu Val Glu Leu Glu Arg Pro Ile Glu Asp Ala Asp Val Val Leu Asp
225                 230                 235                 240
acg cgc tac ggg ggc cct gaa tac ggc ttg ccg tcg gaa ggg acg ctc        768
Thr Arg Tyr Gly Gly Pro Glu Tyr Gly Leu Pro Ser Glu Gly Thr Leu
                245                 250                 255
gaa gcg att cga ctg tgc gcg aag acc gag gga atg ctg acc gac ccg        816
Glu Ala Ile Arg Leu Cys Ala Lys Thr Glu Gly Met Leu Thr Asp Pro
            260                 265                 270
gtt tat gaa ggc aag tcg atg cac ggg atg atc gac agg gtg cgc cgc        864
Val Tyr Glu Gly Lys Ser Met His Gly Met Ile Asp Arg Val Arg Arg
        275                 280                 285
ggc gag ttt ccg gaa ggg tcc cgg gtc ttg tat gcg cac ctc ggt ggc        912
Gly Glu Phe Pro Glu Gly Ser Arg Val Leu Tyr Ala His Leu Gly Gly
    290                 295                 300
gtc ccc gca ttg aac gca tac agc ttc ctg ttc aag aac ggt tga            957
Val Pro Ala Leu Asn Ala Tyr Ser Phe Leu Phe Lys Asn Gly
305                 310                 315
```

<210> 233
<211> 318
<212> PRT
<213> Burkholderia cenocepacia PC184

<400> 233

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

```
Gly Glu Phe Pro Glu Gly Ser Arg Val Leu Tyr Ala His Leu Gly Gly
    290                 295                 300
Val Pro Ala Leu Asn Ala Tyr Ser Phe Leu Phe Lys Asn Gly
305                 310                 315

<210> 234
<211> 1017
<212> DNA
<213> Burkholderia cenocepacia PC184

<220>
<221> CDS
<222> (1)..(1017)

<400> 234
atg aat ctg caa cgc ttc ccc cgt tat ccg ctg acg ttc ggc ccg acg      48
Met Asn Leu Gln Arg Phe Pro Arg Tyr Pro Leu Thr Phe Gly Pro Thr
1               5                   10                  15
ccc atc cag ccg ctc aag cgc ctg agc gcc cat ctc ggc ggc aag gtc      96
Pro Ile Gln Pro Leu Lys Arg Leu Ser Ala His Leu Gly Gly Lys Val
            20                  25                  30
gag ctg tat gcg aag cgc gag gac tgc aac agc ggc ctc gca ttc ggc     144
Glu Leu Tyr Ala Lys Arg Glu Asp Cys Asn Ser Gly Leu Ala Phe Gly
        35                  40                  45
ggc aac aag acg cgc aag ctc gaa tat ctc gtt ccc gac gcg ctc gcg     192
Gly Asn Lys Thr Arg Lys Leu Glu Tyr Leu Val Pro Asp Ala Leu Ala
    50                  55                  60
caa ggt gcc gac acg ctc gta tcg atc ggc ggc gtg cag tcg aat cag     240
Gln Gly Ala Asp Thr Leu Val Ser Ile Gly Gly Val Gln Ser Asn Gln
65                  70                  75                  80
aca cgc cag gtc gcg gct gtc gcc gcg cat ctc gga atg aaa tgc gtg     288
Thr Arg Gln Val Ala Ala Val Ala Ala His Leu Gly Met Lys Cys Val
                85                  90                  95
ctc gtg cag gag cac tgg gtc aac tat gaa gat ccg gtg tac gac cgg     336
Leu Val Gln Glu His Trp Val Asn Tyr Glu Asp Pro Val Tyr Asp Arg
            100                 105                 110
gtc ggc aac atc cag tta tcg cgg atg atg ggc gcc gac gtg cgg ctc     384
Val Gly Asn Ile Gln Leu Ser Arg Met Met Gly Ala Asp Val Arg Leu
        115                 120                 125
gta tcc gac ggt ttc gac atc ggc att cgc cgc agt tgg gaa gaa gcg     432
Val Ser Asp Gly Phe Asp Ile Gly Ile Arg Arg Ser Trp Glu Glu Ala
    130                 135                 140
atg gag agc gtg cga cag gcg ggg ggc aag ccg tat ccg att ccg gcc     480
Met Glu Ser Val Arg Gln Ala Gly Gly Lys Pro Tyr Pro Ile Pro Ala
145                 150                 155                 160
ggc tgc tcc gag cat ccg ctc ggc ggg ctc ggg ttc gtc ggc ttc gcg     528
Gly Cys Ser Glu His Pro Leu Gly Gly Leu Gly Phe Val Gly Phe Ala
                165                 170                 175
gaa gag gtg cgg gcg cag gaa gcg cag ctc ggc ttc aag ttc gac tac     576
Glu Glu Val Arg Ala Gln Glu Ala Gln Leu Gly Phe Lys Phe Asp Tyr
            180                 185                 190
gtc gtc gtc tgc tcg gtg acg ggc agc acg cag gcg gga atg gtc gtg     624
Val Val Val Cys Ser Val Thr Gly Ser Thr Gln Ala Gly Met Val Val
        195                 200                 205
ggc ttc gcg gcc gac gga cgc gcg gac cgc gtg atc ggc atc gac gca     672
Gly Phe Ala Ala Asp Gly Arg Ala Asp Arg Val Ile Gly Ile Asp Ala
    210                 215                 220
tcg gcg aag ccg gaa cag aca cgc gaa cag atc acg cgc atc gca cgg     720
Ser Ala Lys Pro Glu Gln Thr Arg Glu Gln Ile Thr Arg Ile Ala Arg
225                 230                 235                 240
cat acg gcc gag ctg gtc gga ctg ggc cgc gat atc gtc gaa cag gac     768
```

```
His Thr Ala Glu Leu Val Gly Leu Gly Arg Asp Ile Val Glu Gln Asp
                245                 250                 255
gtc gtg ctc gac acg cgt tac ggc ggg ccc gaa tat ggg ctg ccg agc      816
Val Val Leu Asp Thr Arg Tyr Gly Gly Pro Glu Tyr Gly Leu Pro Ser
            260                 265                 270
gac ggc acg ctg gaa gcg att cgg ctg tgc gca cgg ctg gaa ggc atg      864
Asp Gly Thr Leu Glu Ala Ile Arg Leu Cys Ala Arg Leu Glu Gly Met
        275                 280                 285
ctg acc gat ccc gtt tat gaa ggg aaa tcg atg cac ggg atg atc gac      912
Leu Thr Asp Pro Val Tyr Glu Gly Lys Ser Met His Gly Met Ile Asp
    290                 295                 300
aag gtg cgg ctc ggg gaa ttc gag ccg ggg tcg aag gtg ctg tat gcg      960
Lys Val Arg Leu Gly Glu Phe Glu Pro Gly Ser Lys Val Leu Tyr Ala
305                 310                 315                 320
cac ttg ggc ggg gtg cca gcg ttg agc gcg tac cac ggg att ttt cgt     1008
His Leu Gly Gly Val Pro Ala Leu Ser Ala Tyr His Gly Ile Phe Arg
                325                 330                 335
aac ggg tga                                                        1017
Asn Gly
```

<210> 235
<211> 338
<212> PRT
<213> Burkholderia cenocepacia PC184

<400> 235

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

```
Asp Gly Thr Leu Glu Ala Ile Arg Leu Cys Ala Arg Leu Glu Gly Met
        275                 280                 285
Leu Thr Asp Pro Val Tyr Glu Gly Lys Ser Met His Gly Met Ile Asp
    290                 295                 300
Lys Val Arg Leu Gly Glu Phe Glu Pro Gly Ser Lys Val Leu Tyr Ala
305                 310                 315                 320
His Leu Gly Gly Val Pro Ala Leu Ser Ala Tyr His Gly Ile Phe Arg
                325                 330                 335
Asn Gly
```

<210> 236
<211> 1017
<212> DNA
<213> Burkholderia dolosa AUO158

<220>
<221> CDS
<222> (1)..(1017)

<400> 236

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

```
ggc ttc gcg gcc gac gga cgc gcg gat cgc gtg atc ggc atc gat gcg        672
Gly Phe Ala Ala Asp Gly Arg Ala Asp Arg Val Ile Gly Ile Asp Ala
    210                 215                 220
tcg gcg acg ccc gag cgc acg cgc gaa cag atc acg cgg atc gcg cgg        720
Ser Ala Thr Pro Glu Arg Thr Arg Glu Gln Ile Thr Arg Ile Ala Arg
225                 230                 235                 240
cac acg gcc gag ctg gtc gat ctc ggg cgc gac atc ggc gac cgc gac        768
His Thr Ala Glu Leu Val Asp Leu Gly Arg Asp Ile Gly Asp Arg Asp
                245                 250                 255
gtc gtg ctc gac acg cgc tat gcg ggc ccg gaa tac ggg ctg ccg aac        816
Val Val Leu Asp Thr Arg Tyr Ala Gly Pro Glu Tyr Gly Leu Pro Asn
            260                 265                 270
gac ggc acg ctc gac gcg att cgt ctg tgc gcg cgg ctc gaa ggc gtg        864
Asp Gly Thr Leu Asp Ala Ile Arg Leu Cys Ala Arg Leu Glu Gly Val
        275                 280                 285
ctg acc gat ccc gtg tac gaa ggc aaa tcg atg cac ggg atg atc gac        912
Leu Thr Asp Pro Val Tyr Glu Gly Lys Ser Met His Gly Met Ile Asp
    290                 295                 300
aag gta cgg cgc ggc gaa ttc gag ccc gga tcg aag gtg ctg tat gcg        960
Lys Val Arg Arg Gly Glu Phe Glu Pro Gly Ser Lys Val Leu Tyr Ala
305                 310                 315                 320
cac ctc ggc ggc gtg ccg gcg ttg agc gcg tat gcg ggg atc ttc gcg       1008
His Leu Gly Gly Val Pro Ala Leu Ser Ala Tyr Ala Gly Ile Phe Ala
                325                 330                 335
aac ggg tga                                                          1017
Asn Gly
```

<210> 237
<211> 338
<212> PRT
<213> Burkholderia dolosa AUO158

<400> 237

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

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

<210> 238
<211> 1092
<212> DNA
<213> Polaromonas naphthalenivorans CJ2

<220>
<221> CDS
<222> (1)..(1092)
<223> transl_table=11

<400> 238

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

```
                165                 170                 175
gga ggc aag ccc ttc gcc att cca gct ggc tgc tcc gaa cat cct tat      576
Gly Gly Lys Pro Phe Ala Ile Pro Ala Gly Cys Ser Glu His Pro Tyr
            180                 185                 190
ggt ggg ctg ggc ttt gtc ggc ttt gcc gaa gag gtg cgg gcg cag gaa      624
Gly Gly Leu Gly Phe Val Gly Phe Ala Glu Glu Val Arg Ala Gln Glu
        195                 200                 205
gcc gag ctg ggc ttc aag ttc gac tac atc gtc gtc tgc tcg gtc acc      672
Ala Glu Leu Gly Phe Lys Phe Asp Tyr Ile Val Val Cys Ser Val Thr
    210                 215                 220
ggc agc acg cag gcc ggc atg gtg gtt ggt ttt gcc gca gat ggt cgt      720
Gly Ser Thr Gln Ala Gly Met Val Val Gly Phe Ala Ala Asp Gly Arg
225                 230                 235                 240
gcc gac cgg gtg ata ggc att gat gcc tcc gcc aag cct gag caa acc      768
Ala Asp Arg Val Ile Gly Ile Asp Ala Ser Ala Lys Pro Glu Gln Thr
                245                 250                 255
agt gcg caa atc ctg cgc att gcg cag aac acc gcc agg ctg gtc gag      816
Ser Ala Gln Ile Leu Arg Ile Ala Gln Asn Thr Ala Arg Leu Val Glu
            260                 265                 270
ctg gac cgt gac atc act gcg aaa gac gtg gtg ctc gat acc cgc tac      864
Leu Asp Arg Asp Ile Thr Ala Lys Asp Val Val Leu Asp Thr Arg Tyr
        275                 280                 285
ggc ggg ccc gag tac ggc ctg ccg agc gaa ggc acg ctg gaa gcc atc      912
Gly Gly Pro Glu Tyr Gly Leu Pro Ser Glu Gly Thr Leu Glu Ala Ile
    290                 295                 300
cgc ctg tgt gcc cgg cag gag ggc atg ctg acc gac ccg gtc tat gaa      960
Arg Leu Cys Ala Arg Gln Glu Gly Met Leu Thr Asp Pro Val Tyr Glu
305                 310                 315                 320
ggc aag tcc atg cac ggc atg atc gac atg gtg cgc cgc ggt gag ttc     1008
Gly Lys Ser Met His Gly Met Ile Asp Met Val Arg Arg Gly Glu Phe
                325                 330                 335
ccc gag ggt tcc cgg gtg ctg tat gcc cat ctg ggt ggt gta cct gcg     1056
Pro Glu Gly Ser Arg Val Leu Tyr Ala His Leu Gly Gly Val Pro Ala
            340                 345                 350
ctc aat gcc tac agc ttc ctg ttt cgc aac ggc tga                    1092
Leu Asn Ala Tyr Ser Phe Leu Phe Arg Asn Gly
        355                 360
```

<210> 239
<211> 363
<212> PRT
<213> Polaromonas naphthalenivorans CJ2

<400> 239

```
Met Pro Ser Phe Phe Ala Ala Ile Thr Val His Ala Met Gly Leu Ser
1               5                   10                  15
Pro Glu Pro Arg Ser Met Pro Leu Thr Leu Asn Leu Gln Lys Phe Pro
            20                  25                  30
Arg His Ser Leu Thr Phe Gly Pro Thr Pro Ile Gln Pro Leu Lys Arg
        35                  40                  45
Leu Ser Ala His Leu Ser Gly Lys Ile Glu Leu Tyr Ala Lys Arg Glu
    50                  55                  60
Asp Cys Asn Ser Gly Leu Ala Phe Gly Gly Asn Lys Thr Arg Lys Leu
65                  70                  75                  80
Glu Tyr Leu Ile Pro Glu Ala Leu Ala Gln Gly Cys Asp Thr Leu Val
                85                  90                  95
Ser Ile Gly Gly Ile Gln Ser Asn Gln Thr Arg Gln Val Ala Ala Val
            100                 105                 110
Ala Ala His Leu Gly Met Lys Cys Val Leu Val Gln Glu Asn Trp Val
        115                 120                 125
Asn Tyr Ser Asp Ala Val Tyr Asp Arg Val Gly Asn Ile Glu Met Ser
```

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

<210> 240
<211> 1020
<212> DNA
<213> Burkholderia mallei 10229

<220>
<221> CDS
<222> (1)..(1020)

<400> 240

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atg aac acg acg acg ctc tcg acg aaa ctg aac gcc ttc gcc cgc ctg      48
Met Asn Thr Thr Thr Leu Ser Thr Lys Leu Asn Ala Phe Ala Arg Leu
1               5                   10                  15
aac ctg atc gac gcg ccg acg ccg ctg cag tac ttg ccg cgc ctg tcc      96
Asn Leu Ile Asp Ala Pro Thr Pro Leu Gln Tyr Leu Pro Arg Leu Ser
            20                  25                  30
gcg cac gtc ggc cgc gac atc cac gtg aag cgc gac gac tgc acg ccg     144
Ala His Val Gly Arg Asp Ile His Val Lys Arg Asp Asp Cys Thr Pro
        35                  40                  45
ctc gcg atg ggc ggc aac aag ctg cgc aag ctc gaa ttc ctc gcc gcg     192
Leu Ala Met Gly Gly Asn Lys Leu Arg Lys Leu Glu Phe Leu Ala Ala
    50                  55                  60
gac gcg ctc ggc caa aac gcg gac gtg ctg gtg acc gcg ggc gcg atc     240
Asp Ala Leu Gly Gln Asn Ala Asp Val Leu Val Thr Ala Gly Ala Ile
65                  70                  75                  80
cag tcg aat cac gtc cgg cag acg gcc gcg ctc gtc gcg cag ctc ggc     288
Gln Ser Asn His Val Arg Gln Thr Ala Ala Leu Val Ala Gln Leu Gly
                85                  90                  95
ctc ggc tgt gtc gcg ctg ctc gaa aac ccg atc gca gcc gcg cgc gac     336
Leu Gly Cys Val Ala Leu Leu Glu Asn Pro Ile Ala Ala Ala Arg Asp
            100                 105                 110
```

```
gat tat ctg caa agc ggc aac cgg ctg ctg ctc gat ctg ttc gac gtg        384
Asp Tyr Leu Gln Ser Gly Asn Arg Leu Leu Leu Asp Leu Phe Asp Val
        115                 120                 125
cgc gcg cac gtc gtc gac ggg ctc gac gac gtc gac cgg caa ctc gaa        432
Arg Ala His Val Val Asp Gly Leu Asp Asp Val Asp Arg Gln Leu Glu
    130                 135                 140
gcc gcc gcg cgg cgg ctg cgc gac gaa ggg cgg cgc ccg tac gtg atc        480
Ala Ala Ala Arg Arg Leu Arg Asp Glu Gly Arg Arg Pro Tyr Val Ile
145                 150                 155                 160
ccg atc ggc gga tcg aat ccg ctc ggc gcg ctc ggc tac gtg cgc gcg        528
Pro Ile Gly Gly Ser Asn Pro Leu Gly Ala Leu Gly Tyr Val Arg Ala
                165                 170                 175
ggc ctc gag ctc gcg cag cag atc cgc gcg gcc gag cgc gat ttc gcg        576
Gly Leu Glu Leu Ala Gln Gln Ile Arg Ala Ala Glu Arg Asp Phe Ala
            180                 185                 190
gct gtc gtg ctc gcg tcc ggc agc gcc ggc acg cac gcg ggc ctc gcg        624
Ala Val Val Leu Ala Ser Gly Ser Ala Gly Thr His Ala Gly Leu Ala
        195                 200                 205
ttc gcg ctc gcg cac gcg ttg ccc ggg ctg ccg gtg atc ggc gtg acg        672
Phe Ala Leu Ala His Ala Leu Pro Gly Leu Pro Val Ile Gly Val Thr
    210                 215                 220
gta tcg cgc acc gac gcg cag cag cgc ccg aag gtg cgg cat ctg ctc        720
Val Ser Arg Thr Asp Ala Gln Gln Arg Pro Lys Val Arg His Leu Leu
225                 230                 235                 240
gac ggc atg agc ggg ctg ctc gac gtc gcg ttg ccg gcg ggc gcg cgc        768
Asp Gly Met Ser Gly Leu Leu Asp Val Ala Leu Pro Ala Gly Ala Arg
                245                 250                 255
atc gat ctg tgg gac gac tac ttc gcg ccg cgc tac ggc gag ccc aat        816
Ile Asp Leu Trp Asp Asp Tyr Phe Ala Pro Arg Tyr Gly Glu Pro Asn
            260                 265                 270
cgc gcg ggc atc gac gcg ctg cgg ctg ctc gcg cga acc gag ggg ctg        864
Arg Ala Gly Ile Asp Ala Leu Arg Leu Leu Ala Arg Thr Glu Gly Leu
        275                 280                 285
ctg ctc gat ccg gtg tac acg ggc aag gcg atg gcg ggt ctc atc gac        912
Leu Leu Asp Pro Val Tyr Thr Gly Lys Ala Met Ala Gly Leu Ile Asp
    290                 295                 300
ggc gtc gcg cgc ggc cgc ttc gac gga aac ggc ccg gtg ctg ttc gtg        960
Gly Val Ala Arg Gly Arg Phe Asp Gly Asn Gly Pro Val Leu Phe Val
305                 310                 315                 320
cat acg ggc ggc gcg ccc gcg ctg ttc gcg tat cag gac gcg tgc cgc       1008
His Thr Gly Gly Ala Pro Ala Leu Phe Ala Tyr Gln Asp Ala Cys Arg
                325                 330                 335
gcg agc cga tga                                                      1020
Ala Ser Arg
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<210> 241
<211> 339
<212> PRT
<213> Burkholderia mallei 10229

<400> 241

```
Met Asn Thr Thr Thr Leu Ser Thr Lys Leu Asn Ala Phe Ala Arg Leu
1               5                   10                  15
Asn Leu Ile Asp Ala Pro Thr Pro Leu Gln Tyr Leu Pro Arg Leu Ser
            20                  25                  30
Ala His Val Gly Arg Asp Ile His Val Lys Arg Asp Asp Cys Thr Pro
        35                  40                  45
Leu Ala Met Gly Gly Asn Lys Leu Arg Lys Leu Glu Phe Leu Ala Ala
    50                  55                  60
Asp Ala Leu Gly Gln Asn Ala Asp Val Leu Val Thr Ala Gly Ala Ile
```

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

<210> 242
<211> 957
<212> DNA
<213> Roseovarius sp. 217

<220>
<221> CDS
<222> (1)..(957)
<223> transl_table=11

<400> 242

```
atg aac cgg ctg acc gag cat ctg gga ggt cca cgt ttg tgg gtg aag        48
Met Asn Arg Leu Thr Glu His Leu Gly Gly Pro Arg Leu Trp Val Lys
1               5                   10                  15
cgt gac gat tgc aca ggc ctg tcg tcg ggc gga aac aag aca cgc aag        96
Arg Asp Asp Cys Thr Gly Leu Ser Ser Gly Gly Asn Lys Thr Arg Lys
            20                  25                  30
ctc gaa ttc ctg atg gcc gat gct ttg gcg cag ggc gtg gat acg atc       144
Leu Glu Phe Leu Met Ala Asp Ala Leu Ala Gln Gly Val Asp Thr Ile
        35                  40                  45
atc acc caa ggt gcc acc caa tcc aac cac gcg cgc cag act gcg gcg       192
Ile Thr Gln Gly Ala Thr Gln Ser Asn His Ala Arg Gln Thr Ala Ala
    50                  55                  60
gcg gct gcg cgg ttc gga atg gcc tgc cat atc ctc ctt gag gat cgg       240
Ala Ala Ala Arg Phe Gly Met Ala Cys His Ile Leu Leu Glu Asp Arg
```

```
65                  70                  75                  80
acg ggg tct gac gat ccg cag tat acg ctg aac gga aac gtt ctt ctt      288
Thr Gly Ser Asp Asp Pro Gln Tyr Thr Leu Asn Gly Asn Val Leu Leu
                85                  90                  95
gac cgg ctg cat ggt gcg acc gtg gcc aag cgt cgg ggc ggc tcg gat      336
Asp Arg Leu His Gly Ala Thr Val Ala Lys Arg Arg Gly Gly Ser Asp
            100                 105                 110
atg gcg tcc gag atg gag aca ttg gca gac aag ctg cgc gca gac ggg      384
Met Ala Ser Glu Met Glu Thr Leu Ala Asp Lys Leu Arg Ala Asp Gly
        115                 120                 125
cgg agg cct tac atc att ccc ggc ggt ggc tcg aac agc acg ggc gcg      432
Arg Arg Pro Tyr Ile Ile Pro Gly Gly Gly Ser Asn Ser Thr Gly Ala
    130                 135                 140
ctt ggt tat gtg aat tgc gcc ttg gag att gct gag cag tcg gca acc      480
Leu Gly Tyr Val Asn Cys Ala Leu Glu Ile Ala Glu Gln Ser Ala Thr
145                 150                 155                 160
atg ggg cta aag att gat gcg ctg gtg cat gcg acg ggc agt tcg ggc      528
Met Gly Leu Lys Ile Asp Ala Leu Val His Ala Thr Gly Ser Ser Gly
                165                 170                 175
act cag gcg ggg ttg gta gca ggt ctc gcg gcg ctt gaa agt gat atc      576
Thr Gln Ala Gly Leu Val Ala Gly Leu Ala Ala Leu Glu Ser Asp Ile
            180                 185                 190
tat ctt ctc ggc att ggc gtg cgc gcg cct cag gaa aag cag gaa agc      624
Tyr Leu Leu Gly Ile Gly Val Arg Ala Pro Gln Glu Lys Gln Glu Ser
        195                 200                 205
atg gtc ttt gac ctc gca cag cgc acg ggt gcg cgc atg gga ttt gaa      672
Met Val Phe Asp Leu Ala Gln Arg Thr Gly Ala Arg Met Gly Phe Glu
    210                 215                 220
gag gcg att cgt cga gag ggt gtc cgg gcg aac tgc gat tac gtg ggc      720
Glu Ala Ile Arg Arg Glu Gly Val Arg Ala Asn Cys Asp Tyr Val Gly
225                 230                 235                 240
gcg gga tac ggc att ccg acg caa ggc atg atc gag agc gtc cgg ctt      768
Ala Gly Tyr Gly Ile Pro Thr Gln Gly Met Ile Glu Ser Val Arg Leu
                245                 250                 255
ttg gca gag atc gag ggg ctg ctg ttc gac ccg gtc tat tcc ggc aaa      816
Leu Ala Glu Ile Glu Gly Leu Leu Phe Asp Pro Val Tyr Ser Gly Lys
            260                 265                 270
ggg cta gac ggt ctg att gat ctg aca cgc aag ggg gcc ttt gat ggc      864
Gly Leu Asp Gly Leu Ile Asp Leu Thr Arg Lys Gly Ala Phe Asp Gly
        275                 280                 285
atg gag aat gtc gtc ttt ctg cat act ggc ggt tca gcc gcg ctt ttc      912
Met Glu Asn Val Val Phe Leu His Thr Gly Gly Ser Ala Ala Leu Phe
    290                 295                 300
gca tat ccc gac gtg ttt gat ctg ccg ggc tac cag ata aac tga          957
Ala Tyr Pro Asp Val Phe Asp Leu Pro Gly Tyr Gln Ile Asn
305                 310                 315
```

<210> 243
<211> 318
<212> PRT
<213> Roseovarius sp. 217

<400> 243

```
Met Asn Arg Leu Thr Glu His Leu Gly Gly Pro Arg Leu Trp Val Lys
1               5                   10                  15
Arg Asp Asp Cys Thr Gly Leu Ser Ser Gly Gly Asn Lys Thr Arg Lys
            20                  25                  30
Leu Glu Phe Leu Met Ala Asp Ala Leu Ala Gln Gly Val Asp Thr Ile
        35                  40                  45
Ile Thr Gln Gly Ala Thr Gln Ser Asn His Ala Arg Gln Thr Ala Ala
    50                  55                  60
```

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

<210> 244
<211> 1017
<212> DNA
<213> Roseovarius sp. 217

<220>
<221> CDS
<222> (1)..(1017)
<223> transl_table=11

<400> 244

```
atg cat ctt gcc cgc tat ccc cgc cgc ttt ctc gcc cat ctg cca acg      48
Met His Leu Ala Arg Tyr Pro Arg Arg Phe Leu Ala His Leu Pro Thr
1               5                   10                  15
cca ctg gag cgg ctg gat cgt ttg acc aag gaa ttg aac ggg ccg gaa      96
Pro Leu Glu Arg Leu Asp Arg Leu Thr Lys Glu Leu Asn Gly Pro Glu
            20                  25                  30
atc tgg atc aag cgc gac gat tgc acc ggc ctc agc acc ggt ggc aac     144
Ile Trp Ile Lys Arg Asp Asp Cys Thr Gly Leu Ser Thr Gly Gly Asn
        35                  40                  45
aag acc cgc aag ctc gag ttc ctg atg gcc gag gcc gaa ttg cag ggc     192
Lys Thr Arg Lys Leu Glu Phe Leu Met Ala Glu Ala Glu Leu Gln Gly
    50                  55                  60
gcg gat atg gtg atg acc cag ggc gcc acc cag tcc aac cac gcg cgc     240
Ala Asp Met Val Met Thr Gln Gly Ala Thr Gln Ser Asn His Ala Arg
65                  70                  75                  80
caa acg gcg gcc ttt gcg gcc aag ctg ggc atg gat tgc cac ctg cta     288
Gln Thr Ala Ala Phe Ala Ala Lys Leu Gly Met Asp Cys His Leu Leu
```

```
                85                  90                  95
ctt gag gac aga acc ggc tcc aac aac gcc aac tac aac aat ggc ggc       336
Leu Glu Asp Arg Thr Gly Ser Asn Asn Ala Asn Tyr Asn Asn Gly Gly
            100                 105                 110
aac gtc ctt ctg gac cat atg cac ggc gcg acc acg gaa aag cgc ccc       384
Asn Val Leu Leu Asp His Met His Gly Ala Thr Thr Glu Lys Arg Pro
        115                 120                 125
ggc ggc ggc gat atg aat gcc gag atg gaa aag gtc gcg gac aag ttc       432
Gly Gly Gly Asp Met Asn Ala Glu Met Glu Lys Val Ala Asp Lys Phe
    130                 135                 140
cgc gcc gag ggg cgc aat gtc tat acc atc ccc ggt ggt ggg tcg aac       480
Arg Ala Glu Gly Arg Asn Val Tyr Thr Ile Pro Gly Gly Gly Ser Asn
145                 150                 155                 160
ccg acg ggc gcg cta ggc tat gtc aac tgc gcc ttt gag atg ctg gcg       528
Pro Thr Gly Ala Leu Gly Tyr Val Asn Cys Ala Phe Glu Met Leu Ala
                165                 170                 175
cag ttc aat gat cgg gcg ctc aag gtg gat cac att gtc cat gcc acc       576
Gln Phe Asn Asp Arg Ala Leu Lys Val Asp His Ile Val His Ala Thr
            180                 185                 190
gga agt gca ggc acg cag gcg ggg ctg atc acc ggg ctc aaa gcg atg       624
Gly Ser Ala Gly Thr Gln Ala Gly Leu Ile Thr Gly Leu Lys Ala Met
        195                 200                 205
aat gcg cag att ccg ctc ctc gga att ggc gtg cgc gcg ccc aag gca       672
Asn Ala Gln Ile Pro Leu Leu Gly Ile Gly Val Arg Ala Pro Lys Ala
    210                 215                 220
aag cag gaa gag aac gtc tat aac ctc gcc tgt gcc act gct gaa aag       720
Lys Gln Glu Glu Asn Val Tyr Asn Leu Ala Cys Ala Thr Ala Glu Lys
225                 230                 235                 240
ctg ggc tgc gcc gga gtg gtc aag cgc gag gat gtg gtc gcc aat acc       768
Leu Gly Cys Ala Gly Val Val Lys Arg Glu Asp Val Val Ala Asn Thr
                245                 250                 255
gat tac gtc ggc gaa ggc tat ggt att cct aca gaa tcc ggc atc gag       816
Asp Tyr Val Gly Glu Gly Tyr Gly Ile Pro Thr Glu Ser Gly Ile Glu
            260                 265                 270
gca att cac atg ttt gcc gag ttg gag gcg atc ctg ctc gat ccg gtc       864
Ala Ile His Met Phe Ala Glu Leu Glu Ala Ile Leu Leu Asp Pro Val
        275                 280                 285
tat tcg gcc aag ggg gct gcg ggc ttt atc gac ctg atc cgc aag ggg       912
Tyr Ser Ala Lys Gly Ala Ala Gly Phe Ile Asp Leu Ile Arg Lys Gly
    290                 295                 300
cat ttc aag aaa ggc gag cgt gtt gtg ttt ctg cat acc ggg ggt tct       960
His Phe Lys Lys Gly Glu Arg Val Val Phe Leu His Thr Gly Gly Ser
305                 310                 315                 320
gtt gcg ctc ttc ggt tat gac agc gcc ttt gat ttc tcg ggc cgc tgg      1008
Val Ala Leu Phe Gly Tyr Asp Ser Ala Phe Asp Phe Ser Gly Arg Trp
                325                 330                 335
aag aag taa                                                         1017
Lys Lys
```

<210> 245
<211> 338
<212> PRT
<213> Roseovarius sp. 217

<400> 245

```
Met His Leu Ala Arg Tyr Pro Arg Arg Phe Leu Ala His Leu Pro Thr
1               5                   10                  15
Pro Leu Glu Arg Leu Asp Arg Leu Thr Lys Glu Leu Asn Gly Pro Glu
            20                  25                  30
Ile Trp Ile Lys Arg Asp Asp Cys Thr Gly Leu Ser Thr Gly Gly Asn
```

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

<210> 246
<211> 909
<212> DNA
<213> Cellulophaga sp. MED134

<220>
<221> CDS
<222> (1)..(909)
<223> transl_table=11

<400> 246

```
gtg aat ttt act tca aaa aat caa ttt gtc ttt gag caa aat ggc tgt      48
Met Asn Phe Thr Ser Lys Asn Gln Phe Val Phe Glu Gln Asn Gly Cys
1               5                   10                  15
acg ctt ttc ata aag cgt gag gac gag tta cac ccc acc gtt tct ggt      96
Thr Leu Phe Ile Lys Arg Glu Asp Glu Leu His Pro Thr Val Ser Gly
            20                  25                  30
aat aag ttt aga aag ctt aag tat aac cta ctt caa gcc aga gca ctt     144
Asn Lys Phe Arg Lys Leu Lys Tyr Asn Leu Leu Gln Ala Arg Ala Leu
        35                  40                  45
ggt cac gat aca tta ctc acc ttt ggt ggt gca tac tca aat cat att     192
```

```
Gly His Asp Thr Leu Leu Thr Phe Gly Gly Ala Tyr Ser Asn His Ile
    50                  55                  60
gct gca acc gcg gcg gcg ggt aaa cta gaa ggt ttt aaa act gta ggg      240
Ala Ala Thr Ala Ala Ala Gly Lys Leu Glu Gly Phe Lys Thr Val Gly
65                  70                  75                  80
gtt ata agg ggt gag gag ttg ggc cgt gat ctt aaa aaa aca cta gct      288
Val Ile Arg Gly Glu Glu Leu Gly Arg Asp Leu Lys Lys Thr Leu Ala
                85                  90                  95
caa aac cct acg ctt gca ttt gcc cac tct tgt ggg atg gaa ttt cat      336
Gln Asn Pro Thr Leu Ala Phe Ala His Ser Cys Gly Met Glu Phe His
            100                 105                 110
ttt gtt act agg gct gag tat aag gag aag gat aaa tta cgc ttt cgc      384
Phe Val Thr Arg Ala Glu Tyr Lys Glu Lys Asp Lys Leu Arg Phe Arg
        115                 120                 125
gaa agc gta aaa aaa acc ttt aat aac cca ttt att ata ccc gaa gga      432
Glu Ser Val Lys Lys Thr Phe Asn Asn Pro Phe Ile Ile Pro Glu Gly
    130                 135                 140
ggt aca aat gcg ctt gca ata aaa gga tgt gaa gag att cta act aca      480
Gly Thr Asn Ala Leu Ala Ile Lys Gly Cys Glu Glu Ile Leu Thr Thr
145                 150                 155                 160
gag gac agt cag ttt gat tat ata agt tgc cct ata gga acg gcg ggt      528
Glu Asp Ser Gln Phe Asp Tyr Ile Ser Cys Pro Ile Gly Thr Ala Gly
                165                 170                 175
acg ata tct ggt atc ata aat agt gct ggt aaa cat caa aag gta ctt      576
Thr Ile Ser Gly Ile Ile Asn Ser Ala Gly Lys His Gln Lys Val Leu
            180                 185                 190
ggt ttc ccc gcg cta aaa gga gat tgg gta cgt gat gag gta gca caa      624
Gly Phe Pro Ala Leu Lys Gly Asp Trp Val Arg Asp Glu Val Ala Gln
        195                 200                 205
tat gtg gat agt gag caa tgg gaa atc ata gcc gac tat cat tgt gga      672
Tyr Val Asp Ser Glu Gln Trp Glu Ile Ile Ala Asp Tyr His Cys Gly
    210                 215                 220
gga tat gca aaa gta aat aga gag tta atc act ttt ata aat gac ttt      720
Gly Tyr Ala Lys Val Asn Arg Glu Leu Ile Thr Phe Ile Asn Asp Phe
225                 230                 235                 240
aag gaa gca tac ggc att ccg ctt gat cct gtg tat acg ggt aag atg      768
Lys Glu Ala Tyr Gly Ile Pro Leu Asp Pro Val Tyr Thr Gly Lys Met
                245                 250                 255
ctt ttt ggg ctt tca gac ttg atg aat cgt ggg tat ttc cca gag aat      816
Leu Phe Gly Leu Ser Asp Leu Met Asn Arg Gly Tyr Phe Pro Glu Asn
            260                 265                 270
tct cgt att tta gcc att cat acg gga ggt tta caa ggc atc tcg ggt      864
Ser Arg Ile Leu Ala Ile His Thr Gly Gly Leu Gln Gly Ile Ser Gly
        275                 280                 285
atg aat act cga ctt gca aaa aag gga ctc cca ctc ata caa tag           909
Met Asn Thr Arg Leu Ala Lys Lys Gly Leu Pro Leu Ile Gln
    290                 295                 300
```

<210> 247
<211> 302
<212> PRT
<213> Cellulophaga sp. MED134

<400> 247

```
Met Asn Phe Thr Ser Lys Asn Gln Phe Val Phe Glu Gln Asn Gly Cys
1               5                   10                  15
Thr Leu Phe Ile Lys Arg Glu Asp Glu Leu His Pro Thr Val Ser Gly
            20                  25                  30
Asn Lys Phe Arg Lys Leu Lys Tyr Asn Leu Leu Gln Ala Arg Ala Leu
        35                  40                  45
Gly His Asp Thr Leu Leu Thr Phe Gly Gly Ala Tyr Ser Asn His Ile
```

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

<210> 248
<211> 939
<212> DNA
<213> Tenacibaculum sp. MED152

<220>
<221> CDS
<222> (1)..(939)
<223> transl_table=11

<400> 248

```
atg gac ttt aat aaa ccc tat att tcc gag aat cat aaa ata gag cta      48
Met Asp Phe Asn Lys Pro Tyr Ile Ser Glu Asn His Lys Ile Glu Leu
1               5                   10                  15
cct att tta aca cag aaa aat gtg gcg ctt tat ata aaa aga gaa gat      96
Pro Ile Leu Thr Gln Lys Asn Val Ala Leu Tyr Ile Lys Arg Glu Asp
            20                  25                  30
gaa att cat cct ttt gta tca ggt aat aaa ttc aga aaa tta aaa tac     144
Glu Ile His Pro Phe Val Ser Gly Asn Lys Phe Arg Lys Leu Lys Tyr
        35                  40                  45
aac tta gcc gaa gct aaa aag caa aat aaa gct aca tta tta act ttt     192
Asn Leu Ala Glu Ala Lys Lys Gln Asn Lys Ala Thr Leu Leu Thr Phe
    50                  55                  60
gga ggc gca ttt tca aat cat ata gta gca aca gct gtt gct ggt aat     240
Gly Gly Ala Phe Ser Asn His Ile Val Ala Thr Ala Val Ala Gly Asn
65                  70                  75                  80
ctc aat ggt ttt aaa act att ggt att att aga ggt gaa gaa ttg gct     288
Leu Asn Gly Phe Lys Thr Ile Gly Ile Ile Arg Gly Glu Glu Leu Ala
                85                  90                  95
```

```
aat gat tta gaa aaa aca cta gct gaa aat gct act tta aga gag gct        336
Asn Asp Leu Glu Lys Thr Leu Ala Glu Asn Ala Thr Leu Arg Glu Ala
            100                 105                 110
cat cta aat gga atg act ttt aga ttt att tct aga gct gat tat aga        384
His Leu Asn Gly Met Thr Phe Arg Phe Ile Ser Arg Ala Asp Tyr Arg
        115                 120                 125
aat aaa gaa caa aca aat ttt ata gca gat tta agt aaa gaa ttt ggc        432
Asn Lys Glu Gln Thr Asn Phe Ile Ala Asp Leu Ser Lys Glu Phe Gly
    130                 135                 140
gat ttt tat ttg att cct gaa gga ggt aca aac caa ctg gct ata aaa        480
Asp Phe Tyr Leu Ile Pro Glu Gly Gly Thr Asn Gln Leu Ala Ile Lys
145                 150                 155                 160
ggt tgt gaa gaa att tta aca aat caa gac gca att ttc gat tat att        528
Gly Cys Glu Glu Ile Leu Thr Asn Gln Asp Ala Ile Phe Asp Tyr Ile
                165                 170                 175
tgt ttg gct gtt gga act gga ggt act att tct gga gtt ata aat tca        576
Cys Leu Ala Val Gly Thr Gly Gly Thr Ile Ser Gly Val Ile Asn Ser
            180                 185                 190
ttg caa gat cat caa aaa tgt ttg gga ttt cct gct tta aaa gga att        624
Leu Gln Asp His Gln Lys Cys Leu Gly Phe Pro Ala Leu Lys Gly Ile
        195                 200                 205
ttt tta gaa gag gaa atc aaa aaa tat gta aaa tca gaa gag aat tgg        672
Phe Leu Glu Glu Glu Ile Lys Lys Tyr Val Lys Ser Glu Glu Asn Trp
    210                 215                 220
agt tta caa acc gat tat cat ttt gga ggt tat gca aaa tat aat gat        720
Ser Leu Gln Thr Asp Tyr His Phe Gly Gly Tyr Ala Lys Tyr Asn Asp
225                 230                 235                 240
gat tta att cgt ttt ata aac acc ttt aaa aac caa aca gat att tta        768
Asp Leu Ile Arg Phe Ile Asn Thr Phe Lys Asn Gln Thr Asp Ile Leu
                245                 250                 255
tta gac cct gtt tat aca gca aaa atg gtt tac ggt gtt tta gat tta        816
Leu Asp Pro Val Tyr Thr Ala Lys Met Val Tyr Gly Val Leu Asp Leu
            260                 265                 270
ata ggt aaa aat cat ttt cca gtt aaa act aaa ata ctt gca att cat        864
Ile Gly Lys Asn His Phe Pro Val Lys Thr Lys Ile Leu Ala Ile His
        275                 280                 285
aca gga ggt tta caa ggt att gtt ggt ttc aat aaa aag tta gca gca        912
Thr Gly Gly Leu Gln Gly Ile Val Gly Phe Asn Lys Lys Leu Ala Ala
    290                 295                 300
aaa aat caa tct tta ata caa caa taa                                    939
Lys Asn Gln Ser Leu Ile Gln Gln
305                 310
```

<210> 249
<211> 312
<212> PRT
<213> Tenacibaculum sp. MED152

<400> 249

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

```
Asn Asp Leu Glu Lys Thr Leu Ala Glu Asn Ala Thr Leu Arg Glu Ala
            100                 105                 110
His Leu Asn Gly Met Thr Phe Arg Phe Ile Ser Arg Ala Asp Tyr Arg
        115                 120                 125
Asn Lys Glu Gln Thr Asn Phe Ile Ala Asp Leu Ser Lys Glu Phe Gly
    130                 135                 140
Asp Phe Tyr Leu Ile Pro Glu Gly Gly Thr Asn Gln Leu Ala Ile Lys
145                 150                 155                 160
Gly Cys Glu Glu Ile Leu Thr Asn Gln Asp Ala Ile Phe Asp Tyr Ile
                165                 170                 175
Cys Leu Ala Val Gly Thr Gly Gly Thr Ile Ser Gly Val Ile Asn Ser
            180                 185                 190
Leu Gln Asp His Gln Lys Cys Leu Gly Phe Pro Ala Leu Lys Gly Ile
        195                 200                 205
Phe Leu Glu Glu Glu Ile Lys Lys Tyr Val Lys Ser Glu Glu Asn Trp
    210                 215                 220
Ser Leu Gln Thr Asp Tyr His Phe Gly Gly Tyr Ala Lys Tyr Asn Asp
225                 230                 235                 240
Asp Leu Ile Arg Phe Ile Asn Thr Phe Lys Asn Gln Thr Asp Ile Leu
                245                 250                 255
Leu Asp Pro Val Tyr Thr Ala Lys Met Val Tyr Gly Val Leu Asp Leu
            260                 265                 270
Ile Gly Lys Asn His Phe Pro Val Lys Thr Lys Ile Leu Ala Ile His
        275                 280                 285
Thr Gly Gly Leu Gln Gly Ile Val Gly Phe Asn Lys Lys Leu Ala Ala
    290                 295                 300
Lys Asn Gln Ser Leu Ile Gln Gln
305                 310
```

<210> 250
<211> 948
<212> DNA
<213> Flavobacterium sp. MED217

<220>
<221> CDS
<222> (1)..(948)
<223> transl_table=11

<400> 250

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atg agt gat gta ggt ttt ttt gag aat gat ttt tat gac ctg act ata        48
Met Ser Asp Val Gly Phe Phe Glu Asn Asp Phe Tyr Asp Leu Thr Ile
1               5                   10                  15
agt gca tta aat gga ttt gta gga aac gaa ttt aac cta gaa gta gct        96
Ser Ala Leu Asn Gly Phe Val Gly Asn Glu Phe Asn Leu Glu Val Ala
            20                  25                  30
atc aaa cgc gaa gat caa att gac aca ttt gtt tct ggc aat aag ttt       144
Ile Lys Arg Glu Asp Gln Ile Asp Thr Phe Val Ser Gly Asn Lys Phe
        35                  40                  45
aga aag ctc aag tat aat ttg att gaa gct caa aac ctg cgt caa aaa       192
Arg Lys Leu Lys Tyr Asn Leu Ile Glu Ala Gln Asn Leu Arg Gln Lys
    50                  55                  60
aca ctt ctt acc ttt ggc gga gca ttt tct aat cat atc gcg gct acc       240
Thr Leu Leu Thr Phe Gly Gly Ala Phe Ser Asn His Ile Ala Ala Thr
65                  70                  75                  80
gcc aga gcc ggt cag cgc tgt ggt ttt aaa acg atc gga gtc ata cgc       288
Ala Arg Ala Gly Gln Arg Cys Gly Phe Lys Thr Ile Gly Val Ile Arg
                85                  90                  95
ggt gaa gaa ttg ggc att acc tta gat caa acg ctt cag caa aac cct       336
Gly Glu Glu Leu Gly Ile Thr Leu Asp Gln Thr Leu Gln Gln Asn Pro
            100                 105                 110
```

```
acc ttg aag ttt gct tat gaa tgc gga atg caa ttt gaa ttc gtt aca       384
Thr Leu Lys Phe Ala Tyr Glu Cys Gly Met Gln Phe Glu Phe Val Thr
        115                 120                 125
cgt aaa gct tat cgg gaa aaa gaa agc gca gca ttc aac caa atg ctt       432
Arg Lys Ala Tyr Arg Glu Lys Glu Ser Ala Ala Phe Asn Gln Met Leu
    130                 135                 140
aag gag caa ttt ggt gat ttt tat agc att cca gag gga gga aca aat       480
Lys Glu Gln Phe Gly Asp Phe Tyr Ser Ile Pro Glu Gly Gly Thr Asn
145                 150                 155                 160
gca ctc gct gta aaa ggc tgt aaa gag att tta tca gaa aac aca aaa       528
Ala Leu Ala Val Lys Gly Cys Lys Glu Ile Leu Ser Glu Asn Thr Lys
                165                 170                 175
gat ttt gat tac atc gct tgt gct gtg gga aca gga gga act att gcg       576
Asp Phe Asp Tyr Ile Ala Cys Ala Val Gly Thr Gly Gly Thr Ile Ala
            180                 185                 190
ggc att gta gaa gcc agt ctt ccg cat caa aag gtt tta ggt ttt ccg       624
Gly Ile Val Glu Ala Ser Leu Pro His Gln Lys Val Leu Gly Phe Pro
        195                 200                 205
gct tta aaa ggt gat ttt cta aat gct gaa att aaa aaa tat act tca       672
Ala Leu Lys Gly Asp Phe Leu Asn Ala Glu Ile Lys Lys Tyr Thr Ser
    210                 215                 220
aaa gcc aat tgg gaa ctt atc aat acg tat cat ttt gga ggc tat gca       720
Lys Ala Asn Trp Glu Leu Ile Asn Thr Tyr His Phe Gly Gly Tyr Ala
225                 230                 235                 240
aaa gtg aat gag gag ctt gtt cag ttt ata aat gat ttt aaa aag cag       768
Lys Val Asn Glu Glu Leu Val Gln Phe Ile Asn Asp Phe Lys Lys Gln
                245                 250                 255
cac ggg att cag cta gat cct gtg tat acc ggt aaa atg atg ttt ggt       816
His Gly Ile Gln Leu Asp Pro Val Tyr Thr Gly Lys Met Met Phe Gly
            260                 265                 270
ctt aca gat ctt atg cgc aat ggg ttt ttc tct aaa aat acc cgt att       864
Leu Thr Asp Leu Met Arg Asn Gly Phe Phe Ser Lys Asn Thr Arg Ile
        275                 280                 285
tta gcc gtt cat act gga ggc ctg caa ggt att gcc gga atg aat gct       912
Leu Ala Val His Thr Gly Gly Leu Gln Gly Ile Ala Gly Met Asn Ala
    290                 295                 300
aaa ctt tca aaa aaa gga tat cct cag att att tga                       948
Lys Leu Ser Lys Lys Gly Tyr Pro Gln Ile Ile
305                 310                 315
```

<210> 251
<211> 315
<212> PRT
<213> Flavobacterium sp. MED217

<400> 251

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

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

<210> 252
<211> 876
<212> DNA
<213> Campylobacter jejuni subsp. jejuni 260.94

<220>
<221> CDS
<222> (1)..(876)
<223> transl_table=11

<400> 252

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ttg aat ttc att aaa aca att agt cct ata caa aaa atc aat ttt aac      48
Met Asn Phe Ile Lys Thr Ile Ser Pro Ile Gln Lys Ile Asn Phe Asn
1               5                   10                  15
gga ttt gaa ttt tat att aaa aga gat gat tta tta ggg gaa att aat      96
Gly Phe Glu Phe Tyr Ile Lys Arg Asp Asp Leu Leu Gly Glu Ile Asn
            20                  25                  30
gga aat aaa gct agg aaa ctt gct ttt tat atc cat caa aga tat cct     144
Gly Asn Lys Ala Arg Lys Leu Ala Phe Tyr Ile His Gln Arg Tyr Pro
        35                  40                  45
aaa aat caa tct ttt gta agt tat gga gga agc caa agt aat gct ttg     192
Lys Asn Gln Ser Phe Val Ser Tyr Gly Gly Ser Gln Ser Asn Ala Leu
    50                  55                  60
gcg gca tta agt att ttt gct aaa caa aga tca tat aag ctt gtt ttt     240
Ala Ala Leu Ser Ile Phe Ala Lys Gln Arg Ser Tyr Lys Leu Val Phe
65                  70                  75                  80
gct tgt gaa aaa att tct act ttt ctt aag aat aat cct tgt gga aac     288
Ala Cys Glu Lys Ile Ser Thr Phe Leu Lys Asn Asn Pro Cys Gly Asn
                85                  90                  95
tat gct tta gct tta gaa aat ggt gtt gat ttt gta gaa aat atc cat     336
Tyr Ala Leu Ala Leu Glu Asn Gly Val Asp Phe Val Glu Asn Ile His
            100                 105                 110
tct tta tcc tta aag caa ttt gct ttg tct ttg tgt aaa aaa gat gat     384
Ser Leu Ser Leu Lys Gln Phe Ala Leu Ser Leu Cys Lys Lys Asp Asp
        115                 120                 125
```

```
att ttt ata gaa caa ggc ata gct aat tta gaa gct caa tat ggc tat       432
Ile Phe Ile Glu Gln Gly Ile Ala Asn Leu Glu Ala Gln Tyr Gly Tyr
    130                 135                 140
atg gaa ctt gct caa gaa att caa atg caa agt caa agt tta aag ctt       480
Met Glu Leu Ala Gln Glu Ile Gln Met Gln Ser Gln Ser Leu Lys Leu
145                 150                 155                 160
gat ttt gat att ttt tta cct tcg ggt aca ggc act tcg gca gct ttt       528
Asp Phe Asp Ile Phe Leu Pro Ser Gly Thr Gly Thr Ser Ala Ala Phe
                165                 170                 175
ttg gca aag tat tct aaa ttt aaa gta ttt act tgc gct tgt gta ggt       576
Leu Ala Lys Tyr Ser Lys Phe Lys Val Phe Thr Cys Ala Cys Val Gly
            180                 185                 190
gat att aaa tat ctt aaa aaa caa att tta aca tta gat cca agc tat       624
Asp Ile Lys Tyr Leu Lys Lys Gln Ile Leu Thr Leu Asp Pro Ser Tyr
        195                 200                 205
gat ttt tca aat tta gaa ttt tta aca agt gat aaa aaa tat cac ttt       672
Asp Phe Ser Asn Leu Glu Phe Leu Thr Ser Asp Lys Lys Tyr His Phe
    210                 215                 220
gct aag ccg tat aaa gaa ttt tat gag ctt tat atg gat tta aag tta       720
Ala Lys Pro Tyr Lys Glu Phe Tyr Glu Leu Tyr Met Asp Leu Lys Leu
225                 230                 235                 240
aag tgc aat ata gaa ttt gac ttg ttg tat gat att tta gga tta agt       768
Lys Cys Asn Ile Glu Phe Asp Leu Leu Tyr Asp Ile Leu Gly Leu Ser
                245                 250                 255
ata gca tta aaa caa gag tgg aaa aaa cca ttg ctt tat ata cat caa       816
Ile Ala Leu Lys Gln Glu Trp Lys Lys Pro Leu Leu Tyr Ile His Gln
            260                 265                 270
ggt gga att tta gga aat tcc act atg tta gag aga tat aaa ttt aaa       864
Gly Gly Ile Leu Gly Asn Ser Thr Met Leu Glu Arg Tyr Lys Phe Lys
        275                 280                 285
aaa tta gtt taa                                                      876
Lys Leu Val
    290
```

<210> 253
<211> 291
<212> PRT
<213> Campylobacter jejuni subsp. jejuni 260.94

<400> 253

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

```
                165                 170                 175
Leu Ala Lys Tyr Ser Lys Phe Lys Val Phe Thr Cys Ala Cys Val Gly
            180                 185                 190
Asp Ile Lys Tyr Leu Lys Lys Gln Ile Leu Thr Leu Asp Pro Ser Tyr
        195                 200                 205
Asp Phe Ser Asn Leu Glu Phe Leu Thr Ser Asp Lys Lys Tyr His Phe
    210                 215                 220
Ala Lys Pro Tyr Lys Glu Phe Tyr Glu Leu Tyr Met Asp Leu Lys Leu
225                 230                 235                 240
Lys Cys Asn Ile Glu Phe Asp Leu Leu Tyr Asp Ile Leu Gly Leu Ser
                245                 250                 255
Ile Ala Leu Lys Gln Glu Trp Lys Lys Pro Leu Leu Tyr Ile His Gln
            260                 265                 270
Gly Gly Ile Leu Gly Asn Ser Thr Met Leu Glu Arg Tyr Lys Phe Lys
        275                 280                 285
Lys Leu Val
    290
```

<210> 254
<211> 900
<212> DNA
<213> Marinomonas sp. MED121

<220>
<221> CDS
<222> (1)..(900)
<223> transl_table=11

<400> 254

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

```
                165                 170                 175
ggt gca acc agt gca ggt ttt tta gcc aat gat aat gtt cct aat atg       576
Gly Ala Thr Ser Ala Gly Phe Leu Ala Asn Asp Asn Val Pro Asn Met
            180                 185                 190
ctt gtc ttt ccc gcg tta aaa gga ggg gag gcc ttg cta tca gat att       624
Leu Val Phe Pro Ala Leu Lys Gly Gly Glu Ala Leu Leu Ser Asp Ile
        195                 200                 205
cac tcc ctt gcg ctg caa caa aac cct gac agt cac ttg caa cgt tta       672
His Ser Leu Ala Leu Gln Gln Asn Pro Asp Ser His Leu Gln Arg Leu
    210                 215                 220
tct att gtg ggt gaa tat cac cat ggc ggt tac gcg aga ctg cca agt       720
Ser Ile Val Gly Glu Tyr His His Gly Gly Tyr Ala Arg Leu Pro Ser
225                 230                 235                 240
gaa tta aag gac tat att gag caa ctg cat caa ctt aac cct cat tta       768
Glu Leu Lys Asp Tyr Ile Glu Gln Leu His Gln Leu Asn Pro His Leu
                245                 250                 255
agg tta gac cct gtt tat acg gcc aaa ctt gtc tat ggg gta gag caa       816
Arg Leu Asp Pro Val Tyr Thr Ala Lys Leu Val Tyr Gly Val Glu Gln
            260                 265                 270
gaa ata cgc aaa ggt aag ttg acg aat caa aag ctg ttg ctt att cat       864
Glu Ile Arg Lys Gly Lys Leu Thr Asn Gln Lys Leu Leu Leu Ile His
        275                 280                 285
aca gga ggg ctg cag ggt tgg cgc gga tat caa taa                       900
Thr Gly Gly Leu Gln Gly Trp Arg Gly Tyr Gln
    290                 295
```

<210> 255
<211> 299
<212> PRT
<213> Marinomonas sp. MED121

<400> 255

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

```
225                 230                 235                 240
Glu Leu Lys Asp Tyr Ile Glu Gln Leu His Gln Leu Asn Pro His Leu
                245                 250                 255
Arg Leu Asp Pro Val Tyr Thr Ala Lys Leu Val Tyr Gly Val Glu Gln
            260                 265                 270
Glu Ile Arg Lys Gly Lys Leu Thr Asn Gln Lys Leu Leu Leu Ile His
        275                 280                 285
Thr Gly Gly Leu Gln Gly Trp Arg Gly Tyr Gln
    290                 295
```

<210> 256
<211> 1008
<212> DNA
<213> gamma proteobacterium KT 71

<220>
<221> CDS
<222> (1)..(1008)
<223> transl_table=11

<400> 256

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

```
Asn Ser Gln Val Pro Val Leu Gly Ile Gly Val Arg Ala Pro Lys Glu
    210                 215                 220
aaa cag gag gac aac gtt ttt tta ctg gca gag cgc acc gcc gaa tta        720
Lys Gln Glu Asp Asn Val Phe Leu Leu Ala Glu Arg Thr Ala Glu Leu
225                 230                 235                 240
ctc ggg ata ccg ggt gcc gtt cag cgt aaa cac gtg gag gca aat tgc        768
Leu Gly Ile Pro Gly Ala Val Gln Arg Lys His Val Glu Ala Asn Cys
                245                 250                 255
gac tat gtg ggt gaa ggc tac ggc ata cct acc gag ggc acc atc gag        816
Asp Tyr Val Gly Glu Gly Tyr Gly Ile Pro Thr Glu Gly Thr Ile Glu
            260                 265                 270
gcc atc gag atc ttt gcc cgc acc gag agc att ctc ctg gac ccc gtc        864
Ala Ile Glu Ile Phe Ala Arg Thr Glu Ser Ile Leu Leu Asp Pro Val
        275                 280                 285
tat tcc gga aaa ggt gct gca ggt ctt gtt gat ctt gtt cgt aaa ggg        912
Tyr Ser Gly Lys Gly Ala Ala Gly Leu Val Asp Leu Val Arg Lys Gly
    290                 295                 300
cat ttc caa aaa gat cag aac atc gtg ttt ata cac acg ggg ggc gcc        960
His Phe Gln Lys Asp Gln Asn Ile Val Phe Ile His Thr Gly Gly Ala
305                 310                 315                 320
cag gca ctg ttt gcc tat cgc gac gcc ttt ggc tac ggc aat cgc           1005
Gln Ala Leu Phe Ala Tyr Arg Asp Ala Phe Gly Tyr Gly Asn Arg
                325                 330                 335
taa                                                                   1008
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<210> 257
<211> 335
<212> PRT
<213> gamma proteobacterium KT 71

<400> 257

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

```
Lys Gln Glu Asp Asn Val Phe Leu Leu Ala Glu Arg Thr Ala Glu Leu
225                 230                 235                 240
Leu Gly Ile Pro Gly Ala Val Gln Arg Lys His Val Glu Ala Asn Cys
                245                 250                 255
Asp Tyr Val Gly Glu Gly Tyr Gly Ile Pro Thr Glu Gly Thr Ile Glu
            260                 265                 270
Ala Ile Glu Ile Phe Ala Arg Thr Glu Ser Ile Leu Leu Asp Pro Val
        275                 280                 285
Tyr Ser Gly Lys Gly Ala Ala Gly Leu Val Asp Leu Val Arg Lys Gly
    290                 295                 300
His Phe Gln Lys Asp Gln Asn Ile Val Phe Ile His Thr Gly Gly Ala
305                 310                 315                 320
Gln Ala Leu Phe Ala Tyr Arg Asp Ala Phe Gly Tyr Gly Asn Arg
                325                 330                 335
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<210> 258
<211> 978
<212> DNA
<213> gamma proteobacterium KT 71

<220>
<221> CDS
<222> (1)..(978)
<223> transl_table=11

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<400> 258
atg cac ccc ctc agc aat ttc gca gcg gcg gtt ggt gtt ccc gag ctt      48
Met His Pro Leu Ser Asn Phe Ala Ala Ala Val Gly Val Pro Glu Leu
1               5                   10                  15
tgg atg aaa cga gat gac ctc acg ggc ttg gaa gga ggc ggc aac aaa      96
Trp Met Lys Arg Asp Asp Leu Thr Gly Leu Glu Gly Gly Gly Asn Lys
            20                  25                  30
acg cgc aag ctg gaa ttt ctg gta gga gac gcg ctg gcc aaa ggc gcc     144
Thr Arg Lys Leu Glu Phe Leu Val Gly Asp Ala Leu Ala Lys Gly Ala
        35                  40                  45
gac atg ttg gtg acc gtt ggg gcg att caa tcg aat cat acg cgt cag     192
Asp Met Leu Val Thr Val Gly Ala Ile Gln Ser Asn His Thr Arg Gln
    50                  55                  60
act gcc gcc gcc gca gcc aag tcc ggt ctc aaa tgc tca ctg ctg cat     240
Thr Ala Ala Ala Ala Ala Lys Ser Gly Leu Lys Cys Ser Leu Leu His
65                  70                  75                  80
tat gcg tgg acc aaa gat gct agt cct caa tac cga ata gtg ggc aac     288
Tyr Ala Trp Thr Lys Asp Ala Ser Pro Gln Tyr Arg Ile Val Gly Asn
                85                  90                  95
tta ctg ata agt cat ctt ata ggc gcg gat ctg tac gtg gat gaa acg     336
Leu Leu Ile Ser His Leu Ile Gly Ala Asp Leu Tyr Val Asp Glu Thr
            100                 105                 110
gag cga ccg att gag gat cag ggt ccc ctc gac gaa ttc atg gcc ttt     384
Glu Arg Pro Ile Glu Asp Gln Gly Pro Leu Asp Glu Phe Met Ala Phe
        115                 120                 125
ctc cgg gcg cag ggt cat aag cct tac ctg ata ccc ggc ggc gcg tcg     432
Leu Arg Ala Gln Gly His Lys Pro Tyr Leu Ile Pro Gly Gly Ala Ser
    130                 135                 140
gag cat cga ctc gga tgt ttt ggg tac atc aag tgt gct gcg gaa att     480
Glu His Arg Leu Gly Cys Phe Gly Tyr Ile Lys Cys Ala Ala Glu Ile
145                 150                 155                 160
gct tcg cag atg gat gca gcc gac atc cgc ttt gac tac ctt gtg cac     528
Ala Ser Gln Met Asp Ala Ala Asp Ile Arg Phe Asp Tyr Leu Val His
                165                 170                 175
tgc acg ggc tcc agt agc acc cag gcg gga ctg ctg gcg gga ttt gcc     576
Cys Thr Gly Ser Ser Ser Thr Gln Ala Gly Leu Leu Ala Gly Phe Ala
```

```
          180                 185                 190
gct ttg ggc ata gag acc cgc atc gtc ggc ata tct gat gat ggt gaa       624
Ala Leu Gly Ile Glu Thr Arg Ile Val Gly Ile Ser Asp Asp Gly Glu
      195                 200                 205
gta gcc ata aag aaa gcg aga gtg ctg gag ctg gcc aac gcg gcc tta       672
Val Ala Ile Lys Lys Ala Arg Val Leu Glu Leu Ala Asn Ala Ala Leu
  210                 215                 220
aag gag ttg gac cta agt gca cgc gtt aac gcg cag gac gtc gag atc       720
Lys Glu Leu Asp Leu Ser Ala Arg Val Asn Ala Gln Asp Val Glu Ile
225                 230                 235                 240
atc gcc tcc agc aac aat gat tac gga gcg ccc gat gag gag atc att       768
Ile Ala Ser Ser Asn Asn Asp Tyr Gly Ala Pro Asp Glu Glu Ile Ile
                245                 250                 255
aac agc att cgc ctc ctg gct ggc aaa gaa ggc tta atc gcc gac ccc       816
Asn Ser Ile Arg Leu Leu Ala Gly Lys Glu Gly Leu Ile Ala Asp Pro
            260                 265                 270
gtc tat gag ggc cgg gca gtt cat ggg ctt tta aag ttg atc gag gat       864
Val Tyr Glu Gly Arg Ala Val His Gly Leu Leu Lys Leu Ile Glu Asp
        275                 280                 285
gga cgc ctg gac agg aac aca aag gtg ctg ctc atg cac ctg ggc ggt       912
Gly Arg Leu Asp Arg Asn Thr Lys Val Leu Leu Met His Leu Gly Gly
    290                 295                 300
tct ccc gcg att cac gcc tac gca ggg cat ttc gga tcc att cag ttg       960
Ser Pro Ala Ile His Ala Tyr Ala Gly His Phe Gly Ser Ile Gln Leu
305                 310                 315                 320
agc cca ttt cag gcc tga                                               978
Ser Pro Phe Gln Ala
                325
```

<210> 259
<211> 325
<212> PRT
<213> gamma proteobacterium KT 71

<400> 259

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

```
Val Ala Ile Lys Lys Ala Arg Val Leu Glu Leu Ala Asn Ala Ala Leu
    210                 215                 220
Lys Glu Leu Asp Leu Ser Ala Arg Val Asn Ala Gln Asp Val Glu Ile
225                 230                 235                 240
Ile Ala Ser Ser Asn Asn Asp Tyr Gly Ala Pro Asp Glu Glu Ile Ile
                245                 250                 255
Asn Ser Ile Arg Leu Leu Ala Gly Lys Glu Gly Leu Ile Ala Asp Pro
            260                 265                 270
Val Tyr Glu Gly Arg Ala Val His Gly Leu Leu Lys Leu Ile Glu Asp
        275                 280                 285
Gly Arg Leu Asp Arg Asn Thr Lys Val Leu Leu Met His Leu Gly Gly
    290                 295                 300
Ser Pro Ala Ile His Ala Tyr Ala Gly His Phe Gly Ser Ile Gln Leu
305                 310                 315                 320
Ser Pro Phe Gln Ala
                325
```

<210> 260
<211> 927
<212> DNA
<213> Flavobacteriales bacterium HTCC2170

<220>
<221> CDS
<222> (1)..(927)
<223> transl_table=11

<400> 260

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

```
gtt ggt acg ggc gga act ata tct gga ttg atc aat tcc atc aag cca        576
Val Gly Thr Gly Gly Thr Ile Ser Gly Leu Ile Asn Ser Ile Lys Pro
            180                 185                 190
aaa caa cgg gtc ctt ggt ttt cct gct ttg aaa gga gat ttt tta aga        624
Lys Gln Arg Val Leu Gly Phe Pro Ala Leu Lys Gly Asp Phe Leu Arg
        195                 200                 205
gaa gat att tgt aaa ttt gcg gca aac cgt gat tgg gat ttg caa ctg        672
Glu Asp Ile Cys Lys Phe Ala Ala Asn Arg Asp Trp Asp Leu Gln Leu
    210                 215                 220
gat tac aat ttt ggt ggt tat gcc aag gta act cct gaa ctt atc agg        720
Asp Tyr Asn Phe Gly Gly Tyr Ala Lys Val Thr Pro Glu Leu Ile Arg
225                 230                 235                 240
ttt ata aat gag ttc aaa aaa acg aca gat ata cct ttg gat cca gtt        768
Phe Ile Asn Glu Phe Lys Lys Thr Thr Asp Ile Pro Leu Asp Pro Val
                245                 250                 255
tat act ggc aaa atg atg ttt gga ata gtt gag atg gtc aag aat gat        816
Tyr Thr Gly Lys Met Met Phe Gly Ile Val Glu Met Val Lys Asn Asp
            260                 265                 270
gtt ttt aga gag ggt aca aaa cta ttg gcg ata cat act ggt ggt tta        864
Val Phe Arg Glu Gly Thr Lys Leu Leu Ala Ile His Thr Gly Gly Leu
        275                 280                 285
caa gga ata gaa ggg atg aac cgt ata ttg aaa aag aaa gat tta cca        912
Gln Gly Ile Glu Gly Met Asn Arg Ile Leu Lys Lys Lys Asp Leu Pro
    290                 295                 300
tta att gat tta tga                                                   927
Leu Ile Asp Leu
305
```

<210> 261
<211> 308
<212> PRT
<213> Flavobacteriales bacterium HTCC2170

<400> 261

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

```
    210                 215                 220
Asp Tyr Asn Phe Gly Gly Tyr Ala Lys Val Thr Pro Glu Leu Ile Arg
225                 230                 235                 240
Phe Ile Asn Glu Phe Lys Lys Thr Thr Asp Ile Pro Leu Asp Pro Val
                245                 250                 255
Tyr Thr Gly Lys Met Met Phe Gly Ile Val Glu Met Val Lys Asn Asp
            260                 265                 270
Val Phe Arg Glu Gly Thr Lys Leu Leu Ala Ile His Thr Gly Gly Leu
        275                 280                 285
Gln Gly Ile Glu Gly Met Asn Arg Ile Leu Lys Lys Lys Asp Leu Pro
    290                 295                 300
Leu Ile Asp Leu
305
```

<210> 262
<211> 924
<212> DNA
<213> Alteromonas macleodii 'Deep ecotype'

<220>
<221> CDS
<222> (1)..(924)
<223> transl_table=11

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<400> 262
gtg cta tcc ctt gaa gat ttc aaa act tca ctc aca ctt cct tcg cct      48
Met Leu Ser Leu Glu Asp Phe Lys Thr Ser Leu Thr Leu Pro Ser Pro
1               5                   10                  15
gta gaa ccg ttt ttt cca aaa tgg aaa ggg gct gag aag gta tcg ctc      96
Val Glu Pro Phe Phe Pro Lys Trp Lys Gly Ala Glu Lys Val Ser Leu
            20                  25                  30
ttc gtt aag cga gac gac gcc ata cac cct att atg tcg ggg aac aaa     144
Phe Val Lys Arg Asp Asp Ala Ile His Pro Ile Met Ser Gly Asn Lys
        35                  40                  45
tgg cgc aag tta agt aac gct ctt ccc cct tct cta ccc aag gca ata     192
Trp Arg Lys Leu Ser Asn Ala Leu Pro Pro Ser Leu Pro Lys Ala Ile
    50                  55                  60
gtg agt ttc ggg ggc ggt ttc tct aat cac ctc cac gcc cta ggc ttt     240
Val Ser Phe Gly Gly Gly Phe Ser Asn His Leu His Ala Leu Gly Phe
65                  70                  75                  80
atc tgc ttt aag ttg ggt atc cct ttc acc gcg att att cga ggt gac     288
Ile Cys Phe Lys Leu Gly Ile Pro Phe Thr Ala Ile Ile Arg Gly Asp
                85                  90                  95
tat tcg gct acc ccc tca ccg atg att aaa gac ttg ata cag tgg caa     336
Tyr Ser Ala Thr Pro Ser Pro Met Ile Lys Asp Leu Ile Gln Trp Gln
            100                 105                 110
act cac att gaa tat gtg gac cgt ata acc tac aaa aaa cgt agc gat     384
Thr His Ile Glu Tyr Val Asp Arg Ile Thr Tyr Lys Lys Arg Ser Asp
        115                 120                 125
agc gct tat tta aat gaa cta aag ctg cag ttt ccc gat gcg att atc     432
Ser Ala Tyr Leu Asn Glu Leu Lys Leu Gln Phe Pro Asp Ala Ile Ile
    130                 135                 140
atc cca gag ggc gga agc caa gcc caa gcg ctt caa ggg ata aaa gat     480
Ile Pro Glu Gly Gly Ser Gln Ala Gln Ala Leu Gln Gly Ile Lys Asp
145                 150                 155                 160
ttg gtc gat gaa atc gag gta gac ttt gat ttt atc gtc gcg cca gtc     528
Leu Val Asp Glu Ile Glu Val Asp Phe Asp Phe Ile Val Ala Pro Val
                165                 170                 175
gca agc ggc gca acc ttg gcg gga att ata aat gca tta aat aaa cgt     576
Ala Ser Gly Ala Thr Leu Ala Gly Ile Ile Asn Ala Leu Asn Lys Arg
            180                 185                 190
```

```
aat cgt aca acg gct act gac ttt cgt tct ctt cat aaa gtc att ggc        624
Asn Arg Thr Thr Ala Thr Asp Phe Arg Ser Leu His Lys Val Ile Gly
        195                 200                 205
ata ggc gta cta aaa ggt gaa ggc tat tta gag ggg ttg gtt cag aaa        672
Ile Gly Val Leu Lys Gly Glu Gly Tyr Leu Glu Gly Leu Val Gln Lys
    210                 215                 220
ttt ctt ccg ata tct aaa cac cag aca agt tgg cat att gat cat aac        720
Phe Leu Pro Ile Ser Lys His Gln Thr Ser Trp His Ile Asp His Asn
225                 230                 235                 240
tat cat ttt ggt ggc tac gcc aaa gcg cca aat gag ctt caa acc ttt        768
Tyr His Phe Gly Gly Tyr Ala Lys Ala Pro Asn Glu Leu Gln Thr Phe
                245                 250                 255
tgc aac gac ttc aat gac aac atg gaa ttt aaa ata gag cca gtt tac        816
Cys Asn Asp Phe Asn Asp Asn Met Glu Phe Lys Ile Glu Pro Val Tyr
            260                 265                 270
tca ggc aaa gcc ttc tgg gca gtt aaa gat atg ttg gct aaa ggt aag        864
Ser Gly Lys Ala Phe Trp Ala Val Lys Asp Met Leu Ala Lys Gly Lys
        275                 280                 285
ttc gaa gac cgt tct cgc att gtt gta ttg cac acg ggc ggt ttg caa        912
Phe Glu Asp Arg Ser Arg Ile Val Val Leu His Thr Gly Gly Leu Gln
    290                 295                 300
                                                                      924
ggt gca agg taa
Gly Ala Arg
305
```

<210> 263
<211> 307
<212> PRT
<213> Alteromonas macleodii 'Deep ecotype'

<400> 263

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

```
Tyr His Phe Gly Gly Tyr Ala Lys Ala Pro Asn Glu Leu Gln Thr Phe
                245                 250                 255
Cys Asn Asp Phe Asn Asp Asn Met Glu Phe Lys Ile Glu Pro Val Tyr
            260                 265                 270
Ser Gly Lys Ala Phe Trp Ala Val Lys Asp Met Leu Ala Lys Gly Lys
        275                 280                 285
Phe Glu Asp Arg Ser Arg Ile Val Val Leu His Thr Gly Gly Leu Gln
    290                 295                 300
Gly Ala Arg
305

<210> 264
<211> 927
<212> DNA
<213> Polaribacter irgensii 23-P

<220>
<221> CDS
<222> (1)..(927)
<223> transl_table=11

<400> 264
ttg att aaa gaa act aaa aat caa caa gtt att ctt cca att tta gaa      48
Met Ile Lys Glu Thr Lys Asn Gln Gln Val Ile Leu Pro Ile Leu Glu
1               5                   10                  15
gaa aaa aaa gtg acg ctt ttt ata aaa aga gaa gat tta att cac cct      96
Glu Lys Lys Val Thr Leu Phe Ile Lys Arg Glu Asp Leu Ile His Pro
            20                  25                  30
tac gtt tcg gga aac aag ttt cga aaa tta aag tac aat cta caa gaa     144
Tyr Val Ser Gly Asn Lys Phe Arg Lys Leu Lys Tyr Asn Leu Gln Glu
        35                  40                  45
gca aaa aaa cta aaa aag aaa tca tta ctt acc ttt gga ggg gca ttt     192
Ala Lys Lys Leu Lys Lys Lys Ser Leu Leu Thr Phe Gly Gly Ala Phe
    50                  55                  60
tcc aat cat att tta gca acg gca gtt gcg gga aag ttg gca ggt ttt     240
Ser Asn His Ile Leu Ala Thr Ala Val Ala Gly Lys Leu Ala Gly Phe
65                  70                  75                  80
aag acc ttt gga gtt att agg gga gat gag ttg ggt aaa aac ctt gta     288
Lys Thr Phe Gly Val Ile Arg Gly Asp Glu Leu Gly Lys Asn Leu Val
                85                  90                  95
aaa act tta gaa ggg aat gca act tta agg aag gca cac gaa aac gga     336
Lys Thr Leu Glu Gly Asn Ala Thr Leu Arg Lys Ala His Glu Asn Gly
            100                 105                 110
atg aag ttg cag ttt gtg aca cga gag caa tat cgg cag aaa gcc tca     384
Met Lys Leu Gln Phe Val Thr Arg Glu Gln Tyr Arg Gln Lys Ala Ser
        115                 120                 125
ttt gga ttt att gaa aag atg aaa aat aaa tgg ggg gat ttt tat tta     432
Phe Gly Phe Ile Glu Lys Met Lys Asn Lys Trp Gly Asp Phe Tyr Leu
    130                 135                 140
att ccc gag gga gga aca aac ggt tta gca gta gca ggt tgt gaa gaa     480
Ile Pro Glu Gly Gly Thr Asn Gly Leu Ala Val Ala Gly Cys Glu Glu
145                 150                 155                 160
att tta aca aaa gaa gat tcg gaa ttt aat tat att tgc agc gcc gtg     528
Ile Leu Thr Lys Glu Asp Ser Glu Phe Asn Tyr Ile Cys Ser Ala Val
                165                 170                 175
gga aca gga ggt act att tct ggt ttg ata aag tca tta cag aag cac     576
Gly Thr Gly Gly Thr Ile Ser Gly Leu Ile Lys Ser Leu Gln Lys His
            180                 185                 190
caa aaa gta ata ggc ttc cct gct ttg aaa gga aat ttt tta tct gaa     624
Gln Lys Val Ile Gly Phe Pro Ala Leu Lys Gly Asn Phe Leu Ser Glu
        195                 200                 205
```

```
gag att aaa aaa tat aca att aga aaa gac aac tgg agt ttg caa act       672
Glu Ile Lys Lys Tyr Thr Ile Arg Lys Asp Asn Trp Ser Leu Gln Thr
    210                 215                 220
gcg tat cat ttt gga ggg tac gca aag cac act gca gaa tta att gac       720
Ala Tyr His Phe Gly Gly Tyr Ala Lys His Thr Ala Glu Leu Ile Asp
225                 230                 235                 240
ttt atc aat agc ttt aag gag acc aca gga att cta tta gac cct gtt       768
Phe Ile Asn Ser Phe Lys Glu Thr Thr Gly Ile Leu Leu Asp Pro Val
                245                 250                 255
tat act ggt aaa atg cta ttt gga att tta gac tta att aaa aat gac       816
Tyr Thr Gly Lys Met Leu Phe Gly Ile Leu Asp Leu Ile Lys Asn Asp
            260                 265                 270
ggt ttt gag gaa ggg agt cat att tta gca att cat acg gga gga atc       864
Gly Phe Glu Glu Gly Ser His Ile Leu Ala Ile His Thr Gly Gly Ile
        275                 280                 285
caa ggt att gaa ggg ttt aac caa aaa tta atg gat aaa aac gaa caa       912
Gln Gly Ile Glu Gly Phe Asn Gln Lys Leu Met Asp Lys Asn Glu Gln
    290                 295                 300
atc ata gcc ctt taa                                                  927
Ile Ile Ala Leu
305
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<210> 265
<211> 308
<212> PRT
<213> Polaribacter irgensii 23-P

<400> 265

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

```
          260                 265                 270
Gly Phe Glu Glu Gly Ser His Ile Leu Ala Ile His Thr Gly Gly Ile
       275                 280                 285
Gln Gly Ile Glu Gly Phe Asn Gln Lys Leu Met Asp Lys Asn Glu Gln
    290                 295                 300
Ile Ile Ala Leu
305

<210> 266
<211> 906
<212> DNA
<213> Robiginitalea biformata HTCC2501

<220>
<221> CDS
<222> (1)..(906)
<223> transl_table=11

<400> 266
atg tcg gag gca gcc acc tgc gag att gac ctt ccc ata ctt cgg gag      48
Met Ser Glu Ala Ala Thr Cys Glu Ile Asp Leu Pro Ile Leu Arg Glu
1               5                  10                  15
cgg gac gtc cgg ctt tgg atc cgt cgg gaa gat gaa tta ttt ccg ggt      96
Arg Asp Val Arg Leu Trp Ile Arg Arg Glu Asp Glu Leu Phe Pro Gly
            20                  25                  30
ctg tcc ggg aac aaa tac cga aaa ctc aag tac aac att cgg gag atg     144
Leu Ser Gly Asn Lys Tyr Arg Lys Leu Lys Tyr Asn Ile Arg Glu Met
        35                  40                  45
caa cgg ggc ggg cac caa acc ctg ctc acc ttc ggg ggt gcc ttt tcc     192
Gln Arg Gly Gly His Gln Thr Leu Leu Thr Phe Gly Gly Ala Phe Ser
    50                  55                  60
aac cat atc cac gcc gtg gct gcc gcg gga cgg cag ttc ggg ttt cgg     240
Asn His Ile His Ala Val Ala Ala Ala Gly Arg Gln Phe Gly Phe Arg
65                  70                  75                  80
gcc atc gga gtc atc cgc ggg gac gag ctg gcg gtt tcc ccc ctg aac     288
Ala Ile Gly Val Ile Arg Gly Asp Glu Leu Ala Val Ser Pro Leu Asn
                85                  90                  95
cct acg ttg gcg gat gcc cgg gat gca ggc atg cat ttg cat ttt gtc     336
Pro Thr Leu Ala Asp Ala Arg Asp Ala Gly Met His Leu His Phe Val
            100                 105                 110
tcc cgt cgg gac tat gcc cgg cga caa tcc ccg gaa tac ctt cag gaa     384
Ser Arg Arg Asp Tyr Ala Arg Arg Gln Ser Pro Glu Tyr Leu Gln Glu
        115                 120                 125
cta ctg ggg caa ttt ggc ccg gct tac ctg ctc ccg gaa ggg ggg aca     432
Leu Leu Gly Gln Phe Gly Pro Ala Tyr Leu Leu Pro Glu Gly Gly Thr
    130                 135                 140
aac ccg gcg gcc gtc cgg ggc tgt gcc gaa atc ctc ggc gag gcc gat     480
Asn Pro Ala Ala Val Arg Gly Cys Ala Glu Ile Leu Gly Glu Ala Asp
145                 150                 155                 160
gcc gga ttc gac cgg gtt tgc tgc ccc gta ggc acc ggg ggt acc ctg     528
Ala Gly Phe Asp Arg Val Cys Cys Pro Val Gly Thr Gly Gly Thr Leu
                165                 170                 175
gcc gga ctg gcg gct gca gca gtg ccg ggg cag cag gtc cgc gga tat     576
Ala Gly Leu Ala Ala Ala Ala Val Pro Gly Gln Gln Val Arg Gly Tyr
            180                 185                 190
gca tcg cta aag gca tcc ggc ctg gaa gcc agc ttg cgg gac tgg att     624
Ala Ser Leu Lys Ala Ser Gly Leu Glu Ala Ser Leu Arg Asp Trp Ile
        195                 200                 205
ccg ggg aaa cac tgg aca ctg tcc ggg gag ttt cat ttt ggg ggg tat     672
Pro Gly Lys His Trp Thr Leu Ser Gly Glu Phe His Phe Gly Gly Tyr
    210                 215                 220
```

```
gcc cga atc gat gcc cgc ctg gtc cgt ttt atc aat gat ttc cga acc        720
Ala Arg Ile Asp Ala Arg Leu Val Arg Phe Ile Asn Asp Phe Arg Thr
225                 230                 235                 240
gaa acc ggg gtg ccc ctg gac ccg gta tat acg ggc aaa atg ctc tac        768
Glu Thr Gly Val Pro Leu Asp Pro Val Tyr Thr Gly Lys Met Leu Tyr
                245                 250                 255
ggc atc ctg gag gag acc cga cgg ggg cag ttt caa ccg ggg acg cgg        816
Gly Ile Leu Glu Glu Thr Arg Arg Gly Gln Phe Gln Pro Gly Thr Arg
            260                 265                 270
atc ctc gcc atc cac acc ggg ggg ttg cag gga atc cgg ggc atg aac        864
Ile Leu Ala Ile His Thr Gly Gly Leu Gln Gly Ile Arg Gly Met Asn
        275                 280                 285
ctg aaa ttg ggg aaa aag ggc tta cct ttg ttg caa cta tga                906
Leu Lys Leu Gly Lys Lys Gly Leu Pro Leu Leu Gln Leu
    290                 295                 300
```

<210> 267
<211> 301
<212> PRT
<213> Robiginitalea biformata HTCC2501

<400> 267

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Met Ser Glu Ala Ala Thr Cys Glu Ile Asp Leu Pro Ile Leu Arg Glu
1               5                   10                  15
Arg Asp Val Arg Leu Trp Ile Arg Arg Glu Asp Glu Leu Phe Pro Gly
            20                  25                  30
Leu Ser Gly Asn Lys Tyr Arg Lys Leu Lys Tyr Asn Ile Arg Glu Met
        35                  40                  45
Gln Arg Gly Gly His Gln Thr Leu Leu Thr Phe Gly Gly Ala Phe Ser
    50                  55                  60
Asn His Ile His Ala Val Ala Ala Ala Gly Arg Gln Phe Gly Phe Arg
65                  70                  75                  80
Ala Ile Gly Val Ile Arg Gly Asp Glu Leu Ala Val Ser Pro Leu Asn
                85                  90                  95
Pro Thr Leu Ala Asp Ala Arg Asp Ala Gly Met His Leu His Phe Val
            100                 105                 110
Ser Arg Arg Asp Tyr Ala Arg Arg Gln Ser Pro Glu Tyr Leu Gln Glu
        115                 120                 125
Leu Leu Gly Gln Phe Gly Pro Ala Tyr Leu Leu Pro Glu Gly Gly Thr
    130                 135                 140
Asn Pro Ala Ala Val Arg Gly Cys Ala Glu Ile Leu Gly Glu Ala Asp
145                 150                 155                 160
Ala Gly Phe Asp Arg Val Cys Cys Pro Val Gly Thr Gly Gly Thr Leu
                165                 170                 175
Ala Gly Leu Ala Ala Ala Ala Val Pro Gly Gln Gln Val Arg Gly Tyr
            180                 185                 190
Ala Ser Leu Lys Ala Ser Gly Leu Glu Ala Ser Leu Arg Asp Trp Ile
        195                 200                 205
Pro Gly Lys His Trp Thr Leu Ser Gly Glu Phe His Phe Gly Gly Tyr
    210                 215                 220
Ala Arg Ile Asp Ala Arg Leu Val Arg Phe Ile Asn Asp Phe Arg Thr
225                 230                 235                 240
Glu Thr Gly Val Pro Leu Asp Pro Val Tyr Thr Gly Lys Met Leu Tyr
                245                 250                 255
Gly Ile Leu Glu Glu Thr Arg Arg Gly Gln Phe Gln Pro Gly Thr Arg
            260                 265                 270
Ile Leu Ala Ile His Thr Gly Gly Leu Gln Gly Ile Arg Gly Met Asn
        275                 280                 285
Leu Lys Leu Gly Lys Lys Gly Leu Pro Leu Leu Gln Leu
    290                 295                 300
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<210> 268
<211> 1008
<212> DNA
<213> marine actinobacterium PHSC20C1

<220>
<221> CDS
<222> (1)..(1008)
<223> transl_table=11

<400> 268
atg ggc att gca gac ttt gaa cgc tac ccc ctc acc ttc ggt ccc agc 48
Met Gly Ile Ala Asp Phe Glu Arg Tyr Pro Leu Thr Phe Gly Pro Ser
1 5 10 15
ccg gtg cac cca ctc caa cgc ctg agc gcc cac ctc ggc gga gcg acc 96
Pro Val His Pro Leu Gln Arg Leu Ser Ala His Leu Gly Gly Ala Thr
20 25 30
gtg tgg gcc aaa cga gaa gac gta aat agc ggc cta gcc ttc gga ggc 144
Val Trp Ala Lys Arg Glu Asp Val Asn Ser Gly Leu Ala Phe Gly Gly
35 40 45
aac aag acc cgc aaa ctc gaa tac att gtt ccc gac gcc atc gcc cag 192
Asn Lys Thr Arg Lys Leu Glu Tyr Ile Val Pro Asp Ala Ile Ala Gln
50 55 60
ggc gca gat aca ctc gtt tcc atc ggc ggc tac cag tcc aac cac aca 240
Gly Ala Asp Thr Leu Val Ser Ile Gly Gly Tyr Gln Ser Asn His Thr
65 70 75 80
cgt caa gtt gcc gca gtc gcc gca aag atc ggc atg aag gct gtg ctt 288
Arg Gln Val Ala Ala Val Ala Ala Lys Ile Gly Met Lys Ala Val Leu
85 90 95
gtg caa gaa aat tgg gtc gac tgg ccc gac ccg ctc agc gac cgt gtc 336
Val Gln Glu Asn Trp Val Asp Trp Pro Asp Pro Leu Ser Asp Arg Val
100 105 110
ggc aac atc caa ctc tct cga atc atg ggg gcg gat gtt cgg ctc gac 384
Gly Asn Ile Gln Leu Ser Arg Ile Met Gly Ala Asp Val Arg Leu Asp
115 120 125
aac tcc ggc ttc gac atc ggc att cgc gac agt tgg aaa aac gcg atc 432
Asn Ser Gly Phe Asp Ile Gly Ile Arg Asp Ser Trp Lys Asn Ala Ile
130 135 140
gct gat gtg gaa gcc tct ggc ggc aag ccg tac gcc atc ccg gct gga 480
Ala Asp Val Glu Ala Ser Gly Gly Lys Pro Tyr Ala Ile Pro Ala Gly
145 150 155 160
gca tcc gaa cac cac ctg ggc ggt ctc ggg ttc gca aac tgg gcc tac 528
Ala Ser Glu His His Leu Gly Gly Leu Gly Phe Ala Asn Trp Ala Tyr
165 170 175
gag gtg gaa gtg caa gag cgt gaa ctt gga gtg ttc ttt gac acg atc 576
Glu Val Glu Val Gln Glu Arg Glu Leu Gly Val Phe Phe Asp Thr Ile
180 185 190
gtt gtt tgc acc gtc acc gga tca acg cac gcg gga atg att gca ggc 624
Val Val Cys Thr Val Thr Gly Ser Thr His Ala Gly Met Ile Ala Gly
195 200 205
ttt gcc ggg caa gat cgc cca cgc cgt gta atc gga atc gat gcc tca 672
Phe Ala Gly Gln Asp Arg Pro Arg Arg Val Ile Gly Ile Asp Ala Ser
210 215 220
gcg act ctc gag aag acg cga gat caa gtc gcg agg atc gca cgt cac 720
Ala Thr Leu Glu Lys Thr Arg Asp Gln Val Ala Arg Ile Ala Arg His
225 230 235 240
aca gcg caa ttg atc ggt ctc gaa cgt gaa ctg cgg gat gac gag atc 768
Thr Ala Gln Leu Ile Gly Leu Glu Arg Glu Leu Arg Asp Asp Glu Ile
245 250 255
tcg gtt ctc gaa ggc tgg gct ggc gac ctc tat gga atc ccc gtc gat 816
Ser Val Leu Glu Gly Trp Ala Gly Asp Leu Tyr Gly Ile Pro Val Asp

```
          260                 265                 270
tcg act ctc gaa gca atc cgc ttg ggc gga acg ctt gaa gga atg atc      864
Ser Thr Leu Glu Ala Ile Arg Leu Gly Gly Thr Leu Glu Gly Met Ile
      275                 280                 285
acc gac acc gtc tac gag gga aag tct ctt gcc ggc ctc atc gag tta      912
Thr Asp Thr Val Tyr Glu Gly Lys Ser Leu Ala Gly Leu Ile Glu Leu
  290                 295                 300
gtc tcc agc cgc gac att cct gca gac agc aac gtg ctc tac gct cac      960
Val Ser Ser Arg Asp Ile Pro Ala Asp Ser Asn Val Leu Tyr Ala His
305                 310                 315                 320
ctc ggt ggc caa ctc tcg ctc aac gcc tac agc gga cta ttt cgc          1005
Leu Gly Gly Gln Leu Ser Leu Asn Ala Tyr Ser Gly Leu Phe Arg
                325                 330                 335
taa                                                                  1008
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<210> 269
<211> 335
<212> PRT
<213> marine actinobacterium PHSC20C1

<400> 269

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

```
Val Ser Ser Arg Asp Ile Pro Ala Asp Ser Asn Val Leu Tyr Ala His
305                 310                 315                 320
Leu Gly Gly Gln Leu Ser Leu Asn Ala Tyr Ser Gly Leu Phe Arg
                325                 330                 335

<210> 270
<211> 1005
<212> DNA
<213> Desulfotomaculum reducens MI-1

<220>
<221> CDS
<222> (1)..(1005)
<223> transl_table=11

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

```
tta gag ata aaa caa gaa atc ccg agg gaa gct gta agt gta tac gat        768
Leu Glu Ile Lys Gln Glu Ile Pro Arg Glu Ala Val Ser Val Tyr Asp
                245                 250                 255
gat tat gtt ggc cct ggt tat tcc ttg cct act ccg gaa atg gtt gaa        816
Asp Tyr Val Gly Pro Gly Tyr Ser Leu Pro Thr Pro Glu Met Val Glu
            260                 265                 270
gcg gta caa cta ttg gcc aga aca gaa ggt att ttg ctt gac cct gta        864
Ala Val Gln Leu Leu Ala Arg Thr Glu Gly Ile Leu Leu Asp Pro Val
        275                 280                 285
tac act ggt aaa gca atg tct ggc tta ata gga ctt gtt cgt aag ggc        912
Tyr Thr Gly Lys Ala Met Ser Gly Leu Ile Gly Leu Val Arg Lys Gly
    290                 295                 300
ttt ttc aag aaa gac cag aat gtc cta ttc atc cat act ggt ggt tct        960
Phe Phe Lys Lys Asp Gln Asn Val Leu Phe Ile His Thr Gly Gly Ser
305                 310                 315                 320
cct gcg tta tat gct tat acg tca act atc ctg ggc aac gat taa           1005
Pro Ala Leu Tyr Ala Tyr Thr Ser Thr Ile Leu Gly Asn Asp
                325                 330
```

<210> 271
<211> 334
<212> PRT
<213> Desulfotomaculum reducens MI-1

<400> 271

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

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

<210> 272
<211> 1005
<212> DNA
<213> Desulfotomaculum reducens MI-1

<220>
<221> CDS
<222> (1)..(1005)
<223> transl_table=11

<400> 272

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

```
Asp Gln Glu Glu Leu Val Tyr Ser Val Ile Gln Lys Thr Ala Ala Leu
225                 230                 235                 240
tta gag ata aaa caa gaa atc ccg agg gaa gct gta agt gta tac gat      768
Leu Glu Ile Lys Gln Glu Ile Pro Arg Glu Ala Val Ser Val Tyr Asp
                245                 250                 255
gat tac gtt ggc cct ggc tat tcc ttg cct act ccg gaa atg gtt gaa      816
Asp Tyr Val Gly Pro Gly Tyr Ser Leu Pro Thr Pro Glu Met Val Glu
            260                 265                 270
gcg gta caa cta ttg gcc aga aca gaa ggt att ttg ctt gac cct gta      864
Ala Val Gln Leu Leu Ala Arg Thr Glu Gly Ile Leu Leu Asp Pro Val
        275                 280                 285
tac act ggt aaa gca atg tct ggc tta ata gga ctt gtt cgt aag ggc      912
Tyr Thr Gly Lys Ala Met Ser Gly Leu Ile Gly Leu Val Arg Lys Gly
    290                 295                 300
ttt ttc aag aaa gac cag aat gtt cta ttc atc cat act ggt ggt tct      960
Phe Phe Lys Lys Asp Gln Asn Val Leu Phe Ile His Thr Gly Gly Ser
305                 310                 315                 320
cct gct tta tat gct tac acg tca act atc ctg ggc aac gat taa         1005
Pro Ala Leu Tyr Ala Tyr Thr Ser Thr Ile Leu Gly Asn Asp
                325                 330
```

<210> 273
<211> 334
<212> PRT
<213> Desulfotomaculum reducens MI-1

<400> 273

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

```
Ala Val Gln Leu Leu Ala Arg Thr Glu Gly Ile Leu Leu Asp Pro Val
        275                 280                 285
Tyr Thr Gly Lys Ala Met Ser Gly Leu Ile Gly Leu Val Arg Lys Gly
    290                 295                 300
Phe Phe Lys Lys Asp Gln Asn Val Leu Phe Ile His Thr Gly Gly Ser
305                 310                 315                 320
Pro Ala Leu Tyr Ala Tyr Thr Ser Thr Ile Leu Gly Asn Asp
                325                 330
```

<210> 274
<211> 924
<212> DNA
<213> Oceanospirillum sp. MED92

<220>
<221> CDS
<222> (1)..(924)
<223> transl_table=11

<400> 274

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

```
   210                 215                 220
ttg gat ctg gag ggg cat ttt ggt ggc tat ggg aag gtc agt gat cag      720
Leu Asp Leu Glu Gly His Phe Gly Gly Tyr Gly Lys Val Ser Asp Gln
225                 230                 235                 240
ctg ctg caa ttc atg cag tct ttt gaa gtg aat aat cag atc cag cta      768
Leu Leu Gln Phe Met Gln Ser Phe Glu Val Asn Asn Gln Ile Gln Leu
                245                 250                 255
gat cca atc tat acg gct aag atg atg ctg cgg att ttt cag cgg atc      816
Asp Pro Ile Tyr Thr Ala Lys Met Met Leu Arg Ile Phe Gln Arg Ile
            260                 265                 270
gag ctt ggg gaa tat agc cgt ggg agc cgt cta ttg gcg atc cat acc      864
Glu Leu Gly Glu Tyr Ser Arg Gly Ser Arg Leu Leu Ala Ile His Thr
        275                 280                 285
ggg ggg ctg caa gga aga agg gga gca ggt tgt tca gcg gta ccg gct      912
Gly Gly Leu Gln Gly Arg Arg Gly Ala Gly Cys Ser Ala Val Pro Ala
    290                 295                 300
aat tgc aca taa                                                     924
Asn Cys Thr
305
```

<210> 275
<211> 307
<212> PRT
<213> Oceanospirillum sp. MED92

<400> 275

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

```
      275                 280                 285
Gly Gly Leu Gln Gly Arg Arg Gly Ala Gly Cys Ser Ala Val Pro Ala
   290                 295                 300
Asn Cys Thr
305

<210> 276
<211> 996
<212> DNA
<213> Bacillus weihenstephanensis KBAB4

<220>
<221> CDS
<222> (1)..(996)
<223> transl_table=11

<400> 276
atg aat tta gct aaa ttt ccg aga aaa aaa tat aca gaa tca tat aca        48
Met Asn Leu Ala Lys Phe Pro Arg Lys Lys Tyr Thr Glu Ser Tyr Thr
1               5                  10                  15
cca att gaa aaa tta aac aat ttt tct gaa gca ctt ggt ggg cca act        96
Pro Ile Glu Lys Leu Asn Asn Phe Ser Glu Ala Leu Gly Gly Pro Thr
            20                  25                  30
att tat ttt aaa cga gat gat tta ctt ggt tta aca gct ggc ggt aat       144
Ile Tyr Phe Lys Arg Asp Asp Leu Leu Gly Leu Thr Ala Gly Gly Asn
        35                  40                  45
aag acg aga aag tta gag ttt cta gtt gcg gat gca cag gca aag ggt       192
Lys Thr Arg Lys Leu Glu Phe Leu Val Ala Asp Ala Gln Ala Lys Gly
    50                  55                  60
gca gat acg tta att aca gct ggt ggt att cag tca aac cat tgc cgt       240
Ala Asp Thr Leu Ile Thr Ala Gly Gly Ile Gln Ser Asn His Cys Arg
65                  70                  75                  80
cta aca ctt gca gct gcg gta aaa gaa aaa atg aaa tgt att ctt gtg       288
Leu Thr Leu Ala Ala Ala Val Lys Glu Lys Met Lys Cys Ile Leu Val
                85                  90                  95
cta gaa gaa ggg ctt gag cca gaa gaa aag cca gac ttt aac gga aac       336
Leu Glu Glu Gly Leu Glu Pro Glu Glu Lys Pro Asp Phe Asn Gly Asn
            100                 105                 110
tat ttc tta tat cat tta tta ggt gct gaa aac gta att gtt gtg cca       384
Tyr Phe Leu Tyr His Leu Leu Gly Ala Glu Asn Val Ile Val Val Pro
        115                 120                 125
aac gga gca gat ctt atg gaa gag atg cat aaa gta gcg aaa gaa gtt       432
Asn Gly Ala Asp Leu Met Glu Glu Met His Lys Val Ala Lys Glu Val
    130                 135                 140
agt gaa aaa ggt aat aca cca tat gta ata cca gtt ggt gga tca aat       480
Ser Glu Lys Gly Asn Thr Pro Tyr Val Ile Pro Val Gly Gly Ser Asn
145                 150                 155                 160
cct act ggt gca atg gga tac att gct tgt gcg caa gaa att atg gcg       528
Pro Thr Gly Ala Met Gly Tyr Ile Ala Cys Ala Gln Glu Ile Met Ala
                165                 170                 175
caa tca ttc gag caa gga att gat ttc agt tca gtt gtt tgt gta agt       576
Gln Ser Phe Glu Gln Gly Ile Asp Phe Ser Ser Val Val Cys Val Ser
            180                 185                 190
ggt agc gct ggt atg cat gct ggt tta att act ggt ttt tct gga acg       624
Gly Ser Ala Gly Met His Ala Gly Leu Ile Thr Gly Phe Ser Gly Thr
        195                 200                 205
caa agc aaa att cct gta atc gga att aac gta agt aga gga aaa gcg       672
Gln Ser Lys Ile Pro Val Ile Gly Ile Asn Val Ser Arg Gly Lys Ala
    210                 215                 220
gag caa gaa gag aaa gta gca aaa ctt gta gat gaa act tca gct cac       720
Glu Gln Glu Glu Lys Val Ala Lys Leu Val Asp Glu Thr Ser Ala His
```

```
225                 230                 235                 240
gtt ggt atc cca aac tct att tca cgc gag gca gtt aca tgc ttt gat      768
Val Gly Ile Pro Asn Ser Ile Ser Arg Glu Ala Val Thr Cys Phe Asp
                245                 250                 255
gaa tat gta gga cca gga tac gct tta cca aca cca gaa atg gtt gaa      816
Glu Tyr Val Gly Pro Gly Tyr Ala Leu Pro Thr Pro Glu Met Val Glu
            260                 265                 270
gca gta cag tta ctt gcg aaa aca gaa ggt att tta ctt gac cca gtt      864
Ala Val Gln Leu Leu Ala Lys Thr Glu Gly Ile Leu Leu Asp Pro Val
        275                 280                 285
tat aca ggt aaa gca gta gca gga tta att gat tta att aga aaa ggc      912
Tyr Thr Gly Lys Ala Val Ala Gly Leu Ile Asp Leu Ile Arg Lys Gly
    290                 295                 300
aaa ttt aat aaa gaa gac aac att tta ttc gta cat tca ggt ggt tca      960
Lys Phe Asn Lys Glu Asp Asn Ile Leu Phe Val His Ser Gly Gly Ser
305                 310                 315                 320
cca gct tta tat gcg aat acg tct cta ttt gcg taa                     996
Pro Ala Leu Tyr Ala Asn Thr Ser Leu Phe Ala
                325                 330
```

<210> 277
<211> 331
<212> PRT
<213> Bacillus weihenstephanensis KBAB4

<400> 277

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

```
       275                 280                 285
Tyr Thr Gly Lys Ala Val Ala Gly Leu Ile Asp Leu Ile Arg Lys Gly
    290                 295                 300
Lys Phe Asn Lys Glu Asp Asn Ile Leu Phe Val His Ser Gly Gly Ser
305                 310                 315                 320
Pro Ala Leu Tyr Ala Asn Thr Ser Leu Phe Ala
                325                 330
```

<210> 278
<211> 996
<212> DNA
<213> Xanthobacter autotrophicus Py2

<220>
<221> CDS
<222> (1)..(996)
<223> transl_table=11

<400> 278

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

```
gcc gcc gag gcg cgc gtt cgc gtc aag gat ctc gcc gat cag gcg gcc        720
Ala Ala Glu Ala Arg Val Arg Val Lys Asp Leu Ala Asp Gln Ala Ala
225                 230                 235                 240
gat cat ctc ggc ctc ggc cgc gcc gtg ccg gcc gac gac gtg atc atc        768
Asp His Leu Gly Leu Gly Arg Ala Val Pro Ala Asp Asp Val Ile Ile
                245                 250                 255
cat gac ggc ttc atc ggc gcg ggc tac ggc atc gcc tcg ccg gcg ggc        816
His Asp Gly Phe Ile Gly Ala Gly Tyr Gly Ile Ala Ser Pro Ala Gly
            260                 265                 270
atg tcc gcg ctc gag cgg gcg gcg cgc tgc gag ggc gtg gtg ctg gat        864
Met Ser Ala Leu Glu Arg Ala Ala Arg Cys Glu Gly Val Val Leu Asp
        275                 280                 285
ccc gtc tat acg ggc aag gcc atg gcc ggc tat ggc gcg ctg gtc ggg        912
Pro Val Tyr Thr Gly Lys Ala Met Ala Gly Tyr Gly Ala Leu Val Gly
    290                 295                 300
gca ggg cgc tat ggc gag gcc gcc acc gtt ctg ttc ctg cac agc ggc        960
Ala Gly Arg Tyr Gly Glu Ala Ala Thr Val Leu Phe Leu His Ser Gly
305                 310                 315                 320
ggg ctg ccc agc ctg ttc gtc gat gga acc gcg tga                        996
Gly Leu Pro Ser Leu Phe Val Asp Gly Thr Ala
                325                 330
```

<210> 279
<211> 331
<212> PRT
<213> Xanthobacter autotrophicus Py2

<400> 279

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

```
            260                 265                 270
Met Ser Ala Leu Glu Arg Ala Ala Arg Cys Glu Gly Val Val Leu Asp
        275                 280                 285
Pro Val Tyr Thr Gly Lys Ala Met Ala Gly Tyr Gly Ala Leu Val Gly
    290                 295                 300
Ala Gly Arg Tyr Gly Glu Ala Ala Thr Val Leu Phe Leu His Ser Gly
305                 310                 315                 320
Gly Leu Pro Ser Leu Phe Val Asp Gly Thr Ala
                325                 330
```

<210> 280
<211> 996
<212> DNA
<213> Xanthobacter autotrophicus Py2

<220>
<221> CDS
<222> (1)..(996)
<223> transl_table=11

<400> 280

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

```
Leu Leu Gly Ala Ser Trp Arg Val Glu Gly Ile Thr Val Ser Arg Pro
    210                 215                 220
gcc gcc gag gcc cgc gtc cgc gtc aag gat ctc gcc gat cag gcg gcc      720
Ala Ala Glu Ala Arg Val Arg Val Lys Asp Leu Ala Asp Gln Ala Ala
225                 230                 235                 240
gat cat ctg ggc ctt gcc cgc tcc gtc gcg gcc gac gac gtg gtc atc      768
Asp His Leu Gly Leu Ala Arg Ser Val Ala Ala Asp Asp Val Val Ile
                245                 250                 255
cac gac ggc ttc atc ggc gcg ggt tac ggc atc gcc tcg ccc gcg ggc      816
His Asp Gly Phe Ile Gly Ala Gly Tyr Gly Ile Ala Ser Pro Ala Gly
            260                 265                 270
atg tcc gcg atc gaa cgc gcg gcg cgc tca gag ggc gtg gtg ctg gac      864
Met Ser Ala Ile Glu Arg Ala Ala Arg Ser Glu Gly Val Val Leu Asp
        275                 280                 285
ccc gtc tat acg ggc aag gcc atg gcc ggc tat ggc gcg ctg ctc ggc      912
Pro Val Tyr Thr Gly Lys Ala Met Ala Gly Tyr Gly Ala Leu Leu Gly
    290                 295                 300
gcg ggg cgc tat ggc gat gcc acc acc gtt ctg ttc ctg cac agc ggc      960
Ala Gly Arg Tyr Gly Asp Ala Thr Thr Val Leu Phe Leu His Ser Gly
305                 310                 315                 320
ggg ctg cca agc ctg ttc gtc gat gga aat gcg tga                       996
Gly Leu Pro Ser Leu Phe Val Asp Gly Asn Ala
                325                 330
```

<210> 281
<211> 331
<212> PRT
<213> Xanthobacter autotrophicus Py2

```
<400> 281
Met Glu Gln Pro Asp Met Arg Leu Met Glu Pro Pro Arg Leu Val Leu
1               5                   10                  15
Asn Pro Thr Val Thr Pro Leu Leu Pro Ala Pro Gln Leu Thr Gly Thr
            20                  25                  30
Leu Gly Gly Pro Glu Ile Trp Ile Lys Arg Asp Asp Leu Ile Pro Phe
        35                  40                  45
Gly Cys Gly Gly Asn Lys Ile Arg Gly Leu Glu Leu Ile Val Ala Asp
    50                  55                  60
Ala Leu Arg Ala Gly Ala Asp Thr Leu Val Thr Gly Ala Gly Thr Leu
65                  70                  75                  80
Ser Asn His Val Arg Ala Thr Ala Ala Ala Ala Ala Phe Ala Gly Leu
                85                  90                  95
Gly Met Ser Ala Val Tyr Trp Gly Asp Pro Pro Gln Lys Ala Lys Gly
            100                 105                 110
Asn His Leu Leu Ser Val Leu Trp Gly Ala Arg Thr Arg Phe Thr Gly
        115                 120                 125
Ser Ser Asp Arg Asn Ser Val Asp Ala Met Leu Glu Val Glu Ala Ala
    130                 135                 140
Asp Ile Arg Ala Ala Gly Gly Arg Pro Tyr Val Ile Pro Arg Gly Gly
145                 150                 155                 160
Ala Cys Ala Leu Gly Val Ile Gly His Val His Ala Val Gly Glu Val
                165                 170                 175
Met Ala Gln Cys Arg Gln Ala Gly Ile Arg Pro Asp Cys Val Val Met
            180                 185                 190
Ala Val Gly Ser Gly Gly Thr Leu Ala Gly Trp Leu Leu Gly Ser Arg
        195                 200                 205
Leu Leu Gly Ala Ser Trp Arg Val Glu Gly Ile Thr Val Ser Arg Pro
    210                 215                 220
Ala Ala Glu Ala Arg Val Arg Val Lys Asp Leu Ala Asp Gln Ala Ala
225                 230                 235                 240
Asp His Leu Gly Leu Ala Arg Ser Val Ala Ala Asp Asp Val Val Ile
```

```
                245                 250                 255
His Asp Gly Phe Ile Gly Ala Gly Tyr Gly Ile Ala Ser Pro Ala Gly
            260                 265                 270
Met Ser Ala Ile Glu Arg Ala Ala Arg Ser Glu Gly Val Val Leu Asp
        275                 280                 285
Pro Val Tyr Thr Gly Lys Ala Met Ala Gly Tyr Gly Ala Leu Leu Gly
    290                 295                 300
Ala Gly Arg Tyr Gly Asp Ala Thr Thr Val Leu Phe Leu His Ser Gly
305                 310                 315                 320
Gly Leu Pro Ser Leu Phe Val Asp Gly Asn Ala
                325                 330
```

<210> 282
<211> 966
<212> DNA
<213> Flavobacteria bacterium BBFL7

<220>
<221> CDS
<222> (1)..(966)
<223> transl_table=11

<400> 282

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atg aat ctc ttt gat gtt aca aat gca gtt aac caa tca ttt aaa gat      48
Met Asn Leu Phe Asp Val Thr Asn Ala Val Asn Gln Ser Phe Lys Asp
1               5                   10                  15
tat aat gac ggt aaa acg cga gta gat ata aaa cgt gaa gat tta tta      96
Tyr Asn Asp Gly Lys Thr Arg Val Asp Ile Lys Arg Glu Asp Leu Leu
            20                  25                  30
cat gag tta gtt tct ggt aat aaa ttg cgc aaa tta aaa tac aat att     144
His Glu Leu Val Ser Gly Asn Lys Leu Arg Lys Leu Lys Tyr Asn Ile
        35                  40                  45
tta gaa gcc cag cga caa ggt cat aat acc tta cta act tat gga gga     192
Leu Glu Ala Gln Arg Gln Gly His Asn Thr Leu Leu Thr Tyr Gly Gly
    50                  55                  60
gcg ttt tct aat cat att gca gcc aca gcg gct gct ggg aat att tgt     240
Ala Phe Ser Asn His Ile Ala Ala Thr Ala Ala Ala Gly Asn Ile Cys
65                  70                  75                  80
ggg ttt aag acg ata gga gtt att aga gga gaa gaa tta ggt cat aat     288
Gly Phe Lys Thr Ile Gly Val Ile Arg Gly Glu Glu Leu Gly His Asn
                85                  90                  95
cta gag aaa aca cta ggc gga aac aag act tta agt acc gca cac gca     336
Leu Glu Lys Thr Leu Gly Gly Asn Lys Thr Leu Ser Thr Ala His Ala
            100                 105                 110
tta ggc atg caa ttt aaa ttt gta tct cgt tct aat tat cga gaa aaa     384
Leu Gly Met Gln Phe Lys Phe Val Ser Arg Ser Asn Tyr Arg Glu Lys
        115                 120                 125
tat gat gat aaa ttt cag aaa gtt tta aac gca gag tat gga cat gta     432
Tyr Asp Asp Lys Phe Gln Lys Val Leu Asn Ala Glu Tyr Gly His Val
    130                 135                 140
tat cat att ccg gaa gga gga act aat cat ctt gca gtt aaa gga act     480
Tyr His Ile Pro Glu Gly Gly Thr Asn His Leu Ala Val Lys Gly Thr
145                 150                 155                 160
gaa gaa atc tta aca gtt aag gat aaa gat tac tat gat tat ata tgt     528
Glu Glu Ile Leu Thr Val Lys Asp Lys Asp Tyr Tyr Asp Tyr Ile Cys
                165                 170                 175
gtt gca gca gga act ggt ggc act gcg gct gga atc att aat agt aca     576
Val Ala Ala Gly Thr Gly Gly Thr Ala Ala Gly Ile Ile Asn Ser Thr
            180                 185                 190
gca cca cat caa aaa gta cta gtg ttc tct gca tta aaa ggt gat ttt     624
Ala Pro His Gln Lys Val Leu Val Phe Ser Ala Leu Lys Gly Asp Phe
```

```
       195                 200                 205
atg ttt gat gaa att gct cgg tac aca cat cgt gaa aat ttt atg gtg      672
Met Phe Asp Glu Ile Ala Arg Tyr Thr His Arg Glu Asn Phe Met Val
    210                 215                 220
ttt gat gaa aat aga ttc ggt ggt tat gct agg tct agt gat gga ttg      720
Phe Asp Glu Asn Arg Phe Gly Gly Tyr Ala Arg Ser Ser Asp Gly Leu
225                 230                 235                 240
ata aag ttt atg aat gga cgc ttt cgc gaa agc gta aca tca gaa aat      768
Ile Lys Phe Met Asn Gly Arg Phe Arg Glu Ser Val Thr Ser Glu Asn
                245                 250                 255
cct aag gga ata cca ctt gaa cct att tat acc gga aaa atg atg tat      816
Pro Lys Gly Ile Pro Leu Glu Pro Ile Tyr Thr Gly Lys Met Met Tyr
            260                 265                 270
cga tta gaa cat ctt gtt aag act ggc gtt ata tct gga gaa act cgt      864
Arg Leu Glu His Leu Val Lys Thr Gly Val Ile Ser Gly Glu Thr Arg
        275                 280                 285
att tta gcc atc cat act ggc ggt ttg caa agt gtc aca gga tac aat      912
Ile Leu Ala Ile His Thr Gly Gly Leu Gln Ser Val Thr Gly Tyr Asn
    290                 295                 300
gca atg cta gaa aaa aaa ggc aaa att acc tta gat tat atc aat gaa      960
Ala Met Leu Glu Lys Lys Gly Lys Ile Thr Leu Asp Tyr Ile Asn Glu
305                 310                 315                 320
att taa                                                             966
Ile
```

<210> 283
<211> 321
<212> PRT
<213> Flavobacteria bacterium BBFL7

<400> 283

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

```
225                 230                 235                 240
Ile Lys Phe Met Asn Gly Arg Phe Arg Glu Ser Val Thr Ser Glu Asn
                245                 250                 255
Pro Lys Gly Ile Pro Leu Glu Pro Ile Tyr Thr Gly Lys Met Met Tyr
            260                 265                 270
Arg Leu Glu His Leu Val Lys Thr Gly Val Ile Ser Gly Glu Thr Arg
        275                 280                 285
Ile Leu Ala Ile His Thr Gly Gly Leu Gln Ser Val Thr Gly Tyr Asn
    290                 295                 300
Ala Met Leu Glu Lys Lys Gly Lys Ile Thr Leu Asp Tyr Ile Asn Glu
305                 310                 315                 320
Ile
```

<210> 284
<211> 993
<212> DNA
<213> marine gamma proteobacterium HTCC2207

<220>
<221> CDS
<222> (1)..(993)
<223> transl_table=11

<400> 284

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

```
acc cag gcg ggt tta atg ctg ggt tgc caa ttg cat cag atc aat act        624
Thr Gln Ala Gly Leu Met Leu Gly Cys Gln Leu His Gln Ile Asn Thr
        195                 200                 205
cag gta aaa gct tat gcg gtt tgc gat aac gct gag tat ttc act cgc        672
Gln Val Lys Ala Tyr Ala Val Cys Asp Asn Ala Glu Tyr Phe Thr Arg
    210                 215                 220
aaa gtg cgc gga gat cta gag caa tgg cag agt cat tac agc ccg caa        720
Lys Val Arg Gly Asp Leu Glu Gln Trp Gln Ser His Tyr Ser Pro Gln
225                 230                 235                 240
acg gat att tca ggc ctg gtc gcc gat acc tct gat gag tat ata ggt        768
Thr Asp Ile Ser Gly Leu Val Ala Asp Thr Ser Asp Glu Tyr Ile Gly
                245                 250                 255
cca gcg tat ggg gtt gcc ggt gaa gaa gtc ttt gag tgt att aaa gag        816
Pro Ala Tyr Gly Val Ala Gly Glu Glu Val Phe Glu Cys Ile Lys Glu
            260                 265                 270
gtt gct gct cta gaa ggt att ttg ctc gac ccg gtt tat acc ggc aaa        864
Val Ala Ala Leu Glu Gly Ile Leu Leu Asp Pro Val Tyr Thr Gly Lys
        275                 280                 285
gca ttc ttc ggc atg atc gaa gat atc aaa aaa gga aaa ttc tcc caa        912
Ala Phe Phe Gly Met Ile Glu Asp Ile Lys Lys Gly Lys Phe Ser Gln
    290                 295                 300
tgg gac ggt gat gat atc gtc ttt gtc cac acc gga ggg cta ttt gga        960
Trp Asp Gly Asp Asp Ile Val Phe Val His Thr Gly Gly Leu Phe Gly
305                 310                 315                 320
tta ttc gct caa cag cat cga ctg ggc tat tag                            993
Leu Phe Ala Gln Gln His Arg Leu Gly Tyr
                325                 330
```

<210> 285
<211> 330
<212> PRT
<213> marine gamma proteobacterium HTCC2207

<400> 285

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

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

<210> 286
<211> 909
<212> DNA
<213> Flavobacterium johnsoniae UW101

<220>
<221> CDS
<222> (1)..(909)
<223> transl_table=11

<400> 286

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

```
Gly Leu Ile Asn Asn Ala Leu Pro Asn Gln Lys Ile Leu Gly Phe Pro
            180                 185                 190
gcg tta aaa ggt gac ttt tta aac gat gaa att cgt att ttt gca aaa      624
Ala Leu Lys Gly Asp Phe Leu Asn Asp Glu Ile Arg Ile Phe Ala Lys
        195                 200                 205
aaa gat aac tgg aat tta att tct gac tat cat tgt gga ggt tat ggc      672
Lys Asp Asn Trp Asn Leu Ile Ser Asp Tyr His Cys Gly Gly Tyr Gly
    210                 215                 220
aag ata aat tta gaa tta att gaa ttt att aat tct ttt ttt gaa gaa      720
Lys Ile Asn Leu Glu Leu Ile Glu Phe Ile Asn Ser Phe Phe Glu Glu
225                 230                 235                 240
aca aaa gtg ccc tta gat cca att tat aca gga aag atg gtt ttt ggc      768
Thr Lys Val Pro Leu Asp Pro Ile Tyr Thr Gly Lys Met Val Phe Gly
                245                 250                 255
gtt ata gat tta ata aac aaa aat tat ttt cct gcg cat tca aaa att      816
Val Ile Asp Leu Ile Asn Lys Asn Tyr Phe Pro Ala His Ser Lys Ile
            260                 265                 270
tta ctc att cac aca ggc gga ttg cag gga att gac gga atg aat ata      864
Leu Leu Ile His Thr Gly Gly Leu Gln Gly Ile Asp Gly Met Asn Ile
        275                 280                 285
aag ttg aag cag aag aaa tta cca ata ctc aaa acc aat gat taa          909
Lys Leu Lys Gln Lys Lys Leu Pro Ile Leu Lys Thr Asn Asp
    290                 295                 300
```

<210> 287
<211> 302
<212> PRT
<213> Flavobacterium johnsoniae UW101

<400> 287

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

```
                245                 250                 255
Val Ile Asp Leu Ile Asn Lys Asn Tyr Phe Pro Ala His Ser Lys Ile
            260                 265                 270
Leu Leu Ile His Thr Gly Gly Leu Gln Gly Ile Asp Gly Met Asn Ile
        275                 280                 285
Lys Leu Lys Gln Lys Lys Leu Pro Ile Leu Lys Thr Asn Asp
    290                 295                 300

<210> 288
<211> 951
<212> DNA
<213> Psychroflexus torquis ATCC 700755

<220>
<221> CDS
<222> (1)..(951)
<223> transl_table=11

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

```
tcc aat tgg tca ctt caa acc gac ttt cat ttt gga ggc tat gct aaa        720
Ser Asn Trp Ser Leu Gln Thr Asp Phe His Phe Gly Gly Tyr Ala Lys
225                 230                 235                 240
gta aat tca gaa ttg ata gac ttc ata aat tcc ttt caa agt aaa tat        768
Val Asn Ser Glu Leu Ile Asp Phe Ile Asn Ser Phe Gln Ser Lys Tyr
                245                 250                 255
caa att caa ctg gac ccc att tat acc ggg aag atg ttt tac ggc att        816
Gln Ile Gln Leu Asp Pro Ile Tyr Thr Gly Lys Met Phe Tyr Gly Ile
            260                 265                 270
ttc gaa tta ata tcc tca ggt ttt ttt tcc aaa aat act cgt att tta        864
Phe Glu Leu Ile Ser Ser Gly Phe Phe Ser Lys Asn Thr Arg Ile Leu
        275                 280                 285
gca att cat acg gga ggc ctt caa ggt att gaa ggt ata aac cgt agc        912
Ala Ile His Thr Gly Gly Leu Gln Gly Ile Glu Gly Ile Asn Arg Ser
    290                 295                 300
cta aaa caa aaa gga ctt caa acc att acc ctt tta tga                    951
Leu Lys Gln Lys Gly Leu Gln Thr Ile Thr Leu Leu
305                 310                 315
```

<210> 289
<211> 316
<212> PRT
<213> Psychroflexus torquis ATCC 700755

<400> 289

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

```
Ala Ile His Thr Gly Gly Leu Gln Gly Ile Glu Gly Ile Asn Arg Ser
    290                 295                 300
Leu Lys Gln Lys Gly Leu Gln Thr Ile Thr Leu Leu
305                 310                 315

<210> 290
<211> 933
<212> DNA
<213> Pseudomonas aeruginosa PA7

<220>
<221> CDS
<222> (1)..(933)

<400> 290
ttg ccg ttt ccc gac tgg tcc ccg cac gcc acc ctg caa cgc atc gaa        48
Met Pro Phe Pro Asp Trp Ser Pro His Ala Thr Leu Gln Arg Ile Glu
1               5                   10                  15
acc gac tgg ctg gcc cgc gcc ggg gtc gaa ctg gcg ctg ctg cgc ctg        96
Thr Asp Trp Leu Ala Arg Ala Gly Val Glu Leu Ala Leu Leu Arg Leu
            20                  25                  30
gac cag gtc gat ccg ctg att tcc ggc aac aag ggt ttc aag ctc gcc       144
Asp Gln Val Asp Pro Leu Ile Ser Gly Asn Lys Gly Phe Lys Leu Ala
        35                  40                  45
ccg tac ctg gcg cag gcc cgc gag cgc ggg ttg gac ggc ctg atc agc       192
Pro Tyr Leu Ala Gln Ala Arg Glu Arg Gly Leu Asp Gly Leu Ile Ser
    50                  55                  60
ctc ggc ggc gcc cat tcc aac cac ctg cat gcg ctg gcc ggc gcc gct       240
Leu Gly Gly Ala His Ser Asn His Leu His Ala Leu Ala Gly Ala Ala
65                  70                  75                  80
gcg cgt ttc ggc ttc cgc tgc gtc ggc ctg gta cgc gga aac gaa gtc       288
Ala Arg Phe Gly Phe Arg Cys Val Gly Leu Val Arg Gly Asn Glu Val
                85                  90                  95
gat acg ccg acg gta cgc gac ctg cgc agt ctc ggc atg gaa ctg cac       336
Asp Thr Pro Thr Val Arg Asp Leu Arg Ser Leu Gly Met Glu Leu His
            100                 105                 110
tgg ctc ggc tac ggc ggc tat cgc cag cgg cac gcc ggc ggt ttc tgg       384
Trp Leu Gly Tyr Gly Gly Tyr Arg Gln Arg His Ala Gly Gly Phe Trp
        115                 120                 125
gcg ccc tgg cgg gag cgt tat ccc ggg ttg ctg ccg gtc gcc gag ggc       432
Ala Pro Trp Arg Glu Arg Tyr Pro Gly Leu Leu Pro Val Ala Glu Gly
    130                 135                 140
ggt ggc ggg ctg ctg ggc gcg cgt ggt tgc agc ggg ctg gtg gag cgc       480
Gly Gly Gly Leu Leu Gly Ala Arg Gly Cys Ser Gly Leu Val Glu Arg
145                 150                 155                 160
ata gcg acc cag ttg ccg acg ctc ggc tgg gac gat tac gac gcc gtc       528
Ile Ala Thr Gln Leu Pro Thr Leu Gly Trp Asp Asp Tyr Asp Ala Val
                165                 170                 175
tgg gtg gcc gcc ggc acc ggt acg aca ctg gcc ggc ctg gtg ctt ggc       576
Trp Val Ala Ala Gly Thr Gly Thr Thr Leu Ala Gly Leu Val Leu Gly
            180                 185                 190
gag gcc ggg cgg cat ccg gtg gtg ggc gcc ctg gcg gtg ccg gag gac       624
Glu Ala Gly Arg His Pro Val Val Gly Ala Leu Ala Val Pro Glu Asp
        195                 200                 205
cac ggc gtc gcc gcg cag gtg gcg acg act ctc gcc gca gcg ggc gtc       672
His Gly Val Ala Ala Gln Val Ala Thr Thr Leu Ala Ala Ala Gly Val
    210                 215                 220
gcc gat gcc ggc tat cgc ctg ctg gac gcc agc cgc ggc ggc ttc gcc       720
Ala Asp Ala Gly Tyr Arg Leu Leu Asp Ala Ser Arg Gly Gly Phe Ala
225                 230                 235                 240
cgc ctc gat ggc gcg ctg gcg cgg ttc atc gtc ggc ttc gag acg gcc       768
```

```
Arg Leu Asp Gly Ala Leu Ala Arg Phe Ile Val Gly Phe Glu Thr Ala
                245                 250                 255
agt ggc gtc gcc ctg gaa ccg ctg tac acc ggc aag ctg ctg ctc gcc      816
Ser Gly Val Ala Leu Glu Pro Leu Tyr Thr Gly Lys Leu Leu Leu Ala
            260                 265                 270
ctg cgc ggg gca gtg gag cgc ggc gag gtg gct cgt ggc agc cgc ctg      864
Leu Arg Gly Ala Val Glu Arg Gly Glu Val Ala Arg Gly Ser Arg Leu
        275                 280                 285
gtg gcg cta cac acc gga ggc ctg cag ggg cgc cgg gcg ctg cag gag      912
Val Ala Leu His Thr Gly Gly Leu Gln Gly Arg Arg Ala Leu Gln Glu
    290                 295                 300
cgt ctg ctg gca ctg ctc tga                                        933
Arg Leu Leu Ala Leu Leu
305                 310
```

<210> 291
<211> 310
<212> PRT
<213> Pseudomonas aeruginosa PA7

<400> 291

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

<210> 292
<211> 1020
<212> DNA
<213> Rhizobium meliloti

<220>
<221> CDS
<222> (1)..(1020)
<223> transl_table=11

<400> 292

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

```
Glu Ile Val Ile Asn Pro Asp Tyr Ala Tyr Pro Ala Tyr Gly Val Pro
            260                 265                 270
tcg gag gag acc aac gag gcg atc cgg ctc gcg gcg cgc acc gag gcg      864
Ser Glu Glu Thr Asn Glu Ala Ile Arg Leu Ala Ala Arg Thr Glu Ala
        275                 280                 285
atg att acc gac ccg gtc tat gag gga aag tcg atg cag ggg atg atc      912
Met Ile Thr Asp Pro Val Tyr Glu Gly Lys Ser Met Gln Gly Met Ile
    290                 295                 300
gat ctc gcg cgc aag ggc ttc ttc ccc gag ggc tcg aag gtg ctc tac      960
Asp Leu Ala Arg Lys Gly Phe Phe Pro Glu Gly Ser Lys Val Leu Tyr
305                 310                 315                 320
gcc cat ctc ggc ggc gcc ccg gcg ctc aac ggc tat agc tat tac tac     1008
Ala His Leu Gly Gly Ala Pro Ala Leu Asn Gly Tyr Ser Tyr Tyr Tyr
                325                 330                 335
agg gac ggc tga                                                     1020
Arg Asp Gly
```

<210> 293
<211> 339
<212> PRT
<213> Rhizobium meliloti

<400> 293

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

```
   290                 295                 300
Asp Leu Ala Arg Lys Gly Phe Phe Pro Glu Gly Ser Lys Val Leu Tyr
305                 310                 315                 320
Ala His Leu Gly Gly Ala Pro Ala Leu Asn Gly Tyr Ser Tyr Tyr Tyr
                325                 330                 335
Arg Asp Gly
```

<210> 294
<211> 1056
<212> DNA
<213> Aspergillus oryzae

<220>
<221> CDS
<222> (1)..(1056)

<400> 294

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

```
Tyr Pro Gly Glu Lys Lys Lys Arg Val Ile Gly Ile Asp Gly Ser Ala
225                 230                 235                 240
aag ccc gtg gag acg aag gcg cag gtg ttg cgg att gcc agg aac acg      768
Lys Pro Val Glu Thr Lys Ala Gln Val Leu Arg Ile Ala Arg Asn Thr
                245                 250                 255
gct gtg cag att gga ttg aag gaa gag gat att acc gag aag gat atg      816
Ala Val Gln Ile Gly Leu Lys Glu Glu Asp Ile Thr Glu Lys Asp Met
            260                 265                 270
att ctc aat gag gac tat cat gcc ggc act tat ggc att ccc gat aag      864
Ile Leu Asn Glu Asp Tyr His Ala Gly Thr Tyr Gly Ile Pro Asp Lys
        275                 280                 285
gcg acg tgg gag gcc att gag tat gcc gcg cgg atg gag gcg ttt att      912
Ala Thr Trp Glu Ala Ile Glu Tyr Ala Ala Arg Met Glu Ala Phe Ile
    290                 295                 300
acg gat cca gta tac gag gga aag agt ttt gcg gga atg gtg gac ttg      960
Thr Asp Pro Val Tyr Glu Gly Lys Ser Phe Ala Gly Met Val Asp Leu
305                 310                 315                 320
att aag aaa ggg gag att acg ggc aat gtg ctg tat gcg cat ctg ggt     1008
Ile Lys Lys Gly Glu Ile Thr Gly Asn Val Leu Tyr Ala His Leu Gly
                325                 330                 335
ggg cag ttg gcc ctc aac gct tac tcg cgc ctt ggg gag acg aaa          1053
Gly Gln Leu Ala Leu Asn Ala Tyr Ser Arg Leu Gly Glu Thr Lys
            340                 345                 350
tag                                                                 1056
```

<210> 295
<211> 351
<212> PRT
<213> Aspergillus oryzae

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

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

<210> 296
<211> 1206
<212> DNA
<213> Aspergillus oryzae

<220>
<221> CDS
<222> (1)..(1206)

<400> 296

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

```
Leu Glu Gly Leu Arg Ala Gln Gly Lys Val Pro Tyr Trp Ile Pro Ser
            180                 185                 190
ggg gct agt ttg cat ccc ttg ggt ggg ctg ggg tat gcg cgg tgc gca      624
Gly Ala Ser Leu His Pro Leu Gly Gly Leu Gly Tyr Ala Arg Cys Ala
        195                 200                 205
ttt gaa att gcg gcg cag gaa aag gag caa ctg gga gaa aat ggc cgg      672
Phe Glu Ile Ala Ala Gln Glu Lys Glu Gln Leu Gly Glu Asn Gly Arg
    210                 215                 220
ttc gat tat gta ttt gtt gcg tgt ggg agt gga agt acc gtg gga ggc      720
Phe Asp Tyr Val Phe Val Ala Cys Gly Ser Gly Ser Thr Val Gly Gly
225                 230                 235                 240
ttg att gcg ggg ttc aaa tta ctg cag aaa atc gag gca cag cga cag      768
Leu Ile Ala Gly Phe Lys Leu Leu Gln Lys Ile Glu Ala Gln Arg Gln
                245                 250                 255
gat gaa aat gca gag agg gtt att ggt cgt aag gtc atc ggg atc ttg      816
Asp Glu Asn Ala Glu Arg Val Ile Gly Arg Lys Val Ile Gly Ile Leu
            260                 265                 270
aat tcc cct acc aag ccg cga gaa tat cat gaa ggt cga gtg ctc aac      864
Asn Ser Pro Thr Lys Pro Arg Glu Tyr His Glu Gly Arg Val Leu Asn
        275                 280                 285
ttt gcc cgg cgt gcg gca tat ctc att gga ctg gac cct gag cgg gac      912
Phe Ala Arg Arg Ala Ala Tyr Leu Ile Gly Leu Asp Pro Glu Arg Asp
    290                 295                 300
gtc aca ccg gaa gat gtc cag tta gac gat cgg ttt gct ggc aca gcc      960
Val Thr Pro Glu Asp Val Gln Leu Asp Asp Arg Phe Ala Gly Thr Ala
305                 310                 315                 320
tac gga gaa ctg gac cag aca tcc aag aag acc ctg gca ttt cta gcg     1008
Tyr Gly Glu Leu Asp Gln Thr Ser Lys Lys Thr Leu Ala Phe Leu Ala
                325                 330                 335
cag gaa gaa ggg gtc atc gtt gat cct gtg tac aca gtc aag gtt atg     1056
Gln Glu Glu Gly Val Ile Val Asp Pro Val Tyr Thr Val Lys Val Met
            340                 345                 350
aga ggc gta atg cac tgg gta cag gtg ggc gaa ctc atc aga gac tgg     1104
Arg Gly Val Met His Trp Val Gln Val Gly Glu Leu Ile Arg Asp Trp
        355                 360                 365
tca cgc cgc ctt gag agc tcg ccc agc gaa ggt cga gta aat gca cta     1152
Ser Arg Arg Leu Glu Ser Ser Pro Ser Glu Gly Arg Val Asn Ala Leu
    370                 375                 380
ttt atc cac acc ggt ggg cag tcg gcc cta agt gcg tat gca gac atc     1200
Phe Ile His Thr Gly Gly Gln Ser Ala Leu Ser Ala Tyr Ala Asp Ile
385                 390                 395                 400
gag tga                                                            1206
Glu
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<210> 297
<211> 401
<212> PRT
<213> Aspergillus oryzae

<400> 297

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

```
Leu His Gly Pro Gly Glu Arg Ser Glu Ala Lys Ala Thr Thr Thr Leu
                85                  90                  95
Val Thr Glu Gly Ala Ile Gln Ser Asn His Thr Val Gln Val Ala Ser
            100                 105                 110
Val Ala Arg Arg Leu Gly Leu Glu Ala Ile Val Ile Leu His Lys Ala
        115                 120                 125
Thr Gly Gly Gly Leu Thr Ala Ser Ser Asp Lys Asp Val Phe Leu Arg
    130                 135                 140
Thr Gly Asn Val Gln Ile Ala Arg Leu Leu Gly Ala Glu Val Arg Met
145                 150                 155                 160
Leu Glu Asp Ser Ser Thr Val Asp Asn Ser Asp Pro Ile Thr Pro Ile
                165                 170                 175
Leu Glu Gly Leu Arg Ala Gln Gly Lys Val Pro Tyr Trp Ile Pro Ser
            180                 185                 190
Gly Ala Ser Leu His Pro Leu Gly Gly Leu Gly Tyr Ala Arg Cys Ala
        195                 200                 205
Phe Glu Ile Ala Ala Gln Glu Lys Glu Gln Leu Gly Glu Asn Gly Arg
    210                 215                 220
Phe Asp Tyr Val Phe Val Ala Cys Gly Ser Gly Ser Thr Val Gly Gly
225                 230                 235                 240
Leu Ile Ala Gly Phe Lys Leu Leu Gln Lys Ile Glu Ala Gln Arg Gln
                245                 250                 255
Asp Glu Asn Ala Glu Arg Val Ile Gly Arg Lys Val Ile Gly Ile Leu
            260                 265                 270
Asn Ser Pro Thr Lys Pro Arg Glu Tyr His Glu Gly Arg Val Leu Asn
        275                 280                 285
Phe Ala Arg Arg Ala Ala Tyr Leu Ile Gly Leu Asp Pro Glu Arg Asp
    290                 295                 300
Val Thr Pro Glu Asp Val Gln Leu Asp Asp Arg Phe Ala Gly Thr Ala
305                 310                 315                 320
Tyr Gly Glu Leu Asp Gln Thr Ser Lys Lys Thr Leu Ala Phe Leu Ala
                325                 330                 335
Gln Glu Glu Gly Val Ile Val Asp Pro Val Tyr Thr Val Lys Val Met
            340                 345                 350
Arg Gly Val Met His Trp Val Gln Val Gly Glu Leu Ile Arg Asp Trp
        355                 360                 365
Ser Arg Arg Leu Glu Ser Ser Pro Ser Glu Gly Arg Val Asn Ala Leu
    370                 375                 380
Phe Ile His Thr Gly Gly Gln Ser Ala Leu Ser Ala Tyr Ala Asp Ile
385                 390                 395                 400
Glu
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<210> 298
<211> 1116
<212> DNA
<213> Neurospora crassa

<220>
<221> CDS
<222> (1)..(1116)

<400> 298

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atg gcc gac tta cta ctc ccc gaa ccg ttc gcc agc atc cct cgg gag        48
Met Ala Asp Leu Leu Leu Pro Glu Pro Phe Ala Ser Ile Pro Arg Glu
1               5                   10                  15
ccg cta acc ttt gga cct tct ccg atc cag cct ctc ccc cgc atc tcc        96
Pro Leu Thr Phe Gly Pro Ser Pro Ile Gln Pro Leu Pro Arg Ile Ser
            20                  25                  30
caa gcc ctc ggt gga aag gtc aac gtc ttt gct aaa cgc gag gac ctc       144
Gln Ala Leu Gly Gly Lys Val Asn Val Phe Ala Lys Arg Glu Asp Leu
```

```
       35                  40                  45
aac tcc ggt ctt gcc ttt gga ggc aac aag acc aga aag cta gac agc      192
Asn Ser Gly Leu Ala Phe Gly Gly Asn Lys Thr Arg Lys Leu Asp Ser
    50                  55                  60
ttg act aac aag tcc ggc ccc tcg gcc ccc aga tac ctc gtc ccc gac      240
Leu Thr Asn Lys Ser Gly Pro Ser Ala Pro Arg Tyr Leu Val Pro Asp
65                  70                  75                  80
gcc atc tcc cga ggc tgc gac acc ctc gtc tcc atc ggg ggc atc caa      288
Ala Ile Ser Arg Gly Cys Asp Thr Leu Val Ser Ile Gly Gly Ile Gln
                85                  90                  95
tcc aac cac acg cgc caa gtc gcc gcc gcc gcc tcc aag ctc ggc ctg      336
Ser Asn His Thr Arg Gln Val Ala Ala Ala Ala Ser Lys Leu Gly Leu
            100                 105                 110
cac gcc gct ctc gtc caa gaa cac tgg gtc ccc gac tgg acc gat ccc      384
His Ala Ala Leu Val Gln Glu His Trp Val Pro Asp Trp Thr Asp Pro
        115                 120                 125
ggc tac gac aaa gtc ggc aac atc cag ctc tcc cgg ctg atg ggg gcc      432
Gly Tyr Asp Lys Val Gly Asn Ile Gln Leu Ser Arg Leu Met Gly Ala
    130                 135                 140
gac gtc cgt ctt gaa ccg cta gcc ggg ttc ggg atc gag cac aag cag      480
Asp Val Arg Leu Glu Pro Leu Ala Gly Phe Gly Ile Glu His Lys Gln
145                 150                 155                 160
acg ctg gcg aaa ctc aaa gat gat ctg gag aag gag ggg aga aag ccg      528
Thr Leu Ala Lys Leu Lys Asp Asp Leu Glu Lys Glu Gly Arg Lys Pro
                165                 170                 175
tat tat atc ccg gct ggg gcg tcg gat cac cct ctt gga ggg ctg ggg      576
Tyr Tyr Ile Pro Ala Gly Ala Ser Asp His Pro Leu Gly Gly Leu Gly
            180                 185                 190
ttc gcg agg tgg gcg ttt gag gtg gtg gcg cag gag gag gag ttg ggg      624
Phe Ala Arg Trp Ala Phe Glu Val Val Ala Gln Glu Glu Glu Leu Gly
        195                 200                 205
att cat ttc gac acg gtg gtg gtc tgt gcg gtg aca ggg tcg acg atg      672
Ile His Phe Asp Thr Val Val Val Cys Ala Val Thr Gly Ser Thr Met
    210                 215                 220
gcg ggc atg gtg gcc ggg ttt aag ttg gtt gag atg ttg gaa cgc cac      720
Ala Gly Met Val Ala Gly Phe Lys Leu Val Glu Met Leu Glu Arg His
225                 230                 235                 240
tcg gaa agg ctg ggc aag gtg aat aag agg agg gtg att ggg att gat      768
Ser Glu Arg Leu Gly Lys Val Asn Lys Arg Arg Val Ile Gly Ile Asp
                245                 250                 255
gcg tcc gcc aag gtt gag cag acg aga gcg cag gtg ctg agg att gcg      816
Ala Ser Ala Lys Val Glu Gln Thr Arg Ala Gln Val Leu Arg Ile Ala
            260                 265                 270
aaa cag aca gcg gcc aag att ggg ttg aag gag gag gat atc acg gag      864
Lys Gln Thr Ala Ala Lys Ile Gly Leu Lys Glu Glu Asp Ile Thr Glu
        275                 280                 285
tcg gat atc gtg ctg gat gat cgg tac cat gcg ggg gtt tat ggc gtg      912
Ser Asp Ile Val Leu Asp Asp Arg Tyr His Ala Gly Val Tyr Gly Val
    290                 295                 300
ccg gac gag aaa acg att gag gct atc aag ttt ggg gcg cgg acg gag      960
Pro Asp Glu Lys Thr Ile Glu Ala Ile Lys Phe Gly Ala Arg Thr Glu
305                 310                 315                 320
gcg ttc att acc gat ccc gtg tat gag ggc aaa agt ctg gcg ggc atg     1008
Ala Phe Ile Thr Asp Pro Val Tyr Glu Gly Lys Ser Leu Ala Gly Met
                325                 330                 335
atg gac atg att aag aat ggg gag att gag gcg gga agc aat gtg ctg     1056
Met Asp Met Ile Lys Asn Gly Glu Ile Glu Ala Gly Ser Asn Val Leu
            340                 345                 350
tat gcg cac ctt gga ggg caa ttg gca ctg aat gcg tac tcc gct ttg     1104
Tyr Ala His Leu Gly Gly Gln Leu Ala Leu Asn Ala Tyr Ser Ala Leu
        355                 360                 365
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ggg ttg gaa taa
Gly Leu Glu
370

<210> 299
<211> 371
<212> PRT
<213> Neurospora crassa

<400> 299
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1 5 10 15
Pro Leu Thr Phe Gly Pro Ser Pro Ile Gln Pro Leu Pro Arg Ile Ser
20 25 30
Gln Ala Leu Gly Gly Lys Val Asn Val Phe Ala Lys Arg Glu Asp Leu
35 40 45
Asn Ser Gly Leu Ala Phe Gly Gly Asn Lys Thr Arg Lys Leu Asp Ser
50 55 60
Leu Thr Asn Lys Ser Gly Pro Ser Ala Pro Arg Tyr Leu Val Pro Asp
65 70 75 80
Ala Ile Ser Arg Gly Cys Asp Thr Leu Val Ser Ile Gly Gly Ile Gln
85 90 95
Ser Asn His Thr Arg Gln Val Ala Ala Ala Ala Ser Lys Leu Gly Leu
100 105 110
His Ala Ala Leu Val Gln Glu His Trp Val Pro Asp Trp Thr Asp Pro
115 120 125
Gly Tyr Asp Lys Val Gly Asn Ile Gln Leu Ser Arg Leu Met Gly Ala
130 135 140
Asp Val Arg Leu Glu Pro Leu Ala Gly Phe Gly Ile Glu His Lys Gln
145 150 155 160
Thr Leu Ala Lys Leu Lys Asp Asp Leu Glu Lys Glu Gly Arg Lys Pro
165 170 175
Tyr Tyr Ile Pro Ala Gly Ala Ser Asp His Pro Leu Gly Gly Leu Gly
180 185 190
Phe Ala Arg Trp Ala Phe Glu Val Val Ala Gln Glu Glu Glu Leu Gly
195 200 205
Ile His Phe Asp Thr Val Val Val Cys Ala Val Thr Gly Ser Thr Met
210 215 220
Ala Gly Met Val Ala Gly Phe Lys Leu Val Glu Met Leu Glu Arg His
225 230 235 240
Ser Glu Arg Leu Gly Lys Val Asn Lys Arg Arg Val Ile Gly Ile Asp
245 250 255
Ala Ser Ala Lys Val Glu Gln Thr Arg Ala Gln Val Leu Arg Ile Ala
260 265 270
Lys Gln Thr Ala Ala Lys Ile Gly Leu Lys Glu Glu Asp Ile Thr Glu
275 280 285
Ser Asp Ile Val Leu Asp Asp Arg Tyr His Ala Gly Val Tyr Gly Val
290 295 300
Pro Asp Glu Lys Thr Ile Glu Ala Ile Lys Phe Gly Ala Arg Thr Glu
305 310 315 320
Ala Phe Ile Thr Asp Pro Val Tyr Glu Gly Lys Ser Leu Ala Gly Met
325 330 335
Met Asp Met Ile Lys Asn Gly Glu Ile Glu Ala Gly Ser Asn Val Leu
340 345 350
Tyr Ala His Leu Gly Gly Gln Leu Ala Leu Asn Ala Tyr Ser Ala Leu
355 360 365
Gly Leu Glu
370

<210> 300
<211> 1014

<212> DNA
<213> Rhizobium loti

<220>
<221> CDS
<222> (1)..(1014)
<223> transl_table=11

<400> 300

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

```
Glu Thr Lys Glu Ala Ile Arg Leu Cys Ala Arg Leu Glu Gly Met Ile
        275                 280                 285
acc gat ccc gtc tat gag ggc aaa tcg atg caa ggg atg att gac ctc      912
Thr Asp Pro Val Tyr Glu Gly Lys Ser Met Gln Gly Met Ile Asp Leu
    290                 295                 300
gtt caa aaa ggc ttt ttt cct gag ggc tcg agg ata ctc tac gcg cat      960
Val Gln Lys Gly Phe Phe Pro Glu Gly Ser Arg Ile Leu Tyr Ala His
305                 310                 315                 320
ctc ggc ggc gcg ccg gcc atc aac ggt tat ggc tac acc ttt cgc aat     1008
Leu Gly Gly Ala Pro Ala Ile Asn Gly Tyr Gly Tyr Thr Phe Arg Asn
                325                 330                 335
ggc tga                                                            1014
Gly
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<210> 301
<211> 337
<212> PRT
<213> Rhizobium loti

<400> 301

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

Gly

<210> 302
<211> 1149
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (1)..(1149)

<400> 302
atg tct gca aca tcc gta cct tca atg gcg gat ttt ctc acc aaa aaa 48
Met Ser Ala Thr Ser Val Pro Ser Met Ala Asp Phe Leu Thr Lys Lys
1 5 10 15
cct tac tct cct cct tct tgg gct tct cat ctt cgt ccg ctt cct tct 96
Pro Tyr Ser Pro Pro Ser Trp Ala Ser His Leu Arg Pro Leu Pro Ser
20 25 30
cac act ttc tcc ctc gct cac ctt cct act ccg atc cat cga tgg aat 144
His Thr Phe Ser Leu Ala His Leu Pro Thr Pro Ile His Arg Trp Asn
35 40 45
ctt cct ggt ctt cct aat ggc aca gaa ctc tgg atc aag cga gat gat 192
Leu Pro Gly Leu Pro Asn Gly Thr Glu Leu Trp Ile Lys Arg Asp Asp
50 55 60
ttc acc gga atg gaa ttg agt gga aac aaa gta cga aaa ctc gaa ttc 240
Phe Thr Gly Met Glu Leu Ser Gly Asn Lys Val Arg Lys Leu Glu Phe
65 70 75 80
tta atg gcg gaa gct gtt gat caa cac gct gat act gta atc act atc 288
Leu Met Ala Glu Ala Val Asp Gln His Ala Asp Thr Val Ile Thr Ile
85 90 95
ggc ggt att cag agc aat cat tgt cgt gct aca gcc act gca tct aac 336
Gly Gly Ile Gln Ser Asn His Cys Arg Ala Thr Ala Thr Ala Ser Asn
100 105 110
tat ctt aat ctc aat tct cat ctt att ctc cgt act tcc aag ctt ctt 384
Tyr Leu Asn Leu Asn Ser His Leu Ile Leu Arg Thr Ser Lys Leu Leu
115 120 125
gct gat gaa gat cct gga ttg gtt ggg aat ctc ctt gtc gag cgt ctc 432
Ala Asp Glu Asp Pro Gly Leu Val Gly Asn Leu Leu Val Glu Arg Leu
130 135 140
gtt gga gct aat gtt cat cta atc tct aaa gaa gag tat tct tcc att 480
Val Gly Ala Asn Val His Leu Ile Ser Lys Glu Glu Tyr Ser Ser Ile
145 150 155 160
ggg agt gag gct ctt act aat gct ctg aaa gag aaa ctg gaa aaa gaa 528
Gly Ser Glu Ala Leu Thr Asn Ala Leu Lys Glu Lys Leu Glu Lys Glu
165 170 175
gga aag aaa ccc tat gtt att cca gtc ggt gga tcg aac tct ttg gga 576
Gly Lys Lys Pro Tyr Val Ile Pro Val Gly Gly Ser Asn Ser Leu Gly
180 185 190
act tgg ggt tat ata gaa gca gca agg gaa att gag gag cag ctg aat 624
Thr Trp Gly Tyr Ile Glu Ala Ala Arg Glu Ile Glu Glu Gln Leu Asn
195 200 205
tat aga ccc gat gac ctg aaa ttt gat gat att gtg gta gca tgt ggc 672
Tyr Arg Pro Asp Asp Leu Lys Phe Asp Asp Ile Val Val Ala Cys Gly
210 215 220
agt ggt ggt aca att gct ggt att tca ttg ggg tct tgg ttg gga gct 720
Ser Gly Gly Thr Ile Ala Gly Ile Ser Leu Gly Ser Trp Leu Gly Ala
225 230 235 240
cta aaa gcc aag gtt cat gct ttc tcg gtt tgc gat gat cct gat tac 768

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Leu Lys Ala Lys Val His Ala Phe Ser Val Cys Asp Asp Pro Asp Tyr
                245                 250                 255
ttc tat gac ttt gtc caa ggg ctt ctg gat gga ctt cac gct ggt gtt        816
Phe Tyr Asp Phe Val Gln Gly Leu Leu Asp Gly Leu His Ala Gly Val
            260                 265                 270
aac tct cgt gat atc gtc aac atc cac aat gcc aaa gga aaa gga tat        864
Asn Ser Arg Asp Ile Val Asn Ile His Asn Ala Lys Gly Lys Gly Tyr
        275                 280                 285
gcc atg aac acg tca gag gag ctt gag ttt gta aag aaa gta gca agt        912
Ala Met Asn Thr Ser Glu Glu Leu Glu Phe Val Lys Lys Val Ala Ser
    290                 295                 300
tca act ggt gtt att ctt gat ccg gtt tac agt ggg aaa gct gcg tat        960
Ser Thr Gly Val Ile Leu Asp Pro Val Tyr Ser Gly Lys Ala Ala Tyr
305                 310                 315                 320
ggt ttg ata aat gag atc acc aaa gat ccc aaa tgt tgg gag gga agg       1008
Gly Leu Ile Asn Glu Ile Thr Lys Asp Pro Lys Cys Trp Glu Gly Arg
                325                 330                 335
aag ata ttg ttc ata cac act ggt ggg ctt ctt ggg ttg tat gat aag       1056
Lys Ile Leu Phe Ile His Thr Gly Gly Leu Leu Gly Leu Tyr Asp Lys
            340                 345                 350
gtt gat caa atg gca tct ctg atg ggt aat tgg tcc cgg atg gat gtt       1104
Val Asp Gln Met Ala Ser Leu Met Gly Asn Trp Ser Arg Met Asp Val
        355                 360                 365
tca gaa tcc gtt cca aga aaa gat ggt gtt ggg aaa atg ttc tag           1149
Ser Glu Ser Val Pro Arg Lys Asp Gly Val Gly Lys Met Phe
    370                 375                 380
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<210> 303
<211> 382
<212> PRT
<213> Arabidopsis thaliana

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<400> 303
Met Ser Ala Thr Ser Val Pro Ser Met Ala Asp Phe Leu Thr Lys Lys
1               5                   10                  15
Pro Tyr Ser Pro Pro Ser Trp Ala Ser His Leu Arg Pro Leu Pro Ser
            20                  25                  30
His Thr Phe Ser Leu Ala His Leu Pro Thr Pro Ile His Arg Trp Asn
        35                  40                  45
Leu Pro Gly Leu Pro Asn Gly Thr Glu Leu Trp Ile Lys Arg Asp Asp
    50                  55                  60
Phe Thr Gly Met Glu Leu Ser Gly Asn Lys Val Arg Lys Leu Glu Phe
65                  70                  75                  80
Leu Met Ala Glu Ala Val Asp Gln His Ala Asp Thr Val Ile Thr Ile
                85                  90                  95
Gly Gly Ile Gln Ser Asn His Cys Arg Ala Thr Ala Thr Ala Ser Asn
            100                 105                 110
Tyr Leu Asn Leu Asn Ser His Leu Ile Leu Arg Thr Ser Lys Leu Leu
        115                 120                 125
Ala Asp Glu Asp Pro Gly Leu Val Gly Asn Leu Leu Val Glu Arg Leu
    130                 135                 140
Val Gly Ala Asn Val His Leu Ile Ser Lys Glu Glu Tyr Ser Ser Ile
145                 150                 155                 160
Gly Ser Glu Ala Leu Thr Asn Ala Leu Lys Glu Lys Leu Glu Lys Glu
                165                 170                 175
Gly Lys Lys Pro Tyr Val Ile Pro Val Gly Gly Ser Asn Ser Leu Gly
            180                 185                 190
Thr Trp Gly Tyr Ile Glu Ala Ala Arg Glu Ile Glu Glu Gln Leu Asn
        195                 200                 205
Tyr Arg Pro Asp Asp Leu Lys Phe Asp Asp Ile Val Val Ala Cys Gly
    210                 215                 220
```

```
Ser Gly Gly Thr Ile Ala Gly Ile Ser Leu Gly Ser Trp Leu Gly Ala
225                 230                 235                 240
Leu Lys Ala Lys Val His Ala Phe Ser Val Cys Asp Asp Pro Asp Tyr
                245                 250                 255
Phe Tyr Asp Phe Val Gln Gly Leu Leu Asp Gly Leu His Ala Gly Val
            260                 265                 270
Asn Ser Arg Asp Ile Val Asn Ile His Asn Ala Lys Gly Lys Gly Tyr
        275                 280                 285
Ala Met Asn Thr Ser Glu Glu Leu Glu Phe Val Lys Lys Val Ala Ser
    290                 295                 300
Ser Thr Gly Val Ile Leu Asp Pro Val Tyr Ser Gly Lys Ala Ala Tyr
305                 310                 315                 320
Gly Leu Ile Asn Glu Ile Thr Lys Asp Pro Lys Cys Trp Glu Gly Arg
                325                 330                 335
Lys Ile Leu Phe Ile His Thr Gly Gly Leu Leu Gly Leu Tyr Asp Lys
            340                 345                 350
Val Asp Gln Met Ala Ser Leu Met Gly Asn Trp Ser Arg Met Asp Val
        355                 360                 365
Ser Glu Ser Val Pro Arg Lys Asp Gly Val Gly Lys Met Phe
    370                 375                 380
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<210> 304
<211> 1083
<212> DNA
<213> Penicillium citrinum

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

<400> 304

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atg aca gac cca aac cca gtc acc ctc cca acc ccc ttc tcc aca atc      48
Met Thr Asp Pro Asn Pro Val Thr Leu Pro Thr Pro Phe Ser Thr Ile
1               5                  10                  15
ccc cga acc ccc ctc ctc cta ggc ccc tca cca atc cac ccc ctc ccc      96
Pro Arg Thr Pro Leu Leu Leu Gly Pro Ser Pro Ile His Pro Leu Pro
            20                  25                  30
cgc aca aca gcc gat ctc gcc aaa aac aac ccc cac ccc ctg gta aca     144
Arg Thr Thr Ala Asp Leu Ala Lys Asn Asn Pro His Pro Leu Val Thr
        35                  40                  45
atc tac gcc aaa cgc gac gac cta aac tcc ggc tac gcc tac ggg ggc     192
Ile Tyr Ala Lys Arg Asp Asp Leu Asn Ser Gly Tyr Ala Tyr Gly Gly
    50                  55                  60
aac aaa acc cgc aag cta gag tat cta ctc gcg gac gcc caa gcc caa     240
Asn Lys Thr Arg Lys Leu Glu Tyr Leu Leu Ala Asp Ala Gln Ala Gln
65                  70                  75                  80
ggc tgc acg acc ctc gtc tcc atc ggc ggc gtg caa agc aac cac acg     288
Gly Cys Thr Thr Leu Val Ser Ile Gly Gly Val Gln Ser Asn His Thr
                85                  90                  95
cgc caa gtc gcc gcc gtc gcc gca cgc tcg ggc cta aaa gcc cgt ctc     336
Arg Gln Val Ala Ala Val Ala Ala Arg Ser Gly Leu Lys Ala Arg Leu
            100                 105                 110
gtg cag gag cac tgg gtc gac tgg aca gac ccg ggc tac gag agc acg     384
Val Gln Glu His Trp Val Asp Trp Thr Asp Pro Gly Tyr Glu Ser Thr
        115                 120                 125
ggc aac atc cag ctg tcg cgg ctg atg ggc gcg gat gtg cgg ctc gac     432
Gly Asn Ile Gln Leu Ser Arg Leu Met Gly Ala Asp Val Arg Leu Asp
    130                 135                 140
ccg tcc ggg ttc ggg atc gag cat aag aat acc gtg cag agg gtt gtg     480
Pro Ser Gly Phe Gly Ile Glu His Lys Asn Thr Val Gln Arg Val Val
145                 150                 155                 160
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```
gag gag gcg agg ggt gat ggg gag aaa ccc tac tat att cct gct ggg        528
Glu Glu Ala Arg Gly Asp Gly Glu Lys Pro Tyr Tyr Ile Pro Ala Gly
                165                 170                 175
gcg tcg gac cat ccg ctt ggt gga ctt ggg ttt gcg cgg tgg gcg ttt        576
Ala Ser Asp His Pro Leu Gly Gly Leu Gly Phe Ala Arg Trp Ala Phe
            180                 185                 190
gag gtt cgg gag cag gag ggg gag atg ggg gtt ttc ttt gat acg gtg        624
Glu Val Arg Glu Gln Glu Gly Glu Met Gly Val Phe Phe Asp Thr Val
        195                 200                 205
ctt gtt tgt gct gtt acg ggg tcg act ttt gcc ggg atg att gct ggg        672
Leu Val Cys Ala Val Thr Gly Ser Thr Phe Ala Gly Met Ile Ala Gly
    210                 215                 220
ttt aag ttg ctt gag cgg ttg tat cct gcg gat gcg aag agg agg gtt        720
Phe Lys Leu Leu Glu Arg Leu Tyr Pro Ala Asp Ala Lys Arg Arg Val
225                 230                 235                 240
gtt ggg att gat gct tcg gcg acg gtt gag gcg acc cgg gcg cag gtt        768
Val Gly Ile Asp Ala Ser Ala Thr Val Glu Ala Thr Arg Ala Gln Val
                245                 250                 255
ttg agg att gcg aag aat act gct gct aag att ggg ctt agt gag gat        816
Leu Arg Ile Ala Lys Asn Thr Ala Ala Lys Ile Gly Leu Ser Glu Asp
            260                 265                 270
gat att acg gag gat gat gtt atg ctt gat gat cgg tac cat gct ggt        864
Asp Ile Thr Glu Asp Asp Val Met Leu Asp Asp Arg Tyr His Ala Gly
        275                 280                 285
atc tat ggt gtt cct gat cgt cag act tgg gat gcg att gag tac gcg        912
Ile Tyr Gly Val Pro Asp Arg Gln Thr Trp Asp Ala Ile Glu Tyr Ala
    290                 295                 300
gcg aag atg gag gcg ttt att act gat cct gtc tat gaa ggg aag agc        960
Ala Lys Met Glu Ala Phe Ile Thr Asp Pro Val Tyr Glu Gly Lys Ser
305                 310                 315                 320
ttt gcc ggc atg atg gat atg att cgt cgt ggg gag atc aag ggg gga       1008
Phe Ala Gly Met Met Asp Met Ile Arg Arg Gly Glu Ile Lys Gly Gly
                325                 330                 335
aat atc ctg tat gcg cac ctc ggt gga cag ttg gct ttg aat gct tac       1056
Asn Ile Leu Tyr Ala His Leu Gly Gly Gln Leu Ala Leu Asn Ala Tyr
            340                 345                 350
tcc gag ctt ggt cgg acc aat gaa tag                                  1083
Ser Glu Leu Gly Arg Thr Asn Glu
        355                 360
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<210> 305
<211> 360
<212> PRT
<213> Penicillium citrinum

<400> 305

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

```
        115                 120                 125
Gly Asn Ile Gln Leu Ser Arg Leu Met Gly Ala Asp Val Arg Leu Asp
    130                 135                 140
Pro Ser Gly Phe Gly Ile Glu His Lys Asn Thr Val Gln Arg Val Val
145                 150                 155                 160
Glu Glu Ala Arg Gly Asp Gly Glu Lys Pro Tyr Tyr Ile Pro Ala Gly
                165                 170                 175
Ala Ser Asp His Pro Leu Gly Gly Leu Gly Phe Ala Arg Trp Ala Phe
            180                 185                 190
Glu Val Arg Glu Gln Glu Gly Glu Met Gly Val Phe Phe Asp Thr Val
        195                 200                 205
Leu Val Cys Ala Val Thr Gly Ser Thr Phe Ala Gly Met Ile Ala Gly
    210                 215                 220
Phe Lys Leu Leu Glu Arg Leu Tyr Pro Ala Asp Ala Lys Arg Arg Val
225                 230                 235                 240
Val Gly Ile Asp Ala Ser Ala Thr Val Glu Ala Thr Arg Ala Gln Val
                245                 250                 255
Leu Arg Ile Ala Lys Asn Thr Ala Ala Lys Ile Gly Leu Ser Glu Asp
            260                 265                 270
Asp Ile Thr Glu Asp Asp Val Met Leu Asp Asp Arg Tyr His Ala Gly
        275                 280                 285
Ile Tyr Gly Val Pro Asp Arg Gln Thr Trp Asp Ala Ile Glu Tyr Ala
    290                 295                 300
Ala Lys Met Glu Ala Phe Ile Thr Asp Pro Val Tyr Glu Gly Lys Ser
305                 310                 315                 320
Phe Ala Gly Met Met Asp Met Ile Arg Arg Gly Glu Ile Lys Gly Gly
                325                 330                 335
Asn Ile Leu Tyr Ala His Leu Gly Gly Gln Leu Ala Leu Asn Ala Tyr
            340                 345                 350
Ser Glu Leu Gly Arg Thr Asn Glu
        355                 360
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<210> 306
<211> 1245
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (1)..(1245)

<400> 306

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atg aga gga cga agc ttg aca ctc tca aga gta aag ctc gag ctt gcg      48
Met Arg Gly Arg Ser Leu Thr Leu Ser Arg Val Lys Leu Glu Leu Ala
1               5                   10                  15
aga aga agc atg tct gca aca tcc gta cct tca atg gcg gat ttt ctc      96
Arg Arg Ser Met Ser Ala Thr Ser Val Pro Ser Met Ala Asp Phe Leu
            20                  25                  30
acc aaa aaa cct tac tct cct cct tct tgg gct tct cat ctt cgt ccg     144
Thr Lys Lys Pro Tyr Ser Pro Pro Ser Trp Ala Ser His Leu Arg Pro
        35                  40                  45
ctt cct tct cac act ttc tcc ctc gct cac ctt cct act ccg atc cat     192
Leu Pro Ser His Thr Phe Ser Leu Ala His Leu Pro Thr Pro Ile His
    50                  55                  60
cga tgg aat ctt cct ggt ctt cct aat ggc aca gaa ctc tgg atc aag     240
Arg Trp Asn Leu Pro Gly Leu Pro Asn Gly Thr Glu Leu Trp Ile Lys
65                  70                  75                  80
cga gat gat ttc acc gga atg gaa ttg agt gga aac aaa gta cga aaa     288
Arg Asp Asp Phe Thr Gly Met Glu Leu Ser Gly Asn Lys Val Arg Lys
                85                  90                  95
ctc gaa ttc tta atg gcg gaa gct gtt gat caa cac gct gat act gta     336
```

```
Leu Glu Phe Leu Met Ala Glu Ala Val Asp Gln His Ala Asp Thr Val
            100                 105                 110
atc act atc ggc ggt att cag agc aat cat tgt cgt gct aca gcc act      384
Ile Thr Ile Gly Gly Ile Gln Ser Asn His Cys Arg Ala Thr Ala Thr
        115                 120                 125
gca tct aac tat ctt aat ctc aat tct cat ctt att ctc cgt act tcc      432
Ala Ser Asn Tyr Leu Asn Leu Asn Ser His Leu Ile Leu Arg Thr Ser
    130                 135                 140
aag ctt ctt gct gat gaa gat cct gga ttg gtt ggg aat ctc ctt gtc      480
Lys Leu Leu Ala Asp Glu Asp Pro Gly Leu Val Gly Asn Leu Leu Val
145                 150                 155                 160
gag cgt ctc gtt gga gct aat gtt cat cta atc tct aaa gaa gag tat      528
Glu Arg Leu Val Gly Ala Asn Val His Leu Ile Ser Lys Glu Glu Tyr
                165                 170                 175
tct tcc att ggg agt gag gct ctt act aat gct ctg aaa gag aaa ctg      576
Ser Ser Ile Gly Ser Glu Ala Leu Thr Asn Ala Leu Lys Glu Lys Leu
            180                 185                 190
gaa aaa gaa gga aag aaa ccc tat gtt att cca gtc ggt gga tcg aac      624
Glu Lys Glu Gly Lys Lys Pro Tyr Val Ile Pro Val Gly Gly Ser Asn
        195                 200                 205
tct ttg gga act tgg ggt tat ata gaa gca gca agg gaa att gag gag      672
Ser Leu Gly Thr Trp Gly Tyr Ile Glu Ala Ala Arg Glu Ile Glu Glu
    210                 215                 220
cag ctg aat tat aga ccc gat gac ctg aaa ttt gat gat att gtg gta      720
Gln Leu Asn Tyr Arg Pro Asp Asp Leu Lys Phe Asp Asp Ile Val Val
225                 230                 235                 240
gca tgt ggc agt ggt ggt aca att gct ggt att tca ttg ggg tct tgg      768
Ala Cys Gly Ser Gly Gly Thr Ile Ala Gly Ile Ser Leu Gly Ser Trp
                245                 250                 255
ttg gga gct cta aaa gcc aag ttg aca gat ggc tca gtt aag ttt cca      816
Leu Gly Ala Leu Lys Ala Lys Leu Thr Asp Gly Ser Val Lys Phe Pro
            260                 265                 270
ttc att gta cag gtt cat gct ttc tcg gtt tgc gat gat cct gat tac      864
Phe Ile Val Gln Val His Ala Phe Ser Val Cys Asp Asp Pro Asp Tyr
        275                 280                 285
ttc tat gac ttt gtc caa ggg ctt ctg gat gga ctt cac gct ggt gtt      912
Phe Tyr Asp Phe Val Gln Gly Leu Leu Asp Gly Leu His Ala Gly Val
    290                 295                 300
aac tct cgt gat atc gtc aac atc cac aat gcc aaa gga aaa gga tat      960
Asn Ser Arg Asp Ile Val Asn Ile His Asn Ala Lys Gly Lys Gly Tyr
305                 310                 315                 320
gcc atg aac acg tca gag gag ctt gag ttt gta aag aaa gta gca agt     1008
Ala Met Asn Thr Ser Glu Glu Leu Glu Phe Val Lys Lys Val Ala Ser
                325                 330                 335
tca act ggt gtt att ctt gat ccg gtt tac agt ggg aaa gct gcg tat     1056
Ser Thr Gly Val Ile Leu Asp Pro Val Tyr Ser Gly Lys Ala Ala Tyr
            340                 345                 350
ggt ttg ata aat gag atc acc aaa gat ccc aaa tgt tgg gag gga agg     1104
Gly Leu Ile Asn Glu Ile Thr Lys Asp Pro Lys Cys Trp Glu Gly Arg
        355                 360                 365
aag ata ttg ttc ata cac act ggt ggg ctt ctt ggg ttg tat gat aag     1152
Lys Ile Leu Phe Ile His Thr Gly Gly Leu Leu Gly Leu Tyr Asp Lys
    370                 375                 380
gtt gat caa atg gca tct ctg atg ggt aat tgg tcc cgg atg gat gtt     1200
Val Asp Gln Met Ala Ser Leu Met Gly Asn Trp Ser Arg Met Asp Val
385                 390                 395                 400
tca gaa tcc gtt cca aga aaa gat ggt gtt ggg aaa atg ttc tag         1245
Ser Glu Ser Val Pro Arg Lys Asp Gly Val Gly Lys Met Phe
                405                 410
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<210> 307

<211> 414
<212> PRT
<213> Arabidopsis thaliana

<400> 307
Met Arg Gly Arg Ser Leu Thr Leu Ser Arg Val Lys Leu Glu Leu Ala
1 5 10 15
Arg Arg Ser Met Ser Ala Thr Ser Val Pro Ser Met Ala Asp Phe Leu
20 25 30
Thr Lys Lys Pro Tyr Ser Pro Pro Ser Trp Ala Ser His Leu Arg Pro
35 40 45
Leu Pro Ser His Thr Phe Ser Leu Ala His Leu Pro Thr Pro Ile His
50 55 60
Arg Trp Asn Leu Pro Gly Leu Pro Asn Gly Thr Glu Leu Trp Ile Lys
65 70 75 80
Arg Asp Asp Phe Thr Gly Met Glu Leu Ser Gly Asn Lys Val Arg Lys
85 90 95
Leu Glu Phe Leu Met Ala Glu Ala Val Asp Gln His Ala Asp Thr Val
100 105 110
Ile Thr Ile Gly Gly Ile Gln Ser Asn His Cys Arg Ala Thr Ala Thr
115 120 125
Ala Ser Asn Tyr Leu Asn Leu Asn Ser His Leu Ile Leu Arg Thr Ser
130 135 140
Lys Leu Leu Ala Asp Glu Asp Pro Gly Leu Val Gly Asn Leu Leu Val
145 150 155 160
Glu Arg Leu Val Gly Ala Asn Val His Leu Ile Ser Lys Glu Glu Tyr
165 170 175
Ser Ser Ile Gly Ser Glu Ala Leu Thr Asn Ala Leu Lys Glu Lys Leu
180 185 190
Glu Lys Glu Gly Lys Lys Pro Tyr Val Ile Pro Val Gly Gly Ser Asn
195 200 205
Ser Leu Gly Thr Trp Gly Tyr Ile Glu Ala Ala Arg Glu Ile Glu Glu
210 215 220
Gln Leu Asn Tyr Arg Pro Asp Asp Leu Lys Phe Asp Asp Ile Val Val
225 230 235 240
Ala Cys Gly Ser Gly Gly Thr Ile Ala Gly Ile Ser Leu Gly Ser Trp
245 250 255
Leu Gly Ala Leu Lys Ala Lys Leu Thr Asp Gly Ser Val Lys Phe Pro
260 265 270
Phe Ile Val Gln Val His Ala Phe Ser Val Cys Asp Asp Pro Asp Tyr
275 280 285
Phe Tyr Asp Phe Val Gln Gly Leu Leu Asp Gly Leu His Ala Gly Val
290 295 300
Asn Ser Arg Asp Ile Val Asn Ile His Asn Ala Lys Gly Lys Gly Tyr
305 310 315 320
Ala Met Asn Thr Ser Glu Glu Leu Glu Phe Val Lys Lys Val Ala Ser
325 330 335
Ser Thr Gly Val Ile Leu Asp Pro Val Tyr Ser Gly Lys Ala Ala Tyr
340 345 350
Gly Leu Ile Asn Glu Ile Thr Lys Asp Pro Lys Cys Trp Glu Gly Arg
355 360 365
Lys Ile Leu Phe Ile His Thr Gly Gly Leu Leu Gly Leu Tyr Asp Lys
370 375 380
Val Asp Gln Met Ala Ser Leu Met Gly Asn Trp Ser Arg Met Asp Val
385 390 395 400
Ser Glu Ser Val Pro Arg Lys Asp Gly Val Gly Lys Met Phe
405 410

<210> 308
<211> 1014
<212> DNA

<213> Bradyrhizobium japonicum

<220>
<221> CDS
<222> (1)..(1014)
<223> transl_table=11

<400> 308

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atg ctg gaa aaa ttc gcg cgc tat ccg ctg acc ttc ggc ccg acg ccc        48
Met Leu Glu Lys Phe Ala Arg Tyr Pro Leu Thr Phe Gly Pro Thr Pro
1               5                  10                  15
atc gag aag ctg gag cgg ctg tcg aaa cat ctc ggc ggc aat gtc gag        96
Ile Glu Lys Leu Glu Arg Leu Ser Lys His Leu Gly Gly Asn Val Glu
            20                  25                  30
atc tat gcc aag cgc gag gac tgc aac tcc ggc ctc gcc tat ggc ggc       144
Ile Tyr Ala Lys Arg Glu Asp Cys Asn Ser Gly Leu Ala Tyr Gly Gly
        35                  40                  45
aac aag ctg cgc aag ctc gaa tac atc atc ccg gac gcg atc gcc tcg       192
Asn Lys Leu Arg Lys Leu Glu Tyr Ile Ile Pro Asp Ala Ile Ala Ser
    50                  55                  60
aac gcc gac acg ctg gtc tcg atc ggc ggc gtg cag tcc aac cac acc       240
Asn Ala Asp Thr Leu Val Ser Ile Gly Gly Val Gln Ser Asn His Thr
65                  70                  75                  80
cgc atg atc gcc gcc gtc gcc gcc aag atc ggc atg aag tgc cgc ctg       288
Arg Met Ile Ala Ala Val Ala Ala Lys Ile Gly Met Lys Cys Arg Leu
                85                  90                  95
gtg cag gaa gcg tgg gtg ccg cac gag gac gcc gtc tat gac cgc gtc       336
Val Gln Glu Ala Trp Val Pro His Glu Asp Ala Val Tyr Asp Arg Val
            100                 105                 110
ggc aac atc atg ctc tcg cgc atc atg ggc gcc gac gtg cgc ctg gtc       384
Gly Asn Ile Met Leu Ser Arg Ile Met Gly Ala Asp Val Arg Leu Val
        115                 120                 125
gac gac ggc ttc gac atc ggc atc cgc aag agc tgg gag cag gcg atc       432
Asp Asp Gly Phe Asp Ile Gly Ile Arg Lys Ser Trp Glu Gln Ala Ile
    130                 135                 140
gag gaa gtg aag gcc gcg ggc ggc aag cct tac gcg att ccc gcc ggc       480
Glu Glu Val Lys Ala Ala Gly Gly Lys Pro Tyr Ala Ile Pro Ala Gly
145                 150                 155                 160
gcc tcc gtg cac aaa tat ggc ggg ctc ggc tat gtc ggc ttc gcc gag       528
Ala Ser Val His Lys Tyr Gly Gly Leu Gly Tyr Val Gly Phe Ala Glu
                165                 170                 175
gaa gtg cgt aag cag gaa gcc gag ctc ggc ttc aag ttc gac tac atc       576
Glu Val Arg Lys Gln Glu Ala Glu Leu Gly Phe Lys Phe Asp Tyr Ile
            180                 185                 190
gtg gtc tgc acc gtc acc ggc tcg acc cat gcc ggc atg ctg gtc ggc       624
Val Val Cys Thr Val Thr Gly Ser Thr His Ala Gly Met Leu Val Gly
        195                 200                 205
ttc gcc gcc gac ggc cgc gcg cga aag gtg atc ggc atc gac ggg tcg       672
Phe Ala Ala Asp Gly Arg Ala Arg Lys Val Ile Gly Ile Asp Gly Ser
    210                 215                 220
ttc acc ccg gcg cag acc aag gcg cag gtg ctc tcg atc gcc cag aac       720
Phe Thr Pro Ala Gln Thr Lys Ala Gln Val Leu Ser Ile Ala Gln Asn
225                 230                 235                 240
acg gcc aag ctc gtc gag ctc ggc aag gac atc gtc gca gac gac gtc       768
Thr Ala Lys Leu Val Glu Leu Gly Lys Asp Ile Val Ala Asp Asp Val
                245                 250                 255
gtg ctg atc gag gac tac gcc tat ccc gcc tat ggc gtg ccg tcg gaa       816
Val Leu Ile Glu Asp Tyr Ala Tyr Pro Ala Tyr Gly Val Pro Ser Glu
            260                 265                 270
gag acc aag gag gcg atc cgc ctc acc gcg cgt ctc gaa gcc atg atc       864
Glu Thr Lys Glu Ala Ile Arg Leu Thr Ala Arg Leu Glu Ala Met Ile
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       275                 280                 285
acc gac ccc gtc tac gag ggc aag tcg atg cag ggc ctg atc gac ctc      912
Thr Asp Pro Val Tyr Glu Gly Lys Ser Met Gln Gly Leu Ile Asp Leu
    290                 295                 300
acg cag aaa ggc tat ttc gag aag ggc gcg aag gtc ctc tac gcg cat      960
Thr Gln Lys Gly Tyr Phe Glu Lys Gly Ala Lys Val Leu Tyr Ala His
305                 310                 315                 320
ctc ggc ggt gcc ccg gcg ctc aac ggc tac ggc tac gcg ttc aga aac     1008
Leu Gly Gly Ala Pro Ala Leu Asn Gly Tyr Gly Tyr Ala Phe Arg Asn
                325                 330                 335
ggc tag                                                             1014
Gly
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<210> 309
<211> 337
<212> PRT
<213> Bradyrhizobium japonicum

<400> 309

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

<210> 310
<211> 1017
<212> DNA
<213> Burkholderia mallei

<220>
<221> CDS
<222> (1)..(1017)
<223> transl_table=11

<400> 310
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Met Asn Leu Gln Lys Phe Ser Arg Tyr Pro Leu Thr Phe Gly Pro Thr
1 5 10 15
ccg atc cag ccg ctc aag cgg ctt tcc gcg cat ctc ggc ggc aag gtc 96
Pro Ile Gln Pro Leu Lys Arg Leu Ser Ala His Leu Gly Gly Lys Val
20 25 30
gag ctg tac gcg aag cgc gac gac tgc aac agc ggc ctc gcg ttc ggc 144
Glu Leu Tyr Ala Lys Arg Asp Asp Cys Asn Ser Gly Leu Ala Phe Gly
35 40 45
ggc aac aag acg cgc aag ctc gaa tac ctg atc ccg gac gcg ctc gcg 192
Gly Asn Lys Thr Arg Lys Leu Glu Tyr Leu Ile Pro Asp Ala Leu Ala
50 55 60
caa ggc tgc gac acg ctc gtg tcg atc ggc ggc atc cag tcg aac cag 240
Gln Gly Cys Asp Thr Leu Val Ser Ile Gly Gly Ile Gln Ser Asn Gln
65 70 75 80
acg cgc cag gtc gcg gcg gtg gcc gcg cat ctc ggc atg aag tgc gtg 288
Thr Arg Gln Val Ala Ala Val Ala Ala His Leu Gly Met Lys Cys Val
85 90 95
ctc gtg cag gag aac tgg gtc aac tat cac gac gcc gtc tac gat cgc 336
Leu Val Gln Glu Asn Trp Val Asn Tyr His Asp Ala Val Tyr Asp Arg
100 105 110
gtc ggc aac atc cag atg tcg cgc atg atg ggc gcc gac gtg cgc ctc 384
Val Gly Asn Ile Gln Met Ser Arg Met Met Gly Ala Asp Val Arg Leu
115 120 125
gtg ccg gac ggc ttc gac atc ggc ttt cgc aag agc tgg gag gac gcg 432
Val Pro Asp Gly Phe Asp Ile Gly Phe Arg Lys Ser Trp Glu Asp Ala
130 135 140
ctc gcc gat gtc cgc gcg agg ggc ggc aag ccg tat gcg att ccg gcc 480
Leu Ala Asp Val Arg Ala Arg Gly Gly Lys Pro Tyr Ala Ile Pro Ala
145 150 155 160
ggc tgc tcc gac cat ccg ctc ggc ggc ctc ggc ttc gtc ggc ttt gcc 528
Gly Cys Ser Asp His Pro Leu Gly Gly Leu Gly Phe Val Gly Phe Ala
165 170 175
gag gaa gtg cgc gcg cag gag gcc gag ctc ggt ttc caa ttc gat tac 576
Glu Glu Val Arg Ala Gln Glu Ala Glu Leu Gly Phe Gln Phe Asp Tyr
180 185 190
gtc gtg gtg tgc tcg gtg acg ggc agc acg cag gcc ggg atg gtc gtc 624
Val Val Val Cys Ser Val Thr Gly Ser Thr Gln Ala Gly Met Val Val
195 200 205
ggc ttc gcg gcg gac ggg cgc gcg gac cgc gtg atc ggc gtc gac gcg 672
Gly Phe Ala Ala Asp Gly Arg Ala Asp Arg Val Ile Gly Val Asp Ala
210 215 220
tcg gcg aag ccc gcg cag acg cgc gag cag atc ctt cgg atc gcg aag 720
Ser Ala Lys Pro Ala Gln Thr Arg Glu Gln Ile Leu Arg Ile Ala Lys
225 230 235 240
cat acc gcc gat cgc gtc gag ctg ggc cgc gac atc acg agc gcc gac 768

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His Thr Ala Asp Arg Val Glu Leu Gly Arg Asp Ile Thr Ser Ala Asp
                245                 250                 255
gtc gtg ctc gac gag cgc ttc ggc ggc ccc gag tac ggg ctg ccg aac      816
Val Val Leu Asp Glu Arg Phe Gly Gly Pro Glu Tyr Gly Leu Pro Asn
            260                 265                 270
gag ggc acg ctc gag gcg atc cgg ctg tgc gcg aag ctc gaa ggc gtg      864
Glu Gly Thr Leu Glu Ala Ile Arg Leu Cys Ala Lys Leu Glu Gly Val
        275                 280                 285
ctg acc gat ccc gtc tac gaa ggc aag tcg atg cac ggg atg atc gag      912
Leu Thr Asp Pro Val Tyr Glu Gly Lys Ser Met His Gly Met Ile Glu
    290                 295                 300
aag gtg cgg ctc ggc gaa ttc ccg gcc ggc tcg aag gtg ctg tac gcg      960
Lys Val Arg Leu Gly Glu Phe Pro Ala Gly Ser Lys Val Leu Tyr Ala
305                 310                 315                 320
cat ctc ggc ggc gtg ccc gcg ctg aac gcg tac agc ttt ttg ttc cgc     1008
His Leu Gly Gly Val Pro Ala Leu Asn Ala Tyr Ser Phe Leu Phe Arg
                325                 330                 335
gac ggc tga                                                        1017
Asp Gly
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<210> 311
<211> 338
<212> PRT
<213> Burkholderia mallei

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<400> 311
Met Asn Leu Gln Lys Phe Ser Arg Tyr Pro Leu Thr Phe Gly Pro Thr
1               5                   10                  15
Pro Ile Gln Pro Leu Lys Arg Leu Ser Ala His Leu Gly Gly Lys Val
            20                  25                  30
Glu Leu Tyr Ala Lys Arg Asp Asp Cys Asn Ser Gly Leu Ala Phe Gly
        35                  40                  45
Gly Asn Lys Thr Arg Lys Leu Glu Tyr Leu Ile Pro Asp Ala Leu Ala
    50                  55                  60
Gln Gly Cys Asp Thr Leu Val Ser Ile Gly Gly Ile Gln Ser Asn Gln
65                  70                  75                  80
Thr Arg Gln Val Ala Ala Val Ala Ala His Leu Gly Met Lys Cys Val
                85                  90                  95
Leu Val Gln Glu Asn Trp Val Asn Tyr His Asp Ala Val Tyr Asp Arg
            100                 105                 110
Val Gly Asn Ile Gln Met Ser Arg Met Met Gly Ala Asp Val Arg Leu
        115                 120                 125
Val Pro Asp Gly Phe Asp Ile Gly Phe Arg Lys Ser Trp Glu Asp Ala
    130                 135                 140
Leu Ala Asp Val Arg Ala Arg Gly Gly Lys Pro Tyr Ala Ile Pro Ala
145                 150                 155                 160
Gly Cys Ser Asp His Pro Leu Gly Gly Leu Gly Phe Val Gly Phe Ala
                165                 170                 175
Glu Glu Val Arg Ala Gln Glu Ala Glu Leu Gly Phe Gln Phe Asp Tyr
            180                 185                 190
Val Val Val Cys Ser Val Thr Gly Ser Thr Gln Ala Gly Met Val Val
        195                 200                 205
Gly Phe Ala Ala Asp Gly Arg Ala Asp Arg Val Ile Gly Val Asp Ala
    210                 215                 220
Ser Ala Lys Pro Ala Gln Thr Arg Glu Gln Ile Leu Arg Ile Ala Lys
225                 230                 235                 240
His Thr Ala Asp Arg Val Glu Leu Gly Arg Asp Ile Thr Ser Ala Asp
                245                 250                 255
Val Val Leu Asp Glu Arg Phe Gly Gly Pro Glu Tyr Gly Leu Pro Asn
            260                 265                 270
```

```
Glu Gly Thr Leu Glu Ala Ile Arg Leu Cys Ala Lys Leu Glu Gly Val
        275                 280                 285
Leu Thr Asp Pro Val Tyr Glu Gly Lys Ser Met His Gly Met Ile Glu
    290                 295                 300
Lys Val Arg Leu Gly Glu Phe Pro Ala Gly Ser Lys Val Leu Tyr Ala
305                 310                 315                 320
His Leu Gly Gly Val Pro Ala Leu Asn Ala Tyr Ser Phe Leu Phe Arg
                325                 330                 335
Asp Gly


<210> 312
<211> 1038
<212> DNA
<213> Cryptococcus neoformans

<220>
<221> CDS
<222> (1)..(1038)

<400> 312
atg tct acg ccc gct tac cta aca aag ctc gag tct atc ccc aag gag      48
Met Ser Thr Pro Ala Tyr Leu Thr Lys Leu Glu Ser Ile Pro Lys Glu
1               5                   10                  15
aag ttc ctc ttc ggt cct tct ccc atc tca tac ctt ccc aat ctc acc      96
Lys Phe Leu Phe Gly Pro Ser Pro Ile Ser Tyr Leu Pro Asn Leu Thr
            20                  25                  30
gcc gtt ctc ggt ggg aag gtc aag ctt tac gcc aag cgt gag gac tgc     144
Ala Val Leu Gly Gly Lys Val Lys Leu Tyr Ala Lys Arg Glu Asp Cys
        35                  40                  45
aac tcc ggc ctg gcc tac ggt ggt aac aaa gtc cga aag ctg gag tat     192
Asn Ser Gly Leu Ala Tyr Gly Gly Asn Lys Val Arg Lys Leu Glu Tyr
    50                  55                  60
ctc gtt gcg gat gcc aag gcc aaa ggt tgt aac act ctc gtc tcc gtc     240
Leu Val Ala Asp Ala Lys Ala Lys Gly Cys Asn Thr Leu Val Ser Val
65                  70                  75                  80
ggt ggt gtg caa tcc aat cac acc agg gct gtg acc gct gtg gcc gtc     288
Gly Gly Val Gln Ser Asn His Thr Arg Ala Val Thr Ala Val Ala Val
                85                  90                  95
gct tct gga ctc aaa gcc gtc aca gtg caa gag aag tgg gtc ccc atc     336
Ala Ser Gly Leu Lys Ala Val Thr Val Gln Glu Lys Trp Val Pro Ile
            100                 105                 110
gac ccc cct ctt tac tct gag aca ggc aac atc ctt ctc tcc cga tta     384
Asp Pro Pro Leu Tyr Ser Glu Thr Gly Asn Ile Leu Leu Ser Arg Leu
        115                 120                 125
atg ggc ggc gac gtt aga ctt aac cag gag act ttc gat atc aga cac     432
Met Gly Gly Asp Val Arg Leu Asn Gln Glu Thr Phe Asp Ile Arg His
    130                 135                 140
aaa aag gct acc gaa gat gct ttc aag gac gtg gaa gcc aag ggc ggc     480
Lys Lys Ala Thr Glu Asp Ala Phe Lys Asp Val Glu Ala Lys Gly Gly
145                 150                 155                 160
aag cca tac tac atc cct gct ggc gct tct gac cac cca ctc ggt gga     528
Lys Pro Tyr Tyr Ile Pro Ala Gly Ala Ser Asp His Pro Leu Gly Gly
                165                 170                 175
ttg ggt ttc aca aac tgg gtc gtt gag ctc gcc aag caa gaa aaa gaa     576
Leu Gly Phe Thr Asn Trp Val Val Glu Leu Ala Lys Gln Glu Lys Glu
            180                 185                 190
ctc ggc gtc ttc ttc gac gtc gtc atc gtc tgc tcc gtc act ggt tct     624
Leu Gly Val Phe Phe Asp Val Val Ile Val Cys Ser Val Thr Gly Ser
        195                 200                 205
tct cac gcc ggt acc gtc gtc ggt gcc gtt gca gaa gga agg aag cgc     672
```

```
Ser His Ala Gly Thr Val Val Gly Ala Val Ala Glu Gly Arg Lys Arg
    210                 215                 220
aag att atc ggt att gac gcg agt ggt aag ccc gaa gcg aca aga aac      720
Lys Ile Ile Gly Ile Asp Ala Ser Gly Lys Pro Glu Ala Thr Arg Asn
225                 230                 235                 240
cag gtc ttg aag att gca agg aat act gcg gcc ttg ttg gat gag cgt      768
Gln Val Leu Lys Ile Ala Arg Asn Thr Ala Ala Leu Leu Asp Glu Arg
                245                 250                 255
ttg gag att aag gag gag gac gtc atc ttg gac gac agg ttc cac gct      816
Leu Glu Ile Lys Glu Glu Asp Val Ile Leu Asp Asp Arg Phe His Ala
            260                 265                 270
ggt atc tat ggt att cct gac gat gag acc atc gcc gcc atg aag ttg      864
Gly Ile Tyr Gly Ile Pro Asp Asp Glu Thr Ile Ala Ala Met Lys Leu
        275                 280                 285
gct gcc caa acc gat gcg ttc atc acc gac cct gta tac gaa ggc aag      912
Ala Ala Gln Thr Asp Ala Phe Ile Thr Asp Pro Val Tyr Glu Gly Lys
    290                 295                 300
tcc atg gcg gga atg atc cga ctt gtg aag gaa ggt gcc att aag gaa      960
Ser Met Ala Gly Met Ile Arg Leu Val Lys Glu Gly Ala Ile Lys Glu
305                 310                 315                 320
gga tcg aac gtg ttg tat atc cac ctc ggt gga caa ccg gcg tta aac     1008
Gly Ser Asn Val Leu Tyr Ile His Leu Gly Gly Gln Pro Ala Leu Asn
                325                 330                 335
gcc tat agc tca tat ttc cct cat gct tag                             1038
Ala Tyr Ser Ser Tyr Phe Pro His Ala
            340                 345
```

<210> 313
<211> 345
<212> PRT
<213> Cryptococcus neoformans

<400> 313

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

```
Lys Ile Ile Gly Ile Asp Ala Ser Gly Lys Pro Glu Ala Thr Arg Asn
225                 230                 235                 240
Gln Val Leu Lys Ile Ala Arg Asn Thr Ala Ala Leu Leu Asp Glu Arg
                245                 250                 255
Leu Glu Ile Lys Glu Glu Asp Val Ile Leu Asp Asp Arg Phe His Ala
            260                 265                 270
Gly Ile Tyr Gly Ile Pro Asp Asp Glu Thr Ile Ala Ala Met Lys Leu
        275                 280                 285
Ala Ala Gln Thr Asp Ala Phe Ile Thr Asp Pro Val Tyr Glu Gly Lys
    290                 295                 300
Ser Met Ala Gly Met Ile Arg Leu Val Lys Glu Gly Ala Ile Lys Glu
305                 310                 315                 320
Gly Ser Asn Val Leu Tyr Ile His Leu Gly Gly Gln Pro Ala Leu Asn
                325                 330                 335
Ala Tyr Ser Ser Tyr Phe Pro His Ala
            340                 345
```

<210> 314
<211> 1017
<212> DNA
<213> Enterobacter cloacae

<220>
<221> CDS
<222> (1)..(1017)
<223> transl_table=11

<400> 314

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

```
aaa aaa ttg cgg cag cag gaa aag gaa ctg ggc ttc aag ttt aac tac        576
Lys Lys Leu Arg Gln Gln Glu Lys Glu Leu Gly Phe Lys Phe Asn Tyr
            180                 185                 190
atc gtg gtc tgc tcg gtg acc ggc agt acg cag gcg ggc atg gtt gtc        624
Ile Val Val Cys Ser Val Thr Gly Ser Thr Gln Ala Gly Met Val Val
        195                 200                 205
ggt ttc gcg gct gac ggt cgt tct aag aat gtg att ggt gtc gat gct        672
Gly Phe Ala Ala Asp Gly Arg Ser Lys Asn Val Ile Gly Val Asp Ala
    210                 215                 220
tcg gcc aag ccg gaa cag acc aag gca cag atc ctg cgc atc gcc aga        720
Ser Ala Lys Pro Glu Gln Thr Lys Ala Gln Ile Leu Arg Ile Ala Arg
225                 230                 235                 240
cac acg gct gag ctg gtg gag ttg ggg cgc gag att acg gaa gag gac        768
His Thr Ala Glu Leu Val Glu Leu Gly Arg Glu Ile Thr Glu Glu Asp
                245                 250                 255
gtg gtg ctc gat acg cgt ttc gcc tac ccg gaa tat ggc ttg ccc aac        816
Val Val Leu Asp Thr Arg Phe Ala Tyr Pro Glu Tyr Gly Leu Pro Asn
            260                 265                 270
gaa ggt aca ttg gaa gca atc cga ctg tgc ggc agc ctt gaa ggg gtg        864
Glu Gly Thr Leu Glu Ala Ile Arg Leu Cys Gly Ser Leu Glu Gly Val
        275                 280                 285
ctg aca gat ccg gtg tac gaa ggt aaa tcg atg cac ggc atg att gaa        912
Leu Thr Asp Pro Val Tyr Glu Gly Lys Ser Met His Gly Met Ile Glu
    290                 295                 300
atg gtc cgt cgt ggc gaa ttc cct gaa ggc tcc aag gtg ctt tac gca        960
Met Val Arg Arg Gly Glu Phe Pro Glu Gly Ser Lys Val Leu Tyr Ala
305                 310                 315                 320
cac ctg ggt ggg gcg ccg gcg ctg aac gcc tac agc ttc cta ttc cgt       1008
His Leu Gly Gly Ala Pro Ala Leu Asn Ala Tyr Ser Phe Leu Phe Arg
                325                 330                 335
gat ggc tga                                                          1017
Asp Gly
```

<210> 315
<211> 338
<212> PRT
<213> Enterobacter cloacae

<400> 315

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

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

<210> 316
<211> 1017
<212> DNA
<213> Pseudomonas fluorescens

<220>
<221> CDS
<222> (1)..(1017)
<223> transl_table=11

<400> 316

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atg aac ctg aat cgt ttt aaa cgt tat ccg ctg acc ttc ggt cct tct      48
Met Asn Leu Asn Arg Phe Lys Arg Tyr Pro Leu Thr Phe Gly Pro Ser
1               5                   10                  15
ccg atc acg ccc ttg aaa cgc ctc agc gaa cac ctg ggc ggt aag gtc      96
Pro Ile Thr Pro Leu Lys Arg Leu Ser Glu His Leu Gly Gly Lys Val
            20                  25                  30
gag ttg tat gcc aaa cgt gaa gac tgc aac agt ggc ctg gcc ttt ggc     144
Glu Leu Tyr Ala Lys Arg Glu Asp Cys Asn Ser Gly Leu Ala Phe Gly
        35                  40                  45
ggc aac aag acg cgc aag ctc gaa tac ctg att ccc gag gcg ctc gaa     192
Gly Asn Lys Thr Arg Lys Leu Glu Tyr Leu Ile Pro Glu Ala Leu Glu
    50                  55                  60
cag ggc tgc gac acc ttg gtg tcc atc ggc ggg atc cag tcg aac cag     240
Gln Gly Cys Asp Thr Leu Val Ser Ile Gly Gly Ile Gln Ser Asn Gln
65                  70                  75                  80
acc cgc cag gtc gcc gct gtc gct gcc cac ctc ggt atg aag tgt gtg     288
Thr Arg Gln Val Ala Ala Val Ala Ala His Leu Gly Met Lys Cys Val
                85                  90                  95
ctg gtc cag gaa aac tgg gtg aac tac tcc gac gcc gtg tat gac cgg     336
Leu Val Gln Glu Asn Trp Val Asn Tyr Ser Asp Ala Val Tyr Asp Arg
            100                 105                 110
gtc ggc aat atc gag atg tcc cgc atc atg ggg gct gac gta cga ctg     384
Val Gly Asn Ile Glu Met Ser Arg Ile Met Gly Ala Asp Val Arg Leu
        115                 120                 125
gac gct gca ggg ttc gac atc ggt att cgg ccc agt tgg gag aag gcc     432
Asp Ala Ala Gly Phe Asp Ile Gly Ile Arg Pro Ser Trp Glu Lys Ala
```

```
   130                 135                 140
atg aac gac gtg gtg gaa cgg ggt ggc aag ccg ttc ccg ata ccg gcg        480
Met Asn Asp Val Val Glu Arg Gly Gly Lys Pro Phe Pro Ile Pro Ala
145                 150                 155                 160
ggt tgt tcc gaa cat ccc tac ggc ggg ctt ggg ttc gtc ggc ttt gcc        528
Gly Cys Ser Glu His Pro Tyr Gly Gly Leu Gly Phe Val Gly Phe Ala
                165                 170                 175
gag gaa gtg cgg gaa cag gaa aaa caa ctg ggg ttc aag ttc gac tac        576
Glu Glu Val Arg Glu Gln Glu Lys Gln Leu Gly Phe Lys Phe Asp Tyr
            180                 185                 190
atc gtg gtc tgc tcc gtg acc ggc agt acc cag gcc ggc atg gtc gtc        624
Ile Val Val Cys Ser Val Thr Gly Ser Thr Gln Ala Gly Met Val Val
        195                 200                 205
ggt ttt gcc gcg gac ggc cgt tcg aag aac gtt atc ggc att gat gcc        672
Gly Phe Ala Ala Asp Gly Arg Ser Lys Asn Val Ile Gly Ile Asp Ala
    210                 215                 220
tcg gcc aag ccc gag aag acc aag gca cag atc ctg cgt atc gcc cgg        720
Ser Ala Lys Pro Glu Lys Thr Lys Ala Gln Ile Leu Arg Ile Ala Arg
225                 230                 235                 240
cac acc gcc gag ctg gtg gaa ctg ggg cgt gag atc acc gaa gac gac        768
His Thr Ala Glu Leu Val Glu Leu Gly Arg Glu Ile Thr Glu Asp Asp
                245                 250                 255
gtg gtg ctc gat aca ccg ttc gcc tac ccg gaa tat ggt ttg ccc aac        816
Val Val Leu Asp Thr Pro Phe Ala Tyr Pro Glu Tyr Gly Leu Pro Asn
            260                 265                 270
gaa ggt acg ctg gaa gcc att cgc ctg tgc ggc agc ctt gaa ggt gtg        864
Glu Gly Thr Leu Glu Ala Ile Arg Leu Cys Gly Ser Leu Glu Gly Val
        275                 280                 285
ttg acc gac cca gtg tat gaa ggc aaa tcc atg cac ggg atg atc gaa        912
Leu Thr Asp Pro Val Tyr Glu Gly Lys Ser Met His Gly Met Ile Glu
    290                 295                 300
atg gtc cgc cgt ggc gag ttc ccc gaa ggc tcg aaa gtg ctt tac gcg        960
Met Val Arg Arg Gly Glu Phe Pro Glu Gly Ser Lys Val Leu Tyr Ala
305                 310                 315                 320
cac ctg ggt ggg gca cct gcg ctg aac gcc tac agc ttc ctg ttc cgc       1008
His Leu Gly Gly Ala Pro Ala Leu Asn Ala Tyr Ser Phe Leu Phe Arg
                325                 330                 335
aac ggc tga                                                          1017
Asn Gly
```

<210> 317
<211> 338
<212> PRT
<213> Pseudomonas fluorescens

<400> 317

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

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

<210> 318
<211> 1017
<212> DNA
<213> Pseudomonas putida

<220>
<221> CDS
<222> (1)..(1017)
<223> transl_table=11

<400> 318

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atg aac ctg aat cgt ttt gaa cgt tat ccg ttg acc ttc ggt cca tcc        48
Met Asn Leu Asn Arg Phe Glu Arg Tyr Pro Leu Thr Phe Gly Pro Ser
1               5                   10                  15
ccc atc act ccc ttg aaa cgc ctc agc gag cac ctg ggc ggc aag gtg        96
Pro Ile Thr Pro Leu Lys Arg Leu Ser Glu His Leu Gly Gly Lys Val
            20                  25                  30
gaa ctg tat gcc aag cgt gaa gac tgc aat agc ggc ctg gcc ttc ggc       144
Glu Leu Tyr Ala Lys Arg Glu Asp Cys Asn Ser Gly Leu Ala Phe Gly
        35                  40                  45
ggg aac aaa acg cgc aag ctc gaa tat ctg att ccc gag gcc atc gag       192
Gly Asn Lys Thr Arg Lys Leu Glu Tyr Leu Ile Pro Glu Ala Ile Glu
    50                  55                  60
caa ggc tgc gac acc ttg gtg tcc atc ggc ggt atc cag tcg aac cag       240
Gln Gly Cys Asp Thr Leu Val Ser Ile Gly Gly Ile Gln Ser Asn Gln
65                  70                  75                  80
acc cgc cag gtc gct gcg gtc gcc gcc cac ttg ggt atg aag tgt gtg       288
Thr Arg Gln Val Ala Ala Val Ala Ala His Leu Gly Met Lys Cys Val
                85                  90                  95
ctt gtg cag gaa aac tgg gtg aac tac tcc gac gct gta tat gac cgc       336
```

```
Leu Val Gln Glu Asn Trp Val Asn Tyr Ser Asp Ala Val Tyr Asp Arg
            100                 105                 110
gtc ggc aac atc gag atg tcg cgg atc atg gga gcg gat gtg cgg ctt      384
Val Gly Asn Ile Glu Met Ser Arg Ile Met Gly Ala Asp Val Arg Leu
        115                 120                 125
gat gct gca ggt ttc gac att gga att cgg ccg agc tgg gaa aag gcc      432
Asp Ala Ala Gly Phe Asp Ile Gly Ile Arg Pro Ser Trp Glu Lys Ala
    130                 135                 140
atg agc gat gtc gtg gag cgc ggc ggc aaa ccg ttt cca att ccg gcg      480
Met Ser Asp Val Val Glu Arg Gly Gly Lys Pro Phe Pro Ile Pro Ala
145                 150                 155                 160
ggc tgt tcc gag cat ccc tat gga ggg ctc ggg ttt gtc ggc ttc gct      528
Gly Cys Ser Glu His Pro Tyr Gly Gly Leu Gly Phe Val Gly Phe Ala
                165                 170                 175
gag gaa gtg cgg cag cag gaa aag gag ttg ggc ttc aag ttt gac tac      576
Glu Glu Val Arg Gln Gln Glu Lys Glu Leu Gly Phe Lys Phe Asp Tyr
            180                 185                 190
atc gtg gtc tgc tcg gtg acc ggc agt acc cag gcc ggc atg gtc gtc      624
Ile Val Val Cys Ser Val Thr Gly Ser Thr Gln Ala Gly Met Val Val
        195                 200                 205
ggt ttc gcg gct gac ggt cgc tcg aaa aac gtg atc ggg gtc gat gct      672
Gly Phe Ala Ala Asp Gly Arg Ser Lys Asn Val Ile Gly Val Asp Ala
    210                 215                 220
tcg gcg aaa ccg gag caa acc aag gcg cag atc ctg cgt atc gct cga      720
Ser Ala Lys Pro Glu Gln Thr Lys Ala Gln Ile Leu Arg Ile Ala Arg
225                 230                 235                 240
cat acc gct gaa ctg gtg gag ctg ggg cgc gaa atc act gaa gag gat      768
His Thr Ala Glu Leu Val Glu Leu Gly Arg Glu Ile Thr Glu Glu Asp
                245                 250                 255
gtg gtg ctc gat acg cgt ttc gcc tat ccg gaa tat ggc ttg ccc aac      816
Val Val Leu Asp Thr Arg Phe Ala Tyr Pro Glu Tyr Gly Leu Pro Asn
            260                 265                 270
gaa ggg acg ctg gaa gcg att cgc ctg tgc ggc agt ctt gag ggg gtg      864
Glu Gly Thr Leu Glu Ala Ile Arg Leu Cys Gly Ser Leu Glu Gly Val
        275                 280                 285
ttg acc gat ccg gtc tac gag ggc aaa tcc atg cac ggc atg att gaa      912
Leu Thr Asp Pro Val Tyr Glu Gly Lys Ser Met His Gly Met Ile Glu
    290                 295                 300
atg gta cgc cgc ggg gaa ttc cct gac ggc tcc aaa gtt ctt tat gcc      960
Met Val Arg Arg Gly Glu Phe Pro Asp Gly Ser Lys Val Leu Tyr Ala
305                 310                 315                 320
cac ctg ggc ggc gca cct gcg ttg aac gcc tac agc ttc ttg ttt cgc     1008
His Leu Gly Gly Ala Pro Ala Leu Asn Ala Tyr Ser Phe Leu Phe Arg
                325                 330                 335
aac ggc tga                                                        1017
Asn Gly
```

<210> 319
<211> 338
<212> PRT
<213> Pseudomonas putida

<400> 319

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Met Asn Leu Asn Arg Phe Glu Arg Tyr Pro Leu Thr Phe Gly Pro Ser
1               5                   10                  15
Pro Ile Thr Pro Leu Lys Arg Leu Ser Glu His Leu Gly Gly Lys Val
            20                  25                  30
Glu Leu Tyr Ala Lys Arg Glu Asp Cys Asn Ser Gly Leu Ala Phe Gly
        35                  40                  45
Gly Asn Lys Thr Arg Lys Leu Glu Tyr Leu Ile Pro Glu Ala Ile Glu
```

```
    50                  55                  60
Gln Gly Cys Asp Thr Leu Val Ser Ile Gly Gly Ile Gln Ser Asn Gln
65                  70                  75                  80
Thr Arg Gln Val Ala Ala Val Ala Ala His Leu Gly Met Lys Cys Val
                85                  90                  95
Leu Val Gln Glu Asn Trp Val Asn Tyr Ser Asp Ala Val Tyr Asp Arg
            100                 105                 110
Val Gly Asn Ile Glu Met Ser Arg Ile Met Gly Ala Asp Val Arg Leu
        115                 120                 125
Asp Ala Ala Gly Phe Asp Ile Gly Ile Arg Pro Ser Trp Glu Lys Ala
    130                 135                 140
Met Ser Asp Val Val Glu Arg Gly Gly Lys Pro Phe Pro Ile Pro Ala
145                 150                 155                 160
Gly Cys Ser Glu His Pro Tyr Gly Gly Leu Gly Phe Val Gly Phe Ala
                165                 170                 175
Glu Glu Val Arg Gln Gln Glu Lys Glu Leu Gly Phe Lys Phe Asp Tyr
            180                 185                 190
Ile Val Val Cys Ser Val Thr Gly Ser Thr Gln Ala Gly Met Val Val
        195                 200                 205
Gly Phe Ala Ala Asp Gly Arg Ser Lys Asn Val Ile Gly Val Asp Ala
    210                 215                 220
Ser Ala Lys Pro Glu Gln Thr Lys Ala Gln Ile Leu Arg Ile Ala Arg
225                 230                 235                 240
His Thr Ala Glu Leu Val Glu Leu Gly Arg Glu Ile Thr Glu Glu Asp
                245                 250                 255
Val Val Leu Asp Thr Arg Phe Ala Tyr Pro Glu Tyr Gly Leu Pro Asn
            260                 265                 270
Glu Gly Thr Leu Glu Ala Ile Arg Leu Cys Gly Ser Leu Glu Gly Val
        275                 280                 285
Leu Thr Asp Pro Val Tyr Glu Gly Lys Ser Met His Gly Met Ile Glu
    290                 295                 300
Met Val Arg Arg Gly Glu Phe Pro Asp Gly Ser Lys Val Leu Tyr Ala
305                 310                 315                 320
His Leu Gly Gly Ala Pro Ala Leu Asn Ala Tyr Ser Phe Leu Phe Arg
                325                 330                 335
Asn Gly
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<210> 320
<211> 1017
<212> DNA
<213> Pseudomonas sp

<220>
<221> CDS
<222> (1)..(1017)
<223> transl_table=11

<400> 320

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atg aat ctg aat cgt ttt gaa cgt tat cca ttg acc ttc ggt cct tct      48
Met Asn Leu Asn Arg Phe Glu Arg Tyr Pro Leu Thr Phe Gly Pro Ser
1               5                   10                  15
ccc atc acg ccc ttg aag cgc ctc agt caa cat ctg ggg ggc aag gtc      96
Pro Ile Thr Pro Leu Lys Arg Leu Ser Gln His Leu Gly Gly Lys Val
            20                  25                  30
gag ctg tat gcc aaa cgt gaa gac tgc aac agt ggc ctg gcc ttt ggt     144
Glu Leu Tyr Ala Lys Arg Glu Asp Cys Asn Ser Gly Leu Ala Phe Gly
        35                  40                  45
ggg aac aag acg cgc aag ctc gaa tac ctc att ccc gaa gcg atc gag     192
Gly Asn Lys Thr Arg Lys Leu Glu Tyr Leu Ile Pro Glu Ala Ile Glu
    50                  55                  60
```

```
caa ggc tgc gat acg ctg gtt tcc atc ggc ggc atc cag tcg aac cag        240
Gln Gly Cys Asp Thr Leu Val Ser Ile Gly Gly Ile Gln Ser Asn Gln
65                  70                  75                  80
acc cgt cag gtc gct gcc gtc gct gcc cac ttg ggc atg aag tgc gtg        288
Thr Arg Gln Val Ala Ala Val Ala Ala His Leu Gly Met Lys Cys Val
                85                  90                  95
ttg gtg cag gaa aac tgg gtg aac tat tcc gac gcg gtg tat gac cgc        336
Leu Val Gln Glu Asn Trp Val Asn Tyr Ser Asp Ala Val Tyr Asp Arg
            100                 105                 110
gta ggc aac atc gag atg tcg cgg atc atg ggc gct gat gtg cgg ctt        384
Val Gly Asn Ile Glu Met Ser Arg Ile Met Gly Ala Asp Val Arg Leu
        115                 120                 125
gac gcc gct ggc ttc gat att ggc att cgg cca agt tgg gaa aag gcc        432
Asp Ala Ala Gly Phe Asp Ile Gly Ile Arg Pro Ser Trp Glu Lys Ala
    130                 135                 140
atg agc gat gtc gtg gaa cag ggt ggc aaa ccg ttt ccg att cca gcg        480
Met Ser Asp Val Val Glu Gln Gly Gly Lys Pro Phe Pro Ile Pro Ala
145                 150                 155                 160
ggt tgc tcc gag cat ccc tat ggc ggc ctc ggt ttc gtc ggc ttt gcc        528
Gly Cys Ser Glu His Pro Tyr Gly Gly Leu Gly Phe Val Gly Phe Ala
                165                 170                 175
gaa gag gtg cgg cag cag gaa aag gaa ctg ggc ttc aag ttt gac tac        576
Glu Glu Val Arg Gln Gln Glu Lys Glu Leu Gly Phe Lys Phe Asp Tyr
            180                 185                 190
atc gtg gtc tgc tcg gtg acc ggc agt acg cag gcg ggc atg gtt gtt        624
Ile Val Val Cys Ser Val Thr Gly Ser Thr Gln Ala Gly Met Val Val
        195                 200                 205
ggt ttc gcg gct gac ggt cgt tcg aag aat gtg att ggt atc gat gct        672
Gly Phe Ala Ala Asp Gly Arg Ser Lys Asn Val Ile Gly Ile Asp Ala
    210                 215                 220
tcg gcc aag ccg gaa cag acc aag gca cag atc ctg cgc atc gcc cga        720
Ser Ala Lys Pro Glu Gln Thr Lys Ala Gln Ile Leu Arg Ile Ala Arg
225                 230                 235                 240
cac acc gct gag ttg gtg gag ttg ggg cgc gag att acg gaa gag gac        768
His Thr Ala Glu Leu Val Glu Leu Gly Arg Glu Ile Thr Glu Glu Asp
                245                 250                 255
gtg gtg ctc gat acg cgt ttt gcc tac ccg gaa tat ggc ttg ccc aac        816
Val Val Leu Asp Thr Arg Phe Ala Tyr Pro Glu Tyr Gly Leu Pro Asn
            260                 265                 270
gaa ggc aca ttg gaa gcc atc cga ctg tgc ggc agc ctt gaa ggc gtg        864
Glu Gly Thr Leu Glu Ala Ile Arg Leu Cys Gly Ser Leu Glu Gly Val
        275                 280                 285
ctg aca gac ccg gta tat gaa ggt aaa tcg atg cac ggc atg att gaa        912
Leu Thr Asp Pro Val Tyr Glu Gly Lys Ser Met His Gly Met Ile Glu
    290                 295                 300
atg gtc cgt cgt ggt gaa ttc ccc gaa ggt tcc aaa gtg ctt tac gca        960
Met Val Arg Arg Gly Glu Phe Pro Glu Gly Ser Lys Val Leu Tyr Ala
305                 310                 315                 320
cac ttg ggt ggg gcg ccg gcg ctg aac gcc tac agc ttc ctg ttt cgt       1008
His Leu Gly Gly Ala Pro Ala Leu Asn Ala Tyr Ser Phe Leu Phe Arg
                325                 330                 335
aac ggc taa                                                          1017
Asn Gly
```

<210> 321
<211> 338
<212> PRT
<213> Pseudomonas sp

<400> 321

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Met Asn Leu Asn Arg Phe Glu Arg Tyr Pro Leu Thr Phe Gly Pro Ser
1               5                  10                  15
Pro Ile Thr Pro Leu Lys Arg Leu Ser Gln His Leu Gly Gly Lys Val
            20                  25                  30
Glu Leu Tyr Ala Lys Arg Glu Asp Cys Asn Ser Gly Leu Ala Phe Gly
        35                  40                  45
Gly Asn Lys Thr Arg Lys Leu Glu Tyr Leu Ile Pro Glu Ala Ile Glu
    50                  55                  60
Gln Gly Cys Asp Thr Leu Val Ser Ile Gly Gly Ile Gln Ser Asn Gln
65                  70                  75                  80
Thr Arg Gln Val Ala Ala Val Ala Ala His Leu Gly Met Lys Cys Val
                85                  90                  95
Leu Val Gln Glu Asn Trp Val Asn Tyr Ser Asp Ala Val Tyr Asp Arg
            100                 105                 110
Val Gly Asn Ile Glu Met Ser Arg Ile Met Gly Ala Asp Val Arg Leu
        115                 120                 125
Asp Ala Ala Gly Phe Asp Ile Gly Ile Arg Pro Ser Trp Glu Lys Ala
    130                 135                 140
Met Ser Asp Val Val Glu Gln Gly Gly Lys Pro Phe Pro Ile Pro Ala
145                 150                 155                 160
Gly Cys Ser Glu His Pro Tyr Gly Gly Leu Gly Phe Val Gly Phe Ala
                165                 170                 175
Glu Glu Val Arg Gln Gln Glu Lys Glu Leu Gly Phe Lys Phe Asp Tyr
            180                 185                 190
Ile Val Val Cys Ser Val Thr Gly Ser Thr Gln Ala Gly Met Val Val
        195                 200                 205
Gly Phe Ala Ala Asp Gly Arg Ser Lys Asn Val Ile Gly Ile Asp Ala
    210                 215                 220
Ser Ala Lys Pro Glu Gln Thr Lys Ala Gln Ile Leu Arg Ile Ala Arg
225                 230                 235                 240
His Thr Ala Glu Leu Val Glu Leu Gly Arg Glu Ile Thr Glu Glu Asp
                245                 250                 255
Val Val Leu Asp Thr Arg Phe Ala Tyr Pro Glu Tyr Gly Leu Pro Asn
            260                 265                 270
Glu Gly Thr Leu Glu Ala Ile Arg Leu Cys Gly Ser Leu Glu Gly Val
        275                 280                 285
Leu Thr Asp Pro Val Tyr Glu Gly Lys Ser Met His Gly Met Ile Glu
    290                 295                 300
Met Val Arg Arg Gly Glu Phe Pro Glu Gly Ser Lys Val Leu Tyr Ala
305                 310                 315                 320
His Leu Gly Gly Ala Pro Ala Leu Asn Ala Tyr Ser Phe Leu Phe Arg
                325                 330                 335
Asn Gly
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<210> 322
<211> 1017
<212> DNA
<213> Pseudomonas syringae pv

<220>
<221> CDS
<222> (1)..(1017)
<223> transl_table=11

<400> 322
atg aac ctc agc aag ttc aaa cgc tac cct ctg acc ttc ggc ccc tcg 48
Met Asn Leu Ser Lys Phe Lys Arg Tyr Pro Leu Thr Phe Gly Pro Ser
1   5   10   15
ccc atc acc ccg ctg aaa cgc ttg agc gag cac ctg ggt ggc aag gtc 96
Pro Ile Thr Pro Leu Lys Arg Leu Ser Glu His Leu Gly Gly Lys Val

```
          20                  25                  30
gat ctg tac gcc aag cgc gaa gac tgc aat agc ggc ctg gcc ttt ggc        144
Asp Leu Tyr Ala Lys Arg Glu Asp Cys Asn Ser Gly Leu Ala Phe Gly
        35                  40                  45
ggc aac aag acc cgc aag ctg gaa tac ctg gtg ccg gaa gcc atc gag        192
Gly Asn Lys Thr Arg Lys Leu Glu Tyr Leu Val Pro Glu Ala Ile Glu
    50                  55                  60
ggc ggc tac gac acg ctg gtg tcg atc ggc ggc att cag tcc aac cag        240
Gly Gly Tyr Asp Thr Leu Val Ser Ile Gly Gly Ile Gln Ser Asn Gln
65                  70                  75                  80
acc cgc cag gtg gcg gca gtc gcg gcg cat ctg ggc atg aag tgc gtg        288
Thr Arg Gln Val Ala Ala Val Ala Ala His Leu Gly Met Lys Cys Val
                85                  90                  95
ctg gtt cag gaa aac tgg gtc aac tac tcc gat gcg ctg tat gac cgg        336
Leu Val Gln Glu Asn Trp Val Asn Tyr Ser Asp Ala Leu Tyr Asp Arg
            100                 105                 110
gtc ggc aac atc gaa atg tcg cgc atc atg ggc gcc gat gtg cgc ctg        384
Val Gly Asn Ile Glu Met Ser Arg Ile Met Gly Ala Asp Val Arg Leu
        115                 120                 125
gac tcg gcc ggt ttt gat atc ggc att cgc ccg agc tgg gaa aag gcc        432
Asp Ser Ala Gly Phe Asp Ile Gly Ile Arg Pro Ser Trp Glu Lys Ala
    130                 135                 140
atg gcc gat gta gtc gaa agc ggc ggc aag ccg ttc ccg att cct gcg        480
Met Ala Asp Val Val Glu Ser Gly Gly Lys Pro Phe Pro Ile Pro Ala
145                 150                 155                 160
gga tgt tcg gaa cat ccc tac ggc ggc ctt ggg ttc gtg cgc ttt gcc        528
Gly Cys Ser Glu His Pro Tyr Gly Gly Leu Gly Phe Val Arg Phe Ala
                165                 170                 175
gat gaa gta cgc cag caa gaa gaa gaa ctg ggc ttc aag ttc gac tac        576
Asp Glu Val Arg Gln Gln Glu Glu Glu Leu Gly Phe Lys Phe Asp Tyr
            180                 185                 190
atc gtc gtc tgc tcg gtc acc ggc agc acc cac gcc ggt atg ctg gtc        624
Ile Val Val Cys Ser Val Thr Gly Ser Thr His Ala Gly Met Leu Val
        195                 200                 205
ggc ttc gct gcc gat ggc cgt gcg caa cgg gta atc ggc atc gac gcc        672
Gly Phe Ala Ala Asp Gly Arg Ala Gln Arg Val Ile Gly Ile Asp Ala
    210                 215                 220
tcg gcc aaa ccg gac aaa acc cgc gag cag gta ctg cgt atc gcc cag        720
Ser Ala Lys Pro Asp Lys Thr Arg Glu Gln Val Leu Arg Ile Ala Gln
225                 230                 235                 240
aac acc gca aaa ctg gtc gac ctg ggc cgc gaa atc acc gcc gaa gac        768
Asn Thr Ala Lys Leu Val Asp Leu Gly Arg Glu Ile Thr Ala Glu Asp
                245                 250                 255
gtg gtg ctc gac acc cgc tac gcc tac ccc gaa tac ggc ctg ccc aac        816
Val Val Leu Asp Thr Arg Tyr Ala Tyr Pro Glu Tyr Gly Leu Pro Asn
            260                 265                 270
gac ggc acc ctc gaa gcc ata cgc ctc tgc gcc cgc ctc gaa ggc gtg        864
Asp Gly Thr Leu Glu Ala Ile Arg Leu Cys Ala Arg Leu Glu Gly Val
        275                 280                 285
ctg acc gac ccg gtc tac gag ggc aaa tcc atg cac ggc atg atc gac        912
Leu Thr Asp Pro Val Tyr Glu Gly Lys Ser Met His Gly Met Ile Asp
    290                 295                 300
atg gtc cgc aac ggc gaa ttc ccc gaa ggc tcg aaa gtg ctc tac gcg        960
Met Val Arg Asn Gly Glu Phe Pro Glu Gly Ser Lys Val Leu Tyr Ala
305                 310                 315                 320
cac ctg ggc ggc gta ccg gcg ctg aac gcg tac agc ttt ttg ttc aag       1008
His Leu Gly Gly Val Pro Ala Leu Asn Ala Tyr Ser Phe Leu Phe Lys
                325                 330                 335
gat ggt tga                                                           1017
Asp Gly
```

<210> 323
<211> 338
<212> PRT
<213> Pseudomonas syringae pv

<400> 323
Met Asn Leu Ser Lys Phe Lys Arg Tyr Pro Leu Thr Phe Gly Pro Ser
1 5 10 15
Pro Ile Thr Pro Leu Lys Arg Leu Ser Glu His Leu Gly Gly Lys Val
20 25 30
Asp Leu Tyr Ala Lys Arg Glu Asp Cys Asn Ser Gly Leu Ala Phe Gly
35 40 45
Gly Asn Lys Thr Arg Lys Leu Glu Tyr Leu Val Pro Glu Ala Ile Glu
50 55 60
Gly Gly Tyr Asp Thr Leu Val Ser Ile Gly Gly Ile Gln Ser Asn Gln
65 70 75 80
Thr Arg Gln Val Ala Ala Val Ala Ala His Leu Gly Met Lys Cys Val
85 90 95
Leu Val Gln Glu Asn Trp Val Asn Tyr Ser Asp Ala Leu Tyr Asp Arg
100 105 110
Val Gly Asn Ile Glu Met Ser Arg Ile Met Gly Ala Asp Val Arg Leu
115 120 125
Asp Ser Ala Gly Phe Asp Ile Gly Ile Arg Pro Ser Trp Glu Lys Ala
130 135 140
Met Ala Asp Val Val Glu Ser Gly Gly Lys Pro Phe Pro Ile Pro Ala
145 150 155 160
Gly Cys Ser Glu His Pro Tyr Gly Gly Leu Gly Phe Val Arg Phe Ala
165 170 175
Asp Glu Val Arg Gln Gln Glu Glu Glu Leu Gly Phe Lys Phe Asp Tyr
180 185 190
Ile Val Val Cys Ser Val Thr Gly Ser Thr His Ala Gly Met Leu Val
195 200 205
Gly Phe Ala Ala Asp Gly Arg Ala Gln Arg Val Ile Gly Ile Asp Ala
210 215 220
Ser Ala Lys Pro Asp Lys Thr Arg Glu Gln Val Leu Arg Ile Ala Gln
225 230 235 240
Asn Thr Ala Lys Leu Val Asp Leu Gly Arg Glu Ile Thr Ala Glu Asp
245 250 255
Val Val Leu Asp Thr Arg Tyr Ala Tyr Pro Glu Tyr Gly Leu Pro Asn
260 265 270
Asp Gly Thr Leu Glu Ala Ile Arg Leu Cys Ala Arg Leu Glu Gly Val
275 280 285
Leu Thr Asp Pro Val Tyr Glu Gly Lys Ser Met His Gly Met Ile Asp
290 295 300
Met Val Arg Asn Gly Glu Phe Pro Glu Gly Ser Lys Val Leu Tyr Ala
305 310 315 320
His Leu Gly Gly Val Pro Ala Leu Asn Ala Tyr Ser Phe Leu Phe Lys
325 330 335
Asp Gly

<210> 324
<211> 1017
<212> DNA
<213> Pseudomonas sp

<220>
<221> CDS
<222> (1)..(1017)
<223> transl_table=11

<400> 324

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atg aac ctg caa cga ttc cct cgt tac ccg ctg act ttc ggg ccg acg        48
Met Asn Leu Gln Arg Phe Pro Arg Tyr Pro Leu Thr Phe Gly Pro Thr
1               5                  10                  15
cca atc caa ccg cta gcg cgt ctg agc aag cac ctc ggc ggc aaa gtg        96
Pro Ile Gln Pro Leu Ala Arg Leu Ser Lys His Leu Gly Gly Lys Val
            20                  25                  30
cat ctg tat gcg aaa cgc gaa gac tgc aac agc ggc ctg gcg ttc ggt       144
His Leu Tyr Ala Lys Arg Glu Asp Cys Asn Ser Gly Leu Ala Phe Gly
        35                  40                  45
ggc aac aag aca cgc aag ctc gaa tat ctg atc cct gaa gcg ctt gct       192
Gly Asn Lys Thr Arg Lys Leu Glu Tyr Leu Ile Pro Glu Ala Leu Ala
    50                  55                  60
cag ggt tgc gac acg ctc gtg tcg atc ggc ggc att cag tcg aac cag       240
Gln Gly Cys Asp Thr Leu Val Ser Ile Gly Gly Ile Gln Ser Asn Gln
65                  70                  75                  80
acg cgc cag gtg gcg gcc gtg gcg gct cat ctg ggc atg aag tgc gtg       288
Thr Arg Gln Val Ala Ala Val Ala Ala His Leu Gly Met Lys Cys Val
                85                  90                  95
ctg gtg cag gag aac tgg gtc aac tat tcg gac gca gtc tac gac cgc       336
Leu Val Gln Glu Asn Trp Val Asn Tyr Ser Asp Ala Val Tyr Asp Arg
            100                 105                 110
gtc ggc aac atc cag atg tcg cgc att ctc ggc gcc gat gtt cgc ctc       384
Val Gly Asn Ile Gln Met Ser Arg Ile Leu Gly Ala Asp Val Arg Leu
        115                 120                 125
gtg ccc gac ggc ttc gac atc ggt ttt cgc agg agc tgg gag gat gcg       432
Val Pro Asp Gly Phe Asp Ile Gly Phe Arg Arg Ser Trp Glu Asp Ala
    130                 135                 140
ctg gaa agc gtg cgg gcg gcc ggc ggc aag ccg tat gcg att ccg gca       480
Leu Glu Ser Val Arg Ala Ala Gly Gly Lys Pro Tyr Ala Ile Pro Ala
145                 150                 155                 160
ggc tgc tcg gat cac ccg ctc ggc ggc ctg ggt ttc gtc ggc ttc gcg       528
Gly Cys Ser Asp His Pro Leu Gly Gly Leu Gly Phe Val Gly Phe Ala
                165                 170                 175
gag gag gtg cgg gcg cag gaa gcc gaa ttg ggc ttc aaa ttc gac tat       576
Glu Glu Val Arg Ala Gln Glu Ala Glu Leu Gly Phe Lys Phe Asp Tyr
            180                 185                 190
gtc gtc gtg tgt tcc gtg acc ggc agc acg cag gcc ggc atg gtg gtg       624
Val Val Val Cys Ser Val Thr Gly Ser Thr Gln Ala Gly Met Val Val
        195                 200                 205
ggc ttc gcc gct gac ggc cgc gcc gat cgc gtg atc ggc gtc gac gct       672
Gly Phe Ala Ala Asp Gly Arg Ala Asp Arg Val Ile Gly Val Asp Ala
    210                 215                 220
tcg gcc aaa ccc gcg cag acg cgc gag cag atc acc cgc atc gcg aga       720
Ser Ala Lys Pro Ala Gln Thr Arg Glu Gln Ile Thr Arg Ile Ala Arg
225                 230                 235                 240
cag acc gcg gag aaa gtc ggc ctg gag cgc gat atc atg cgg gcc gac       768
Gln Thr Ala Glu Lys Val Gly Leu Glu Arg Asp Ile Met Arg Ala Asp
                245                 250                 255
gtg gtg ctc gac gag cgc ttc gcg ggt ccg gaa tac gga ttg ccg aac       816
Val Val Leu Asp Glu Arg Phe Ala Gly Pro Glu Tyr Gly Leu Pro Asn
            260                 265                 270
gaa ggc acg ctg gaa gcg atc cgc ttg tgc gcg cgc acg gag ggc atg       864
Glu Gly Thr Leu Glu Ala Ile Arg Leu Cys Ala Arg Thr Glu Gly Met
        275                 280                 285
ctg acc gat ccc gtc tac gaa ggc aaa tcg atg cac ggc atg atc gaa       912
Leu Thr Asp Pro Val Tyr Glu Gly Lys Ser Met His Gly Met Ile Glu
    290                 295                 300
atg gtg cgc aac ggc gaa ttt ccg gaa ggc tcg cgc gtg ctg tat gcg       960
Met Val Arg Asn Gly Glu Phe Pro Glu Gly Ser Arg Val Leu Tyr Ala
```

```
305                 310                 315                 320
cac ctc ggc ggg gtg ccg gcg ttg aac ggc tac agc ttt atc ttc cga      1008
His Leu Gly Gly Val Pro Ala Leu Asn Gly Tyr Ser Phe Ile Phe Arg
                325                 330                 335
gac ggc tga                                                       1017
Asp Gly
```

<210> 325
<211> 338
<212> PRT
<213> Pseudomonas sp

<400> 325

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Met Asn Leu Gln Arg Phe Pro Arg Tyr Pro Leu Thr Phe Gly Pro Thr
1               5                  10                  15
Pro Ile Gln Pro Leu Ala Arg Leu Ser Lys His Leu Gly Gly Lys Val
            20                  25                  30
His Leu Tyr Ala Lys Arg Glu Asp Cys Asn Ser Gly Leu Ala Phe Gly
        35                  40                  45
Gly Asn Lys Thr Arg Lys Leu Glu Tyr Leu Ile Pro Glu Ala Leu Ala
    50                  55                  60
Gln Gly Cys Asp Thr Leu Val Ser Ile Gly Gly Ile Gln Ser Asn Gln
65                  70                  75                  80
Thr Arg Gln Val Ala Ala Val Ala Ala His Leu Gly Met Lys Cys Val
                85                  90                  95
Leu Val Gln Glu Asn Trp Val Asn Tyr Ser Asp Ala Val Tyr Asp Arg
            100                 105                 110
Val Gly Asn Ile Gln Met Ser Arg Ile Leu Gly Ala Asp Val Arg Leu
        115                 120                 125
Val Pro Asp Gly Phe Asp Ile Gly Phe Arg Arg Ser Trp Glu Asp Ala
    130                 135                 140
Leu Glu Ser Val Arg Ala Ala Gly Gly Lys Pro Tyr Ala Ile Pro Ala
145                 150                 155                 160
Gly Cys Ser Asp His Pro Leu Gly Gly Leu Gly Phe Val Gly Phe Ala
                165                 170                 175
Glu Glu Val Arg Ala Gln Glu Ala Glu Leu Gly Phe Lys Phe Asp Tyr
            180                 185                 190
Val Val Val Cys Ser Val Thr Gly Ser Thr Gln Ala Gly Met Val Val
        195                 200                 205
Gly Phe Ala Ala Asp Gly Arg Ala Asp Arg Val Ile Gly Val Asp Ala
    210                 215                 220
Ser Ala Lys Pro Ala Gln Thr Arg Glu Gln Ile Thr Arg Ile Ala Arg
225                 230                 235                 240
Gln Thr Ala Glu Lys Val Gly Leu Glu Arg Asp Ile Met Arg Ala Asp
                245                 250                 255
Val Val Leu Asp Glu Arg Phe Ala Gly Pro Glu Tyr Gly Leu Pro Asn
            260                 265                 270
Glu Gly Thr Leu Glu Ala Ile Arg Leu Cys Ala Arg Thr Glu Gly Met
        275                 280                 285
Leu Thr Asp Pro Val Tyr Glu Gly Lys Ser Met His Gly Met Ile Glu
    290                 295                 300
Met Val Arg Asn Gly Glu Phe Pro Glu Gly Ser Arg Val Leu Tyr Ala
305                 310                 315                 320
His Leu Gly Gly Val Pro Ala Leu Asn Gly Tyr Ser Phe Ile Phe Arg
                325                 330                 335
Asp Gly
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<210> 326
<211> 993

<212> DNA
<213> Pyrococcus abyssi

<220>
<221> CDS
<222> (1)..(993)
<223> transl_table=11

<400> 326

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

```
Ser Val Gly Thr Met Glu Gly Leu Leu Leu Asp Pro Val Tyr Thr Gly
        275                 280                 285
aag gca ttc tac ggc ctg atg gat ctt gcg aag aaa gga gat ctc gga        912
Lys Ala Phe Tyr Gly Leu Met Asp Leu Ala Lys Lys Gly Asp Leu Gly
    290                 295                 300
gag agc gtt ctc ttt ata cac acg ggt ggt ctc cca ggg ata ttc cac        960
Glu Ser Val Leu Phe Ile His Thr Gly Gly Leu Pro Gly Ile Phe His
305                 310                 315                 320
tat ggt gag gaa atg ctt gaa ttg ttg gta tga                            993
Tyr Gly Glu Glu Met Leu Glu Leu Leu Val
                325                 330
```

<210> 327
<211> 330
<212> PRT
<213> Pyrococcus abyssi

<400> 327

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

<210> 328
<211> 1017
<212> DNA
<213> Ralstonia solanacearum

<220>
<221> CDS
<222> (1)..(1017)
<223> transl_table=11

<400> 328

```
atg aac ctg aac aag cat ccc cgc cat ccg ctg acc ttc ggc ccc acg      48
Met Asn Leu Asn Lys His Pro Arg His Pro Leu Thr Phe Gly Pro Thr
1               5                  10                  15
ccc atc cag ccg ctc aag cgg ctg tcg gcc cac ctc ggc ggc aag gtc      96
Pro Ile Gln Pro Leu Lys Arg Leu Ser Ala His Leu Gly Gly Lys Val
            20                  25                  30
gag ctt tac gcc aag cgt gag gac tgc aac agc ggc ctg gcc ttc ggc     144
Glu Leu Tyr Ala Lys Arg Glu Asp Cys Asn Ser Gly Leu Ala Phe Gly
        35                  40                  45
ggc aac aag acg cgc aag ctc gaa tac ctg gtg ccg gag gtg ctg gcc     192
Gly Asn Lys Thr Arg Lys Leu Glu Tyr Leu Val Pro Glu Val Leu Ala
    50                  55                  60
ggc ggc tac gac aca ctg gtc tcg atc ggc ggc atc cag tcg aac cag     240
Gly Gly Tyr Asp Thr Leu Val Ser Ile Gly Gly Ile Gln Ser Asn Gln
65                  70                  75                  80
acg cgc cag gtc gcg gcg gtg gcc gcg cac ctg ggg ctg aag tgc gtg     288
Thr Arg Gln Val Ala Ala Val Ala Ala His Leu Gly Leu Lys Cys Val
                85                  90                  95
ctg gtg cag gag aac tgg gtc aac tat gcc gat gcg gtc tac gac cgg     336
Leu Val Gln Glu Asn Trp Val Asn Tyr Ala Asp Ala Val Tyr Asp Arg
            100                 105                 110
gtg ggc aac atc gag ctg tcg cgc atc ctg ggc gcg gac gtg cgg ctg     384
Val Gly Asn Ile Glu Leu Ser Arg Ile Leu Gly Ala Asp Val Arg Leu
        115                 120                 125
gac gcg gcc ggg ttc gac atc ggc atc cgc ccg agc tgg gag cag gcc     432
Asp Ala Ala Gly Phe Asp Ile Gly Ile Arg Pro Ser Trp Glu Gln Ala
    130                 135                 140
atg gag gac gtg cgc cgc gcg ggc ggc aag ccg ttc ccg atc ccg gcc     480
Met Glu Asp Val Arg Arg Ala Gly Gly Lys Pro Phe Pro Ile Pro Ala
145                 150                 155                 160
ggc tgc tcg gag cat ccg ctc ggt ggc ctg ggc ttc gtc ggc ttt gcc     528
Gly Cys Ser Glu His Pro Leu Gly Gly Leu Gly Phe Val Gly Phe Ala
                165                 170                 175
gag gag gtg cgc cag cag gag gcc gag ttc ggt ttc cgc ttc gac tac     576
Glu Glu Val Arg Gln Gln Glu Ala Glu Phe Gly Phe Arg Phe Asp Tyr
            180                 185                 190
atc gtg gtg tgc tcc gtc acg ggc agc aca cag gcg ggc atg gtg gtg     624
Ile Val Val Cys Ser Val Thr Gly Ser Thr Gln Ala Gly Met Val Val
        195                 200                 205
ggt ttc gcg gcg gac ggg cgc gcc gac cgg gtg atc ggc atc gac gca     672
Gly Phe Ala Ala Asp Gly Arg Ala Asp Arg Val Ile Gly Ile Asp Ala
    210                 215                 220
tcg gcc aag ccg gag cag acg cgc gag cag atc ctg cgg atc gct cgc     720
Ser Ala Lys Pro Glu Gln Thr Arg Glu Gln Ile Leu Arg Ile Ala Arg
225                 230                 235                 240
gat acc gcc aag ctg gtc gag ctc ggc cgc gac atc acg gaa gac gac     768
Asp Thr Ala Lys Leu Val Glu Leu Gly Arg Asp Ile Thr Glu Asp Asp
                245                 250                 255
gtg gtg ctc gac acg cgc tac ggc ggc ccc gaa tac ggc ttg ccg aac     816
Val Val Leu Asp Thr Arg Tyr Gly Gly Pro Glu Tyr Gly Leu Pro Asn
```

```
            260                 265                 270
gaa ggc acg ctg gag gcg atc cgg ctg tgc gcg cgc cag gag ggc atg      864
Glu Gly Thr Leu Glu Ala Ile Arg Leu Cys Ala Arg Gln Glu Gly Met
        275                 280                 285
ctg acc gac ccg gtg tac gag ggc aag tcg atg cac ggc atg atc gac      912
Leu Thr Asp Pro Val Tyr Glu Gly Lys Ser Met His Gly Met Ile Asp
    290                 295                 300
cgg gtg cgc ggc ggc gag ttt ccc gag ggt tcg cgc gtg ctg tac gcc      960
Arg Val Arg Gly Gly Glu Phe Pro Glu Gly Ser Arg Val Leu Tyr Ala
305                 310                 315                 320
cac ctg ggc ggc gtg ccg gcg ctc aat gcg tac agc ttc ctc ttc cgc     1008
His Leu Gly Gly Val Pro Ala Leu Asn Ala Tyr Ser Phe Leu Phe Arg
                325                 330                 335
aac ggt tga                                                        1017
Asn Gly
```

<210> 329
<211> 338
<212> PRT
<213> Ralstonia solanacearum

<400> 329

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

```
Arg Val Arg Gly Gly Glu Phe Pro Glu Gly Ser Arg Val Leu Tyr Ala
305                 310                 315                 320
His Leu Gly Gly Val Pro Ala Leu Asn Ala Tyr Ser Phe Leu Phe Arg
                325                 330                 335
Asn Gly


<210> 330
<211> 1014
<212> DNA
<213> Rhizobium loti

<220>
<221> CDS
<222> (1)..(1014)
<223> transl_table=11

<400> 330
atg ctg gaa aaa ttc gag cgt tac ccg ctc acc ttt gga ctc aca ccc      48
Met Leu Glu Lys Phe Glu Arg Tyr Pro Leu Thr Phe Gly Leu Thr Pro
1               5                   10                  15
atc gag aag ctc gac cgg ctc ggc aag cat ctg ggt ggc aag gtc gaa      96
Ile Glu Lys Leu Asp Arg Leu Gly Lys His Leu Gly Gly Lys Val Glu
            20                  25                  30
atc tac gcc aaa cgc gag gac tgc aac tcc ggt ctg gcg ttc ggc ggc     144
Ile Tyr Ala Lys Arg Glu Asp Cys Asn Ser Gly Leu Ala Phe Gly Gly
        35                  40                  45
aac aag ctg cgc aag ctc gaa tac gtc atc ccc gac gcg atc gcg tca     192
Asn Lys Leu Arg Lys Leu Glu Tyr Val Ile Pro Asp Ala Ile Ala Ser
    50                  55                  60
gat gcc gat acc ctg gtc acc gtc ggc ggc gtg cag tcc aac cac acg     240
Asp Ala Asp Thr Leu Val Thr Val Gly Gly Val Gln Ser Asn His Thr
65                  70                  75                  80
cgc atg gtc gcc gcc gtc gcc gcc aag atc ggc atg aag tgt ctc ctg     288
Arg Met Val Ala Ala Val Ala Ala Lys Ile Gly Met Lys Cys Leu Leu
                85                  90                  95
gtt cac gag agc tgg gtt cca cat gag gat gtc gtc tac gac cgg gtc     336
Val His Glu Ser Trp Val Pro His Glu Asp Val Val Tyr Asp Arg Val
            100                 105                 110
ggc aac att ctc ttg agc cgc atc ttg ggc gca gag gtg cgt ctg gtc     384
Gly Asn Ile Leu Leu Ser Arg Ile Leu Gly Ala Glu Val Arg Leu Val
        115                 120                 125
gac gat ggc ttt gac atc ggt atc cgc cgc agc tgg gaa aaa gcg ctc     432
Asp Asp Gly Phe Asp Ile Gly Ile Arg Arg Ser Trp Glu Lys Ala Leu
    130                 135                 140
tat gag gtc aag gca agg ggc ggc agg ccc tat gcg ata ccg gcc ggg     480
Tyr Glu Val Lys Ala Arg Gly Gly Arg Pro Tyr Ala Ile Pro Ala Gly
145                 150                 155                 160
gcg tct gtt cac ccg aat gga ggc ctc ggc tat gtg ggg ttc gcg gag     528
Ala Ser Val His Pro Asn Gly Gly Leu Gly Tyr Val Gly Phe Ala Glu
                165                 170                 175
gaa gtg cgc gcc cag gag gaa cag ctt ggg ttt gcc ttc gac tac atg     576
Glu Val Arg Ala Gln Glu Glu Gln Leu Gly Phe Ala Phe Asp Tyr Met
            180                 185                 190
gtc gtt tgc acg gtc acc ggt tca acg cat gcc ggc atg ctc gtc gga     624
Val Val Cys Thr Val Thr Gly Ser Thr His Ala Gly Met Leu Val Gly
        195                 200                 205
ttc gcc aag gac ggt cgg cag cgc aac gtg atc ggt atc gat gcc tct     672
Phe Ala Lys Asp Gly Arg Gln Arg Asn Val Ile Gly Ile Asp Ala Ser
    210                 215                 220
gct acc ccg gcc aag acc aag gcg cag gtg ctt agc att gcc cga cat     720
```

```
Ala Thr Pro Ala Lys Thr Lys Ala Gln Val Leu Ser Ile Ala Arg His
225                 230                 235                 240
acg gcg acc ctc gtc gag ctc gga tcg gaa ctt gcc gag gat gac gtg      768
Thr Ala Thr Leu Val Glu Leu Gly Ser Glu Leu Ala Glu Asp Asp Val
                245                 250                 255
gtg ttg ctc gag gac tac gcg cac ccg cgg tac ggc att cca tcc gag      816
Val Leu Leu Glu Asp Tyr Ala His Pro Arg Tyr Gly Ile Pro Ser Glu
            260                 265                 270
gaa acc aag gag gcg atc cgt ctg tgt gcg cgg ctc gag ggt atg att      864
Glu Thr Lys Glu Ala Ile Arg Leu Cys Ala Arg Leu Glu Gly Met Ile
        275                 280                 285
acc gat ccc gtc tat gag ggc aaa tcg atg caa ggg atg att gac ctc      912
Thr Asp Pro Val Tyr Glu Gly Lys Ser Met Gln Gly Met Ile Asp Leu
    290                 295                 300
gtt caa aaa ggt ttt ttt cca gcg ggc tcg agg ata ctt tac gcg cat      960
Val Gln Lys Gly Phe Phe Pro Ala Gly Ser Arg Ile Leu Tyr Ala His
305                 310                 315                 320
ctc ggc ggc gcg ccg gcc atc aac ggt tat ggc tac acc ttt cgc aat     1008
Leu Gly Gly Ala Pro Ala Ile Asn Gly Tyr Gly Tyr Thr Phe Arg Asn
                325                 330                 335
ggc tga                                                            1014
Gly
```

<210> 331
<211> 337
<212> PRT
<213> Rhizobium loti

```
<400> 331
Met Leu Glu Lys Phe Glu Arg Tyr Pro Leu Thr Phe Gly Leu Thr Pro
1               5                   10                  15
Ile Glu Lys Leu Asp Arg Leu Gly Lys His Leu Gly Gly Lys Val Glu
            20                  25                  30
Ile Tyr Ala Lys Arg Glu Asp Cys Asn Ser Gly Leu Ala Phe Gly Gly
        35                  40                  45
Asn Lys Leu Arg Lys Leu Glu Tyr Val Ile Pro Asp Ala Ile Ala Ser
    50                  55                  60
Asp Ala Asp Thr Leu Val Thr Val Gly Gly Val Gln Ser Asn His Thr
65                  70                  75                  80
Arg Met Val Ala Ala Val Ala Ala Lys Ile Gly Met Lys Cys Leu Leu
                85                  90                  95
Val His Glu Ser Trp Val Pro His Glu Asp Val Val Tyr Asp Arg Val
            100                 105                 110
Gly Asn Ile Leu Leu Ser Arg Ile Leu Gly Ala Glu Val Arg Leu Val
        115                 120                 125
Asp Asp Gly Phe Asp Ile Gly Ile Arg Arg Ser Trp Glu Lys Ala Leu
    130                 135                 140
Tyr Glu Val Lys Ala Arg Gly Gly Arg Pro Tyr Ala Ile Pro Ala Gly
145                 150                 155                 160
Ala Ser Val His Pro Asn Gly Gly Leu Gly Tyr Val Gly Phe Ala Glu
                165                 170                 175
Glu Val Arg Ala Gln Glu Glu Gln Leu Gly Phe Ala Phe Asp Tyr Met
            180                 185                 190
Val Val Cys Thr Val Thr Gly Ser Thr His Ala Gly Met Leu Val Gly
        195                 200                 205
Phe Ala Lys Asp Gly Arg Gln Arg Asn Val Ile Gly Ile Asp Ala Ser
    210                 215                 220
Ala Thr Pro Ala Lys Thr Lys Ala Gln Val Leu Ser Ile Ala Arg His
225                 230                 235                 240
Thr Ala Thr Leu Val Glu Leu Gly Ser Glu Leu Ala Glu Asp Asp Val
```

```
                245                 250                 255
Val Leu Leu Glu Asp Tyr Ala His Pro Arg Tyr Gly Ile Pro Ser Glu
            260                 265                 270
Glu Thr Lys Glu Ala Ile Arg Leu Cys Ala Arg Leu Glu Gly Met Ile
        275                 280                 285
Thr Asp Pro Val Tyr Glu Gly Lys Ser Met Gln Gly Met Ile Asp Leu
    290                 295                 300
Val Gln Lys Gly Phe Phe Pro Ala Gly Ser Arg Ile Leu Tyr Ala His
305                 310                 315                 320
Leu Gly Gly Ala Pro Ala Ile Asn Gly Tyr Gly Tyr Thr Phe Arg Asn
                325                 330                 335
Gly
```

<210> 332
<211> 1020
<212> DNA
<213> Rhizobium leguminosarum bv

<220>
<221> CDS
<222> (1)..(1020)
<223> transl_table=11

<400> 332

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

```
tat atc atc gtc tgc gtt gtc acc ggt tca acc cag ggc gga atg atc        624
Tyr Ile Ile Val Cys Val Val Thr Gly Ser Thr Gln Gly Gly Met Ile
        195                 200                 205
gtc ggc ttt gcc gca cta gac agg gcc gac cgg gtg att ggc atc gat        672
Val Gly Phe Ala Ala Leu Asp Arg Ala Asp Arg Val Ile Gly Ile Asp
    210                 215                 220
gcc tcg ggc acc ctc cag cag acg cgg gat cag gtg cgg aag atc gtc        720
Ala Ser Gly Thr Leu Gln Gln Thr Arg Asp Gln Val Arg Lys Ile Val
225                 230                 235                 240
gat gcg acc tcg gaa ctc gtg aac ctt ggt cgg tcg gtg cgt gaa gac        768
Asp Ala Thr Ser Glu Leu Val Asn Leu Gly Arg Ser Val Arg Glu Asp
                245                 250                 255
gag atc gtc atc aac cct gac tac gcc tat ccc gcc tat gga gtg ccc        816
Glu Ile Val Ile Asn Pro Asp Tyr Ala Tyr Pro Ala Tyr Gly Val Pro
            260                 265                 270
tcg gag gag acc aac gag gcg atc cgg ctc gcg gcg cgc acc gag gcg        864
Ser Glu Glu Thr Asn Glu Ala Ile Arg Leu Ala Ala Arg Thr Glu Ala
        275                 280                 285
atg att acc gac cca gtc tat gag gga aag tcg atg cag ggg atg atc        912
Met Ile Thr Asp Pro Val Tyr Glu Gly Lys Ser Met Gln Gly Met Ile
    290                 295                 300
gat ctc gca cgc aag ggc ttc ttt ccc gag ggc tcg aag gtg ctg tac        960
Asp Leu Ala Arg Lys Gly Phe Phe Pro Glu Gly Ser Lys Val Leu Tyr
305                 310                 315                 320
gcc cat ctc ggc ggc gcc ccg gcg ctc aac ggc tat agc tat tac tac       1008
Ala His Leu Gly Gly Ala Pro Ala Leu Asn Gly Tyr Ser Tyr Tyr Tyr
                325                 330                 335
aag gac ggg tga                                                      1020
Lys Asp Gly
```

<210> 333
<211> 339
<212> PRT
<213> Rhizobium leguminosarum bv

<400> 333

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

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

<210> 334
<211> 1017
<212> DNA
<213> Schizosaccharomyces pombe

<220>
<221> CDS
<222> (1)..(1017)

<400> 334

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

```
ggt tgc tcg gaa cat ccc tat ggt ggt cta gga ttc gta ggt tgc gta       528
Gly Cys Ser Glu His Pro Tyr Gly Gly Leu Gly Phe Val Gly Cys Val
                165                 170                 175
gag gaa att tat gag caa gaa aaa caa ctt gga ttc aag ttt gac aag       576
Glu Glu Ile Tyr Glu Gln Glu Lys Gln Leu Gly Phe Lys Phe Asp Lys
            180                 185                 190
ata gtt gtc tgt acc gta act ggt tct tca ttt gct ggt att atc gtt       624
Ile Val Val Cys Thr Val Thr Gly Ser Ser Phe Ala Gly Ile Ile Val
        195                 200                 205
ggt atg gca ttg acc gga aga cag aaa gat gtt att gga att gac gct       672
Gly Met Ala Leu Thr Gly Arg Gln Lys Asp Val Ile Gly Ile Asp Ala
    210                 215                 220
tct gcc act cct gaa aaa acc aag gca cag gtt tta agg att gca caa       720
Ser Ala Thr Pro Glu Lys Thr Lys Ala Gln Val Leu Arg Ile Ala Gln
225                 230                 235                 240
aac act gcc aaa ctt att gga tta gaa aag gaa ttg act gag agc gat       768
Asn Thr Ala Lys Leu Ile Gly Leu Glu Lys Glu Leu Thr Glu Ser Asp
                245                 250                 255
gtc aat att gac aca aga ttt gct cat ccc gct tat gga att cca aat       816
Val Asn Ile Asp Thr Arg Phe Ala His Pro Ala Tyr Gly Ile Pro Asn
            260                 265                 270
gaa ggc acc ata gaa gct atc aag tta tgt ggt gct acg gaa ggt gtc       864
Glu Gly Thr Ile Glu Ala Ile Lys Leu Cys Gly Ala Thr Glu Gly Val
        275                 280                 285
ttg act gat cca gtt tat gaa ggc aag tct atg caa ggt ctt att cat       912
Leu Thr Asp Pro Val Tyr Glu Gly Lys Ser Met Gln Gly Leu Ile His
    290                 295                 300
ctt gtg aga aat aac gaa att gct gaa ggt tct aaa gtt ctt tac atc       960
Leu Val Arg Asn Asn Glu Ile Ala Glu Gly Ser Lys Val Leu Tyr Ile
305                 310                 315                 320
cat tta gga ggt gca cct gcc ttg tca gcc tat agt gca tat ttt aaa      1008
His Leu Gly Gly Ala Pro Ala Leu Ser Ala Tyr Ser Ala Tyr Phe Lys
                325                 330                 335
aat acc taa                                                         1017
Asn Thr
```

<210> 335
<211> 338
<212> PRT
<213> Schizosaccharomyces pombe

<400> 335

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

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

<210> 336
<211> 939
<212> DNA
<213> Thermotoga maritima

<220>
<221> CDS
<222> (1)..(939)
<223> transl_table=11

<400> 336

```
atg aga atc gat ctt tcc ctt aaa ccc aca cct gtt cag ttt ctc aaa      48
Met Arg Ile Asp Leu Ser Leu Lys Pro Thr Pro Val Gln Phe Leu Lys
1               5                   10                  15
aga ctt tcg gaa aaa tac ggg ttc aac atc tac gtt aaa aga gac gat      96
Arg Leu Ser Glu Lys Tyr Gly Phe Asn Ile Tyr Val Lys Arg Asp Asp
            20                  25                  30
ctc aca gag ctt gtg gga tcg ggc aac aaa atc aga aag ctg gag tat     144
Leu Thr Glu Leu Val Gly Ser Gly Asn Lys Ile Arg Lys Leu Glu Tyr
        35                  40                  45
ctt cta tgg gaa gct ctt aaa aaa gga gca acg act gtc ttc acc tgt     192
Leu Leu Trp Glu Ala Leu Lys Lys Gly Ala Thr Thr Val Phe Thr Cys
    50                  55                  60
gga ggt ctt cag tcg aac cat gcc aga gca acg gca tac gtt tcg aga     240
Gly Gly Leu Gln Ser Asn His Ala Arg Ala Thr Ala Tyr Val Ser Arg
65                  70                  75                  80
aga tac ggc ttg aaa cct gtt ctc ttc ctc aga aaa ggg gag aag gta     288
Arg Tyr Gly Leu Lys Pro Val Leu Phe Leu Arg Lys Gly Glu Lys Val
                85                  90                  95
ctg aac gga aat ctt ctc ctc gac att ctc ctc ggt gct gaa ata gtg     336
Leu Asn Gly Asn Leu Leu Leu Asp Ile Leu Leu Gly Ala Glu Ile Val
            100                 105                 110
gag gta tcc ccg gaa gag tac gaa cgc atc gat gag atc ttc gat gtt     384
Glu Val Ser Pro Glu Glu Tyr Glu Arg Ile Asp Glu Ile Phe Asp Val
```

```
       115                 120                 125
cac aaa aag atg aga gaa aag aaa ggt gaa aag gtg tac gtg ata ccc      432
His Lys Lys Met Arg Glu Lys Lys Gly Glu Lys Val Tyr Val Ile Pro
    130                 135                 140
gaa ggg gga tcg aac tcc ctt gga gcc ttt ggc tac ttc aat gcg gtg      480
Glu Gly Gly Ser Asn Ser Leu Gly Ala Phe Gly Tyr Phe Asn Ala Val
145                 150                 155                 160
ctg gag atg aaa gat caa ttg aac ctc gaa tct ttc gat gct att gtg      528
Leu Glu Met Lys Asp Gln Leu Asn Leu Glu Ser Phe Asp Ala Ile Val
                165                 170                 175
tgt gct gtt gga agt ggt gga acc ata gcg ggc ttg tca gct gga att      576
Cys Ala Val Gly Ser Gly Gly Thr Ile Ala Gly Leu Ser Ala Gly Ile
            180                 185                 190
tcc ttt ctg gaa tat cac gta ccc gta gtg ggt gtg aac gtc acc acg      624
Ser Phe Leu Glu Tyr His Val Pro Val Val Gly Val Asn Val Thr Thr
        195                 200                 205
aaa aac tcg gat tat ttt gtg ggg aag gtg aaa aga ata att agt ggt      672
Lys Asn Ser Asp Tyr Phe Val Gly Lys Val Lys Arg Ile Ile Ser Gly
    210                 215                 220
atg gaa gag tac ggc ctg aga gtc aac gaa acc gtt ttc gaa gtg gtg      720
Met Glu Glu Tyr Gly Leu Arg Val Asn Glu Thr Val Phe Glu Val Val
225                 230                 235                 240
gac gat tac aga ggg ccg gga tat gcg att ccg tcc agt gag gat gtg      768
Asp Asp Tyr Arg Gly Pro Gly Tyr Ala Ile Pro Ser Ser Glu Asp Val
                245                 250                 255
gag atc ttg aaa gaa gta gct tcg ata gaa ggc atc atc ctc gat ccg      816
Glu Ile Leu Lys Glu Val Ala Ser Ile Glu Gly Ile Ile Leu Asp Pro
            260                 265                 270
gtc tac acg gca aaa gcc ttc aga gga atg atc gaa atg ttc aga aac      864
Val Tyr Thr Ala Lys Ala Phe Arg Gly Met Ile Glu Met Phe Arg Asn
        275                 280                 285
tca gaa aag aac gtt ctt ttc atc cac acg ggg gga ata ttc ggt ctg      912
Ser Glu Lys Asn Val Leu Phe Ile His Thr Gly Gly Ile Phe Gly Leu
    290                 295                 300
ttc gcg cag agc agg agg ttg gta taa                                  939
Phe Ala Gln Ser Arg Arg Leu Val
305                 310
```

<210> 337
<211> 312
<212> PRT
<213> Thermotoga maritima

<400> 337

```
Met Arg Ile Asp Leu Ser Leu Lys Pro Thr Pro Val Gln Phe Leu Lys
1               5                  10                  15
Arg Leu Ser Glu Lys Tyr Gly Phe Asn Ile Tyr Val Lys Arg Asp Asp
            20                  25                  30
Leu Thr Glu Leu Val Gly Ser Gly Asn Lys Ile Arg Lys Leu Glu Tyr
        35                  40                  45
Leu Leu Trp Glu Ala Leu Lys Lys Gly Ala Thr Thr Val Phe Thr Cys
    50                  55                  60
Gly Gly Leu Gln Ser Asn His Ala Arg Ala Thr Ala Tyr Val Ser Arg
65                  70                  75                  80
Arg Tyr Gly Leu Lys Pro Val Leu Phe Leu Arg Lys Gly Glu Lys Val
                85                  90                  95
Leu Asn Gly Asn Leu Leu Leu Asp Ile Leu Leu Gly Ala Glu Ile Val
            100                 105                 110
Glu Val Ser Pro Glu Glu Tyr Glu Arg Ile Asp Glu Ile Phe Asp Val
        115                 120                 125
His Lys Lys Met Arg Glu Lys Lys Gly Glu Lys Val Tyr Val Ile Pro
```

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

<210> 338
<211> 1017
<212> DNA
<213> Variovorax paradoxus

<220>
<221> CDS
<222> (1)..(1017)
<223> transl_table=11

<400> 338

```
atg aac ctg aag aaa ttc ccc cgc cac gtc ctg acc ttc ggc ccc acg      48
Met Asn Leu Lys Lys Phe Pro Arg His Val Leu Thr Phe Gly Pro Thr
1               5                   10                  15
ccg atc cag ccg ctg aag cgc ctg agc gcc cac ctc ggc ggc aag gtc      96
Pro Ile Gln Pro Leu Lys Arg Leu Ser Ala His Leu Gly Gly Lys Val
            20                  25                  30
gat ctc tac gcc aag cgc gag gac tgc aac agc ggc ctg gcc ttc ggc     144
Asp Leu Tyr Ala Lys Arg Glu Asp Cys Asn Ser Gly Leu Ala Phe Gly
        35                  40                  45
ggc aac aag acg cgc aag ctg gag tac ctg att ccc gag gcg ctc gaa     192
Gly Asn Lys Thr Arg Lys Leu Glu Tyr Leu Ile Pro Glu Ala Leu Glu
    50                  55                  60
ggc ggc tac gac acg ctg gtg tcg atc ggc ggc atc cag tcg aac cag     240
Gly Gly Tyr Asp Thr Leu Val Ser Ile Gly Gly Ile Gln Ser Asn Gln
65                  70                  75                  80
acg cgg cag gtg gcc gcg gtg gct gcg cac ctg ggc ctg aag tgc gtg     288
Thr Arg Gln Val Ala Ala Val Ala Ala His Leu Gly Leu Lys Cys Val
                85                  90                  95
ctg gtg cag gag aac tgg gtc aac tac tcc gac gcg gtg tac gac cgg     336
Leu Val Gln Glu Asn Trp Val Asn Tyr Ser Asp Ala Val Tyr Asp Arg
            100                 105                 110
gtc ggc aac atc gag atg tcg cgc atc atg ggc gcc gac gtg cgc ttg     384
Val Gly Asn Ile Glu Met Ser Arg Ile Met Gly Ala Asp Val Arg Leu
        115                 120                 125
gac gca gcc ggc ttc gac atc ggc atc cgc cag agc tgg gaa cag gcc     432
Asp Ala Ala Gly Phe Asp Ile Gly Ile Arg Gln Ser Trp Glu Gln Ala
```

```
   130                 135                 140
atg gcc gac gtg cgc gcg gcc ggc ggc aag ccc ttc ccg att ccg gcg      480
Met Ala Asp Val Arg Ala Ala Gly Gly Lys Pro Phe Pro Ile Pro Ala
145                 150                 155                 160
ggc tgc tcc gag cat ccg cgc ggt ggc ctc ggc tcc gtg ggc ttt gcc      528
Gly Cys Ser Glu His Pro Arg Gly Gly Leu Gly Ser Val Gly Phe Ala
                165                 170                 175
gaa gaa gtg cgc cag cag gag gcc gaa ctc ggc ttc aag ttc gac tac      576
Glu Glu Val Arg Gln Gln Glu Ala Glu Leu Gly Phe Lys Phe Asp Tyr
            180                 185                 190
ctc gtg gtc tgc tcg gtc acc ggc agc acg cag gcc ggc atg gtg gtg      624
Leu Val Val Cys Ser Val Thr Gly Ser Thr Gln Ala Gly Met Val Val
        195                 200                 205
ggc ttc gcg gcc gac ggc cgc gcc gac cgc gtg atc ggc atc gac gcc      672
Gly Phe Ala Ala Asp Gly Arg Ala Asp Arg Val Ile Gly Ile Asp Ala
    210                 215                 220
tcg gcc aag ccg cag cag acc ttc gaa caa atc ttg cgc atc gca aag      720
Ser Ala Lys Pro Gln Gln Thr Phe Glu Gln Ile Leu Arg Ile Ala Lys
225                 230                 235                 240
aac acg gcc gag ctg gtc gag ctg ggc cgc gac atc acc gag aaa gac      768
Asn Thr Ala Glu Leu Val Glu Leu Gly Arg Asp Ile Thr Glu Lys Asp
                245                 250                 255
gtg gtg ctc gac cgc cgc ttc ggc ggg ccc gag tac ggg ctg ccg aac      816
Val Val Leu Asp Arg Arg Phe Gly Gly Pro Glu Tyr Gly Leu Pro Asn
            260                 265                 270
gaa ggc acg ctg gag gcc att cgg ttg agc gcg cgc ttc gaa ggc atg      864
Glu Gly Thr Leu Glu Ala Ile Arg Leu Ser Ala Arg Phe Glu Gly Met
        275                 280                 285
ctg acc gac ccc gtg tac gag ggc aag tcg atg cac gga atg atc gag      912
Leu Thr Asp Pro Val Tyr Glu Gly Lys Ser Met His Gly Met Ile Glu
    290                 295                 300
aag gtg cgg ctc ggg gag ttt ccg gcg ggc tcg aag gtg ctc tac gca      960
Lys Val Arg Leu Gly Glu Phe Pro Ala Gly Ser Lys Val Leu Tyr Ala
305                 310                 315                 320
cac ctg ggc ggc gtg ccg gcg ctg aac gcc tac agc ttc ctg ttc cgc     1008
His Leu Gly Gly Val Pro Ala Leu Asn Ala Tyr Ser Phe Leu Phe Arg
                325                 330                 335
aac ggc tga                                                        1017
Asn Gly
```

<210> 339
<211> 338
<212> PRT
<213> Variovorax paradoxus

<400> 339

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

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

<210> 340
<211> 993
<212> DNA
<213> Yersinia pestis

<220>
<221> CDS
<222> (1)..(993)
<223> transl_table=11

<400> 340

```
gtg acg ctt caa caa aaa ctg acg caa ttc ccg cgt ctc gat ctg gtc       48
Met Thr Leu Gln Gln Lys Leu Thr Gln Phe Pro Arg Leu Asp Leu Val
1               5                   10                  15
ggt aat gcg acg cca tta gaa aaa ctg tct cgt cta tct gat tat ctg       96
Gly Asn Ala Thr Pro Leu Glu Lys Leu Ser Arg Leu Ser Asp Tyr Leu
            20                  25                  30
gga cgt gaa att tac att aaa cgt gat gat gtc acg cct gtg gcg ctt      144
Gly Arg Glu Ile Tyr Ile Lys Arg Asp Asp Val Thr Pro Val Ala Leu
        35                  40                  45
ggc ggg aat aaa ctg cgc aag cta gaa ttc tta gcc gca gat gcc ttg      192
Gly Gly Asn Lys Leu Arg Lys Leu Glu Phe Leu Ala Ala Asp Ala Leu
    50                  55                  60
aga cag gga gcc gat acg ctg gtt acg gct ggt gct att caa tct aat      240
Arg Gln Gly Ala Asp Thr Leu Val Thr Ala Gly Ala Ile Gln Ser Asn
65                  70                  75                  80
cat gtc cgc caa acc gcc gcc gtg gcc gcg aaa ctg ggg ctg cat tgc      288
His Val Arg Gln Thr Ala Ala Val Ala Ala Lys Leu Gly Leu His Cys
                85                  90                  95
gtt gcg ctg ttg gaa aac ccc att ggt act gag cag gca aac tat ctg      336
```

```
Val Ala Leu Leu Glu Asn Pro Ile Gly Thr Glu Gln Ala Asn Tyr Leu
            100                 105                 110
acc aat ggg aac cgg ctg tta ctg gac cta ttc aat gtt gat gtt gtg       384
Thr Asn Gly Asn Arg Leu Leu Leu Asp Leu Phe Asn Val Asp Val Val
        115                 120                 125
atg tgt gag gca ttg aac gat cca aat cag caa tta gca gaa ttg gct       432
Met Cys Glu Ala Leu Asn Asp Pro Asn Gln Gln Leu Ala Glu Leu Ala
    130                 135                 140
acc cgc gtg gaa gcg cag ggt ttc cgc cca tat gtg gta ccg att ggc       480
Thr Arg Val Glu Ala Gln Gly Phe Arg Pro Tyr Val Val Pro Ile Gly
145                 150                 155                 160
ggt tct aat gcc ttg ggc gcg ctg ggt tat gtg cag tgc tca ctg gaa       528
Gly Ser Asn Ala Leu Gly Ala Leu Gly Tyr Val Gln Cys Ser Leu Glu
                165                 170                 175
att gct gct caa gcc gcg ggc aat gtt gcg ttt agt tcg gtc gtc gtg       576
Ile Ala Ala Gln Ala Ala Gly Asn Val Ala Phe Ser Ser Val Val Val
            180                 185                 190
gcc tct ggc agt gcg gga aca cat gca gga ttg gcg gtt ggt cta cag       624
Ala Ser Gly Ser Ala Gly Thr His Ala Gly Leu Ala Val Gly Leu Gln
        195                 200                 205
cag ttg tta ccc gat gcg gaa tta atc ggt gtg acg gta tca cgt agt       672
Gln Leu Leu Pro Asp Ala Glu Leu Ile Gly Val Thr Val Ser Arg Ser
    210                 215                 220
gcc gat gaa cag cgg cct aaa gtg gca cag att caa caa gcg ttg gcg       720
Ala Asp Glu Gln Arg Pro Lys Val Ala Gln Ile Gln Gln Ala Leu Ala
225                 230                 235                 240
aca tca tta ggg atg acg gac cca ttg gca aaa atc acc ttg tgg gat       768
Thr Ser Leu Gly Met Thr Asp Pro Leu Ala Lys Ile Thr Leu Trp Asp
                245                 250                 255
agt tat ttt gcc ccg caa tat ggg atg cca aac gaa gag ggg ata gcg       816
Ser Tyr Phe Ala Pro Gln Tyr Gly Met Pro Asn Glu Glu Gly Ile Ala
            260                 265                 270
gct att aag ctc ttg gca aga ctg gaa gga ata ttg ttg gac cct gtg       864
Ala Ile Lys Leu Leu Ala Arg Leu Glu Gly Ile Leu Leu Asp Pro Val
        275                 280                 285
tat acc ggt aag gcg atg gcg ggc tta ctt gat ggt att gaa cag caa       912
Tyr Thr Gly Lys Ala Met Ala Gly Leu Leu Asp Gly Ile Glu Gln Gln
    290                 295                 300
aaa ttc tgc gac aaa ggg cca att tta ttt atc cac act ggc ggg gca       960
Lys Phe Cys Asp Lys Gly Pro Ile Leu Phe Ile His Thr Gly Gly Ala
305                 310                 315                 320
cct gcg ctg ttt gct tat cat ccg cag gtg tag                           993
Pro Ala Leu Phe Ala Tyr His Pro Gln Val
                325                 330
```

<210> 341
<211> 330
<212> PRT
<213> Yersinia pestis

<400> 341

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

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

<210> 342
<211> 1406
<212> DNA
<213> Glycine max

<220>
<221> CDS
<222> (68)..(1207)

<400> 342
gaattcccgg atcgacgctt tcgttgaatt ctaaaaggaa agaacagctg agctggtcag 60

```
ataatca atg gca tca tcc ttg ggt ttt gag ttc ctg acg aag aag cct      109
        Met Ala Ser Ser Leu Gly Phe Glu Phe Leu Thr Lys Lys Pro
        1               5                   10
tac agt cct cca tcc tgg gca tcc cat ctc cac cct tta cct tcc cac      157
Tyr Ser Pro Pro Ser Trp Ala Ser His Leu His Pro Leu Pro Ser His
15                  20                  25                  30
ttc ttc tct ctt gcc cat ctt ccc act cca att cac aga tgg aac ctt      205
Phe Phe Ser Leu Ala His Leu Pro Thr Pro Ile His Arg Trp Asn Leu
                35                  40                  45
ccc aat ctg ccc acc aat acc gag ctg tgg atc aag cga gac gac ctt      253
Pro Asn Leu Pro Thr Asn Thr Glu Leu Trp Ile Lys Arg Asp Asp Leu
            50                  55                  60
tcc gga atg cag ctg agt ggt aac aaa gtg agg aaa ttg gag ttc ctg      301
Ser Gly Met Gln Leu Ser Gly Asn Lys Val Arg Lys Leu Glu Phe Leu
        65                  70                  75
atg gcc gat gcc att gcg caa ggc gcc gac tct atc atc aca atc gga      349
```

```
Met Ala Asp Ala Ile Ala Gln Gly Ala Asp Ser Ile Ile Thr Ile Gly
    80                  85                  90
ggc att cag agc aac cac tgt cgc gcc acc gcc gtt gcc gcc aag tat      397
Gly Ile Gln Ser Asn His Cys Arg Ala Thr Ala Val Ala Ala Lys Tyr
95                  100                 105                 110
tta aac ctt gac tgt ttt ctc atc ctc cgc act tct gac ctc ctc gtc      445
Leu Asn Leu Asp Cys Phe Leu Ile Leu Arg Thr Ser Asp Leu Leu Val
                115                 120                 125
gat caa gat cca gga ctt act ggc aat ctt ctc gtc gaa cgt atg gtt      493
Asp Gln Asp Pro Gly Leu Thr Gly Asn Leu Leu Val Glu Arg Met Val
            130                 135                 140
gga gct cac gtt cac ctc atc tcc aaa caa gaa tat gcc aaa att ggc      541
Gly Ala His Val His Leu Ile Ser Lys Gln Glu Tyr Ala Lys Ile Gly
        145                 150                 155
agc gtg aca ctc acc aat gtc cta aaa gaa aaa ttg atc aag gaa ggg      589
Ser Val Thr Leu Thr Asn Val Leu Lys Glu Lys Leu Ile Lys Glu Gly
    160                 165                 170
agg agg cca tat gtt ata ccc gtt ggc gga tca aac tct ttg gga aca      637
Arg Arg Pro Tyr Val Ile Pro Val Gly Gly Ser Asn Ser Leu Gly Thr
175                 180                 185                 190
tgg ggt tat ata gaa gca gta cgg gaa att gag cag cag att cag aag      685
Trp Gly Tyr Ile Glu Ala Val Arg Glu Ile Glu Gln Gln Ile Gln Lys
                195                 200                 205
ggg aca ggc aat gtc aag ttt gat gat att gtt gtt gct tgt ggc agt      733
Gly Thr Gly Asn Val Lys Phe Asp Asp Ile Val Val Ala Cys Gly Ser
            210                 215                 220
ggt ggc aca att gct ggt ctg tca cta gga tcg tca ttg agt gca ttg      781
Gly Gly Thr Ile Ala Gly Leu Ser Leu Gly Ser Ser Leu Ser Ala Leu
        225                 230                 235
aaa gca agg gta cat gca ttc tct gtt tgt gat gac cca gat tac ttc      829
Lys Ala Arg Val His Ala Phe Ser Val Cys Asp Asp Pro Asp Tyr Phe
    240                 245                 250
cac aac ttt gct caa ggc ttg ctt gat gga ctc aag gct ggc gtt agc      877
His Asn Phe Ala Gln Gly Leu Leu Asp Gly Leu Lys Ala Gly Val Ser
255                 260                 265                 270
tca aga gat att gtc cac att caa aac gcc aag ggt ctt ggc tat gca      925
Ser Arg Asp Ile Val His Ile Gln Asn Ala Lys Gly Leu Gly Tyr Ala
                275                 280                 285
atg aat aca tcg gag gag ctt aat ttt gta aaa gaa gtt gct gcc act      973
Met Asn Thr Ser Glu Glu Leu Asn Phe Val Lys Glu Val Ala Ala Thr
            290                 295                 300
act ggt gtt gtt ctt gac cca gta tac agt ggt aag gct gct tat gca     1021
Thr Gly Val Val Leu Asp Pro Val Tyr Ser Gly Lys Ala Ala Tyr Ala
        305                 310                 315
atg ctg aaa gat atg tct gaa aat cca aag aag tgg gaa agg aga aag     1069
Met Leu Lys Asp Met Ser Glu Asn Pro Lys Lys Trp Glu Arg Arg Lys
    320                 325                 330
atc ctc ttc ata cat acg ggt ggc ctc cta gga ttg tat gac aag gtc     1117
Ile Leu Phe Ile His Thr Gly Gly Leu Leu Gly Leu Tyr Asp Lys Val
335                 340                 345                 350
gat cag ttg gct tct ttt gtt ggg aat tgg caa cga atg gat gtc aat     1165
Asp Gln Leu Ala Ser Phe Val Gly Asn Trp Gln Arg Met Asp Val Asn
                355                 360                 365
gaa tct gtt cct agg cag gat ggt att gga aag atg ttc tag agaaggaaaa  1217
Glu Ser Val Pro Arg Gln Asp Gly Ile Gly Lys Met Phe
            370                 375                 379
tgaaaaaacc tgacgttgcc agcatctata ttttgtacta tcttgctcta aataaatttt   1277

atacttatat ttaatagcca tatgctcaca ctgaatcctg cctgaagtta ccataagata   1337

gtaaagttcc aaaaacttaa gtgacaaata aatcaagttt tatttatttt taaaaaaaaa   1397
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aaaaaaaaa 1406

<210> 343
<211> 379
<212> PRT
<213> Glycine max

<400> 343

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

<210> 344
<211> 1315
<212> DNA
<213> Brassica napus

<220>
<221> CDS
<222> (14)..(1138)

<400> 344
tgcagcaaca ccc atg gcg gat ttt ctc acg aaa agt cct tac tct cct 49
Met Ala Asp Phe Leu Thr Lys Ser Pro Tyr Ser Pro
1 5 10
cct tcg tgg gct tct cat ctt cgt ccg ctt cct tcc cac acc ttc tcc 97
Pro Ser Trp Ala Ser His Leu Arg Pro Leu Pro Ser His Thr Phe Ser
15 20 25
ctc gct cac cgt cct act ccg atc cat cga tgg aac ctc ccc ggt ctc 145
Leu Ala His Arg Pro Thr Pro Ile His Arg Trp Asn Leu Pro Gly Leu
30 35 40
ccc aac ggc acc gaa ctc tgg atc aag cga gat gac ttc acg ggg atg 193
Pro Asn Gly Thr Glu Leu Trp Ile Lys Arg Asp Asp Phe Thr Gly Met
45 50 55 60
gaa ttg agc ggg aac aaa gtc cgg aaa ctc gag ttc cta atg gcc gac 241
Glu Leu Ser Gly Asn Lys Val Arg Lys Leu Glu Phe Leu Met Ala Asp
65 70 75
gcc gtg gag cag caa gcc gac acc gtc atc acc atc ggc ggt atc cag 289
Ala Val Glu Gln Gln Ala Asp Thr Val Ile Thr Ile Gly Gly Ile Gln
80 85 90
agc aac cac tgc cgc gcc acc acc gtc gct tct aac tac ctc aat ctg 337
Ser Asn His Cys Arg Ala Thr Thr Val Ala Ser Asn Tyr Leu Asn Leu
95 100 105
gac act cat ctt atc ctc cgc acc tcc aag ctt ctt gcg gat gga gat 385
Asp Thr His Leu Ile Leu Arg Thr Ser Lys Leu Leu Ala Asp Gly Asp
110 115 120
cct ggg ttg gtt ggg aat ctc ctt gtt gag cgc ctc gtt gga gct aac 433
Pro Gly Leu Val Gly Asn Leu Leu Val Glu Arg Leu Val Gly Ala Asn
125 130 135 140
gtt cat ctc atc tcc aag gaa gag tat tcc tcc att ggg agt gag gct 481
Val His Leu Ile Ser Lys Glu Glu Tyr Ser Ser Ile Gly Ser Glu Ala
145 150 155
ctc act agt gcc ttg aaa gag aag ctg gag aaa gaa ggg aaa aag cct 529
Leu Thr Ser Ala Leu Lys Glu Lys Leu Glu Lys Glu Gly Lys Lys Pro
160 165 170
tat gtt att ccc gtt ggt gga tcc aac tct ctg gga act tgg ggt tat 577
Tyr Val Ile Pro Val Gly Gly Ser Asn Ser Leu Gly Thr Trp Gly Tyr
175 180 185
att gaa gca gca agg gaa att gag gag cag ctt aaa tgt aga act gat 625
Ile Glu Ala Ala Arg Glu Ile Glu Glu Gln Leu Lys Cys Arg Thr Asp
190 195 200
agc ctc aag ttt gat gat att gtg gtt gca tgt ggc agt ggt ggt aca 673
Ser Leu Lys Phe Asp Asp Ile Val Val Ala Cys Gly Ser Gly Gly Thr
205 210 215 220
att gct ggt att tca ttg gga tct tgg ttg gga gct ctt aaa gcc aag 721
Ile Ala Gly Ile Ser Leu Gly Ser Trp Leu Gly Ala Leu Lys Ala Lys
225 230 235
gtc cat gct ttc tcg gta tgc gat gat cct gat tac ttt tac gac ttt 769
Val His Ala Phe Ser Val Cys Asp Asp Pro Asp Tyr Phe Tyr Asp Phe
240 245 250
gtc caa ggc ctt ctg gat gga ctt caa gct ggt gtt aac tct cgc gat 817
Val Gln Gly Leu Leu Asp Gly Leu Gln Ala Gly Val Asn Ser Arg Asp
255 260 265

```
att gtt agc atc cac aat gcc aag gga aaa gga tat gca atg aac act       865
Ile Val Ser Ile His Asn Ala Lys Gly Lys Gly Tyr Ala Met Asn Thr
    270                 275                 280
tca gag gag ctt aag ttt tta aag gac ata gct agt gca aca agt gtg       913
Ser Glu Glu Leu Lys Phe Leu Lys Asp Ile Ala Ser Ala Thr Ser Val
285                 290                 295                 300
att ctt gat cct gtt tac agt ggg aaa gct gcg tac ggt ttg ata aat       961
Ile Leu Asp Pro Val Tyr Ser Gly Lys Ala Ala Tyr Gly Leu Ile Asn
                305                 310                 315
gag atg acc aag gat ccc aaa agt tgg gag ggg aag aag ata ttg ttc      1009
Glu Met Thr Lys Asp Pro Lys Ser Trp Glu Gly Lys Lys Ile Leu Phe
            320                 325                 330
ata cac act ggt ggg ctt ctt ggg ttg tat gat aaa gtt gat caa atg      1057
Ile His Thr Gly Gly Leu Leu Gly Leu Tyr Asp Lys Val Asp Gln Met
        335                 340                 345
gct tct ctg atg gga aac tgg agc cgt atg gat gtt caa gaa tcc gtc      1105
Ala Ser Leu Met Gly Asn Trp Ser Arg Met Asp Val Gln Glu Ser Val
    350                 355                 360
cca aga aaa gag ggt gtt ggg aaa atg ttc tag cagaacaaaa acctgattct    1158
Pro Arg Lys Glu Gly Val Gly Lys Met Phe
365                 370             374
gtaataatcc tgtgaagata agacaggttg aacacttgtt tgtgcatttg gtctgataaa    1218

aacgcatcca ttcatgtgat ttctattctg tgtattatgt ttaatagcta tcgatgatta    1278

ataaaatggt gggtccactc tcaaaaaaaa aaaaaaa                             1315
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<210> 345
<211> 374
<212> PRT
<213> Brassica napus

<400> 345

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

```
Asp Asp Ile Val Val Ala Cys Gly Ser Gly Gly Thr Ile Ala Gly Ile
    210                 215                 220
Ser Leu Gly Ser Trp Leu Gly Ala Leu Lys Ala Lys Val His Ala Phe
225                 230                 235                 240
Ser Val Cys Asp Asp Pro Asp Tyr Phe Tyr Asp Phe Val Gln Gly Leu
                245                 250                 255
Leu Asp Gly Leu Gln Ala Gly Val Asn Ser Arg Asp Ile Val Ser Ile
            260                 265                 270
His Asn Ala Lys Gly Lys Gly Tyr Ala Met Asn Thr Ser Glu Glu Leu
        275                 280                 285
Lys Phe Leu Lys Asp Ile Ala Ser Ala Thr Ser Val Ile Leu Asp Pro
    290                 295                 300
Val Tyr Ser Gly Lys Ala Ala Tyr Gly Leu Ile Asn Glu Met Thr Lys
305                 310                 315                 320
Asp Pro Lys Ser Trp Glu Gly Lys Lys Ile Leu Phe Ile His Thr Gly
                325                 330                 335
Gly Leu Leu Gly Leu Tyr Asp Lys Val Asp Gln Met Ala Ser Leu Met
            340                 345                 350
Gly Asn Trp Ser Arg Met Asp Val Gln Glu Ser Val Pro Arg Lys Glu
        355                 360                 365
Gly Val Gly Lys Met Phe
    370
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<210> 346
<211> 1389
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (42)..(1229)

<400> 346

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gtcgcttccg ccgacacctg agtcttgtcg ctgccgccgg g atg gcc gga gtc acc      56
                                                 Met Ala Gly Val Thr
                                                 1               5
gcc acc ggg atg gcc gga gtt ccc gcc acc ttc tcc tca gcc acc gct      104
Ala Thr Gly Met Ala Gly Val Pro Ala Thr Phe Ser Ser Ala Thr Ala
                10                  15                  20
cag atc ggg ggc ttc ctc tcg aag aag cct tac gcg ccg ccg ttg tgg      152
Gln Ile Gly Gly Phe Leu Ser Lys Lys Pro Tyr Ala Pro Pro Leu Trp
            25                  30                  35
gcc acg cac ctc tcc ccc atg cct tgc cat acc ttc tcg ctc ggc cat      200
Ala Thr His Leu Ser Pro Met Pro Cys His Thr Phe Ser Leu Gly His
        40                  45                  50
ttc cca aca ccg att cac aag tgg aat ctg ccc aat ttg ccg gaa gga      248
Phe Pro Thr Pro Ile His Lys Trp Asn Leu Pro Asn Leu Pro Glu Gly
    55                  60                  65
acg gaa gtg tgg atc aag cga gac gat tta tca ggc atg cag ttg agt      296
Thr Glu Val Trp Ile Lys Arg Asp Asp Leu Ser Gly Met Gln Leu Ser
70                  75                  80                  85
gga aac aag gtc cgg aag ctg gag ttc ttg atg gca gat gcc gta gca      344
Gly Asn Lys Val Arg Lys Leu Glu Phe Leu Met Ala Asp Ala Val Ala
                90                  95                  100
caa ggc gca gac tgc gtt att act gtt ggg ggt ata cag agt aac cac      392
Gln Gly Ala Asp Cys Val Ile Thr Val Gly Gly Ile Gln Ser Asn His
            105                 110                 115
tgc cgt gcc aca gcc gtg gct gct aag tat ctc aat ctt gat tgc tac      440
Cys Arg Ala Thr Ala Val Ala Ala Lys Tyr Leu Asn Leu Asp Cys Tyr
        120                 125                 130
ctg ata cta cgt acc tcc aag ctt ctt gtg gat aag gac cct ggt ttg      488
```

```
Leu Ile Leu Arg Thr Ser Lys Leu Leu Val Asp Lys Asp Pro Gly Leu
    135                 140                 145
gtt ggc aat ctt ctt gtc gag aga cta gtt ggg gca cac gtt gat ctt      536
Val Gly Asn Leu Leu Val Glu Arg Leu Val Gly Ala His Val Asp Leu
150                 155                 160                 165
gtg tca aaa gaa gaa tat gga aaa att ggt agt gtg gct tta gct gac      584
Val Ser Lys Glu Glu Tyr Gly Lys Ile Gly Ser Val Ala Leu Ala Asp
                170                 175                 180
ctg ctg aaa aaa agg ctt ctg gaa gaa ggg agg aag ccg tat gtg att      632
Leu Leu Lys Lys Arg Leu Leu Glu Glu Gly Arg Lys Pro Tyr Val Ile
            185                 190                 195
cct gtt ggt gga tca aac tca ttg gga act tgg gga tat att gag gca      680
Pro Val Gly Gly Ser Asn Ser Leu Gly Thr Trp Gly Tyr Ile Glu Ala
        200                 205                 210
ata agg gag att gag cag caa att cag caa tct gct gat gtt cag ttt      728
Ile Arg Glu Ile Glu Gln Gln Ile Gln Gln Ser Ala Asp Val Gln Phe
    215                 220                 225
gat gat att gtt gtt gca tgt ggc agt ggt gga acc atc gct ggc ctt      776
Asp Asp Ile Val Val Ala Cys Gly Ser Gly Gly Thr Ile Ala Gly Leu
230                 235                 240                 245
gct tta gga tcc aga ttg agc agc tta aat aca aaa gtt cat gca ttc      824
Ala Leu Gly Ser Arg Leu Ser Ser Leu Asn Thr Lys Val His Ala Phe
                250                 255                 260
tct gtt tgt gat gac cct gaa tac ttc tat gac tat atc caa ggc ctg      872
Ser Val Cys Asp Asp Pro Glu Tyr Phe Tyr Asp Tyr Ile Gln Gly Leu
            265                 270                 275
att gat gga ctt aat tct ggt ttg gat tca cat gat ata gtt agc atc      920
Ile Asp Gly Leu Asn Ser Gly Leu Asp Ser His Asp Ile Val Ser Ile
        280                 285                 290
gaa aat gct aag ggg tta ggc tat gcc atg aaa aca gct gag gag ctt      968
Glu Asn Ala Lys Gly Leu Gly Tyr Ala Met Lys Thr Ala Glu Glu Leu
    295                 300                 305
aag ttt gtc aaa gac ata gct gca tca aca ggc att atc ctt gat cca     1016
Lys Phe Val Lys Asp Ile Ala Ala Ser Thr Gly Ile Ile Leu Asp Pro
310                 315                 320                 325
gtc tac agt ggg aag gcg gtt tat ggt ttg cta aaa gac atg gct ggc     1064
Val Tyr Ser Gly Lys Ala Val Tyr Gly Leu Leu Lys Asp Met Ala Gly
                330                 335                 340
aat cca gcc aaa tgg aaa ggt cga aaa gtt ctg ttt atc cac aca ggt     1112
Asn Pro Ala Lys Trp Lys Gly Arg Lys Val Leu Phe Ile His Thr Gly
            345                 350                 355
ggt ctt ctt ggg ttg tat gat aag gct gac cag tta tca tct ttg gct     1160
Gly Leu Leu Gly Leu Tyr Asp Lys Ala Asp Gln Leu Ser Ser Leu Ala
        360                 365                 370
ggg agc tgg cgc aga atg gat ctt gaa gat tct gtt cca cgc caa gat     1208
Gly Ser Trp Arg Arg Met Asp Leu Glu Asp Ser Val Pro Arg Gln Asp
    375                 380                 385
ggc act ggt aag atg ttc tga tcagtatggt tcatgtgatt ccatgatggc       1259
Gly Thr Gly Lys Met Phe
390                 395
tcattcctgc aaacattgta tccattacag agttgttact cttatatttg tgcaagaaaa  1319

tgcagaatag atggttcaca ttgtatagag cactgatgca atttaagaat aaagcacatc  1379

ttttttgcca                                                        1389


<210> 347
<211> 395
<212> PRT
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<213> Zea mays

<400> 347
Met Ala Gly Val Thr Ala Thr Gly Met Ala Gly Val Pro Ala Thr Phe
1 5 10 15
Ser Ser Ala Thr Ala Gln Ile Gly Gly Phe Leu Ser Lys Lys Pro Tyr
20 25 30
Ala Pro Pro Leu Trp Ala Thr His Leu Ser Pro Met Pro Cys His Thr
35 40 45
Phe Ser Leu Gly His Phe Pro Thr Pro Ile His Lys Trp Asn Leu Pro
50 55 60
Asn Leu Pro Glu Gly Thr Glu Val Trp Ile Lys Arg Asp Asp Leu Ser
65 70 75 80
Gly Met Gln Leu Ser Gly Asn Lys Val Arg Lys Leu Glu Phe Leu Met
85 90 95
Ala Asp Ala Val Ala Gln Gly Ala Asp Cys Val Ile Thr Val Gly Gly
100 105 110
Ile Gln Ser Asn His Cys Arg Ala Thr Ala Val Ala Ala Lys Tyr Leu
115 120 125
Asn Leu Asp Cys Tyr Leu Ile Leu Arg Thr Ser Lys Leu Leu Val Asp
130 135 140
Lys Asp Pro Gly Leu Val Gly Asn Leu Leu Val Glu Arg Leu Val Gly
145 150 155 160
Ala His Val Asp Leu Val Ser Lys Glu Glu Tyr Gly Lys Ile Gly Ser
165 170 175
Val Ala Leu Ala Asp Leu Leu Lys Lys Arg Leu Leu Glu Glu Gly Arg
180 185 190
Lys Pro Tyr Val Ile Pro Val Gly Gly Ser Asn Ser Leu Gly Thr Trp
195 200 205
Gly Tyr Ile Glu Ala Ile Arg Glu Ile Glu Gln Gln Ile Gln Gln Ser
210 215 220
Ala Asp Val Gln Phe Asp Asp Ile Val Val Ala Cys Gly Ser Gly Gly
225 230 235 240
Thr Ile Ala Gly Leu Ala Leu Gly Ser Arg Leu Ser Ser Leu Asn Thr
245 250 255
Lys Val His Ala Phe Ser Val Cys Asp Asp Pro Glu Tyr Phe Tyr Asp
260 265 270
Tyr Ile Gln Gly Leu Ile Asp Gly Leu Asn Ser Gly Leu Asp Ser His
275 280 285
Asp Ile Val Ser Ile Glu Asn Ala Lys Gly Leu Gly Tyr Ala Met Lys
290 295 300
Thr Ala Glu Glu Leu Lys Phe Val Lys Asp Ile Ala Ala Ser Thr Gly
305 310 315 320
Ile Ile Leu Asp Pro Val Tyr Ser Gly Lys Ala Val Tyr Gly Leu Leu
325 330 335
Lys Asp Met Ala Gly Asn Pro Ala Lys Trp Lys Gly Arg Lys Val Leu
340 345 350
Phe Ile His Thr Gly Gly Leu Leu Gly Leu Tyr Asp Lys Ala Asp Gln
355 360 365
Leu Ser Ser Leu Ala Gly Ser Trp Arg Arg Met Asp Leu Glu Asp Ser
370 375 380
Val Pro Arg Gln Asp Gly Thr Gly Lys Met Phe
385 390 395

<210> 348
<211> 1429
<212> DNA
<213> Zea mays

<220>
<221> CDS

<222> (284)..(1228)

<400> 348

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gtcgcttccg ccgacacctg agtcttgtcg ctgccgccgg gatggccgga gtcaccgcca      60

ccgggatggc cggagttccc gccaccttct cctcaaccac cgctcagatc gggggcttcc     120

tctcgaagaa gccttacgcg ccgccgttgt gggccacgca cctctccccc atgccttgcc     180

ataccttctc gctcggccat ttcccaacac cgattcacaa gtggaatctg cccaatttgc     240

cggaaggaac ggaagtgtgg atcaagcgag acgattatca ggc atg cag ttg agt       295
                                                Met Gln Leu Ser
                                                1

gga aac aag gtc cgg aag ctg gag ttc ttg atg gca gat gcc gta gca       343
Gly Asn Lys Val Arg Lys Leu Glu Phe Leu Met Ala Asp Ala Val Ala
5                   10                  15                  20

caa ggc gca gac tgc gtt att act gtt ggg ggt ata cag agt aac cac       391
Gln Gly Ala Asp Cys Val Ile Thr Val Gly Gly Ile Gln Ser Asn His
                25                  30                  35

tgc cgt gcc aca gcc gtg gct gct aag tat ctc aat ctt gat tgc tac       439
Cys Arg Ala Thr Ala Val Ala Ala Lys Tyr Leu Asn Leu Asp Cys Tyr
            40                  45                  50

ctg ata cta cgt acc tcc aag ctt ctt gtg gat aag gac cct ggt ttg       487
Leu Ile Leu Arg Thr Ser Lys Leu Leu Val Asp Lys Asp Pro Gly Leu
        55                  60                  65

gtt ggc aat ctt ctt gtc gag aga cta gtt ggg gca cac gtt gat ctt       535
Val Gly Asn Leu Leu Val Glu Arg Leu Val Gly Ala His Val Asp Leu
    70                  75                  80

gtg tca aaa gaa gaa tat gga aaa att ggt agt gtg gct tta gct gac       583
Val Ser Lys Glu Glu Tyr Gly Lys Ile Gly Ser Val Ala Leu Ala Asp
85                  90                  95                  100

ctg ctg aaa aaa agg ctt ctg gaa gaa ggg agg aag ccg tat gtg att       631
Leu Leu Lys Lys Arg Leu Leu Glu Glu Gly Arg Lys Pro Tyr Val Ile
                105                 110                 115

cct gtt ggt gga tca aac tca ttg gga act tgg gga tat att gag gca       679
Pro Val Gly Gly Ser Asn Ser Leu Gly Thr Trp Gly Tyr Ile Glu Ala
            120                 125                 130

ata agg gag att gag cag caa att cag caa tct gct gat gtt cag ttt       727
Ile Arg Glu Ile Glu Gln Gln Ile Gln Gln Ser Ala Asp Val Gln Phe
        135                 140                 145

gat gat att gtt gtt gca tgt ggc agt ggt gga acc atc gct ggc ctt       775
Asp Asp Ile Val Val Ala Cys Gly Ser Gly Gly Thr Ile Ala Gly Leu
    150                 155                 160

gct tta gga tcc aga ttg agc agc tta aat aca aaa gtt cat gca ttc       823
Ala Leu Gly Ser Arg Leu Ser Ser Leu Asn Thr Lys Val His Ala Phe
165                 170                 175                 180

tct gtt tgt gat gac cct gaa tac ttc tat gac tat gtc caa ggc ctg       871
Ser Val Cys Asp Asp Pro Glu Tyr Phe Tyr Asp Tyr Val Gln Gly Leu
                185                 190                 195

att gat gga ctt aat tct ggt ttg gat tca cat gat ata gtt agc atc       919
Ile Asp Gly Leu Asn Ser Gly Leu Asp Ser His Asp Ile Val Ser Ile
            200                 205                 210

gaa aat gct aag ggg tta ggc tat gcc atg aac aca gct gag gag ctt       967
Glu Asn Ala Lys Gly Leu Gly Tyr Ala Met Asn Thr Ala Glu Glu Leu
        215                 220                 225

aag ttt gtc aaa gac ata gct gca tca aca ggc att atc ctt gat cca      1015
Lys Phe Val Lys Asp Ile Ala Ala Ser Thr Gly Ile Ile Leu Asp Pro
    230                 235                 240

gtc tac agt ggg aag gcg gtt tat ggt ttg cta aaa gac atg gct ggc      1063
Val Tyr Ser Gly Lys Ala Val Tyr Gly Leu Leu Lys Asp Met Ala Gly
```

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245                 250                 255                 260
aat cca gcc aaa tgg aaa ggt cga aaa gtt ctg ttt atc cac aca ggt      1111
Asn Pro Ala Lys Trp Lys Gly Arg Lys Val Leu Phe Ile His Thr Gly
                265                 270                 275
ggt ctt ctt ggg ttg tat gat aag gct gac cag ttg tca tct ttg gct      1159
Gly Leu Leu Gly Leu Tyr Asp Lys Ala Asp Gln Leu Ser Ser Leu Ala
            280                 285                 290
ggg agc tgg cgc aga atg gat ctt gaa gat tct gtt cca cgc caa gat      1207
Gly Ser Trp Arg Arg Met Asp Leu Glu Asp Ser Val Pro Arg Gln Asp
        295                 300                 305
ggc act ggt aag atg ttc tga tcagtatggt tcatgtgatt ccatgatggc         1258
Gly Thr Gly Lys Met Phe
    310             314
tcattcttgc aaacattgta tccattacag agttgttact cttatatttg tgcaagaaaa    1318

tgcagaatag atggttcaca ttgtatagag cactgatgca atttaagaat aaagcacatc    1378

ttttttgcca tttggaaata aatatttttt atgtggaaaa aaaaaaaaaa a              1429


<210> 349
<211> 314
<212> PRT
<213> Zea mays

<400> 349
Met Gln Leu Ser Gly Asn Lys Val Arg Lys Leu Glu Phe Leu Met Ala
1               5                   10                  15
Asp Ala Val Ala Gln Gly Ala Asp Cys Val Ile Thr Val Gly Gly Ile
            20                  25                  30
Gln Ser Asn His Cys Arg Ala Thr Ala Val Ala Ala Lys Tyr Leu Asn
        35                  40                  45
Leu Asp Cys Tyr Leu Ile Leu Arg Thr Ser Lys Leu Leu Val Asp Lys
    50                  55                  60
Asp Pro Gly Leu Val Gly Asn Leu Leu Val Glu Arg Leu Val Gly Ala
65                  70                  75                  80
His Val Asp Leu Val Ser Lys Glu Glu Tyr Gly Lys Ile Gly Ser Val
                85                  90                  95
Ala Leu Ala Asp Leu Leu Lys Lys Arg Leu Leu Glu Glu Gly Arg Lys
            100                 105                 110
Pro Tyr Val Ile Pro Val Gly Gly Ser Asn Ser Leu Gly Thr Trp Gly
        115                 120                 125
Tyr Ile Glu Ala Ile Arg Glu Ile Glu Gln Gln Ile Gln Gln Ser Ala
    130                 135                 140
Asp Val Gln Phe Asp Asp Ile Val Val Ala Cys Gly Ser Gly Gly Thr
145                 150                 155                 160
Ile Ala Gly Leu Ala Leu Gly Ser Arg Leu Ser Ser Leu Asn Thr Lys
                165                 170                 175
Val His Ala Phe Ser Val Cys Asp Asp Pro Glu Tyr Phe Tyr Asp Tyr
            180                 185                 190
Val Gln Gly Leu Ile Asp Gly Leu Asn Ser Gly Leu Asp Ser His Asp
        195                 200                 205
Ile Val Ser Ile Glu Asn Ala Lys Gly Leu Gly Tyr Ala Met Asn Thr
    210                 215                 220
Ala Glu Glu Leu Lys Phe Val Lys Asp Ile Ala Ala Ser Thr Gly Ile
225                 230                 235                 240
Ile Leu Asp Pro Val Tyr Ser Gly Lys Ala Val Tyr Gly Leu Leu Lys
                245                 250                 255
Asp Met Ala Gly Asn Pro Ala Lys Trp Lys Gly Arg Lys Val Leu Phe
            260                 265                 270
Ile His Thr Gly Gly Leu Leu Gly Leu Tyr Asp Lys Ala Asp Gln Leu
```

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        275                 280                 285
Ser Ser Leu Ala Gly Ser Trp Arg Arg Met Asp Leu Glu Asp Ser Val
    290                 295                 300
Pro Arg Gln Asp Gly Thr Gly Lys Met Phe
305                 310
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<210> 350
<211> 1383
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (42)..(1226)

<400> 350

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gtcgcttccg ccgacacctg agtcttgtcg ctgccgccgg g atg gcc gga gtc acc      56
                                                 Met Ala Gly Val Thr
                                                 1               5
gcc acc ggg atg gcc gga gtt ccc gcc acc ttc tcc tca gcc acc gct      104
Ala Thr Gly Met Ala Gly Val Pro Ala Thr Phe Ser Ser Ala Thr Ala
                10                  15                  20
cag atc ggg ggc ttc ctc tcg aag aag cct tac gcg ccg ccg ttg tgg      152
Gln Ile Gly Gly Phe Leu Ser Lys Lys Pro Tyr Ala Pro Pro Leu Trp
            25                  30                  35
gcc acg cac ctc tcc ccc atg cct tgc cat acc ttc tcg ctc ggc cat      200
Ala Thr His Leu Ser Pro Met Pro Cys His Thr Phe Ser Leu Gly His
        40                  45                  50
ttc cca aca ccg att cac aag tgg aat ctg ccc aat ttg ccg gaa gga      248
Phe Pro Thr Pro Ile His Lys Trp Asn Leu Pro Asn Leu Pro Glu Gly
    55                  60                  65
acg gaa gtg tgg atc aag cga gac gat tta tca ggc atg cag ttg agt      296
Thr Glu Val Trp Ile Lys Arg Asp Asp Leu Ser Gly Met Gln Leu Ser
70                  75                  80                  85
gga aac aag gtc cgg aag ctg gag ttc ttg atg gca gat gcc gta gca      344
Gly Asn Lys Val Arg Lys Leu Glu Phe Leu Met Ala Asp Ala Val Ala
                90                  95                  100
caa ggc gca gac tgc gtt att act gtt ggg ggt ata cag agt aac cac      392
Gln Gly Ala Asp Cys Val Ile Thr Val Gly Gly Ile Gln Ser Asn His
            105                 110                 115
tgc cgt gcc aca gcc gtg gct gct aag tat ctc aat ctt gat tgc tac      440
Cys Arg Ala Thr Ala Val Ala Ala Lys Tyr Leu Asn Leu Asp Cys Tyr
        120                 125                 130
ctg ata cta cgt acc tcc aag ctt ctt gtg gat aag gac cct ggt ttg      488
Leu Ile Leu Arg Thr Ser Lys Leu Leu Val Asp Lys Asp Pro Gly Leu
    135                 140                 145
gtt ggc aat ctt ctt gtc gag aga cta gtt ggg gca cac gtt gat ctt      536
Val Gly Asn Leu Leu Val Glu Arg Leu Val Gly Ala His Val Asp Leu
150                 155                 160                 165
gtg tca aaa gaa gaa tat gga aaa att ggc agt gtg gct tta gct gac      584
Val Ser Lys Glu Glu Tyr Gly Lys Ile Gly Ser Val Ala Leu Ala Asp
                170                 175                 180
ctg ctg aaa aaa agg ctt ctg gaa gaa ggg agg aag ccg tat gtg att      632
Leu Leu Lys Lys Arg Leu Leu Glu Glu Gly Arg Lys Pro Tyr Val Ile
            185                 190                 195
cct gtt ggt gga tca aac tca ttg gga act tgg gga tat att gag gca      680
Pro Val Gly Gly Ser Asn Ser Leu Gly Thr Trp Gly Tyr Ile Glu Ala
        200                 205                 210
ata agg gag att gag cag caa att cag caa tct gct gat gtt cag ttt      728
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Ile Arg Glu Ile Glu Gln Gln Ile Gln Gln Ser Ala Asp Val Gln Phe
    215                 220                 225
gat gat att gtt gtt gca tgt ggc agt ggt gga acc atc gct ggc ctt      776
Asp Asp Ile Val Val Ala Cys Gly Ser Gly Gly Thr Ile Ala Gly Leu
230                 235                 240                 245
gct tta gga tcc aga ttg agc agc tta aat aca aaa gtt cat gca ttc      824
Ala Leu Gly Ser Arg Leu Ser Ser Leu Asn Thr Lys Val His Ala Phe
                250                 255                 260
tct gtt tgt gat gac cct gaa tac ttc tat gac tat gtc caa ggc ctg      872
Ser Val Cys Asp Asp Pro Glu Tyr Phe Tyr Asp Tyr Val Gln Gly Leu
            265                 270                 275
att gat gga ctt aat tct ggt ttg gat tca cat gat ata gtt agc atc      920
Ile Asp Gly Leu Asn Ser Gly Leu Asp Ser His Asp Ile Val Ser Ile
        280                 285                 290
gaa aat gct aag ggg tta ggc tat gcc atg aac aca gct gag gag ctt      968
Glu Asn Ala Lys Gly Leu Gly Tyr Ala Met Asn Thr Ala Glu Glu Leu
    295                 300                 305
aag ttt gtc aaa gac ata gct gca tca aca ggc att gtc ctt gat cca     1016
Lys Phe Val Lys Asp Ile Ala Ala Ser Thr Gly Ile Val Leu Asp Pro
310                 315                 320                 325
gtc tac agt ggg aag gcg gtt tat gga ttg cta aaa gac atg gct ggc     1064
Val Tyr Ser Gly Lys Ala Val Tyr Gly Leu Leu Lys Asp Met Ala Gly
                330                 335                 340
aat cca gcc aaa tgg aaa ggt cga aaa gtt ctg ttt atc cac aca ggt     1112
Asn Pro Ala Lys Trp Lys Gly Arg Lys Val Leu Phe Ile His Thr Gly
            345                 350                 355
ggt ctt ctt ggg ttg tat gat aag gct gac cag ttg tca tct ttg gct     1160
Gly Leu Leu Gly Leu Tyr Asp Lys Ala Asp Gln Leu Ser Ser Leu Ala
        360                 365                 370
ggg agc tgg cgc aga atg gat ctt gaa gat tct gtt cca cgc aaa gat     1208
Gly Ser Trp Arg Arg Met Asp Leu Glu Asp Ser Val Pro Arg Lys Asp
    375                 380                 385
ggc act ggt aag atg ttc tgatcagtat ggtccatgtg attccatgat            1256
Gly Thr Gly Lys Met Phe
390                 395
ggctcattct tgcaaacatt gtatccatta cagagttgtt actcttatat ttgtgcaaga   1316

aaatgcagaa tagatggttc acattgtata gaacactgat gcaatttaag aataaagcac   1376

tctttct                                                            1383


<210>  351
<211>  395
<212>  PRT
<213>  Zea mays

<400>  351

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


<210>  352
<211>  1402
<212>  DNA
<213>  Oryza sativa

<220>
<221>  CDS
<222>  (38)..(1192)

<400>  352
cattcccctc cacgccgccg ccgccgccgc cgcgtgg atg gcc gga gtt tcc gcc      55
                                          Met Ala Gly Val Ser Ala
                                          1               5
gcc tcc gcc gcc ggg aag atc ggg agc ttc ctc tcc aag agg ccg tac      103
Ala Ser Ala Ala Gly Lys Ile Gly Ser Phe Leu Ser Lys Arg Pro Tyr
            10                  15                  20
gcg ccg ccg tcc tgg gcc tcg cac ctg tcc ccc gcc ccc tcg cag acc      151
Ala Pro Pro Ser Trp Ala Ser His Leu Ser Pro Ala Pro Ser Gln Thr
        25                  30                  35
ttc tcg ctc ggc cat ttc ccg acg ccg atc cac aag tgg aat ctg ccc      199
Phe Ser Leu Gly His Phe Pro Thr Pro Ile His Lys Trp Asn Leu Pro
```

```
   40                  45                  50
aat ttg ccg aat ggc acg gag gtg tgg atc aag cga gac gac atc tca      247
Asn Leu Pro Asn Gly Thr Glu Val Trp Ile Lys Arg Asp Asp Ile Ser
55                  60                  65                  70
ggc atg cag ttg agc ggg aac aag gtc cgg aag ctc gag ttc ctg atg      295
Gly Met Gln Leu Ser Gly Asn Lys Val Arg Lys Leu Glu Phe Leu Met
                75                  80                  85
gca gat gcc gtc gcg cag ggc gct gac tgc gtt ata act gta ggt ggc      343
Ala Asp Ala Val Ala Gln Gly Ala Asp Cys Val Ile Thr Val Gly Gly
            90                  95                  100
atc cag agc aat cac tgc cgt gcc acc gca gtg gct gca aag tat ata      391
Ile Gln Ser Asn His Cys Arg Ala Thr Ala Val Ala Ala Lys Tyr Ile
        105                 110                 115
aat ctt gat tgt tat ctg ata ctg cgc aca tcc aag ctt ctt gtg gat      439
Asn Leu Asp Cys Tyr Leu Ile Leu Arg Thr Ser Lys Leu Leu Val Asp
    120                 125                 130
aag gac cct ggt ttg gtt ggg aat ctc ctt gtt gag aga ttg gtg gga      487
Lys Asp Pro Gly Leu Val Gly Asn Leu Leu Val Glu Arg Leu Val Gly
135                 140                 145                 150
gcg cat att gat ctt gtt tca aaa gaa gaa tat gga aaa att ggc agt      535
Ala His Ile Asp Leu Val Ser Lys Glu Glu Tyr Gly Lys Ile Gly Ser
                155                 160                 165
gtg gct tta gcg gac ttg ctg aaa aag aag ctt ttg gaa gaa ggc cga      583
Val Ala Leu Ala Asp Leu Leu Lys Lys Lys Leu Leu Glu Glu Gly Arg
            170                 175                 180
aaa cca tat gtt att cct gtt ggt gga tca aac tct cta gga act tgg      631
Lys Pro Tyr Val Ile Pro Val Gly Gly Ser Asn Ser Leu Gly Thr Trp
        185                 190                 195
gga tat ata gaa gca ata agg gag att gaa cat caa att cag ata tca      679
Gly Tyr Ile Glu Ala Ile Arg Glu Ile Glu His Gln Ile Gln Ile Ser
    200                 205                 210
ggt gat gtt cag ttt gac gac att gtt gtt gca tgt ggc agc ggt gga      727
Gly Asp Val Gln Phe Asp Asp Ile Val Val Ala Cys Gly Ser Gly Gly
215                 220                 225                 230
acc att gct ggt ctt gct tta gga tca aaa ttg agt agc tta aag gca      775
Thr Ile Ala Gly Leu Ala Leu Gly Ser Lys Leu Ser Ser Leu Lys Ala
                235                 240                 245
aaa gtc cat gct ttc tct gtt tgt gat gat cct gga tat ttc cat tcc      823
Lys Val His Ala Phe Ser Val Cys Asp Asp Pro Gly Tyr Phe His Ser
            250                 255                 260
tat gtt caa gac ctg att gat gga ctt cat tct gat ttg cgt tca cat      871
Tyr Val Gln Asp Leu Ile Asp Gly Leu His Ser Asp Leu Arg Ser His
        265                 270                 275
gat tta gtc aac att gaa aat gct aag ggc tta ggt tat gcc atg aac      919
Asp Leu Val Asn Ile Glu Asn Ala Lys Gly Leu Gly Tyr Ala Met Asn
    280                 285                 290
aca gct gag gag ctt aag ttt gtt aaa gat ata gct aca gca aca ggc      967
Thr Ala Glu Glu Leu Lys Phe Val Lys Asp Ile Ala Thr Ala Thr Gly
295                 300                 305                 310
att gtc ctt gat cca gtc tac agt gga aag gca gca tat gga atg ctg     1015
Ile Val Leu Asp Pro Val Tyr Ser Gly Lys Ala Ala Tyr Gly Met Leu
                315                 320                 325
aaa gac atg ggt gct aat cca gct aag tgg gaa ggg cga aaa att ctt     1063
Lys Asp Met Gly Ala Asn Pro Ala Lys Trp Glu Gly Arg Lys Ile Leu
            330                 335                 340
ttt gta cat aca ggt ggt ctt ctt ggt ttg tat gat aag gtt gat gag     1111
Phe Val His Thr Gly Gly Leu Leu Gly Leu Tyr Asp Lys Val Asp Glu
        345                 350                 355
tta tca tct ttg agt ggg agt tgg cgc aga atg gat ctt gaa gaa tct     1159
Leu Ser Ser Leu Ser Gly Ser Trp Arg Arg Met Asp Leu Glu Glu Ser
    360                 365                 370
```

gtt cca cgc aaa gat gga act ggt aag atg ttc tgattgctat gctccaaaat 1212
Val Pro Arg Lys Asp Gly Thr Gly Lys Met Phe
375 380 385
tgcttccatt gttgttagag gtttcagaca tctcattgtc taaaaagagt attcgcctca 1272

atttgtacga caaaattcaa agcagatggt taatgtaaaa cactgtttgt tatatttaaa 1332

gaataaagca tatatttctg ccatttggaa ataaaggttt atatacattt gatgtaaaaa 1392

aaaaaaaaaa 1402

<210> 353
<211> 385
<212> PRT
<213> Oryza sativa

<400> 353

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

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Glu Gly Arg Lys Ile Leu Phe Val His Thr Gly Gly Leu Leu Gly Leu
            340                 345                 350
Tyr Asp Lys Val Asp Glu Leu Ser Ser Leu Ser Gly Ser Trp Arg Arg
        355                 360                 365
Met Asp Leu Glu Glu Ser Val Pro Arg Lys Asp Gly Thr Gly Lys Met
    370                 375                 380
Phe
385
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<210> 354
<211> 1406
<212> DNA
<213> Glycine max

<220>
<221> CDS
<222> (68)..(1204)

<400> 354

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gaattcccgg atcgacgctt tcgttgaatt ctaaaaggaa agaacagctg agctggtcag     60

aaaatca atg gca tca tcc ttg ggt ttt gag ttc ctg acg aag aag cct      109
        Met Ala Ser Ser Leu Gly Phe Glu Phe Leu Thr Lys Lys Pro
        1               5                   10
tac agt cct cca tcc tgg gca tcc cat ctc cac cct tta cct tcc cac      157
Tyr Ser Pro Pro Ser Trp Ala Ser His Leu His Pro Leu Pro Ser His
15              20                  25                  30
ttc ttc tct ctt gcc cat ctt ccc act cca att cac aga tgg aac ctt      205
Phe Phe Ser Leu Ala His Leu Pro Thr Pro Ile His Arg Trp Asn Leu
                35                  40                  45
ccc aat ctg ccc acc aat acc gag ctg tgg atc aag cga gac gac ctt      253
Pro Asn Leu Pro Thr Asn Thr Glu Leu Trp Ile Lys Arg Asp Asp Leu
            50                  55                  60
tcc gga atg cag ctg agt ggt aac aaa gtg agg aaa ttg gag ttc ctg      301
Ser Gly Met Gln Leu Ser Gly Asn Lys Val Arg Lys Leu Glu Phe Leu
        65                  70                  75
atg gcc gat gcc att gcg caa ggc gcc gac tct atc atc aca atc gga      349
Met Ala Asp Ala Ile Ala Gln Gly Ala Asp Ser Ile Ile Thr Ile Gly
    80                  85                  90
ggc att cag agc aac cac tgt cgc gcc acc gcc gtt gcc gcc aag tat      397
Gly Ile Gln Ser Asn His Cys Arg Ala Thr Ala Val Ala Ala Lys Tyr
95                  100                 105                 110
tta aac ctt gac tgt ttt ctc atc ctc cgc act tct gac ctc ctc gtc      445
Leu Asn Leu Asp Cys Phe Leu Ile Leu Arg Thr Ser Asp Leu Leu Val
                115                 120                 125
gat caa gat cca gga ctt act ggc aat ctt ctc gtc gaa cgt atg gtt      493
Asp Gln Asp Pro Gly Leu Thr Gly Asn Leu Leu Val Glu Arg Met Val
            130                 135                 140
gga gct cac gtt cac ctc atc tcc aaa caa gaa tat gcc aaa att ggc      541
Gly Ala His Val His Leu Ile Ser Lys Gln Glu Tyr Ala Lys Ile Gly
        145                 150                 155
agc gtg aca ctc acc aat gtc cta aaa gaa aaa ttg atc aag gaa ggg      589
Ser Val Thr Leu Thr Asn Val Leu Lys Glu Lys Leu Ile Lys Glu Gly
    160                 165                 170
agg agg cca tat gtt ata ccc gtt ggc gga tca aac tct ttg gga aca      637
Arg Arg Pro Tyr Val Ile Pro Val Gly Gly Ser Asn Ser Leu Gly Thr
175                 180                 185                 190
tgg ggt tat ata gaa gca gta cgg gaa att gag cag cag att cag aag      685
Trp Gly Tyr Ile Glu Ala Val Arg Glu Ile Glu Gln Gln Ile Gln Lys
                195                 200                 205
```

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ggg aca ggc aat gtc aag ttt gat gat att gtt gtt gct tgt ggc agt      733
Gly Thr Gly Asn Val Lys Phe Asp Asp Ile Val Val Ala Cys Gly Ser
            210                 215                 220
ggt ggc aca att gct ggt ctg tca cta gga tcg tca ttg agt gca ttg      781
Gly Gly Thr Ile Ala Gly Leu Ser Leu Gly Ser Ser Leu Ser Ala Leu
        225                 230                 235
aaa gca agg gta cat gca ttc tct gtt tgt gat gac cca gat tac ttc      829
Lys Ala Arg Val His Ala Phe Ser Val Cys Asp Asp Pro Asp Tyr Phe
    240                 245                 250
cac aac ttt gct caa ggc ttg ctt gat gga ctc aag gct ggc gtt agc      877
His Asn Phe Ala Gln Gly Leu Leu Asp Gly Leu Lys Ala Gly Val Ser
255                 260                 265                 270
tca aga gat att gtc cac att caa aac gcc aag ggt ctt ggc tat gca      925
Ser Arg Asp Ile Val His Ile Gln Asn Ala Lys Gly Leu Gly Tyr Ala
                275                 280                 285
atg aat aca tcg gag gag ctt aat ttt gta aaa gaa gtt gct gcc act      973
Met Asn Thr Ser Glu Glu Leu Asn Phe Val Lys Glu Val Ala Ala Thr
            290                 295                 300
act ggt gtt gtt ctt gac cca gta tac agt ggt aag gct gct tat gca     1021
Thr Gly Val Val Leu Asp Pro Val Tyr Ser Gly Lys Ala Ala Tyr Ala
        305                 310                 315
atg ctg aaa gat atg tct gaa aat cca aag aag tgg gaa agg aga aag     1069
Met Leu Lys Asp Met Ser Glu Asn Pro Lys Lys Trp Glu Arg Arg Lys
    320                 325                 330
atc ctc ttc ata cat acg ggt ggc ctc cta gga ttg tat gac aag gtc     1117
Ile Leu Phe Ile His Thr Gly Gly Leu Leu Gly Leu Tyr Asp Lys Val
335                 340                 345                 350
gat cag ttg gct tct ttt gtt ggg aat tgg caa cga atg gat gtc aat     1165
Asp Gln Leu Ala Ser Phe Val Gly Asn Trp Gln Arg Met Asp Val Asn
                355                 360                 365
gaa tct gtt cct agg cag gat ggt att gga aag atg ttc tagagaagga      1214
Glu Ser Val Pro Arg Gln Asp Gly Ile Gly Lys Met Phe
            370                 375
aaatgaaaaa acctgacgtt gccagcatct atattttgta ctatcttgct ctaaataaat   1274

tttatactta tatttaatag ccatatgctc acactgaatc ctgcctgaag ttaccataag   1334

atagtaaagt tccaaaaact taagtgacaa ataaatcaag ttttatttat ttttaaaaaa   1394

aaaaaaaaaa aa                                                       1406


<210>  355
<211>  379
<212>  PRT
<213>  Glycine max

<400>  355

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

```
Gln Ser Asn His Cys Arg Ala Thr Ala Val Ala Ala Lys Tyr Leu Asn
            100                 105                 110
Leu Asp Cys Phe Leu Ile Leu Arg Thr Ser Asp Leu Leu Val Asp Gln
        115                 120                 125
Asp Pro Gly Leu Thr Gly Asn Leu Leu Val Glu Arg Met Val Gly Ala
    130                 135                 140
His Val His Leu Ile Ser Lys Gln Glu Tyr Ala Lys Ile Gly Ser Val
145                 150                 155                 160
Thr Leu Thr Asn Val Leu Lys Glu Lys Leu Ile Lys Glu Gly Arg Arg
                165                 170                 175
Pro Tyr Val Ile Pro Val Gly Gly Ser Asn Ser Leu Gly Thr Trp Gly
            180                 185                 190
Tyr Ile Glu Ala Val Arg Glu Ile Glu Gln Gln Ile Gln Lys Gly Thr
        195                 200                 205
Gly Asn Val Lys Phe Asp Asp Ile Val Val Ala Cys Gly Ser Gly Gly
    210                 215                 220
Thr Ile Ala Gly Leu Ser Leu Gly Ser Ser Leu Ser Ala Leu Lys Ala
225                 230                 235                 240
Arg Val His Ala Phe Ser Val Cys Asp Asp Pro Asp Tyr Phe His Asn
                245                 250                 255
Phe Ala Gln Gly Leu Leu Asp Gly Leu Lys Ala Gly Val Ser Ser Arg
            260                 265                 270
Asp Ile Val His Ile Gln Asn Ala Lys Gly Leu Gly Tyr Ala Met Asn
        275                 280                 285
Thr Ser Glu Glu Leu Asn Phe Val Lys Glu Val Ala Ala Thr Thr Gly
    290                 295                 300
Val Val Leu Asp Pro Val Tyr Ser Gly Lys Ala Ala Tyr Ala Met Leu
305                 310                 315                 320
Lys Asp Met Ser Glu Asn Pro Lys Lys Trp Glu Arg Arg Lys Ile Leu
                325                 330                 335
Phe Ile His Thr Gly Gly Leu Leu Gly Leu Tyr Asp Lys Val Asp Gln
            340                 345                 350
Leu Ala Ser Phe Val Gly Asn Trp Gln Arg Met Asp Val Asn Glu Ser
        355                 360                 365
Val Pro Arg Gln Asp Gly Ile Gly Lys Met Phe
    370                 375
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<210> 356
<211> 1463
<212> DNA
<213> Triticum aestivum

<220>
<221> CDS
<222> (21)..(1280)

<400> 356

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cccacgcgtc cgaatccccc atg ctc ctg aga ccg gcc ctc ccc gtc gcc gtc      53
                       Met Leu Leu Arg Pro Ala Leu Pro Val Ala Val
                       1               5                   10
agt tcc act ctc cca ctc ttc tcc cat ctc gcc gcc gtc cgc cgt cgg      101
Ser Ser Thr Leu Pro Leu Phe Ser His Leu Ala Ala Val Arg Arg Arg
            15                  20                  25
tgc tca atc gcc gcc acg ggc atg gca gga gtc tcc gcc gcc tct ccc      149
Cys Ser Ile Ala Ala Thr Gly Met Ala Gly Val Ser Ala Ala Ser Pro
        30                  35                  40
gcc gca gca cag atc ggc agc ttc ctc tcc aag aag ccc tac gcg ccg      197
Ala Ala Ala Gln Ile Gly Ser Phe Leu Ser Lys Lys Pro Tyr Ala Pro
    45                  50                  55
ccg tcc tgg gcc tcg cac ctc gcc ctc gcc cca tcc cac act ttc tcc      245
```

```
Pro Ser Trp Ala Ser His Leu Ala Leu Ala Pro Ser His Thr Phe Ser
60                  65                  70                  75
ctc ggc cac ttc ccg acc ccg att cac aaa tgg aat ctg cca aat ctg      293
Leu Gly His Phe Pro Thr Pro Ile His Lys Trp Asn Leu Pro Asn Leu
                80                  85                  90
ccg gag ggc act gaa gta tgg atc aag cgg gac gat ctg tcg ggt atg      341
Pro Glu Gly Thr Glu Val Trp Ile Lys Arg Asp Asp Leu Ser Gly Met
            95                  100                 105
cag ctg agc ggg aac aag gtc cgg aag ctc gag ttt ctg ttg tca gat      389
Gln Leu Ser Gly Asn Lys Val Arg Lys Leu Glu Phe Leu Leu Ser Asp
        110                 115                 120
gcc gtc gcg cag ggt gcg gac tgc gtt atc act gtc ggt ggt atc cag      437
Ala Val Ala Gln Gly Ala Asp Cys Val Ile Thr Val Gly Gly Ile Gln
    125                 130                 135
agc aac cac tgc cgt gcg acg gcg gtg gct gcc aag tat ctc aat ctt      485
Ser Asn His Cys Arg Ala Thr Ala Val Ala Ala Lys Tyr Leu Asn Leu
140                 145                 150                 155
gac tgt tat ttg ata ctg cgt act tcc aag ctt ctt gtg gat cag gac      533
Asp Cys Tyr Leu Ile Leu Arg Thr Ser Lys Leu Leu Val Asp Gln Asp
                160                 165                 170
cct ggt ttg gtt ggc aat ctc ctt gtt gag aga ctg ttg gga gcg cac      581
Pro Gly Leu Val Gly Asn Leu Leu Val Glu Arg Leu Leu Gly Ala His
            175                 180                 185
att gat ctc gtc tca aaa gaa gag tat ggg aaa att ggc agt gtg gct      629
Ile Asp Leu Val Ser Lys Glu Glu Tyr Gly Lys Ile Gly Ser Val Ala
        190                 195                 200
tta gcg gac ttg ctt aaa aag agg ctt ttg gag gaa gga cgg aag cca      677
Leu Ala Asp Leu Leu Lys Lys Arg Leu Leu Glu Glu Gly Arg Lys Pro
    205                 210                 215
tat gtg att cct gtt ggt gga tcc aat tca ctt gga act tgg gga tat      725
Tyr Val Ile Pro Val Gly Gly Ser Asn Ser Leu Gly Thr Trp Gly Tyr
220                 225                 230                 235
att gaa gca gta aga gag ctt gag cag caa att cag tta tct ggc gat      773
Ile Glu Ala Val Arg Glu Leu Glu Gln Gln Ile Gln Leu Ser Gly Asp
                240                 245                 250
gtt cag ttt gat gac att gtt gtt gcc tgt ggc agt ggt gga acc att      821
Val Gln Phe Asp Asp Ile Val Val Ala Cys Gly Ser Gly Gly Thr Ile
            255                 260                 265
gct ggt ctt gct tta gga tca aaa ttg agt agc tta acg gca aaa gtc      869
Ala Gly Leu Ala Leu Gly Ser Lys Leu Ser Ser Leu Thr Ala Lys Val
        270                 275                 280
cat gct ttc tct gtt tgc gat gac cct gaa tac ttc tat gat tat gtt      917
His Ala Phe Ser Val Cys Asp Asp Pro Glu Tyr Phe Tyr Asp Tyr Val
    285                 290                 295
caa ggc ctg att gat gga cta caa tct ggc ttg gat tca cat gat ata      965
Gln Gly Leu Ile Asp Gly Leu Gln Ser Gly Leu Asp Ser His Asp Ile
300                 305                 310                 315
gtc agc att caa aat gct aag ggc tta ggt tat gcc atg aac aca gct     1013
Val Ser Ile Gln Asn Ala Lys Gly Leu Gly Tyr Ala Met Asn Thr Ala
                320                 325                 330
gag gag ctt aag ttt gtt aaa gat ata gct act gca aca ggc att gtg     1061
Glu Glu Leu Lys Phe Val Lys Asp Ile Ala Thr Ala Thr Gly Ile Val
            335                 340                 345
ctt gat cca gtc tac agt ggg aag gga gca tat gca atg ctg aaa gac     1109
Leu Asp Pro Val Tyr Ser Gly Lys Gly Ala Tyr Ala Met Leu Lys Asp
        350                 355                 360
atg gct gat aat cca tcc aag tgg aaa ggg cga aaa gtc ctc ttt gtc     1157
Met Ala Asp Asn Pro Ser Lys Trp Lys Gly Arg Lys Val Leu Phe Val
    365                 370                 375
cac aca ggt ggc ctt ctt ggg ttg tat gac aag gtt gat cag atg tca     1205
His Thr Gly Gly Leu Leu Gly Leu Tyr Asp Lys Val Asp Gln Met Ser
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380                 385                 390                 395
tct ttg gct ggg agc tgg cga aga atg gat ctt gaa gaa tca gtc cca     1253
Ser Leu Ala Gly Ser Trp Arg Arg Met Asp Leu Glu Glu Ser Val Pro
                400                 405                 410
cgc aaa gat ggc act ggt aag atg ttc tgattgatat gctccagaaa          1300
Arg Lys Asp Gly Thr Gly Lys Met Phe
            415                 420
ccgctccatt atgggctgga gtttcagaaa tgtcattcat cttaagggta tatgctctta  1360

catttgtaaa agaaaattca gaatagacag ctagcatgga atgttgatat acaagaataa  1420

agtgcatcgt tctgccattt gaaaataaag ctatctgtat tgc                    1463


<210>  357
<211>  420
<212>  PRT
<213>  Triticum aestivum

<400>  357

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

```
Ala Lys Gly Leu Gly Tyr Ala Met Asn Thr Ala Glu Glu Leu Lys Phe
                325                 330                 335
Val Lys Asp Ile Ala Thr Ala Thr Gly Ile Val Leu Asp Pro Val Tyr
            340                 345                 350
Ser Gly Lys Gly Ala Tyr Ala Met Leu Lys Asp Met Ala Asp Asn Pro
        355                 360                 365
Ser Lys Trp Lys Gly Arg Lys Val Leu Phe Val His Thr Gly Gly Leu
    370                 375                 380
Leu Gly Leu Tyr Asp Lys Val Asp Gln Met Ser Ser Leu Ala Gly Ser
385                 390                 395                 400
Trp Arg Arg Met Asp Leu Glu Glu Ser Val Pro Arg Lys Asp Gly Thr
                405                 410                 415
Gly Lys Met Phe
            420
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<210> 358
<211> 31
<212> DNA
<213> Unknown

<220>
<223> AtACCD forward primer

<400> 358
ggggtcgacg aagcaatgag aggacgaagc t 31

<210> 359
<211> 32
<212> DNA
<213> Unknown

<220>
<223> AtACCD reverse primer

<400> 359
gggttaatta acagattttg ttgtgctaga ac 32

<210> 360
<211> 20
<212> DNA
<213> Unknown

<220>
<223> NOS terminator forward primer

<400> 360
tccccgatcg ttcaaacatt 20

<210> 361
<211> 25
<212> DNA
<213> Unknown

<220>
<223> NOS terminator reverse primer

<400> 361
ccatctcata aataacgtca tgcat 25