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(54) Title: ENZYME SYSTEMS FOR SACCHARIFICATION OF PLANT CELL WALL POLYSACCHARIDES

(57) Abstract: The present invention relates to cell wall degradative systems, in particular to systems containing enzymes that bind to and/or depolymerize cellulose. These systems have a number of applications. Some embodiments relate to a method of producing ethanol using the cell wall degradative systems of the present invention.



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ENZYME SYSTEMS FOR SACCHARIFICATION OF PLANT CELL WALL POLYSACCHARIDES

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application is a continuation-in-part of U.S. Application Serial No. 11/121,154 filed May 4, 2005 and claims priority to U.S. Provisional Application No. 60/567,971, filed May 4, 2004, the contents of which are incorporated herein, in their entirety, by reference.

STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH OR DEVELOPMENT

[0002] This invention was made with government support under Contract Number SA7528051E awarded by the National Oceanic and Atmospheric Administration (NOAA) and Contract Number DEB0109869 awarded by the National Science Foundation (NSF). The government has certain rights in the invention.

SEQUENCE LISTING

[0003] The present application contains a lengthy Sequence Listing, which has been submitted via triplicate CD-R in lieu of a printed paper copy, and is hereby incorporated by reference in its entirety. The CD-Rs, recorded on September 14, 2005 in related U.S. Application Serial No. 11/121,154 filed May 4, 2005, are labeled "CRF", "Copy 1," and "Copy 2," respectively, and each contains only one identical 828 KB file (18172121.APP).

BACKGROUND OF THE INVENTION

1. Field of the Invention:

[0004] The invention is generally directed to degradative enzymes and systems. In particular, the present invention is directed to plant cell wall degrading enzymes and associated proteins found in *Microbulbifer degradans*, systems containing such enzymes and/or proteins, and methods of using the systems to obtain ethanol.

2. Background of the Invention:

[0005] Cellulases and related enzymes have been utilized in food, beer, wine, animal feeds, textile production and laundering, pulp and paper industry, and agricultural industries. Various such uses are described in the paper "Cellulases and related enzymes in biotechnology" by M.K. Bhat (Biotechnical Advances 18 (2000) 355-383), the subject matter of which is hereby incorporated by reference in its entirety.

[0006] The cell walls of plants are composed of a heterogeneous mixture of complex polysaccharides that interact through covalent and noncovalent means. Complex polysaccharides of higher plant cell walls include, for example, cellulose (β -1, 4 glucan) which generally makes up 35-50% of carbon found in cell wall components. Cellulose polymers self associate through hydrogen bonding, van der Waals interactions and hydrophobic interactions to form semi-crystalline cellulose microfibrils. These microfibrils also include noncrystalline regions, generally known as amorphous cellulose. The cellulose microfibrils are embedded in a matrix formed of hemicelluloses (including, e.g., xylans, arabinans, and mannans), pectins (e.g., galacturonans and galactans), and various other β -1, 3 and β -1, 4 glucans. These matrix polymers are often substituted with, for example, arabinose, galactose and/or xylose residues to yield highly complex arabinoxylans, arabinogalactans, galactomannans, and xyloglucans. The hemicellulose matrix is, in turn, surrounded by polyphenolic lignin.

[0007] The complexity of the matrix makes it difficult to degrade by microorganisms as lignin and hemicellulose components must be degraded before enzymes can act on the core cellulose microfibrils. Ordinarily, a consortium of different microorganisms is required to degrade cell wall polymers to release the constituent monosaccharides. For saccharification of plant cell walls, the lignin must be permeabilized and hemicellulose removed to allow cellulose-degrading enzymes to act on their substrate. For industrial saccharification of cell walls, large amounts of primarily fungal cellulases are added to processed feedstock that has been treated with dilute sulfuric acid at high temperature and pressure to permeabilize the lignin and partially saccharify the hemicellulose constituents.

[0008] *Saccharophagus degradans* strain 2-40 (herein referred to as "*S. degradans* 2-40" or "2-40") is a representative of an emerging group of marine bacteria that degrade

complex polysaccharides (CP). *S. degradans* has been deposited at the American Type Culture Collection and bears accession number **ATCC** 43961. *S. degradans* 2-40, formerly known and referred to synonymously herein as *Microbulbifer degradans* strain 2-40 ("M. *degradans* 2-40"), is a marine α -proteobacterium that was isolated from decaying *Spartina alterniflora*, a salt marsh cord grass in the Chesapeake Bay watershed. Consistent with its isolation from decaying plant matter, *S. degradans* strain 2-40 is able to degrade many complex polysaccharides, including cellulose, pectin, xylan, and chitin, which are common components of the cell walls of higher plants. *S. degradans* strain 2-40 is also able to depolymerize algal cell wall components, such as agar, agarose, and laminarin, as well as protein, starch, pullulan, and alginic acid. In addition to degrading this plethora of polymers, *S. degradans* strain 2-40 can utilize each of the polysaccharides as the sole carbon source. Therefore, *S. degradans* strain 2-40 is not only an excellent model of microbial degradation of insoluble complex polysaccharides (ICPs) but can also be used as a paradigm for complete metabolism of these ICPs. ICPs are polymerized saccharides that are used for form and structure in animals and plants. They are insoluble in water and therefore are difficult to break down.

[0009] *Microbulbifer degradans* strain 2-40 requires at least 1% sea salts for growth and will tolerate salt concentrations as high as 10%. It is a highly pleomorphic, Gram-negative bacterium that is aerobic, generally rod-shaped, and motile by means of a single polar flagellum. Previous work has determined that 2-40 can degrade at least 10 different carbohydrate polymers (CP), including agar, chitin, alginic acid, carboxymethylcellulose (CMC), β -glucan, laminarin, pectin, pullulan, starch and xylan (Ensor, Stotz et al. 1999). In addition, it has been shown to synthesize a true tyrosinase (Kelley, Coyne et al. 1990). 16S rDNA analysis shows that 2-40 is a member of the gamma-subclass of the phylum *Proteobacteria*, related to *Microbulbifer hydrolyticus* (Gonzalez and Weiner 2000) and to *Teridinibacter* sp., (Distel, Morrill et al. 2002) cellulolytic nitrogen-fixing bacteria that are symbionts of shipworms.

[0010] The agarase, chitinase and alginase systems have been generally characterized. Zymogram activity gels indicate that all three systems are comprised of multiple depolymerases and multiple lines of evidence suggest that at least some of these

depolymerases are attached to the cell surface (Stotz 1994; Whitehead 1997; Chakravorty 1998). Activity assays reveal that the majority of 2-40 enzyme activity resides with the cell fraction during logarithmic growth on CP, while in later growth phases the bulk of the activity is found in the supernatant and cell-bound activity decreases dramatically (Stotz 1994). Growth on CP is also accompanied by dramatic alterations in cell morphology. Glucose-grown cultures of 2-40 are relatively uniform in cell size and shape, with generally smooth and featureless cell surfaces. However, when grown on agarose, alginate, or chitin, 2-40 cells exhibit novel surface structures and features.

[0011] These exo- and extra-cellular structures (ES) include small protuberances, larger bleb-like structures that appear to be released from the cell, fine fimbriae or pili, and a network of fibril-like appendages which may be tubules of some kind. Immunoelectron microscopy has shown that agarases, alginases and/or chitinases are localized in at least some types of 2-40 ES. The surface topology and pattern of immunolocalization of 2-40 enzymes to surface protuberances are very similar to what is seen with cellulolytic members of the genus *Clostridium*.

[0012] The oldest methods studied to convert lignocellulosic materials to saccharides are based on acid hydrolysis (see, e.g., review by Grethlein, Chemical Breakdown Of Cellulosic Materials, J.APPL.CHEM. BIOTECHNOL. 28:296-308 (1978)). This process can involve the use of concentrated or dilute acids. For example, U.S. Patent Nos. 5,221,537 and 5,536,325, incorporated by reference herein in their entireties, describe a two-step process for the acid hydrolysis of lignocellulosic material to glucose. These processes have numerous disadvantages including, for example, recovery of the acid, the specialized materials of construction required, the need to minimize water in the system, and the high production of degradation products which can inhibit the fermentation to ethanol.

[0013] To overcome the problems of the acid hydrolysis process, cellulose conversion processes are being developed using enzymatic hydrolysis. See, for example, U.S. Patent No. 5,916,780, incorporated by reference herein in its entirety, which discloses enzymatic hydrolysis with a pre-treatment step to break down the integrity of the fiber structure and make the cellulose more accessible to attack by

cellulase enzymes in the treatment phase.

[0014] U.S. Patent No. 6,333,181, incorporated by reference herein in its entirety, discloses production of ethanol from lignocellulosic material by treatment of a mixture of lignocellulose, cellulose, and an ethanologenic microorganism with ultrasound.

[0015] There exists a need to identify enzyme systems that use cellulose as a substrate, express the genes encoding the proteins using suitable vectors, identify and isolate the amino acid products (enzymes and non-enzymatic products), and use these products as well as organisms containing these genes for purposes, such as the production of ethanol and uses described in the Bhat paper. There is also a need in the art of using lignocellulosic materials for production of ethanol, to develop more effective treatment methods that result in greater yields of ethanol.

SUMMARY OF THE INVENTION

[0016] One aspect of the present invention is directed to systems of plant wall active carbohydrases and related proteins.

[0017] A further aspect of the invention is directed to a method for the degradation of substances comprising cellulose. The method involves contacting the cellulose containing substances with one or more compounds obtained from *Saccharophagus degradans* strain 2-40.

[0018] Another aspect of the present invention is directed to groups of enzymes that catalyze reactions involving cellulose.

[0019] Another aspect of the present invention is directed to polynucleotides that encode polypeptides with cellulose degrading or cellulose binding activity.

[0020] A further aspect of the invention is directed to chimeric genes and vectors comprising genes that encode polypeptides with cellulose depolymerase activity.

[0021] A further aspect of the invention is directed to a method for the identification of a nucleotide sequence encoding a polypeptide comprising any one of the following activities from *S. degradans*: cellulose depolymerase, or cellulose binding. An *S. degradans* genomic library can be constructed in *E. coli* and screened for the desired activity. Transformed *E. coli* cells with specific activity are created and isolated.

[0022] Another aspect of the invention is directed to a method for producing ethanol from lignocellulosic material, comprising treating lignocellulosic material with an

effective saccharifying amount of one or more compounds listed in Figures 4-11 to obtain saccharides and converting the saccharides to produce ethanol. Conversion of sugars to ethanol and recovery may be accomplished by, but are not limited to, any of the well-established methods known to those of skill in the art. For example, through the use of an ethanologenic microorganism, such as *Zymomonas*, *Erwinia*, *Klebsiella*, *Xanthomonas*, and *Escherichia*, preferably *Escherichia coli* K011 and *Klebsiella oxytoca* P2.

[0023] A further aspect of the invention is directed to a method for producing ethanol from lignocellulosic material, comprising contacting lignocellulosic material with a microorganism expressing an effective saccharifying amount of one or more compounds listed in Figures 4-11 to obtain saccharides and converting the saccharides to produce ethanol.

[0024] A further aspect of the invention is directed to a method for producing ethanol from lignocellulosic material, comprising contacting lignocellulosic material with an ethanologenic microorganism expressing an effective saccharifying amount of one or more compounds listed in Figures 4-11 to produce ethanol. Such an ethanologenic microorganism expresses an effective amount of one or more compounds listed in Figures 4-11 to saccharify the lignocellulosic material and an effective amount of one or more enzymes or enzyme systems which, in turn, catalyze (individually or in concert) the conversion of the saccharides to ethanol.

[0025] Further aspects of the invention are directed to utilization of the cellulose degrading substances in food, beer, wine, animal feeds, textile production and laundering, pulp and paper industry, and agricultural industries.

[0026] The present invention is advantageous in that saccharification of plant cell walls and ethanol production processes including saccharification may be obtained without permeabilizing lignin and/or removing or partially saccharifying the hemicellulose or hemicellulose constituents before the cellulose-degrading enzymes can act on their substrate. The present invention also allows for saccharification and ethanol production processes including saccharification without or with a reduced amount of fungal cellulases, acids (e.g., sulfuric acid), high temperatures, and high pressures in the saccharification process.

[0027] Other aspects, features, and advantages of the invention will become apparent from the following detailed description, which when taken in conjunction with the accompanying figures, which are part of this disclosure, and which illustrate by way of example the principles of this invention.

BRIEF DESCRIPTION OF THE FIGURES

- [0028] Figure 1A shows the chemical formula of cellulose;
- [0029] Figure 1B illustrates the physical structure of cellulose;
- [0030] Figure 2A illustrates the degradation of cellulose fibrils;
- [0031] Figure 2B shows the chemical representation of cellulose degradation to cellobiose and glucose;
- [0032] Figure 3 shows SDS-PAGE and Zymogram analysis of 2-40 culture supernatants;
- [0033] Figure 4 lists the predicted cellulases of *S. degradans* 2-40 (the sequences from Figures 4-10 are disclosed as SEQ ID NOs 1-214, respectively in order of appearance in the appendix);
- [0034] Figure 5 lists the predicted xylanases, xylosidases and related accessories of *M. degradans* 2-40;
- [0035] Figure 6 lists the predicted pectinases and related accessories of *S. degradans* 2-40;
- [0036] Figure 7 lists the arabinanases and arabinogalactanases of *S. degradans* 2-40;
- [0037] Figure 8 lists the mannanases of *S. degradans* 2-40;
- [0038] Figure 9 lists the laminarinases of *S. degradans* 2-40;
- [0039] Figure 10 lists selected carbohydrate-binding module proteins of *S. degradans* 2-40; and
- [0040] Figure 11 lists the recombinant proteins of *S. degradans* 2-40 and a comparison of predicted vs. observed molecular weights thereof.

DETAILED DESCRIPTION

[0041] Analysis of the genome sequence of *S. degradans* 2-40 reveals an abundance of genes coding for enzymes that are predicted to degrade plant-derived carbohydrates. To date, 2-40 is the only sequenced marine bacterium with apparently complete

cellulase and xylanase systems, as well as a number of other systems containing plant-wall active carbohydrases.

[0042] Thus it appears that 2-40 can play a significant role in the marine carbon cycle, functioning as a "super-degrader" that mediates the breakdown of CP from various algal, plantal, and invertebrate sources. The remarkable enzymatic diversity, novel surface features (ES), and the apparent localization of carbohydrases to ES make *S. degradans* 2-40 an intriguing organism in which to study the cell biology of CP metabolism and surface enzyme attachment.

[0043] It has now been discovered that 2-40 has a complete complement of enzymes, suitably positioned, to degrade plant cell walls. This has been accomplished by the following approaches: a) annotation and genomic analysis of 2-40 plant-wall active enzyme systems, b) identification of enzymes and other proteins which contain domains or motifs that may be involved in surface enzyme display, c) the development of testable models based on identified protein motifs, and d) cloning and expression of selected proteins for the production of antibody probes to allow testing of proposed models of surface enzyme display using immunoelectron microscopy.

[0044] These efforts have been greatly facilitated by the recent sequencing of the genome of 2-40, allowing a strategy where genes which code for proteins with potential involvement in surface attachment may be identified based on sequence homology with modules or domains known to function in surface attachment and/or adhesion.

[0045] Enzymatic and non-enzymatic ORFs with compelling sequence elements are identified using BLAST and other amino acid sequence alignment and analysis tools. Genes of interest can be cloned into *E coli*, expressed with in-frame polyhistidine affinity tag fusions and purified by nickel ion chromatography, thus providing the means of identifying and producing recombinant 2-40 proteins for study and antibody probe production.

[0046] The genome sequence of 2-40 was recently obtained in conjunction with the Department of Energy's Joint Genome Initiative (JGI). The finished draft sequence dated January 19, 2005 comprises 5.1Mbp contained in a single contiguous sequence. Automated annotation of open reading frames (ORFs) was performed by the computational genomics division of the Oak Ridge National Laboratory (ORNL), and the

annotated sequence is available on the World Wide Web (<http://genome.ornl.gov/microbial/mdeg>).

[0047] The initial genome annotation has revealed a variety of carbohydrases, including a number of agarases, alginases and chitinases. Remarkably, the genome also contains an abundance of enzymes with predicted roles in the degradation of plant cell wall polymers, including a number of ORFs with homology to cellulases, xylanases, pectinases, and other glucanases and glucosidases. In all, over 180 open reading frames with a probable role in carbohydrate catabolism were identified in the draft genome.

[0048] To begin to define the cellulase, xylanase and pectinase systems of 2-40, genes were initially classified as belonging to one of those systems by BLAST homology. Ambiguous ORFs were tentatively assigned to the class of the best known hit. Other tools used to refine this tentative classification include Pfam (Protein families database of alignments and HMMs; <http://www.sanger.ac.uk/Software/Pfam/>) and SMART (Simple Modular Architecture Research Tool; <http://smart.embl-heidelberg.de/>) which use multiple alignments and hidden Markov models (statistical models of sequence consensus homology) to identify discreet modular domains within a protein sequence. These analyses were relatively successful; however, a number of ORFs remained difficult to classify based on sequence homology alone.

[0049] Enzymes have traditionally been classified by substrate specificity and reaction products. In the pre-genomic era, function was regarded as the most amenable (and perhaps most useful) basis for comparing enzymes and assays for various enzymatic activities have been well-developed for many years, resulting in the familiar EC classification scheme. Cellulases and other O-Glycosyl hydrolases, which act upon glycosidic bonds between two carbohydrate moieties (or a carbohydrate and non-carbohydrate moiety—as occurs in nitrophenol-glycoside derivatives) are designated as EC 3.2.1.-, with the final number indicating the exact type of bond cleaved. According to this scheme an endo-acting cellulase (1,4- β -endoglucanase) is designated EC 3.2.1.4.

[0050] With the advent of widespread genome sequencing projects and the ease of determining the nucleotide sequence of cloned genes, ever-increasing amounts of sequence data have facilitated analyses and comparison of related genes and proteins

on an unprecedented scale. This is particularly true for carbohydrases; it has become clear that classification of such enzymes according to reaction specificity, as is seen in the E.C. nomenclature scheme, is limited by the inability to convey sequence similarity. Additionally, a growing number of carbohydrases have been crystallized and their 3-D structures solved.

[0051] One of the major revelations of carbohydrase sequence and structure analyses is that there are discreet families of enzymes with related sequence, which contain conserved three-dimensional folds that can be predicted based on their amino acid sequence. Further, it has been shown that enzymes with the same three-dimensional fold exhibit the same stereospecificity of hydrolysis, even when they catalyze different reactions (Henrissat, Teeri et al. 1998; Coutinho and Henrissat 1999).

[0052] These findings form the basis of a sequence-based classification of carbohydrase modules which is available in the form of an internet database, the Carbohydrate-Active enZYme server (CAZy), at <http://afmb.cnrs-mrs.fr/CAZY/index.html> (Coutinho and Henrissat 1999; Coutinho and Henrissat 1999).

[0053] CAZy defines four major classes of carbohydrases, based on the type of reaction catalyzed: Glycosyl Hydrolases (GH's), Glycosyltransferases (GT's), Polysaccharide Lyases (PL's), and Carbohydrate Esterases (CE's). GH's cleave glycosidic bonds through hydrolysis. This class includes many familiar polysaccharidases such as cellulases, xylanases, and agarases. GT's generally function in polysaccharide synthesis, catalyzing the formation of new glycosidic bonds through the transfer of a sugar molecule from an activated carrier molecule, such as uridine diphosphate (UDP), to an acceptor molecule. While GT's often function in biosynthesis, there are examples where the mechanism is exploited for bond cleavage, as occurs in the phosphorolytic cleavage of cellobiose and cellodextrins (Lou, Dawson et al. 1996). PL's use a β -elimination mechanism to mediate bond cleavage and are commonly involved in alginate and pectin depolymerization. CE's generally act as deacetylases on O- or N-substituted polysaccharides. Common examples include xylan and chitin deacetylases. Sequence-based families are designated by number within each class, as is seen with GH5: glycosyl hydrolase family 5. Members of GH5 hydrolyze β -1,4 bonds in a retaining fashion, using a double-displacement mechanism which results in retention of the

original bond stereospecificity. Retention or inversion of anomeric configuration is a general characteristic of a given GH family (Henrissat and Bairoch 1993; Coutinho and Henrissat 1999). Many examples of endocellulases, xylanases and mannanases belonging to GH5 have been reported, illustrating the variety of substrate specificity possible within a GH family. Also, GH5s are predominantly endohydrolases—cleaving chains of their respective substrates at random locations internal to the polymer chains. While true for GH5, this generalization does not hold for many other GH families. In addition to carbohydrases, the CAZy server defines numerous families of Carbohydrate Binding Modules (CBM). As with catalytic modules, CBM families are designated based on amino acid sequence similarity and conserved three-dimensional folds.

[0054] The CAZyme structural families have been incorporated into a new classification and nomenclature scheme, developed by Bernard Henrissat and colleagues (Henrissat, Teeri et al. 1998). Traditional gene/protein nomenclature assigns an acronym indicating general function and order of discovery; in this scheme an organism's cellulase genes are designated celA, celB, etc., regardless of their actual mechanism of action on cellulose. Some researchers have attempted to convey more information by naming cellulases as endoglucanases (engA, engB) or cellobiohydrolases (cbhA, cbhB), however this requires determination of function *in vitro* and still fails to convey relatedness of protein sequence and structure. CAZyme nomenclature retains the familiar acronym to indicate the functional system a gene belongs to and incorporates the family number designation. Capital letters after the family number indicate the order of report within a given organism system. An example is provided by two endoglucanases, CenA and CenB, of *Cellulomonas fimi*. In the old nomenclature nothing can be deduced from the names except order of discovery. Naming them Cel6A and Cel9A, respectively, makes it immediately clear that these two cellulases are unrelated in sequence, and so belong to different GH families (where Cel stands for cellulase, and 9 for glycosyl hydrolase family nine). While this scheme does not distinguish between endo- and exo- activity, these designations are not absolute and can be included in discussion of an enzyme when relevant (i.e. the cellobiohydrolase Cel6A, the endoxylanase Xyn10B). Catalytic modules take precedence in naming carbohydrases; since many (or even most) carbohydrases contain at least one CBM,

they are named for their enzymatic module. If more than one catalytic domain is present, they are named in order from N-terminus to C-terminus, i.e. cel9A-cel48A contains a GH9 at the amino-terminus and a GH48 at the carboxy-terminus. Both domains act against cellulose. There are, however, many examples of CBM modules occurring on proteins with no predicted carbohydrase module. In the absence of some other predicted functional domain (like a protease) these proteins are named for the CBM module family. If there are multiple CBM families present, then naming is again from amino to carboxy end, i.e. cbm2D-cbm10A (Henrissat, Teeri et al. 1998). This nomenclature has been widely accepted and will be used in the naming of all 2-40 plant-wall active carbohydrases and related proteins considered as part of this study.

[0055] The cell walls of higher plants are comprised of a variety of carbohydrate polymer (CP) components. These CP interact through covalent and non-covalent means, providing the structural integrity plants required to form rigid cell walls and resist turgor pressure. The major CP found in plants is cellulose, which forms the structural backbone of the cell wall. See Fig. 1A. During cellulose biosynthesis, chains of poly- β -1,4-D-glucose self associate through hydrogen bonding and hydrophobic interactions to form cellulose microfibrils which further self-associate to form larger fibrils. Cellulose microfibrils are somewhat irregular and contain regions of varying crystallinity. The degree of crystallinity of cellulose fibrils depends on how tightly ordered the hydrogen bonding is between its component cellulose chains. Areas with less-ordered bonding, and therefore more accessible glucose chains, are referred to as amorphous regions (Figure 1B). The relative crystallinity and fibril diameter are characteristic of the biological source of the cellulose (Beguin and Aubert 1994; Tomme, Warren et al. 1995; Lynd, Weimer et al. 2002). The irregularity of cellulose fibrils results in a great variety of altered bond angles and steric effects which hinder enzymatic access and subsequent degradation.

[0056] The general model for cellulose depolymerization to glucose involves a minimum of three distinct enzymatic activities (See Figures 2A and 2B). Endoglucanases cleave cellulose chains internally to generate shorter chains and increase the number of accessible ends, which are acted upon by exoglucanases. These exoglucanases are specific for either reducing ends or non-reducing ends and frequently liberate

cellobiose, the dimer of cellulose (cellobiohydrolases). The accumulating cellobiose is cleaved to glucose by cellobiases (β -1,4-glucosidases). In many systems an additional type of enzyme is present: cellodextrinases are β -1,4-glucosidases which cleave glucose monomers from cellulose oligomers, but not from cellobiose. Because of the variable crystallinity and structural complexity of cellulose, and the enzymatic activities required for its degradation, organisms with "complete" cellulase systems synthesize a variety of endo and/or exo-acting β -1,4-glucanases.

[0057] For example, *Cellulomonas fimi* and *Thermomonospora fusca* have each been shown to synthesize six cellulases while *Clostridium thermocellum* has as many as 15 or more (Tomme, Warren et al. 1995). Presumably, the variations in the shape of the substrate-binding pockets and/or active sites of these numerous cellulases facilitate complete cellulose degradation (Warren 1996). Organisms with complete cellulase systems are believed to be capable of efficiently using plant biomass as a carbon and energy source while mediating cellulose degradation. The ecological and evolutionary role of incomplete cellulose systems is less clear, although it is believed that many of these function as members of consortia (such as ruminal communities) which may collectively achieve total or near-total cellulose hydrolysis (Ljungdahl and Eriksson 1985; Tomme, Warren et al. 1995).

[0058] In the plant cell wall, microfibrils of cellulose are embedded in a matrix of hemicelluloses (including xylans, arabinans and mannans), pectins (galacturonans and galactans), and various β -1,3 and β -1,4 glucans. These matrix polymers are often substituted with arabinose, galactose and/or xylose residues, yielding arabinoxylans, galactomannans and xyloglucans—to name a few (Tomme, Warren et al. 1995; Warren 1996; Kosugi, Murashima et al. 2002; Lynd, Weimer et al. 2002). The complexity and sheer number of different glycosyl bonds presented by these non-cellulosic CP requires specific enzyme systems which often rival cellulase systems in enzyme count and complexity. Because of its heterogeneity, plant cell wall degradation often requires consortia of microorganisms (Ljungdahl and Eriksson 1985; Tomme, Warren et al. 1995).

[0059] Objectives —*S. degradans* and *M. degradans* synthesize complete multi-enzyme systems that degrade the major structural polymers of plant cell walls. A) define

cellulase and xylanase systems, determining the activities of genes for which function cannot be predicted by sequence homology; and B) genomic identification and annotation of other plant-degrading enzyme systems by sequence homology (i.e. pectinases, laminarinases, etc.).

[0060] All publications, patents and patent applications are herein expressly incorporated by reference in their entirety to the same extent as if each individual publication, patent or patent application was specifically and indicated individually to be incorporated by reference in its entirety.

[0061] The following examples illustrate but are not intended in any way to limit the scope of the invention.

[0062] Experimental Results

[0063] I: Genomic, proteomic and functional analyses of 2-40 plant-wall active enzymes

[0064] From the ORNL annotation it is clear that the 2-40 genome contains numerous enzymes with predicted activity against plant cell wall polymers. This is particularly surprising since 2-40 is an estuarine bacterium with several complex enzyme systems that degrade common marine polysaccharides such as agar, alginate, and chitin. Defining multienzyme systems based on automated annotations is complicated by the presence of poorly conserved domains and/or novel combinations of domains. There are many examples of this in the plant-wall active enzymes of 2-40. Accordingly, the ORNL annotations of carbohydrase ORFs were manually reviewed with emphasis on the modular composition and then assigned to general groups based on the substrate they were likely to be involved with (i.e. cellulose or xylan degradation). These genomic sequence analyses resulted in a pool of about 25 potential cellulases, 11 xylanases and 17 pectinases.

[0065] When sequence homology is well-conserved, highly accurate predictions of function are possible. Therefore, to verify the presence of functioning cellulase and xylanase systems in *M. degradans*, zymograms and enzyme activity assays were performed as discussed below. Also, attempts were made to identify enzymes from 2-40 culture supernatants using Mass Spectrometry based proteomics.

[0066] Next, more sophisticated genomic analyses were used to predict function where possible and to identify ORFs which require functional characterization to determine

their roles, if any, in the cellulase and xylanase systems. ORFs which belong to other plant wall-active enzyme systems were tentatively classified based on the sequence analyses and functional predictions of B. Henrissat.

[0067] To gain insight into the induction and expression of 2-40 cellulases and xylanases, specific activities were determined for avicel and xylan-grown cells and supernatants by dinitrosalicylic acid reducing-sugar assays (DNSA assays), as discussed in the Experimental Protocols section at the end of this proposal. Xylanase activity was measured for avicel-grown cultures, and vice versa, in order to investigate possible co-induction of activity by these two substrates which occur together in the plant cell wall.

[0068] Growth on either avicel or xylan yields enzymatic activity against both substrates, suggesting co-induction of the cellulase and xylanase systems. As with other 2-40 carbohydrase systems, highest levels of activity were induced by the homologous substrate. The results also reveal some key differences in the expression of these two systems. When grown on avicel, cellulase activity is cell-associated in early growth and accumulates significantly in late-stage supernatants. Cell and supernatant fractions exhibit low levels of xylanase activity that remain roughly equal throughout all growth phases. In contrast, xylan-grown cultures exhibit the majority of xylanase and cellulase activity in the cellular fraction throughout the growth cycle. Cellulase activity does not accumulate in the supernatant and xylanase activity accumulates modestly, but still remains below the cell-bound activity.

[0069] Enzyme activity gels (zymograms) of avicel and xylan grown cell pellets and culture supernatants were analyzed to visualize and identify expressed cellulases and xylanases. The zymograms revealed five xylanolytic bands in xylan-grown supernatants (Figure 3), four of which correspond well with the calculated MW of predicted xylanases (xyl/arb43G-xyn10D: 129.6kDa, xyn10E: 75.2kDa, xyn10C: 42.3kDa, and xyn11A: 30.4kDa; see Table 2). Avicel-grown cultures showed eight active bands with MWs ranging from 30-150kDa in CMC zymograms. CMC is generally a suitable substrate for endocellulase activity. These zymograms clearly demonstrate that 2-40 synthesizes a number of endocellulases of varied size during growth on avicel—indicative of a functioning multienzyme cellulase system. Together, the CMC and xylan zymograms

confirm the results of the genomic analyses and the inducible expression of multienzyme cellulase and xylanase systems in *M degradans* 2-40.

[0070] To identify individual cellulases and xylanases produced during growth on CP, culture supernatants were subjected to proteomic analysis using reversed-phase high-performance liquid chromatography (RP-HPLC) coupled with tandem Mass Spectrometry (MS/MS). The power resulting from separating the peptides on the RP-HPLC column prior to electrospray ionization and MS/MS analysis allows the identification of a great number of proteins from complex samples (Smith, Loo et al. 1990; Shevchenko, Wilm et al. 1996; Jonsson, Aissouni et al. 2001). These analyses confidently identified over 100 different non-enzymatic proteins and a number of carbohydrases, including a xylanase, two xylosidases, a cellulase, and two cellodextrinases. An agarase was identified during additional analyses of agarose-grown supernatant.

[0071] Gel-slice digestion, extraction, and MS/MS analyses performed at the Stanford University Mass Spectrometry facility identified two annotated cellulases from an avicel-grown supernatant sample. One, designated cel5H, has a predicted MW of 67kDa and was identified from a band with an apparent MW of 75kDa. The other, cel9B, has a predicted MW of 89kDa, but an apparent MW of 120kDa. The discrepancy between the predicted and apparent MW of cel9B is consistent with similar instances where certain 2-40 proteins, cloned and expressed in *E coli*, exhibit apparent MWs which are 30-40% higher than their predicted MW.

[0072] The amino acid translations of all gene models in the 2-40 draft genome were analyzed on the CAZy ModO (Carbohydrase Active enZyme Modular Organization) server at AFMB-CRNS. This analysis identified all gene models that contain a catalytic module (GH, GT, PL, or CE) and/or a CBM. In all, the genome contains 222 gene models containing CAZy domains, most of which have modular architecture. Of these, 117 contain a GH module, 39 have GTs, 29 PLs, and 17 CE. Many of these carry one or more CBM from various families. There are also 20 proteins that contain a CBM but no predicted carbohydrase domain.

[0073] Detailed comparisons of 2-40 module sequences to those in the ModO database allowed specific predictions of function for modules where the sequence of the active

site is highly conserved. For example, Cel9B (from the gel slice MS/MS) contains a GH9 module which is predicted to function as an endocellulase, a CBM2 and a CBM10 module.

[0074] When catalytic module sequences are less conserved, only a general mechanism can be predicted. This is the case with gly5M which contains a GH5 predicted to be either a 1,3 or 1,4 glucanase—sequence analysis cannot be certain which, and so the acronym designation “gly” for glycanase.

[0075] The results of this detailed evaluation and analysis were used to assign genes to cellulase, xylanase, pectinase, laminarinase, arabinanase and mannanase systems. Each system was also assigned the relevant accessory enzymes, i.e. cellobiases belong to the cellulase system and xylosidases belong to the xylanase system. Genes with less-conserved GH modules which have the most potential to function as cellulases, xylanases or accessories were identified and designated as needing demonstration of function.

[0076] The results of the ORNL annotation, follow-up annotation analyses, proteomic (mass spectrometry) analyses, CAZyme modular analyses and functional predictions have been incorporated into Figures 4-11, which contain tables that summarize the predicted plant wall active carbohydrases and selected CBM only genes of 2-40.

[0077] The genes chosen for cloning and functional analysis include the carbohydrases gly3C, gly5K, gly5M, gly9C, and gly43M. Because the active site of gly5L is highly homologous to that of gly5K, its activity is inferred from the results obtained from gly5K. Four of the 20 “CBM only” proteins, cbm2A, cbm2B, cbm2C and cbm2D-cbm10A are included in activity assays to investigate their predicted lack of enzymatic function. These four contain CBM2 modules that are predicted to bind to crystalline cellulose. This predicted affinity is the reason for their inclusion in activity assays; those proteins that bind to cellulose are most likely to contain cellulase or xylanase modules which were not detected by sequence analysis. With CBM only proteins, a lack of detected enzyme activity will confirm the absence of a catalytic domain (CD).

[0078] In order to define the complete cellulase and xylanase systems of *M. degradans*, those enzymes which may belong to the systems but cannot be confidently assigned based on sequence homology will be expressed, purified and assayed for activity as

described in the Experimental Protocols. To date, gly3C, gly5K, gly5M, gly9C and gly43M, as well as cbm2A, cbm2B, cbm2C and cbm2D-cbm10A, have been cloned into expression strains as pETBlue2 (Novagen) constructs. This vector places expression under the control an inducible T7 *lac* promoter and incorporates a C-terminal 6xHistidine tag, allowing purification of the recombinant protein by nickel ion affinity. Successful cloning and expression of these proteins was confirmed by western blots using α -HisTag[®] monoclonal antibody (Novagen). All expressed proteins have apparent MWs which are close to, or larger, than their predicted MW (Table 8) except for Cbm2D-Cbm10A which appears to be unstable; two separate attempts to clone and express this protein have resulted in HisTag[®] containing bands which occur near the dye front in western blots, suggesting proteolytic degradation of this gene product. An additional enzyme, Cel5A, has been cloned and expressed for use as an endocellulase positive control in activity assays. Cel5A has a predicted MW of 129 kDa, contains two GH5 modules, and is highly active in HE-cellulose zymograms.

[0079] The major criteria for assigning function will be the substrate acted upon, and the type of activity detected. As such, the various enzyme activity assays will focus on providing a qualitative demonstration of function rather than on rigorously quantifying relative activity levels. The assays required are dictated by the substrate being tested, and are discussed in more detail in Experimental Protocols. For cellulose it is important to distinguish between β -1,4-endoglucanase (endocellulase), β -1,4-exoglucanase (cellobiohydrolase), and β -1,4-glucosidase (cellobiase) activities. This will be accomplished using zymograms to assay for endocellulase, DNSA reducing-sugar assays for cellobiohydrolase, and p-nitrophenol- β -1,4-cellobioside (pnp-cellobiose) for cellobiase activity. The combined results from all three assays will allow definition of function as follows: a positive zymogram indicates endocellulase activity, a negative zymogram combined with a positive DNSA assay and a negative pnp-cellobiose assay indicates an exocellulase, while a negative zymogram and DNSA with a positive pnp-cellobiose result will imply that the enzyme is a cellobiase.

[0080] Xylanase (β -1,4-xylanase), laminarinase (β -1,3-glucanase), and mixed glucanase (β -1,3(4)-glucanase) activity will be determined by xylan, laminarin and barley glucan zymograms, respectively. Unlike cellulose, there do not appear to be any

reports of "xylobiohydrolases" or other exo-acting enzymes which specifically cleave dimers from these substrates. Thus zymograms will suffice for demonstrating depolymerase (endo) activity and pnp-derivatives will detect monosaccharide (exo) cleavage. The pnp-derivatives used in this study will include pnp- α -L-arabinofuranoside, - α -L-arabinopyranoside, - β -L-arabinopyranoside, - β -D-cellobioside, - α -D-xylopyranoside and - β -D-xylopyranoside. These substrates were chosen based on the possible activities of the domains in question. The assays will allow determination of function for any α - and β -arabinosidases, β -cellobiases, β -xylosidases, bifunctional α -arabinosidase/ β -xylosidases, and α -xylosidases—which cleave α -linked xylose substituents from xyloglucans. The pnp-derivative assays will be run in 96-well microtiter plates using a standard curve of p-nitrophenol concentrations, as discussed in Experimental Protocols.

[0081] The combination of assays for β -1,4-, β -1,3-, and β -1,3(4)- glucanase activities, as well as for β -1,4-xylanase and the various exo-glycosidase activities should clearly resolve the function of the ambiguous carbohydrases. Proteins with demonstrated activity will be assigned to the appropriate enzyme system.

[0082] Experimental Protocols

[0083] Zymograms

[0084] All activity gels were prepared as standard SDS-PAGE gels with the appropriate CP substrate incorporated directly into the separating gel. Zymograms are cast with 8% polyacrylamide concentration and the substrate dissolved in dH₂O and/or gel buffer solution to give a final concentration of 0.1% (HE-cellulose), 0.15% (barley β -glucan), or 0.2% (xylan). Gels are run under discontinuous conditions according to the procedure of Laemmli (Laemmli 1970) with the exception of an 8 minute treatment at 95°C in sample buffer containing a final concentration of 2% SDS and 100mM dithiothreitol (DTT). After electrophoresis, gels are incubated at room temperature for 1 hour in 80ml of a renaturing buffer of 20mM PIPES buffer pH 6.8 which contains 2.5% Triton X-100, 2mM DTT and 2.5mM CaCl₂. The calcium was included to assist the refolding of potential calcium-binding domains such as the tsp3s of Lam16A.

[0085] After the 1 hour equilibration, gels were placed in a fresh 80ml portion of renaturing buffer and held overnight at 4°C with gentle rocking. The next morning gels

were equilibrated in 80ml of 20mM PIPES pH6.8 for 1 hour at room temperature, transferred to a clean container, covered with the minimal amount of PIPES buffer and incubated at 37°C for 4 hours. Following incubation gels were stained for 30 minutes with a solution of either 0.25% Congo red in dH₂O (HE-cellulose, β -glucan and xylan) or 0.01% Toluidine blue in 7% acetic acid. Gels were destained with 1M NaCl for Congo red and dH₂O for Toluidine blue until clear bands were visible against a stained background.

[0086] Nelson-Somogyi reducing-sugar assays

[0087] Purified proteins were assayed for activity using a modification of the Nelson-Somogyi reducing sugar method adapted for 96-well microtiter plates, using 50ul reaction volumes (Green, Clausen et al. 1989). Test substrates included avicel, CMC, phosphoric-acid swollen cellulose (PASC), Barley glucan, laminarin, and xylan dissolved at 1% in 20mM PIPES pH 6.8 (Barley glucan and laminarin, 0.5%). Barley glucan, laminarin and xylan assays were incubated 2 hours at 37°C; avicel, CMC and PASC assays were incubated 36 hours at 37°C. Samples were assayed in triplicate, corrected for blank values, and levels estimated from a standard curve. Protein concentration of enzyme assay samples was measured in triplicate using the Pierce BCA protein assay according to the manufacture's instructions. Enzymatic activity was calculated, with one unit (U) defined as 1 μ M of reducing sugar released/minute and reported as specific activity in U/mg protein.

[0088] Exoglycosidase activity assays: pnp-derivatives

[0089] Purified proteins were assayed for activity against pNp derivatives of α -L-arabinofuranoside, - α -L-arabinopyranoside, - β -L-arabinopyranoside, - β -D-cellobioside, - α -D-glucopyranoside, - β -D-glucopyranoside, - α -D-xylopyranoside and - β -D-xylopyranoside. 25 μ l of enzyme solution was added to 125 μ l of 5mM substrate solution in 20mM PIPES pH 6.8, incubated for 30 min at 37°C, and A₄₀₅ was determined. After correcting for blank reactions, readings were compared to a p-nitrophenol standard curve and reported as specific activities in U/mg protein, with one unit (U) defined as 1 μ mol p-Np/min.

[0090] Mass Spectrometry and proteomic analyses

[0091] Stationary-phase supernatants from avicel, CMC, and xylan-grown cultures were

concentrated to ~25X by centrifugal ultrafiltration using microcon or centricon devices (Millipore). Sample protein concentrations were determined by the BCA protein assay. Samples were exchanged into 100mM Tris buffer, pH 8.5, which also contained 8M urea and 10mM DTT. Samples were incubated 2 hours at 37°C with shaking to denature the proteins and reduce disulfide bonds. After reduction, 1M iodoacetate was added to a final concentration of 50mM and the reaction was incubated 30 minutes at 25°C in the dark. This step alkylates the reduced cysteine residues, thereby preventing reformation of disulfide bonds. The samples are then exchanged into 50mM Tris, 1mM CaCl₂, pH 8.5 using microcon devices. The denatured, reduced, and alkylated sample is digested into peptide fragments using proteomics-grade trypsin (Promega) at a 1:50 enzyme (trypsin) to substrate (supernatant) ratio. Typical digestion reactions were around 150µl total volume. Digestions were incubated overnight at 37°C, stopped by addition of 99% formic acid to a final concentration of ~1% and analyzed by RPHPLC-MS/MS at the UMCP College of Life Sciences CORE Mass Spectrometry facility.

[0092] Peptide fragments were loaded onto a Waters 2960 HPLC fitted with a 12cm microbore column containing C₁₈ as the adsorbent and eluted with a linear gradient of increasing acetonitrile (CH₃CN) concentration into an electrospray ionization apparatus. The electrospray apparatus ionized and injected the peptides into a Finnagin LCQ tandem Mass Spectrometer. Automated operating software controlled the solvent gradient and continually scanned the eluted peptides. The program identifies each of the three most abundant ion species in a survey scan, isolates each of them in the Mass Spectrometer's ion trap and fragments them by inducing collisions with helium molecules. The resulting sub-fragment masses are recorded for further analysis by peptide analysis packages like SEQUEST and MASCOT. After the three subscan and collision cycles have completed, the MS takes another survey scan and the cycle repeats until the end of the run, usually about three hours. The raw MS reads are used by the analysis software to generate peptide fragment sequences, which were compared to amino acid sequence translations of all gene models in the 2-40 draft genome. Peptide identity matches were evaluated using accepted thresholds of statistical significance which are specific for each program.

[0093] Cloning and expression of 2-40 proteins in E coli

[0094] The basic cloning and expression system uses pETBlue2 (Novagen) as the vector, *E coli* DH5 α (Invitrogen) as the cloning strain, and *E coli* BL-21(DE3) Tuner® cells (Novagen) for protein expression strain. This system allows the cloning of toxic or otherwise difficult genes because the vector places expression under the control of a T7 *lac* promoter—which is lacking in the cloning strain DH5 α , thereby abolishing even low-level expression during plasmid screening and propagation. After the blue/white screen, plasmids are purified from DH5 α and transformed into the expression host (Tuners). The Tuner strain has the T7 *lac* promoter, allowing IPTG-inducible expression of the vector-coded protein and lacks the *Lon* and *Omp* proteases.

[0095] The nucleotide sequences of gene models were obtained from the DOE JGI's *Microbulbifer degradans* genome web server and entered into the PrimerQuest™ design tool provided on Integrated DNA Technologies web page located at <http://biotools.idtdna.com/Primerquest/>. The design parameters were Optimum T_m 60°C, Optimum Primer Size 20nt, Optimum GC% = 50, and the product size ranges were chosen so that the primers were selected within the first and last 100 nucleotides of each ORF in order to clone as much of the gene as reasonably possible. The cloning and expression vector, pETBlue2, provides a C-terminal 6xHistidine fusion as well as the start and stop codon for protein expression. Thus, careful attention to the frame of the vector and insert sequences is required when adding 5' restriction sites to the PCR primers. The resulting “tailed primers” were between 26 to 30nt long, and their sequences were verified by “virtual cloning” analysis using the PDRAW software package (<http://www.acaclone.com>). This program allows vector and insert DNA sequences to be cut with standard restriction enzymes and ligated together. The amino acid translations of the resulting sequences were examined to detect any frame shifts introduced by errors in primer design. Following this verification, the primers were purchased from Invitrogen (Frederick, MD).

[0096] PCR reactions contained 10pMol of forward and reverse primers, 1 μ l of 10mM DNTPs, 1.5 μ l of 100mM MgCl₂, and 1 μ l Proof Pro® *Pfu* Polymerase in a 50 μ l reaction with 0.5 μ l of 2-40 genomic DNA as the template. PCRs conditions used standard parameters for tailed primers and *Pfu* DNA polymerase. PCR products were cleaned up with the QIAGEN QIAquick PCR Cleanup kit and viewed in 0.8% agarose gels.

Following cleanup and confirmation of size, PCR products and pETBlue2 are digested with appropriate restriction enzymes, usually *AscI* and *ClaI* at 37°C for 1 to 4 hours, cleaned up using the QIAquick kit, and visualized in agarose gels. Clean digestions are ligated using T4 DNA ligase for at least 2 hours in the dark at room temperature. Ligations are then transformed into *E coli* DH5 α by electroporation. Transformants are incubated one hour at 37°C in non-selective media, and then plated onto LB agar containing ampicillin and X-gal. As pETBlue2 carries an Amp^r gene and inserts are cloned into the *lacZ* ORF, white colonies contain the insert sequence. White colonies are picked with toothpicks and patched onto a new LB/Amp/X-gal plate, with three of the patched colonies also being used to inoculate 3ml overnight broths. Plasmids are prepped from broths which correspond to patched colonies which remained white after overnight outgrowth. These plasmid preps are then singly digested with an appropriate restriction enzyme and visualized by agarose electrophoresis for size confirmation.

[0097] The plasmids are then heat-shock transformed into the Tuner® strain, which carries a chromosomal chloramphenicol resistance gene (*Cm^r*). The Transformants are incubated 1 hour at 37°C in non-selective rescue medium, plated on LB agar with Amp and Cm (Tuner medium) and incubated overnight at 37°C. Any colonies thus selected should contain the vector and insert. This is confirmed by patching three colonies onto a Tuner medium plate and inoculating corresponding 3ml overnight broths. The next morning the broths are used to inoculate 25ml broths which are grown to an OD₆₀₀ of around 0.6 (2-3 hours). At this point a 1ml aliquot is removed from the culture, pelleted and resuspended in 1/10 volume 1X SDS-PAGE treatment buffer. This pre-induced sample is frozen at -20°C for later use in western blots. The remaining broth is then amended to 1mM IPTG and incubated 4 hours at 37°C. Induced pellet samples are collected at hourly intervals. These samples and the pre-induced control are run in standard SDS-PAGE gels and electroblotted onto PVDF membrane. The membranes are then processed as western blots using a 1/5000 dilution of monoclonal mouse α -HisTag® primary antibodies followed by HRP-conjugated goat α -mouse IgG secondary antibodies. Bands are visualized colorimetrically using BioRad's Opti-4CN substrate kit. Presence of His tagged bands in the induced samples, but not in uninduced controls, confirms successful expression and comparison of bands from the hourly time points

are used to optimize induction parameters in later, larger-scale purifications.

[0098] Production and purification of recombinant proteins

[0099] Expression strains are grown to an OD₆₀₀ of 0.6 to 0.8 in 500ml or 1 liter broths of tuner medium. At this point a non-induced sample is collected and the remaining culture induced by addition of 100mM IPTG to a final concentration of 1mM. Induction is carried out for four hours at 37°C or for 16 hours at 25°C. Culture pellets are harvested and frozen overnight at -20°C for storage and to aid cell lysis. Pellets are then thawed on ice for 10 minutes and transferred to pre-weighed falcon tubes and weighed. The cells are then rocked for 1 hour at 25°C in 4ml of lysis buffer (8M Urea, 100mM NaH₂PO₄, 25mM Tris, pH 8.0) per gram wet pellet weight. The lysates are centrifuged for 30 minutes at 15,000g to pellet cell debris. The cleared lysate (supernatant) is pipetted into a clean falcon tube, where 1ml of QIAGEN 50% Nickel-NTA resin is added for each 4ml cleared lysate. This mixture is gently agitated for 1 hour at room temperature to facilitate binding between the Ni⁺² ions on the resin and the His tags of the recombinant protein. After binding, the slurry is loaded into a disposable mini column and the flow thru (depleted lysate) is collected and saved for later evaluation. The resin is washed twice with lysis buffer that has been adjusted to pH 7.0; the volume of each of these washes is equal to the original volume of cleared lysate. The flow thru of these two washes is also saved for later analysis in western blots to evaluate purification efficiency.

[00100] At this point the columns contain relatively purified recombinant proteins which are immobilized by the His tags at their C-terminus. This is an ideal situation for refolding, so the column is moved to a 4°C room and a series of renaturation buffers with decreasing urea concentrations are passed through the column. The renaturation buffers contain varying amounts of urea in 25mM Tris pH 7.4, 500mM NaCl, and 20% glycerol. This buffer is prepared as stock solutions containing 6M, 4M, 2M and 1M urea. Aliquots of these can be easily mixed to obtain 5M and 3M urea concentrations thus providing a descending series of urea concentrations in 1M steps. One volume (the original lysate volume) of 6M buffer is passed through the column, followed by one volume of 5M buffer, continuing on to the 1M buffer—which is repeated once to ensure equilibration of the column at 1M urea. At this point the refolded proteins are eluted in 8

fractions of 1/10th original volume using 1M urea, 25mM Tris pH 7.4, 500mM NaCl, 20% glycerol containing 250mM imidazole. The imidazole disrupts the Nickel ion-His tag interaction, thereby releasing the protein from the column.

[00101] Western blots are used to evaluate the amount of His tagged protein in the depleted lysate, the two washes, and the eluted fractions. If there is an abundance of recombinant protein in the depleted lysate and/or washes it is possible to repeat the process and "scavenge" more protein. Eluate fractions that contain the protein of interest are pooled and then concentrated and exchanged into storage buffer (20mM Tris pH 7.4, 10mM NaCl, 10% glycerol) using centricon centrifugal ultrafiltration devices (Millipore). The enzyme preparations are then aliquoted and frozen at -80°C for use in activity assays.

[00102] In various embodiments of this invention, the cellulose degrading enzymes, related proteins and systems containing thereof, of this invention, for example including one or more enzymes or cellulose -binding proteins, have a number of uses. Many possible uses of the cellulases of the present invention are the same as described for other cellulases in the paper "Cellulases and related enzymes in biotechnology" by M.K. Bhat (Biotechnical Advances 18 (2000) 355-383), the subject matter of which is hereby incorporated by reference in its entirety. For examples, the cellulases and systems thereof of this invention can be utilized in food, beer, wine, animal feeds, textile production and laundering, pulp and paper industry, and agricultural industries.

[00103] In one embodiment, these systems can be used to degrade cellulose to produce short chain peptides for use in medicine.

[00104] In other embodiments, these systems are used to break down cellulose in the extraction and/or clarification of fruit and vegetable juices, in the production and preservation of fruit nectars and purees, in altering the texture, flavor and other sensory properties of food, in the extraction of olive oil, in improving the quality of bakery products, in brewing beer and making wine, in preparing monogastric and ruminant feeds, in textile and laundry technologies including "fading" denim material, defibrillation of lyocell, washing garments and the like, preparing paper and pulp products, and in agricultural uses.

[00105] In some embodiments of this invention, cellulose may be used to absorb

environmental pollutants and waste spills. The cellulose may then be degraded by the cellulase degrading systems of the present invention. Bacteria that can metabolize environmental pollutants and can degrade cellulose may be used in bioreactors that degrade toxic materials. Such a bioreactor would be advantageous since there would be no need to add additional nutrients to maintain the bacteria - they would use cellulose as a carbon source.

[00106] In some embodiments of this invention, cellulose degrading enzyme systems can be supplied in dry form, in buffers, as pastes, paints, micelles, etc. Cellulose degrading enzyme systems can also comprise additional components such as metal ions, chelators, detergents, organic ions, inorganic ions, additional proteins such as biotin and albumin.

[00107] In some embodiments of this invention, the cellulose degrading systems of this invention could be applied directly to the cellulose material. For example, a system containing one, some or all of the compounds listed in Figures 4-11 could be directly applied to a plant or other cellulose containing item such that the system would degrade the plant or other cellulose containing item. As another example, 2-40 could be grown on the plant or other cellulose containing item, which would allow the 2-40 to produce the compounds listed in Figures 4-11 in order to degrade the cellulose containing item as the 2-40 grows. An advantage of using the 2-40 or systems of this invention is that the degradation of the cellulose containing plant or item can be conducted in a marine environment, for example under water.

[00108] It is one aspect of the present invention to provide a nucleotide sequence that has a homology selected from 100%, 99%, 98%, 97%, 96%, 95%, 90%, 85%, 80%, or 75% to any of the sequences of the compounds listed in Figures 4-11

[00109] The present invention also covers replacement of between 1 and 20 nucleotides of any of the sequences of the compounds listed in Figures 4-11 with non-natural or non-standard nucleotides for example phosphorothioate, deoxyinosine, deoxyuridine, isocytosine, isoguanosine, ribonucleic acids including 2-O-methyl, and replacement of the phosphodiester backbone with, for example, alkyl chains, aryl groups, and protein nucleic acid (PNA).

[00110] It is another aspect of some embodiments of this invention to provide a

nucleotide sequence that hybridizes to any one of the sequences of the compounds listed in Figures 4-11 under stringency condition of 1 x SSC, 2 x SSC, 3x SSC, 4 x SSC, 5 x SSC, 6 x SSC, 7 x SSC, 8 x SSC, 9 x SSC, or 10 x SSC.

[00111] The scope of this invention covers natural and non-natural alleles of any one of the sequences of the compounds listed in Figures 4-11. In some embodiments of this invention, alleles of any one of any one of the sequences of the compounds listed in Figures 4-11 can comprise replacement of one, two, three, four, or five naturally occurring amino acids with similarly charged, shaped, sized, or situated amino acids (conservative substitutions). The present invention also covers non-natural or non-standard amino acids for example selenocysteine, pyrrolysine, 4-hydroxyproline, 5-hydroxylysine, phosphoserine, phosphotyrosine, and the D-isomers of the 20 standard amino acids.

[00112] Some embodiments of this invention are directed to a method for producing ethanol from lignocellulosic material, comprising treating lignocellulosic material with an effective saccharifying amount of one or more compounds listed in Figures 4-11, preferably cellulase cel5A listed in Figure 4, to obtain saccharides and converting the saccharides to produce ethanol. The treating may be conducted in a marine environment, such as under water. The one or more compounds listed in Figures 4-11 may be present in dry form, in a buffer, or in the form of a paste, paint, or micelle.

[00113] Conversion of sugars to ethanol and recovery may be accomplished by, but are not limited to, any of the well-established methods known to those of skill in the art. For example, through the use of an ethanologenic microorganism, such as *Zymomonas*, *Erwinia*, *Klebsiella*, *Xanthomonas*, and *Escherichia*, preferably *Escherichia coli* K011 and *Klebsiella oxytoca* P2.

[00114] In further aspects of the present invention, the lignocellulosic material is treated with an effective saccharifying amount of all of the compounds listed in Figures 4-11.

[00115] In further aspects of the present invention, the one or more compounds listed in Figures 4-11 are from *Microbulbifer degradans* 2-40.

[00116] In further aspects of the present invention, the one or more compounds

listed in Figures 4-11 are in a system consisting essentially of one or more compounds listed in Figures 4-11 or a system further comprising metal ions, chelators, detergents, organic ions, inorganic ions, or one or more additional proteins, such as biotin and/or albumin.

[00117] Some embodiments of this invention are directed to ethanol produced by treating lignocellulosic material with an effective saccharifying amount of one or more compounds listed in Figures 4-11 to obtain saccharides and converting the saccharides to produce ethanol. Conversion of sugars to ethanol and recovery may be accomplished by, but are not limited to, any of the well-established methods known to those of skill in the art. For example, through the use of an ethanologenic microorganism, such as *Zymomonas*, *Erwinia*, *Klebsiella*, *Xanthomonas*, and *Escherichia*, preferably *Escherichia coli* K011 and *Klebsiella oxytoca* P2.

[00118] Further embodiments of this invention are directed to a method for producing ethanol from lignocellulosic material, comprising contacting lignocellulosic material with a microorganism expressing an effective saccharifying amount of one or more compounds listed in Figures 4-11, preferably cellulase cel5A listed in Figure 4, to obtain saccharides and converting the saccharides to produce ethanol. The contacting may be conducted in a marine environment, such as under water. The microorganism may be *Microbulbifer degradans* 2-40 or a recombinant microorganism containing a chimeric gene comprising at least one polynucleotide encoding a polypeptide comprising an amino acid sequence of at least one of the compounds listed in Figures 4-11; wherein the gene is operably linked to regulatory sequences that allow expression of the amino acid sequence by the microorganism. The recombinant microorganism, may be a bacteria or yeast, such as *Escherichia coli*. In some aspects of the present invention, the recombinant microorganism is an ethanologenic microorganism, such as microorganisms from the species *Zymomonas*, *Erwinia*, *Klebsiella*, *Xanthomonas*, or *Escherichia*, preferably *Escherichia coli* K011 or *Klebsiella oxytoca* P2.

[00119] Further aspects of the present invention are directed to ethanol produced by contacting lignocellulosic material with a microorganism expressing an effective saccharifying amount of one or more compounds listed in Figures 4-11 to obtain saccharides and converting the saccharides to produce ethanol.

[00121] A further aspect of the invention is directed to a method for producing ethanol from lignocellulosic material, comprising contacting lignocellulosic material with an ethanologenic microorganism expressing an effective saccharifying amount of one or more compounds listed in Figures 4-11 to produce ethanol. The ethanologenic microorganism expresses an effective amount of one or more compounds listed in Figures 4-11 to saccharify the lignocellulosic material and an effective amount of one or more enzymes or enzyme systems which, in turn, catalyze (individually or in concert) the conversion of the saccharides (e.g., sugars such as xylose and/or glucose) to ethanol. The one or more enzymes or enzyme systems of the ethanologenic organism may be expressed naturally or by, but not limited to, any of the methods known to those of skill in the art. For example, release of the one or more enzymes or enzyme systems may be obtained through the use of ultrasound. In some aspects of the present invention, the ethanologenic microorganism is transformed in order to be able to express one or more of the compounds listed in Figures 4-11. In some aspects of the present invention, the ethanologenic microorganism is from the species *Zymomonas*, *Erwinia*, *Klebsiella*, *Xanthomonas*, or *Escherichia*, preferably *Escherichia coli* K011 or *Klebsiella oxytoca* P2.

[00122] Additional embodiments of this invention are directed to a use for the production of ethanol from lignocellulosic material of one or more compounds listed in Figures 4-11. Other embodiments are directed to the use of a microorganism or an ethanologenic microorganism expressing an effective saccharifying amount of one or more compounds listed in Figures 4-11 to produce ethanol from lignocellulosic material.

[00123] It is to be understood that while the invention has been described above using specific embodiments, the description and examples are intended to illustrate the structural and functional principles of the present invention and are not intended to limit the scope of the invention. On the contrary, the present invention is intended to encompass all modifications, alterations, and substitutions within the spirit and scope of the appended claims.

[00124] References Cited

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**LISTING OF AMINO ACID SEQUENCES OF THE COMPOUNDS IN FIGURES 4-10,
AND THE CORRESPONDING NUCLEOTIDE SEQUENCES (SEQ ID NOs 1-214,
RESPECTIVELY IN ORDER OF APPEARANCE)**

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 VERSION NZ_AABI02000010.1 GI:28878292
 KEYWORDS WGS.
 SOURCE Microbulbifer degradans 2-40
 ORGANISM Microbulbifer degradans 2-40
 Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
 Microbulbifer.
 REFERENCE 1 (bases 1 to 3504)
 AUTHORS NCBI Microbial Genomes Annotation Project.
 TITLE Direct Submission
 JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
 Information, NIH, Bethesda, MD 20894, USA
 COMMENT On Mar 7, 2003 this sequence version replaced gi:23028613.
 Protein-coding genes were predicted using GeneMark program (kindly
 provided by M. Borodovsky). Functional annotation is based on CDD
 (Conserved Domain Database) and COG (Clusters of Orthologous
 Groups) assignments, it has not yet been subject to manual review.
 DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.
 URL -- <http://www.jgi.doe.gov>
 Contact: Paul Richardson
microbes@cuba.jgi-psf.org.
 COG assignment was automatically updated on Sep 23, 2003.
 FEATURES Location/Qualifiers
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ORIGIN

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LOCUS NZ_AABI02000001 1701 bp DNA linear BCT 23-SEP-2003
 DEFINITION Microbulbifer degradans 2-40 Mdeg_1, whole genome shotgun sequence.
 ACCESSION NZ_AABI02000001 REGION: complement(279610..281310)
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 SOURCE Microbulbifer degradans 2-40
 ORGANISM Microbulbifer degradans 2-40
 Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
 Microbulbifer.
 REFERENCE 1 (bases 1 to 1701)
 AUTHORS NCBI Microbial Genomes Annotation Project.
 TITLE Direct Submission
 JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
 Information, NIH, Bethesda, MD 20894, USA
 COMMENT On Mar 7, 2003 this sequence version replaced gi:23026153.
 Protein-coding genes were predicted using GeneMark program (kindly
 provided by M. Borodovsky). Functional annotation is based on CDD
 (Conserved Domain Database) and COG (Clusters of Orthologous
 Groups) assignments, it has not yet been subject to manual review.
 DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.
 URL -- <http://www.jgi.doe.gov>
 Contact: Paul Richardson
microbes@cuba.jgi-psf.org.
 COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

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ORIGIN

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LOCUS NZ_AABI02000019 1356 bp DNA linear BCT 23-SEP-2003

DEFINITION Microbulbifer degradans 2-40 Mdeg_19, whole genome shotgun sequence.

ACCESSION NZ_AABI02000019 REGION: complement(10740..12095)

VERSION NZ_AABI02000019.1 GI:28878283

KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40

ORGANISM Microbulbifer degradans 2-40

Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae; Microbulbifer.

REFERENCE 1 (bases 1 to 1356)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23029085.

Protein-coding genes were predicted using GeneMark program (kindly provided by M. Borodovsky). Functional annotation is based on CDD (Conserved Domain Database) and COG (Clusters of Orthologous Groups) assignments, it has not yet been subject to manual review. DNA sequence and predicted proteins are available for BLAST at http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson

microbes@cuba.jgi-psf.org.

COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

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ORIGIN

1 atgagaataa taacggcggtt tgcagttatg ctgctatgca taacaggctg tagcggatcg

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181 agctcatcta gctccagctc atcatcaagc tctagcagtt cttcgggcgg cgaagcgctt
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1321 ctatgatcca ttatggaagg ggccagaggg gaataa

LOCUS NZ_AABI02000001 1866 bp DNA linear BCT 23-SEP-2003
 DEFINITION Microbulbifer degradans 2-40 Mdeg_1, whole genome shotgun sequence.
 ACCESSION NZ_AABI02000001 REGION: complement(472006..473871)
 VERSION NZ_AABI02000001.1 GI:28878301
 KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40
 ORGANISM Microbulbifer degradans 2-40
 Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
 Microbulbifer.

REFERENCE 1 (bases 1 to 1866)
 AUTHORS NCBI Microbial Genomes Annotation Project.
 TITLE Direct Submission
 JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
 Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23026153.
 Protein-coding genes were predicted using GeneMark program (kindly
 provided by M. Borodovsky). Functional annotation is based on CDD
 (Conserved Domain Database) and COG (Clusters of Orthologous
 Groups) assignments, it has not yet been subject to manual review.
 DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.
 URL -- <http://www.jgi.doe.gov>
 Contact: Paul Richardson
microbes@cuba.jgi-psf.org.
 COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

source 1..1866
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 gene 1..1866
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 CDS 1..1866
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LOCUS NZ_AABI02000006 2022 bp DNA linear BCT 23-SEP-2003
DEFINITION Microbulbifer degradans 2-40 Mdeg_6, whole genome shotgun sequence.
ACCESSION NZ_AABI02000006 REGION: 82200..84221
VERSION NZ_AABI02000006.1 GI:28878296
KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40
ORGANISM Microbulbifer degradans 2-40
Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
Microbulbifer.

REFERENCE 1 (bases 1 to 2022)
AUTHORS NCBI Microbial Genomes Annotation Project.
TITLE Direct Submission
JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23027577.
Protein-coding genes were predicted using GeneMark program (kindly
provided by M. Borodovsky). Functional annotation is based on CDD
(Conserved Domain Database) and COG (Clusters of Orthologous
Groups) assignments, it has not yet been subject to manual review.
DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.
URL -- <http://www.jgi.doe.gov>
Contact: Paul Richardson
microbes@cuba.jgi-psf.org.
COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

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CDS 1..2022
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LOCUS NZ_AABI02000011 1098 bp DNA linear BCT 23-SEP-2003
 DEFINITION Microbulbifer degradans 2-40 Mdeg_9, whole genome shotgun sequence.
 ACCESSION NZ_AABI02000011 REGION: 115594..116691
 VERSION NZ_AABI02000011.1 GI:28878291
 KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40
 ORGANISM Microbulbifer degradans 2-40
 Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
 Microbulbifer.

REFERENCE 1 (bases 1 to 1098)
 AUTHORS NCBI Microbial Genomes Annotation Project.
 TITLE Direct Submission
 JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
 Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23028020.
 Protein-coding genes were predicted using GeneMark program (kindly
 provided by M. Borodovsky). Functional annotation is based on CDD
 (Conserved Domain Database) and COG (Clusters of Orthologous
 Groups) assignments, it has not yet been subject to manual review.
 DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.
 URL -- <http://www.jgi.doe.gov>
 Contact: Paul Richardson
microbes@cuba.jgi-psf.org.
 COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers
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ORIGIN

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961 cagaaaaaag gcgtttcta cacggtatgg gtattcgacc ccgactggag cccaacaatg
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LOCUS NZ_AABI02000008 1917 bp DNA linear BCT 23-SEP-2003
 DEFINITION Microbulbifer degradans 2-40 Mdeg_7, whole genome shotgun sequence.
 ACCESSION NZ_AABI02000008 REGION: complement(17943..19859)
 VERSION NZ_AABI02000008.1 GI:28878294
 KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40
 ORGANISM Microbulbifer degradans 2-40
 Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
 Microbulbifer.

REFERENCE 1 (bases 1 to 1917)
 AUTHORS NCBI Microbial Genomes Annotation Project.
 TITLE Direct Submission
 JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
 Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23027735.
 Protein-coding genes were predicted using GeneMark program (kindly
 provided by M. Borodovsky). Functional annotation is based on CDD
 (Conserved Domain Database) and COG (Clusters of Orthologous
 Groups) assignments, it has not yet been subject to manual review.
 DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.
 URL -- <http://www.jgi.doe.gov>
 Contact: Paul Richardson
microbes@cuba.jgi-psf.org.
 COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers
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 /organism="Microbulbifer degradans 2-40"
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 ASNNCKYVKVRAIY"

ORIGIN

1 atgactttca caagaatgaa atcatcacac caaggcgcggt gtcgaccaag gtcttcacc
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421 caccacgccg aagaccacaa aagtgaagcc attgctttt ttgaggatat ggcgcgacc
481 tacggcaata aaaaacagct tatttacgaa attataacg agcctttaca aatttcgtg
541 agcaacacaa ttaaaccta cgccgaagat gtaattagag ctattcgcg gatagacccc
601 gacaacttaa ttattgttg tacgccaacg tggcgcaag atgtagacgt agcatcgcaa
661 gacccatta cggctacgc caatattgcc tacacattgc acttttacgc aggcacccac
721 aaacaatctt tacgagacaa agcgcaaacc gcacttaaca acggcatagc gctttcgca
781 acagagtggg gaacagtaaa tgcaaacggt gatggcgctg taaacaccac cgaaacagac
841 aagtggatga cgttcttaa aaccaaccac ataagccag caaactgggc gctaaacgac
901 aaatcagaag gcgcttctgc attaaacccc ggagccagcc ccaatggcaa ctggagcaac
961 gccgacttaa ccacatcggg taagtacgta aaaaacatta tcaaaaactg gaacgacggc
1021 acgccgggag gcagctctc aagctctcc ggcggctcaa ccagttctc ctcaagctca
1081 tctagctcta attccagctc tgggtctggc aaagtaaatt taccgcacg cattgaagcc
1141 gaaaactata acagtgcacc ggtagaaaca actgcaggca atagtggcg cagcgttca
1201 caatgtacat acagagggct aaatgtagac gtacaagacg caagcgaagg cacttgaat
1261 attggctgga cagcagcagg cgaaaaagtt acctacaaca taggcacagc aaataatact
1321 tacaatattg cacttcgac cgcctcgtt gatgcaggca agcgcgtatc ggtatatga
1381 ggcaacaccc tcgccgacac aataagcacc caaggtggcg gctggcaaaa ttggaagacg
1441 caaacatcc ccaatgtata tattcatca aactcagta ttaccgtga attctacgat
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1621 ggtggcagtt gtagcagcta tatagatata ccttgaata ctgcaccga agttacccta
1681 acaagtggcg cctgcgttcg cttaaccaa aaccttcgg gcaaaacct acaagtgtg
1741 gatagcgatg caaactcatc gtgcgattc cggggcacag ttacaacagt aggcggcact
1801 ggcagttta atgtaagcag caactatgt tctctaaga gcctaacagg aaccaaact
1861 acatttaatt cagcaagtaa taacaattgt aagtacgta aagttcgtc ttattag

LOCUS NZ_AABI02000045 1893 bp DNA linear BCT 23-SEP-2003
DEFINITION Microbulbifer degradans 2-40 Mdeg_45, whole genome shotgun
sequence.

ACCESSION NZ_AABI02000045 REGION: complement(268..2160)

VERSION NZ_AABI02000045.1 GI:28878257

KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40

ORGANISM Microbulbifer degradans 2-40

Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
Microbulbifer.

REFERENCE 1 (bases 1 to 1893)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23029974.
Protein-coding genes were predicted using GeneMark program (kindly
provided by M. Borodovsky). Functional annotation is based on CDD
(Conserved Domain Database) and COG (Clusters of Orthologous
Groups) assignments, it has not yet been subject to manual review.
DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.
URL -- <http://www.jgi.doe.gov>
Contact: Paul Richardson
microbes@cuba.jgi-psf.org.
COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

source 1..1893

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/mol_type="genomic DNA"
/strain="2-40"
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gene 1..1893

/gene="Mdeg3677"

CDS 1..1893

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ORIGIN

1 atgaaatcag caaccacaaa tcaatcgagg gcaacgcagta gcgcctttaa aaatatgttg

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121 ctaaccgtag acggcaataa aattcttagc ggtggccagc aagccagttt tgcggtaat
181 agcttatitt ggtctaaca tggctggggc ggtgagaagt attacacggc cggtagcgtt
241 gaatggctaa agcaagactg gggcagtaat ttagttcgcg ccgcaatggg tgcgatgaa
301 aacggcggct acttagaaga cccagcagga aacaaagcga aagtaacaac cgtttagat
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1141 tacgatagcg caccggtaga aaccactgca ggtaatagcg gctcaccac caattgttcg
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1501 aacctaaact tttaaacat taccgaaagc tcgggtaccg aaccacctgt agaaccacc
1561 gttgagccgc cagtagaacc acccgtagac aacggttaact tcccatgtaa cgacggtaac
1621 tctacgcttg ccaacaacgg cgctccatt aaccttaacc aaggagcgtg tgtaataac
1681 aatcacggct ggggcgatat tcgttttagc acctggagcg gcaacggtag cattcgatac
1741 gacgtactag actgcaataa caacgtaatg agtgatattg cacaaaaact taatgacttt
1801 actgctgtag acaccgcaac aatgaactgc gcacactaca ttatgtaaa acaagcccct
1861 agcagctaca ccctgcaatt tggtagctgg tag

LOCUS NZ_AABI02000017 2178 bp DNA linear BCT 23-SEP-2003

DEFINITION Microbulbifer degradans 2-40 Mdeg_17, whole genome shotgun sequence.

ACCESSION NZ_AABI02000017 REGION: complement(88284..90461)

VERSION NZ_AABI02000017.1 GI:28878285

KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40

ORGANISM Microbulbifer degradans 2-40

Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae; Microbulbifer.

REFERENCE 1 (bases 1 to 2178)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23028916.

Protein-coding genes were predicted using GeneMark program (kindly provided by M. Borodovsky). Functional annotation is based on CDD (Conserved Domain Database) and COG (Clusters of Orthologous Groups) assignments, it has not yet been subject to manual review.

DNA sequence and predicted proteins are available for BLAST at

http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson

microbes@cuba.jgi-psf.org.

COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

source 1..2178

/organism="Microbulbifer degradans 2-40"

/mol_type="genomic DNA"

/strain="2-40"

/db_xref="taxon:203122"

gene 1..2178

/gene="Mdeg2776"

CDS 1..2178

/gene="Mdeg2776"

/codon_start=1

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/product="COG2730: Endoglucanase"

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/db_xref="GI:23028996"

/db_xref="COG:COG2730"

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SEVNPDLIFVEGVAGGTGAGVDVPHGDESSNPWNGENFYPAQTAPLNIPKDRLVISP

HTYGPSVFVQRQFMDPNDPECVGLGDEAAEAGCQIVIDYATLAAGWDEHFGFLREQG

FAMVVGEFGGNMDWPNGTRQAEKDMWSHITPGIDRQWQEAQVDYMVEKNIQACYWSIN

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/gene="Mdeg2777"
 CDS complement(570..785)
 /gene="Mdeg2777"
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 /db_xref="GI:23028997"
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ORIGIN

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 121 agtggctacc aagccgatgt tcgtgttaca aacagcggta gcgctgttag tggctggacc
 181 gtaaatata atttgcctc agccccgcaa atgacaaatg gctggaacgc agcttgagt
 241 actagcggca atacaattag tgcatctaatt attagtggga atggcaattt gggtaattgt
 301 cagtcacca gctttgggtt tcagggcaat tcaaatggta acttggaac gccaacgtgt
 361 gtaggtagcg gtacgggggc tctagcagc tctcatcca gctctacttc tagcacaagc
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 2161 gagcttggg gtatttaa

LOCUS NZ_AABI02000001 1833 bp DNA linear BCT 23-SEP-2003
DEFINITION Microbulbifer degradans 2-40 Mdeg_1, whole genome shotgun sequence.
ACCESSION NZ_AABI02000001 REGION: 285915..287747
VERSION NZ_AABI02000001.1 GI:28878301
KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40
ORGANISM Microbulbifer degradans 2-40
Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
Microbulbifer.

REFERENCE 1 (bases 1 to 1833)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23026153.
Protein-coding genes were predicted using GeneMark program (kindly
provided by M. Borodovsky). Functional annotation is based on CDD
(Conserved Domain Database) and COG (Clusters of Orthologous
Groups) assignments, it has not yet been subject to manual review.
DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson

microbes@cuba.jgi-psf.org.

COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

source 1..1833
/organism="Microbulbifer degradans 2-40"
/mol_type="genomic DNA"
/strain="2-40"
/db_xref="taxon:203122"
gene 1..1833
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CDS 1..1833
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ORIGIN

1 atgatgtaca caaacctctt taatttaaaa aagcacctct tcaaaccctc acttaaacta
61 ctggcctgcg ccacattaat tggcggcacc ctaaacgcag ccgctgacgt gccagcaatg
121 tccgtacaag gcaataaagt actggtgggc ggtgaagta aaagcctgg aggtatgagc

181 tattttgggt ctaacaacgg ctggggcggc gagaaatact acaacgcttc taccgttagt
241 tactcaagc aagactggaa ggcattccatt gttcgagctg caatgggggt agaagatgcc
301 ggcggctact tcgatgacct gcagggtctt aagcaaaaag ttctacaat agtagatgcc
361 gccattgcca atgatatgta cgtcattatc gattggcact cacattacgc caacaccac
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541 tacgccgaaa cggtaattga tgccattcgc gcaattgacc cagataacgt gatcgtagta
601 ggcactcctc gctggtcgca gggggtaaaa gaagcgtcat gggaccaat caaccgcaat
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721 gcagcagaag ctatgagtaa tggattgcc ttgttgta ctgaatggg cagcgtaa
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1741 gttaccctta acgtggtgt acaagatttt gggtaggta ttactagtgg tggctcaat
1801 attaactgga taaaagtcga ggcaattcac taa

LOCUS NZ_AABI02000001 2376 bp DNA linear BCT 23-SEP-2003
 DEFINITION Microbulbifer degradans 2-40 Mdeg_1, whole genome shotgun sequence.
 ACCESSION NZ_AABI02000001 REGION: 28883..31258
 VERSION NZ_AABI02000001.1 GI:28878301
 KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40
 ORGANISM *Microbulbifer degradans* 2-40
 Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
 Microbulbifer.

REFERENCE 1 (bases 1 to 2376)
 AUTHORS NCBI Microbial Genomes Annotation Project.
 TITLE Direct Submission
 JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
 Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23026153.
 Protein-coding genes were predicted using GeneMark program (kindly
 provided by M. Borodovsky). Functional annotation is based on CDD
 (Conserved Domain Database) and COG (Clusters of Orthologous
 Groups) assignments, it has not yet been subject to manual review.
 DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.
 URL -- <http://www.jgi.doe.gov>
 Contact: Paul Richardson
microbes@cuba.jgi-psf.org.
 COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

source 1..2376
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 /mol_type="genomic DNA"
 /strain="2-40"
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 gene 1..2376
 /gene="Mdeg0020"
 CDS 1..2376
 /gene="Mdeg0020"
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 /transl_table=11
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 (1,4-beta-cellobiosidase A)"
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ORIGIN

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LOCUS NZ_AABI02000004 1737 bp DNA linear BCT 23-SEP-2003
DEFINITION Microbulbifer degradans 2-40 Mdeg_4, whole genome shotgun sequence.
ACCESSION NZ_AABI02000004 REGION: 239646..241382
VERSION NZ_AABI02000004.1 GI:28878298
KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40
ORGANISM Microbulbifer degradans 2-40
Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
Microbulbifer.

REFERENCE 1 (bases 1 to 1737)
AUTHORS NCBI Microbial Genomes Annotation Project.
TITLE Direct Submission
JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23027141.
Protein-coding genes were predicted using GeneMark program (kindly
provided by M. Borodovsky). Functional annotation is based on CDD
(Conserved Domain Database) and COG (Clusters of Orthologous
Groups) assignments, it has not yet been subject to manual review.
DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.
URL -- <http://www.jgi.doe.gov>
Contact: Paul Richardson
microbes@cuba.jgi-psf.org.
COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

source 1..1737
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/mol_type="genomic DNA"
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gene 1..1737
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CDS 1..1737
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ORIGIN

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181 aaattcgaca taatcgatgt aactagcgtt aaagtagcgt ttacggggag ttaagcgac

241 gtaaaaagct ggagcgcgat gggggacgaa tcttcaagt tggcagact tagcgccctg
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LOCUS NZ_AABI02000004 2604 bp DNA linear BCT 23-SEP-2003
DEFINITION Microbulbifer degradans 2-40 Mdeg_4, whole genome shotgun sequence.
ACCESSION NZ_AABI02000004 REGION: 254535..257138
VERSION NZ_AABI02000004.1 GI:28878298
KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40
ORGANISM Microbulbifer degradans 2-40
Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
Microbulbifer.

REFERENCE 1 (bases 1 to 2604)
AUTHORS NCBI Microbial Genomes Annotation Project.
TITLE Direct Submission
JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23027141.
Protein-coding genes were predicted using GeneMark program (kindly
provided by M. Borodovsky). Functional annotation is based on CDD
(Conserved Domain Database) and COG (Clusters of Orthologous
Groups) assignments, it has not yet been subject to manual review.
DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.
URL -- <http://www.jgi.doe.gov>
Contact: Paul Richardson
microbes@cuba.jgi-psf.org.
COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

source 1..2604
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gene 1..2604
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CDS 1..2604
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 2581 acgccaagct gtttagttaa gtaa

LOCUS NZ_AABI02000001 3219 bp DNA linear BCT 23-SEP-2003
DEFINITION Microbulbifer degradans 2-40 Mdeg_1, whole genome shotgun sequence.
ACCESSION NZ_AABI02000001 REGION: complement(289745..292963)
VERSION NZ_AABI02000001.1 GI:28878301
KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40
ORGANISM Microbulbifer degradans 2-40
Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
Microbulbifer.

REFERENCE 1 (bases 1 to 3219)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23026153.
Protein-coding genes were predicted using GeneMark program (kindly
provided by M. Borodovsky). Functional annotation is based on CDD
(Conserved Domain Database) and COG (Clusters of Orthologous
Groups) assignments, it has not yet been subject to manual review.
DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.
URL -- <http://www.jgi.doe.gov>
Contact: Paul Richardson
microbes@cuba.jgi-psf.org.
COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

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/mol_type="genomic DNA"

/strain="2-40"

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CDS 1..3219

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ORIGIN

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LOCUS NZ_AABI02000040 2589 bp DNA linear BCT 23-SEP-2003
 DEFINITION Microbulbifer degradans 2-40 Mdeg_40, whole genome shotgun
 sequence.

ACCESSION NZ_AABI02000040 REGION: complement(12943..15531)

VERSION NZ_AABI02000040.1 GI:28878262

KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40

ORGANISM Microbulbifer degradans 2-40

Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
 Microbulbifer.

REFERENCE 1 (bases 1 to 2589)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
 Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23029901.
 Protein-coding genes were predicted using GeneMark program (kindly
 provided by M. Borodovsky). Functional annotation is based on CDD
 (Conserved Domain Database) and COG (Clusters of Orthologous
 Groups) assignments, it has not yet been subject to manual review.
 DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson

microbes@cuba.jgi-psf.org.

COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

source 1..2589

/organism="Microbulbifer degradans 2-40"

/mol_type="genomic DNA"

/strain="2-40"

/db_xref="taxon:203122"

gene 1..2589

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CDS 1..2589

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/product="COG1472: Beta-glucosidase-related glycosidases"

/protein_id="ZP_00068210.1"

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ORIGIN

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LOCUS NZ_AABI02000040 2589 bp DNA linear BCT 23-SEP-2003

DEFINITION Microbulbifer degradans 2-40 Mdeg_40, whole genome shotgun sequence.

ACCESSION NZ_AABI02000040 REGION: complement(12943..15531)

VERSION NZ_AABI02000040.1 GI:28878262

KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40

ORGANISM Microbulbifer degradans 2-40

Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae; Microbulbifer.

REFERENCE 1 (bases 1 to 2589)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23029901.

Protein-coding genes were predicted using GeneMark program (kindly provided by M. Borodovsky). Functional annotation is based on CDD (Conserved Domain Database) and COG (Clusters of Orthologous Groups) assignments, it has not yet been subject to manual review.

DNA sequence and predicted proteins are available for BLAST at

http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson

microbes@cuba.jgi-psf.org.

COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

source 1..2589

/organism="Microbulbifer degradans 2-40"

/mol_type="genomic DNA"

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gene 1..2589

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CDS 1..2589

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LOCUS NZ_AABI02000016 1386 bp DNA linear BCT 23-SEP-2003
DEFINITION Microbulbifer degradans 2-40 Mdeg_16, whole genome shotgun
sequence.

ACCESSION NZ_AABI02000016 REGION: complement(53198..54583)

VERSION NZ_AABI02000016.1 GI:28878286

KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40

ORGANISM Microbulbifer degradans 2-40

Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
Microbulbifer.

REFERENCE 1 (bases 1 to 1386)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23028824.
Protein-coding genes were predicted using GeneMark program (kindly
provided by M. Borodovsky). Functional annotation is based on CDD
(Conserved Domain Database) and COG (Clusters of Orthologous
Groups) assignments, it has not yet been subject to manual review.
DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson
microbes@cuba.jgi-psf.org.

COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

source 1..1386

/organism="Microbulbifer degradans 2-40"

/mol_type="genomic DNA"

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/db_xref="taxon:203122"

gene 1..1386

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CDS 1..1386

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Beta-glucosidase/6-phospho-beta-glucosidase/beta-
galactosidase"

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ORIGIN

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961 tcggaagacc aaatggcac cctctccaaa gaccaagct gggaacaaac cgacatggag
1021 tggagcattg tgccctggg ctgtaaaaa ttattaatct ggtaagcga gcgctacaac
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1141 atagccatta acgatacac gcgcgtagat tttaccgcg gttatatga tgcgtgtcac
1201 caagcaatag aggccggcg aaaactaaaa ggctatttg catggacact tatggataac
1261 tacgaatggg aagaaggcta caccaaaccg tttggctaa accatgtaga ttcaccaca
1321 ggcaaacgca cacctaaaca gtctgaatt tggtagca cgtaattaa agatggtggg
1381 ttctag

LOCUS NZ_AABI02000013 1335 bp DNA linear BCT 23-SEP-2003
DEFINITION Microbulbifer degradans 2-40 Mdeg_12, whole genome shotgun
sequence.

ACCESSION NZ_AABI02000013 REGION: 65269..66603

VERSION NZ_AABI02000013.1 GI:28878289

KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40

ORGANISM Microbulbifer degradans 2-40

Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
Microbulbifer.

REFERENCE 1 (bases 1 to 1335)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23028387.
Protein-coding genes were predicted using GeneMark program (kindly
provided by M. Borodovsky). Functional annotation is based on CDD
(Conserved Domain Database) and COG (Clusters of Orthologous
Groups) assignments, it has not yet been subject to manual review.
DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson

microbes@cuba.jgi-psf.org.

COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

source 1..1335

/organism="Microbulbifer degradans 2-40"

/mol_type="genomic DNA"

/strain="2-40"

/db_xref="taxon:203122"

gene 1..1335

/gene="Mdeg2234"

CDS 1..1335

/gene="Mdeg2234"

/codon_start=1

/transl_table=11

/product="COG2723:

Beta-glucosidase/6-phospho-beta-glucosidase/beta-
galactosidase"

/protein_id="ZP_00066838.1"

/db_xref="GI:23028439"

/db_xref="COG:COG2723"

/translation="MNRLTLPPSSRLRSKEFTFGVATSSYQIEGGIDSR LPCNWD TFC
EQPNTIIDNTNGA IACDHINRWQDDIELIANLGVDAYRFSIAWGRVINLDGSLNNEG
VTFYKNILTKLREKNLKAYITLYHWDLPQHLEDAGGWLNRDTAYKFRDYVNLITQALDD
DVFCYTTLNPFCSAYLGYEIGVHAPGIKDLASGRKAAHLLLAHGLAMQVLRKNCPN
SLSGIVLNMSPCYAGSNAQADIDA AKRADDLLFQWYAQPLLTGCYPDAINSLPDNAKP
PICEGDMALISQPLDYLG LNY YTRAVFFADGNGGFTEQVPEGVELTDMGWEVYPQGLT
DLLIDLNQRYTL PPLLITENGAAMVDELVNGEVNDIARINYFQTHLQAVHNAIEQGVD
VRGYFAWSLMDNFEWALGYSKRFGITYVDYQTQKRTLKASGHAFAEFVSSRS"

ORIGIN

1 atgaatagac ttactactacc gcctttctct cgtttgcgca gcaaagagtt tacctttggt

61 gttgcaacgt cgtcttacc aattgaaggc ggcatagatt ctgcctgcc ctgtaattgg

121 gatacgttct gtgagcagcc caataccatt attgataaca ccaacggcgc cattgcttgc

181 gaccacataa atagatggca agacgatata gaacttattg ccaacctagg ggtagatgcc
241 taccgctttt ctattgctg gggccgtgtt attaathtag acggcagcct caataatgaa
301 ggcgttacat ttacaaaaa tttttaact aagcttcgcg aaaagaattt aaaagcttat
361 ataacgctat accactggga ctgccacaa cattagaag atgctggcgg ctggcttaac
421 cgcgataccg cctacaagt tgcgactat gtaaacctta taaccaagc gcttgatgac
481 gatgtatttt gctacacaac gttaaacgag cccttttgca gtgcctacct tggctatgaa
541 attggtgtac acgcaccggg tataaaagac ttagccagtg ggcgcaaagc cgcacaccat
601 ttattacttg ccatggctt agctatgcaa gtgctgcgaa aaaactgccc caatagtta
661 agcggcatag tgtaaacat gagccctgt tacgccgga gcaacgcaca agcagatata
721 gatgcagcaa aacgcgcgga cgatttatta tticagtgtt atgcacaacc gctacttact
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961 ctaaccgata tgggctggga agttaccg caaggcttaa ccgatttact aatagaccta
1021 aaccaacgct ataccctacc cccgttactt attaccgaaa acggcgcagc aatggtggac
1081 gaacttgta acggcgaagt taacgatatt gccgaataa attatttca aaccattta
1141 caagcggfac acaacgcat tgaacaagg gtgatgtac gcggttatt tgctggagc
1201 ctaatggata attttgagt ggcactgggt tacagcaaac gattcggtat tacctatgta
1261 gattaccaa caaaaagcg aacgctaaaa gccagcgcc acgcatttc tgagttgtc
1321 tcgagtagga gctaa

LOCUS NZ_AABI02000009 2601 bp DNA linear BCT 23-SEP-2003
DEFINITION Microbulbifer degradans 2-40 Mdeg_10, whole genome shotgun
sequence.

ACCESSION NZ_AABI02000009 REGION: 594..3194

VERSION NZ_AABI02000009.1 GI:28878293

KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40

ORGANISM Microbulbifer degradans 2-40

Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
Microbulbifer.

REFERENCE 1 (bases 1 to 2601)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23028157.

Protein-coding genes were predicted using GeneMark program (kindly
provided by M. Borodovsky). Functional annotation is based on CDD
(Conserved Domain Database) and COG (Clusters of Orthologous
Groups) assignments, it has not yet been subject to manual review.

DNA sequence and predicted proteins are available for BLAST at

http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson

microbes@cuba.jgi-psf.org.

COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

source 1..2601

/organism="Microbulbifer degradans 2-40"

/mol_type="genomic DNA"

/strain="2-40"

/db_xref="taxon:203122"

gene 1..2601

/gene="Mdeg1959"

CDS 1..2601

/gene="Mdeg1959"

/codon_start=1

/transl_table=11

/product="COG1472: Beta-glucosidase-related glycosidases"

/protein_id="ZP_00066570.1"

/db_xref="GI:23028159"

/db_xref="COG:COG1472"

/translation="MLLSLKNTQLKRSMNMNLKHLFLVALALNIAACNVKEPAATNDN

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DVILGPGVNLARLPLYGRNFEYMGEDPFLASRLAVAEIKAIQENDVAACIKHFALNNQ

ELNRTGVNAKPDERTLREVYLPFAFEAAVKEAGVHTIMGAYNEFRGTNANQSKHLVMDI

LKGEWGYKGVLLTDWNVDINTYDAAVNGLDIEMGTNVDSYDDYMLAQPMIDMIKAGSI

PESVLDDKVRRLRVQLSIGMMDKYRLSGERNTAKHHEAARKIASEGIVLLKNENILP

LNKNKIKNVLVLPNADKVHGLGGGSSEVPALYEITPLQGLKQKLGDNVNITVMRARY

DGVLMPIASDYVTSRHWTGTPAWNMVRYSDAARTQAIGDSAIVDSAYSSPAGTTKEYV

TMTATIKPLKSGEHTLKTSVMGDFELKINGKTTVKHSSTSGDVVTQKIALNGGETYSF

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LPNHQDPVISKVLAANPNTVFLIAGSAVEMPWADKAKAIWGWYGGMEAGNAYADML

FGDTNPSGKMPITLPKALEDTAPIALNDYNPVESLYTEGVFIGYRWFEKQNIPLFPF

GHGLSYTQFKYNNIKLSSANIKGDQTVTVSATITNTGKVAGAEVVQLYLHDEQASVER

PAKELKGFQKVFLKPGESKAVNITLNKRALSFWDENSNDWLAETGKFNVLGASVSDI
RLQTSFYQQ"

ORIGIN

1 atgtctgtaa gcttaaaaaa cactcaactc aaaagaagta tgaacatgaa ccttaaacac
61 ctctttctgg ttgctttggc gctaaatatt gctgcgtgca atgtaaaaga gcccgcggcg
121 acaaatgata accacattag ctaccaagcc gctcggaag cgcgctggc aaaagttgaa
181 gccgaagttg aacgcctgct gccactatta acactagaag aaaaagcctc ttggttcat
241 gcgaacagca aattctctat cgctctatc gagcggctag gcattcacga aatgtggatg
301 tctgatggcc ccacggcgt gcgctatcaa atcgaacgcc acggctgggc accagcaggc
361 tggacagatg acaactccac ttacttacca ccgcttacta ccgtagccgc cagctggaac
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541 gaataatagg gtgaagacc cttctggca tcacgtctg ctgtggcaga aattaaagcc
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661 aatcgaccgc gcgtaaagc caaacccgat gaacgcacat tacggaagt gtatttacc
721 gccttgaag ccgccgttaa agaagcgggc gtgcacacca taatgggggc ctacaatgaa
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1201 gtattgtgc ttggcccaa cgcagacaaa gtgcacggt taggcggtg ctgctcagaa
1261 gtgcagcac ttatgaaat aacccgta caagggtta aacagaagct gggagataat
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2341 ggcgtgaag ttgtacaact gtatttgcac gacgagcaag caagcgtaga acgcccagca
2401 aaagaacta aaggtttcca aaaagtgtt taaagcgg gtgaaagcaa agcggtaat
2461 attacgcta ataaacgcgc ctttcattt tgggatgaa acagcaacga ctggctgca
2521 gaaacaggta aatttaagt gctattggc gcacagtaa cgcataacg cttacaaact
2581 agcttcaat accagcagta a

LOCUS NZ_AABI02000028 2436 bp DNA linear BCT 23-SEP-2003
 DEFINITION Microbulbifer degradans 2-40 Mdeg_28, whole genome shotgun
 sequence.

ACCESSION NZ_AABI02000028 REGION: 14441..16876

VERSION NZ_AABI02000028.1 GI:28878274

KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40

ORGANISM Microbulbifer degradans 2-40

Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
 Microbulbifer.

REFERENCE 1 (bases 1 to 2436)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
 Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23029569.

Protein-coding genes were predicted using GeneMark program (kindly
 provided by M. Borodovsky). Functional annotation is based on CDD
 (Conserved Domain Database) and COG (Clusters of Orthologous
 Groups) assignments, it has not yet been subject to manual review.
 DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson
microbes@cuba.jgi-psf.org.

COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

source 1..2436

/organism="Microbulbifer degradans 2-40"

/mol_type="genomic DNA"

/strain="2-40"

/db_xref="taxon:203122"

gene 1..2436

/gene="Mdeg3326"

CDS 1..2436

/gene="Mdeg3326"

/codon_start=1

/transl_table=11

/product="COG3459: Cellobiose phosphorylase"

/protein_id="ZP_00067911.1"

/db_xref="GI:23029584"

/db_xref="COG:COG3459"

/translation="MKFGHFDDKAREYVITDPKTPYPWINYLGNEDFFSLVSNTGGGY
 SFYKDAKFRRLLTRYRYNNVPVDNNGGKYFYINDSGDVWSPGWKPKVKAELDAYSCAHGLS
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 MTNFQRNFSTGEVEVEDSVIYHKTEFKERRNHAFYSVNAPIQGFDTDRDKWKGLYND
 FDKPDAVFEGEPRNSEAHGWSPIASHYLEVELAPGESKDLIFVLGYIEVAPENKWESK
 GVINKSPAKELIARFDSVEKVDAELTKLADYWANLLSTYSVESGDEKLDRMVNIWNQY
 QCMVTFNMSRSASFFESGIGRGMGFRDSNQDLIGFVHQVPERARERIIDIASTQFEDG
 SAYHQYQPLTKRGNNAGGNFNDPLWLILSTTDYIKETGDFSILEEQVPYDNDASKA
 TSHFEHLKRSFYHTVNNLGPGLPLIGRADWNDCLNLNCFSEDPNESFQTTGNKTGRT
 AESLMIAGLFVLYGNEFVKLCREIGQDGEAAEAQAHAIDQMVEAVKKHGWGDGEWFLRAY
 DYYGKKVGSKENEEGKIFIESQGF CGMAGIGLEDGLVEKSMDSVKEWLD CDYGIVLQQ
 PAFTKYYIEYGEISTYPAGYKENAGIFCHNNPWIMITETLLGRGDKAFEYYRKIAPAY
 LEEISDLHKVEPYAYCQMIAGKDAYLPGEKNSWLTGTASWNFAAITQYILGVKPDYS
 GLAINPCIPSSWDGFKVTRKYRGATYNIIVTNPTHVSKGVKSLTLNGNAIDGYIVPPQ

QAGTVCNVEVTLG"

ORIGIN

1 atgaaatttg ggcactttga cgacaaagca cgcgagtatg taattaccga cccgaaaact
 61 cctacccttg ggataaacta cttaggcaac gaagacttct ttagcctagt atctaact
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 241 tggagccccg gttggaagcc ggtaaaagca gagctagacg catacagctg cgtcacggc
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 661 aaacccgatg ccgttttga aggcgagcct cgcaactccg aagcgcacgg ctggtcgcca
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 1321 gtgccttacg ataatgatgc gagcaaagcc acaagtcatt tgaacattt aaagcgctcg
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 2281 tatcgcgcg caacctata catcatcgta accaaccaca ccatgtaag caaaggcgta
 2341 aaatcgctca ccctaaatgg caacgctatt gatggctaca tagtgccacc gcaacaagct
 2401 ggcaccgtat gtaacgtaga agttacattg ggctaa

LOCUS NZ_AABI02000049 2367 bp DNA linear BCT 23-SEP-2003

DEFINITION Microbulbifer degradans 2-40 Mdeg_48, whole genome shotgun sequence.

ACCESSION NZ_AABI02000049 REGION: complement(7846..10212)

VERSION NZ_AABI02000049.1 GI:28878253

KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40

ORGANISM Microbulbifer degradans 2-40

Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae; Microbulbifer.

REFERENCE 1 (bases 1 to 2367)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23029998.

Protein-coding genes were predicted using GeneMark program (kindly provided by M. Borodovsky). Functional annotation is based on CDD (Conserved Domain Database) and COG (Clusters of Orthologous Groups) assignments, it has not yet been subject to manual review.

DNA sequence and predicted proteins are available for BLAST at

http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson

microbes@cuba.jgi-psf.org.

COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

source 1..2367

/organism="Microbulbifer degradans 2-40"

/mol_type="genomic DNA"

/strain="2-40"

/db_xref="taxon:203122"

gene 1..2367

/gene="Mdeg3704"

CDS 1..2367

/gene="Mdeg3704"

/codon_start=1

/transl_table=11

/product="COG3459: Cellobiose phosphorylase"

/protein_id="ZP_00068287.1"

/db_xref="GI:23030008"

/db_xref="COG:COG3459"

/translation="MLKAINNGERYQLTSPTAMPQSASFLWNKKMMIQVNCRGYAVAQ
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PVGYSWMNQSGDYSQTAGGIIASCVTPTYQKVADYFKNKDFDKTFFLHETAPAAWEV
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RWLLQARDERGLSFIAQGDWCDPMNMVGYKKGKGVSGWLSVATAYALNLWADVCEQRQQ
NSCANEFRQGAKDINA AVNKHWDGEWFGRGITDDGVLFGTSKDKEGRIFLNPQSWAI
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NHA AVFYIFSLLSIGESERAYKLLRQMLPGPDEADLLQRGQLPVFIPNYRGA YYQHP
RTAGRSSQLFNTGT VSWVYRCLIEGVFGLKGSPQGLV VQPQLPVAWQTAEAVREFRGA
TFNVSYRKSSDIKEMEIQLNESVISGNTISDITAGATYQLTVLLPATH"

ORIGIN

1 atgttaaaag ccattaacaa cggcgaacgc tatcaactca ctagccctac cgctatgccg
 61 caaagcgcat cgttttatg gaataaaaa atgatgatac aagtaaattg ccgcggctac
 121 gccgttgcgc aatttatgca gccagaacca gccaaatacg cttacgcacc caatctggaa
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 301 cagctgaaca actttagctt taacgcaggc aagagcgata taagctggca tattgccgct
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 2221 acgtttaacg tgagctaccg caaaagcagc gatataaaag aaatggaaat acagctaaat
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 2341 accgttctat tacctgccac aactaa

LOCUS NZ_AABI02000007 1725 bp DNA linear BCT 23-SEP-2003
DEFINITION Microbulbifer degradans 2-40 Mdeg_8, whole genome shotgun sequence.
ACCESSION NZ_AABI02000007 REGION: 110169..111893
VERSION NZ_AABI02000007.1 GI:28878295
KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40
ORGANISM Microbulbifer degradans 2-40
Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
Microbulbifer.

REFERENCE 1 (bases 1 to 1725)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23027895.
Protein-coding genes were predicted using GeneMark program (kindly
provided by M. Borodovsky). Functional annotation is based on CDD
(Conserved Domain Database) and COG (Clusters of Orthologous
Groups) assignments, it has not yet been subject to manual review.
DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.
URL -- <http://www.jgi.doe.gov>
Contact: Paul Richardson
microbes@cuba.jgi-psf.org.
COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

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gene 1..1725
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CDS 1..1725
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RVGDCNFV"

ORIGIN

1 atgaagaagt taattaagcc tacgctatcg tgggttcag gagttgctt gtcgctgggt
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121 agtgtgcga acgacttcat ggactactgg gatcagatta ccccagagaa tgaaggcaag
181 tggggctcgg tggagcgag tcgcgacaac tattcatgga gcggccaaga tgccgcctac
241 aattttgccc gtgccaacgg catcccattt aaagcacata cttagtatg gggcagtcaa
301 tatcccagct ggataaacia tttaagtaac gcggaaaaag ccgctgagat tgaagagtgg
361 attcgcgatt actgtaaccg ttaccagcc accgatatta tcgatgtgt caatgaagca
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1201 tcggcggatg tgcaattca gattcgtgca gacctagcta acggcaatga cgactcttt
1261 tattacaagc tggactcagg ctcttgaat actcagaaca acgctccac gctggttgg
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1381 ctccgcagag aagatggggc gaaactcgt aaggtaactc tgaatgctt agttggtcag
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1501 tctagtctt caagcagcag cggcgggca gtcgaagtt gtgacggtt taatgaatac
1561 cccagctgga cagcaaaaga ttggtctggg ggtgactata accacgcaa tagcgtgac
1621 tacatgagct atcagggtgt tctatatcga gcaaactgtt acaccgcaac tgttctgga
1681 agtgattct cctggactcg agttggcgat tgcaatttt tgtaa

LOCUS NZ_AABI02000006 1860 bp DNA linear BCT 23-SEP-2003
 DEFINITION Microbulbifer degradans 2-40 Mdeg_6, whole genome shotgun sequence.
 ACCESSION NZ_AABI02000006 REGION: 76803..78662
 VERSION NZ_AABI02000006.1 GI:28878296
 KEYWORDS WGS.
 SOURCE Microbulbifer degradans 2-40
 ORGANISM Microbulbifer degradans 2-40
 Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
 Microbulbifer.
 REFERENCE 1 (bases 1 to 1860)
 AUTHORS NCBI Microbial Genomes Annotation Project.
 TITLE Direct Submission
 JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
 Information, NIH, Bethesda, MD 20894, USA
 COMMENT On Mar 7, 2003 this sequence version replaced gi:23027577.
 Protein-coding genes were predicted using GeneMark program (kindly
 provided by M. Borodovsky). Functional annotation is based on CDD
 (Conserved Domain Database) and COG (Clusters of Orthologous
 Groups) assignments, it has not yet been subject to manual review.
 DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.
 URL -- <http://www.jgi.doe.gov>
 Contact: Paul Richardson
microbes@cuba.jgi-psf.org.
 COG assignment was automatically updated on Sep 23, 2003.
 FEATURES Location/Qualifiers
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 gene 1..1860
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 CDS 1..1860
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CDS complement(558..869)

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ORIGIN

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LOCUS NZ_AABI02000001 1413 bp DNA linear BCT 23-SEP-2003
DEFINITION Microbulbifer degradans 2-40 Mdeg_1, whole genome shotgun sequence.
ACCESSION NZ_AABI02000001 REGION: complement(468091..469503)
VERSION NZ_AABI02000001.1 GI:28878301
KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40
ORGANISM Microbulbifer degradans 2-40
Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
Microbulbifer.

REFERENCE 1 (bases 1 to 1413)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23026153.
Protein-coding genes were predicted using GeneMark program (kindly
provided by M. Borodovsky). Functional annotation is based on CDD
(Conserved Domain Database) and COG (Clusters of Orthologous
Groups) assignments, it has not yet been subject to manual review.
DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.
URL -- <http://www.jgi.doe.gov>
Contact: Paul Richardson
microbes@cuba.jgi-psf.org.
COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

source 1..1413
/organism="Microbulbifer degradans 2-40"
/mol_type="genomic DNA"
/strain="2-40"
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gene 1..1413
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ORIGIN

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541 gagttatgg aacgagcctt tcgcttagct cacgcagcgg acccaaaagc acacttatgt
601 tacaacgatt acaatatgca ctgccgcaa aagcgcgaat tttggttaa gttattcaaa
661 gactacatta agcgcggcgt gcctattcac ggcgtagggt tgcaggggca tggggccta
721 gactaccctt cgctggacga gttggaaaa accatcgtgg ccatggccga tttaggctta
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LOCUS NZ_AABI02000016 3561 bp DNA linear BCT 23-SEP-2003
 DEFINITION Microbulbifer degradans 2-40 Mdeg_16, whole genome shotgun
 sequence.

ACCESSION NZ_AABI02000016 REGION: 34542..38102

VERSION NZ_AABI02000016.1 GI:28878286

KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40

ORGANISM Microbulbifer degradans 2-40

Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
 Microbulbifer.

REFERENCE 1 (bases 1 to 3561)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
 Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23028824.
 Protein-coding genes were predicted using GeneMark program (kindly
 provided by M. Borodovsky). Functional annotation is based on CDD
 (Conserved Domain Database) and COG (Clusters of Orthologous
 Groups) assignments, it has not yet been subject to manual review.
 DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson
microbes@cuba.jgi-psf.org.

COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

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/mol_type="genomic DNA"

/strain="2-40"

/db_xref="taxon:203122"

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CDS 1..3561

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/transl_table=11

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 SSSTSSSSSSGAAPTGNVTYSINVTNDWQSGYCAELTVTNNNTNNAQWQASVSMDSV
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WHGLTFSVGLTQGNLYEVAWWWKLAAGSADTPILTAKRQNDSDSTYNEYTGIVTT
 IANDSEWVLLHGQYTQTGTAFEHFIESESDSVSFYADEFSIGGEVTPKNEVGFFVGN
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 SAFGNNWIIRSFELTRQYCPNSILINDYNVLSWNTQEFIQMATPAVNAGVVDAIGLQ
 AHGLADWSLSDELTKLNQVAALGLPIYISEYDIEKTNDQEQLRVMQTQFPLFYNHPSV
 KGITWGYVVGATWRDGTGLLHSGNTPRPALTWLM DYLN R"

ORIGIN

1 atgttcgaa gacccaatc aacacccatt gtaagcgaa agatttctgc ctatgtaggt
 61 tggggctctgt cgtgttact tagcgtctgc acggcctcga tctctgggc aggtaacct
 121 attgtgtctc atgtatatac cgcagacct gctgcacggg taataaacgg aagagcctat
 181 gtaatggta cccacgatca ggataacaa aatgattacg gtggttgat tgattactac
 241 ctgttctcat cggacgatat ggtaattgg caagatcacg gtattgtgtg gaattctcga
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 541 tactttgtg gaggcgtga tgaaccgag cggttattc gtttaataa cgacatgata
 601 agtaccagt gtgcagccat aagtattgac gtacctaact tcttgaagc gctatacatg
 661 cataagcgca acggcattta ctactatcc tactcgacca acccagcgc ggggatgagc
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3361 atagaaaaaa ctaacgacca agaacagctg cgcgtaatgc aaactcagtt cccgctgttt
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3541 atggattact tgaatagata g

ORIGIN

1 atggtcataa taactatgaa agccgggtta ctctacgca tctattaac tgtactcg
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 541 gtatttattg aagacaacat cgactttact aaatttttaa accgcaaat aaccgccgcg
 601 caagattggg tagagtatta cctaccgca gaaattaccg ataaccatgc aaccggtgaa
 661 gtgggcttgc gcattggctt tggcgctggc cctagggcg aggtgttga tattggcgt
 721 gttagctat tgcattacac caatactgat ataagcgcta tgcctagtac acgccaagt
 781 tacgaaggcc gcgagccaga tgcgcatgg cgtacagcg cgagagagc aattgagcag
 841 caccgcaaag gcgacttga gtaacagta gtggacgatg gcaaccctat cgccaatgcc
 901 accatagatg tagattttca aaaacacgcc tatcatttg gctcgtaac tttggccat
 961 ctattgatgg gcaccagtga agatagcgcc atttaccgcg aaaaagtgt cgagctattt
 1021 aaccaaagtg gccagaaaa cgatttaaag tggggccat gggaaggcga gtggggcaac
 1081 aattttaacc aaactcaaac cctaaacggc ttgcagtggc tgcgcgataa cggcctgtac
 1141 acacgtggcc atgtaatggt ttggccttct aagcgcaact tgccaaactt aatgcagcaa
 1201 tatttaccag aaggcgacc cgccagcgcc aaccagaag caaaacaagt ggtgctggat
 1261 cacatcgatg atatagcaac cgcaacagct aattatttag atgagtggga tgtactaac
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 1801 cgagaaaagc ccaatgcact agcttggaag gagcaaat ttaacgagt gtggaacgac
 1861 ttgacggca cgaccaacgc acagggtaaa ttgatgaac gcggtttta cggcgattac
 1921 caagtaactg taaccgtagg tgaagagcag caaatttta ccttagcct agttaaggc
 1981 ggcaacaaa acttagttt tgatggcaa tag

LOCUS NZ_AABI02000014 828 bp DNA linear BCT 23-SEP-2003
 DEFINITION Microbulbifer degradans 2-40 Mdeg_13, whole genome shotgun
 sequence.

ACCESSION NZ_AABI02000014 REGION: complement(14092..14919)

VERSION NZ_AABI02000014.1 GI:28878288

KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40

ORGANISM Microbulbifer degradans 2-40

Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
 Microbulbifer.

REFERENCE 1 (bases 1 to 828)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
 Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23028504.
 Protein-coding genes were predicted using GeneMark program (kindly
 provided by M. Borodovsky). Functional annotation is based on CDD
 (Conserved Domain Database) and COG (Clusters of Orthologous
 Groups) assignments, it has not yet been subject to manual review.
 DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson

microbes@cuba.jgi-psf.org.

COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

source 1..828

/organism="Microbulbifer degradans 2-40"

/mol_type="genomic DNA"

/strain="2-40"

/db_xref="taxon:203122"

gene 1..828

/gene="Mdeg2305"

CDS 1..828

/gene="Mdeg2305"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/protein_id="ZP_00066908.1"

/db_xref="GI:23028515"

/translation="MNIKTFFPALIASVFLLINASTGYAASITKTLCPADSDNGYGA
 GTFNGKFYSWFELSQEDITDCDTKIGFYNETNRHFRVEWNVAQSWGEDAIGGMGWSSG
 SRDRKIGYNVGQLTTNSSIQKALVAMYGWSCSTSGGNQISQEYYVDTWDGGKFVPWD
 ENANNGNGAPASVGTVSANGATYDVYKVRNRNGAQYCFNGSSRSFDFQFWSVRRTPRAI
 NGNRNMDFRPHANRWDNSDLGFKVDGLSSGYQILAVEIFGDANLRHKGAADITLWPR"

ORIGIN

1 atgaacataa aaacattctt ccccgactt attgcaagt tattttatt aattaacgcc
 61 agcactggct atgcagcaag cattacaaa acgcttgca acccagccga tccgataac
 121 ggctacggtg caggaacctt caatggcaaa tttattctt ggttgagt aagccaagaa
 181 gacattaccg attgcgatac aaaaattggt tttacaacg aaaccaatcg acacttagg
 241 gtggagtga atgtgtctca atcttgggga gaagatgcaa ttggtggaat gggttggagc
 301 tctggctcga gagatagaaa aatagggtac aacgttgcc aacttacaac taattctct
 361 attcaaaaag cattggttgc tatgtatggc tggctctgt ctaccagtgg tggcaaccaa
 421 atatcacaag aatattatgt agtgataca tgggacggcg gcaagttgt gccttgggat
 481 gaaaacgcaa ataattggca cggtgctcca gcacagagt taggaacagt tagcgcta

541 ggtgcaacat acgatgttta taagggtcgc cgcaacggtg cgcaatattg tttaatggc
601 agcagccgct cgttgatca gtttgaggt gtgcgtagaa cgcctagagc gattaacggc
661 aaccgtaata tggattttcg cccgcacgcc aaccgctggg acaacagtga cctaggttt
721 aaagttgacg ggtaagcag cggttaccaa atttagcgg ttgaaatatt tggatgacg
781 aacctaagac ataaagggtc agcagatatt acttatggc cacgctaa

LOCUS NZ_AABI02000010 2304 bp DNA linear BCT 23-SEP-2003
DEFINITION Microbulbifer degradans 2-40 Mdeg_14, whole genome shotgun
sequence.

ACCESSION NZ_AABI02000010 REGION: 110928..113231

VERSION NZ_AABI02000010.1 GI:28878292

KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40

ORGANISM Microbulbifer degradans 2-40

Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
Microbulbifer.

REFERENCE 1 (bases 1 to 2304)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23028613.
Protein-coding genes were predicted using GeneMark program (kindly
provided by M. Borodovsky). Functional annotation is based on CDD
(Conserved Domain Database) and COG (Clusters of Orthologous
Groups) assignments, it has not yet been subject to manual review.
DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson

microbes@cuba.jgi-psf.org.

COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

source 1..2304

/organism="Microbulbifer degradans 2-40"

/mol_type="genomic DNA"

/strain="2-40"

/db_xref="taxon:203122"

gene 1..2304

/gene="Mdeg2474"

CDS 1..2304

/gene="Mdeg2474"

/codon_start=1

/transl_table=11

/product="COG0726: Predicted xylanase/chitin deacetylase"

/protein_id="ZP_00067071.1"

/db_xref="GI:23028683"

/db_xref="COG:COG0726"

/translation="MKSINVCGRRLKQALAAIATAAATLWFTPVDAQTLTSNQTGTHG

GYYYSFWTDSAGTVSMTLGNNGNYSSWSNTGNWVGKGWQTGGRKTVNYSGTFNPSG
NGYLTLYGWTQNPLIEYYIIIESWGTYRPGESGTYGTVNTDGGTYDIYRTQRVNQPSI
EGTATFYQYWSVRQQKRVGGTITGNHFDASHGLNLGTHNYMVMATEGYQSSGNSN
ITVSESGSSSTSSSSSTGGPSGTNIVVRAQGVSGQEHINLIIGGNVADWTLSTSM
QDYTYTGNAAGDLQVEYDNDASGRDVELDYVYVNGEIRQAEDMEYNTATYSGECGGGS
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GQFAQQKSVGEIQNHSYTHSHMLNWSYQQVRDELASTNQAIVNAGGATPTLFRPPYGE
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PLCQTTNDGWGWENSQSCVSQNTCNSQ"

ORIGIN

1 atgaagtcaa tcaatgtatg cggcagacgc ctcaagcaag ccctgcagc aatagcaacc
 61 gctgcagcaa ctctctggt tacgccagt gatgcacaaa cctaacctc aaaccaaact
 121 ggtactcatg gtggttacta ctattcctc tggaccgaca gtgctggcac tgtttctatg
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 1261 tatgttaca acggcaatgc atctggtgat gtagaagtac aattcgacaa cgatgccaac
 1321 ggtcgcgatg ttattctcga ttacgtaata gtaaatggcg aaactcgcca agcgggaagt
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 1441 atgactgca gcggcgaaat tggtttggc cacaccgacg attgcttag tggaaattgc
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 1921 ataacctggg atgtagattc gcgcgattg gatggcgcaa gcgcttcagc tattgccaac
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 2161 ggcagcaata caggaaatgg cggtaatggc ggcattgta actgttacgg caccagcatt
 2221 ccattatgcc aaactaccaa cgacgggtgg ggctgggaaa actcacaag ctgcgttcg
 2281 caaaatacct gtaactcaca ataa

LOCUS NZ_AABI02000001 1083 bp DNA linear BCT 23-SEP-2003
 DEFINITION Microbulbifer degradans 2-40 Mdeg_1, whole genome shotgun sequence.
 ACCESSION NZ_AABI02000001 REGION: complement(131880..132962)
 VERSION NZ_AABI02000001.1 GI:28878301
 KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40

ORGANISM Microbulbifer degradans 2-40

Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
 Microbulbifer.

REFERENCE 1 (bases 1 to 1083)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
 Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23026153.
 Protein-coding genes were predicted using GeneMark program (kindly
 provided by M. Borodovsky). Functional annotation is based on CDD
 (Conserved Domain Database) and COG (Clusters of Orthologous
 Groups) assignments, it has not yet been subject to manual review.
 DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson

microbes@cuba.jgi-psf.org.

COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

source 1..1083

/organism="Microbulbifer degradans 2-40"

/mol_type="genomic DNA"

/strain="2-40"

/db_xref="taxon:203122"

gene 1..1083

/gene="Mdeg0096"

CDS 1..1083

/gene="Mdeg0096"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/protein_id="ZP_00064735.1"

/db_xref="GI:23026249"

/translation="MCLKINRCWVFWLCLCATTAHSETYVPADNDQYLYTGRIDFSD
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 SITSGMGNEGADNGADHLGSEKNNYLAYGAITARNLNAELHTISQSGIGVMVSWF
 PFIMPQFYNQLSAVGNNDSIWDFKQWTPHVVINLQMNDSWLIDREKRLTPIPA
 DAQRIAHYQAFVQSIRAEYPKAQIICALGSM DATANEKWPNYVREAVKNMQDNGD
 NKIDTIFFEYIGY GQHPRVAQHNANADKLTKFIKKMKW"

ORIGIN

1 atgtgcctaa aaataaacgc gtgctgggtg ttgtttgtg tlggtattg cgcaactact
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 121 gattttagcg atataaaagc accctcgcta agctggcccg gcacaagtat aaaagccaac
 181 ttaccggcg aacatttaga ggtagtgta gacgatcaaa acgtaagaa tttttta
 241 gtgattatcg acgtaacga tcgatttcct tatgtgctag aagctaaaca aggtgagcat
 301 cgatatttaa tttctctgc gctaagcaag ggcaagcaca gcgtagaaat ttataaacgt
 361 acagaaggcg aagagggcg aacgctatt aaaggcctt ggtagccga tgatagttat
 421 ttattaaaac cccctaaacg cccaaaacgc agaatagaaa ttatgggtga ctcaattaca

481 agcggatgg gtaacgaagg cgcagataac ggcgccgacc atttgggctc cgaaaaaat
541 aattaccttg cctatggggc tattaccgca cgcaatttaa acgccgagct acataccatt
601 tcgcaaagcg gtattggggg aatggtaagt tggttccgt ttattatgcc gcagttttac
661 aaccagctaa gtgctgttgg taataatgat tccatatggg actttaaaaca atggacgccc
721 catgtagtg taataaacct aatgcaaaac gatagctggc taatagatag agaaaagcgc
781 cttacgcaa ttctgcaga tgcacaacgc atagccatt atcaagcgtt tgtcaaagc
841 attcgtgccg aatacccaa ggcgcaaata atatgcgcac tgggcagtat ggatgaacc
901 gcaaacgaaa aatggccaaa ctacgtgcg gaagctgtaa aaaatatgca agataatggc
961 gataataaaa tcgatactat ttctttgaa tacatcggct acggccaaca cccgcgcgta
1021 gcgcaacaca atgcgaatgc agataagtta actaaattta ttaagaaaaa aatgaaatgg
1081 tag

LOCUS NZ_AABI02000001 2922 bp DNA linear BCT 23-SEP-2003
DEFINITION Microbulbifer degradans 2-40 Mdeg_1, whole genome shotgun sequence.
ACCESSION NZ_AABI02000001 REGION: complement(296895..299816)
VERSION NZ_AABI02000001.1 GI:28878301
KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40
ORGANISM Microbulbifer degradans 2-40
Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
Microbulbifer.

REFERENCE 1 (bases 1 to 2922)
AUTHORS NCBI Microbial Genomes Annotation Project.
TITLE Direct Submission
JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23026153.
Protein-coding genes were predicted using GeneMark program (kindly
provided by M. Borodovsky). Functional annotation is based on CDD
(Conserved Domain Database) and COG (Clusters of Orthologous
Groups) assignments, it has not yet been subject to manual review.
DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.
URL -- <http://www.jgi.doe.gov>
Contact: Paul Richardson
microbes@cuba.jgi-psf.org.
COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

source 1..2922
/organism="Microbulbifer degradans 2-40"
/mol_type="genomic DNA"
/strain="2-40"
/db_xref="taxon:203122"
gene 1..2922
/gene="Mdeg0224"
CDS 1..2922
/gene="Mdeg0224"
/codon_start=1
/transl_table=11
/product="COG1501: Alpha-glucosidases, family 31 of
glycosyl hydrolases"
/protein_id="ZP_00064863.1"
/db_xref="GI:23026377"
/db_xref="COG:COG1501"
/translation="MNYYLNKKRLGQLLTGAIIIPVLYACGSQEKNVEPATVNWHKTS
DGVVVS LQDSEAKK VRLQVINDRIVRVTATPQQDFNNLPNTLMVVAKPEQTAFEVKQN
DASVVLSTADLSAEVSLVTGVVSFKDEHGKVLTTEDVRGNFGAVTRDPGVVDADSF
RQQFTSDENEGYYGLGQQQDGEVNYAGDNVELTTYNLEISIPYVSSKDYALLWNNTS
ISRLGDPNPPEPLKEGFKLFDANGNPGGLTARYFDGDKLLLERVEADLDYQFLAQGSN
RTTPMPDETADAKNLRIEWEGSIESDTNGVHELKMYSSGYAKLYLNGELVDRWRMNW
NPWYHNTKLEMQAGKKVALKLDWQVDGGYMRKQHKPLPVAEQGRLSIASDTAKAIDY
YFVVGDNKDELVSGYRTLTKAVMLPKWVFGFWQSRERYKTQDEIIDALQEYRDRKIP
IDNIVLDWSYWPQDAWGSHDFDEQFFDPVSALVDKVHELNGNIMISWVPKFYPTTDNY
KALNAKGCMFNKNIEQKNLDWIGEGYLNFGFYDAYNPECREMFWAQIRDKINVHGFDAW
WLDAVEPDIHSNLSFEHRKDLMTPNALGTGAEVFNAYALPHAETVYQGERRDDGDKRA
FILTRSGFAGIQRTGSAIWSGDVSRWSDLKEQIAAGVGVGISGMPYWTFDIGGFTPE
DRYRYSAKGSVGHFSMMNESEVPEWQEINLRWFQFGTFVPLFRSHGQNPYREIYNIAD
KGTEVYDSMWYTKTRYRLMPYIYSLVGDAHHKDGTFRALVMDFPSDLNVRDINDQY

MFGPALLVNPVSEFKARSRDVYLPAGADWYDFYTGKHTGGKTIKADAPLAKMPIFVK
 AGSIPTGVEIQHVYDKPDAPYTLNVYTGANGSFEIYEDDGKTYAYEQGAWARIPVSY
 NDKTGELTIGDRVGSFEGMTKEREFVRWISAKRDDAANFDTGVAKAVTYTGKAITIK
 R"

ORIGIN

1 gtgaattatt atttaaaca aaagcgactg gggcaattgc tcaccggcgc ggccattatt
 61 cccgtgctat atgcatgttg ctacacaggaa aaaaacgtag agcccgcaac ggtaattgg
 121 cataaaacaa gcgacggcgt cgtgtgaagc ttgcaagata gcaagcaaa aaaagtgcgc
 181 ttgcaagtca ttaacgatcg gatagtagct gttaccgcta cgccacagca ggatttcaac
 241 aacctgccaa atacgcttat ggtgtggcc aagcccgagc aaacggcgtt tgaagttaa
 301 caaacgatg catctgtgt gttatcaacg gcagatctat ctgccgaagt gtcattagta
 361 actggtgttg taagtttaa agatgagcac ggcaagggtc ttacaacaga agttgatcgc
 421 ggcaattttg gggcggtaac ccgcgaccca ggtgtgttg acgcccattc atttgctatt
 481 cgccaacagt ttacaagcga cgaatatgaa ggctactacg gtttaggtca gcagcaggat
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 721 aatgtaacc ccggcgggt aaccgcacgt tatttgatg gcgataaatt actgctcgag
 781 cgtgtagagg ccgatttaga ttatcaattt ttagcgcaag gtagtaatcg cactacgccc
 841 atgcctgatg aaaccgctga tgcaaaaaat ctgcgtattg aatgggaagg tagtatcgaa
 901 tccgatacca acggtgtgca cgagttaaaa atgtattcca gtggctacgc taaattgtat
 961 tgaatggcg agttagtgt agatcgctgg cgtatgaact ggaacccttg gtatcacaac
 1021 accaagttag aatgcaggc cgttaaaaaa gtgcattaa agttagattg gcaagtagat
 1081 ggtggttata tgcgcataaa acagcataaa ccactgccgg tagcagagca gggacgtttg
 1141 tctattgctt ccgataccgc gaaagccatt gattactact ttgtagttgg cgataacaag
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 1261 gtgtttggtt ttggcgaag ccgcgagcgc tataaacac aagatgaaat tatcgacgcc
 1321 ttgcaagaat accgcgatcg taaaattcct atcgataaca ttgtattaga ttggagttat
 1381 tggcctcagg atgcatgggg tagtcatgat ttgcagagc aattttccc cgacccatct
 1441 gcactagtag ataaagtaca cgagctaaac ggcaatatta tgattccgt atggcctaag
 1501 tttacccta caaccgacaa ctacaaagcg ctacacgcta aaggttgat gtttaataaa
 1561 aacatcgagc agaaaaacct cgattggatt ggcgagggtt acctaaatgg cttttacgat
 1621 gcctataacc cagagtgcg tgaaatgtt tggcgcaaa ttgcgataa gatcaatgtg
 1681 cacggttcg atgctgttg gttagatgcg gtagagccag atatccattc caaccttct
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 1801 aacgcttag ctttgcgca cgcagaaact gttaccaag gcgagcgtag agatgacggt
 1861 gacaagcgcg catttattct aacgcgttct ggtttgcg gtattcagcg caccggttcg
 1921 gctatttga gttgcgatgt ggtatcgcg tggccgact taaaagaaca aattgcagca
 1981 ggtgtggcg tgggcatttc tggatgccc tattggacgt tcgatacgg tggctttact
 2041 ccagaagatc gctaccgtta tagcgccaaa ggttctgtg gtcatttctc tatgatgaac
 2101 gaatcggaag tgcctgaatg gcaagaaatc aatctgcgtt ggtccaatt tggtagctt
 2161 gtgcccgtgt ttaggtccca cggccaaaac ccatacgcg aaatatataa catcgccgat
 2221 aaaggcaccg aggtatacga cagcatggtg tggtagacca aaactcgcta tcgcttaatg
 2281 ccttatattt attcgttagt tggcgatgct caccacaaag acggcacctt tatgcgcgct
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 2401 ggccccgcgc tactctgtaa cctgtgtcg gaatttaaag cgcgttcacg ggatgtgat
 2461 ctacctgagg gcgcagattg gtacgatttc tatacagggtg tgaagcacac aggtggtaaa
 2521 accattaagg ccgatgcacc gcttgccaaa atgcctattt ttgtaaggc cggctctatt
 2581 attccaacag gttagaataa ccagcatgtg tacgataagc ccgatgctcc ttacaccctt
 2641 aacgtgtata ccggtgcgaa tggcagcttc gaaatttatg aagatgacgg caaaacctac
 2701 gcttacgagc aaggggcttg ggcgcgcat cccgtttcgt acaacgataa aaccggtgag
 2761 ctacacattg gcgatcgct aggtagcttt gagggaaatga ccaaagagcg cgaattccgc
 2821 gtgcgctgga tatctgcaa gcgagacgat gccgccaatt tcgatacagg tttggccaaa
 2881 gccgttacct atacgggtaa ggcaataacc attagcgct aa

LOCUS NZ_AABI02000024 2682 bp DNA linear BCT 23-SEP-2003
DEFINITION Microbulbifer degradans 2-40 Mdeg_22, whole genome shotgun
sequence.

ACCESSION NZ_AABI02000024 REGION: complement(16977..19658)

VERSION NZ_AABI02000024.1 GI:28878278

KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40

ORGANISM Microbulbifer degradans 2-40

Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
Microbulbifer.

REFERENCE 1 (bases 1 to 2682)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission.

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23029266.

Protein-coding genes were predicted using GeneMark program (kindly
provided by M. Borodovsky). Functional annotation is based on CDD
(Conserved Domain Database) and COG (Clusters of Orthologous
Groups) assignments, it has not yet been subject to manual review.
DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson

microbes@cuba.jgi-psf.org.

COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

source 1..2682

/organism="Microbulbifer degradans 2-40"

/mol_type="genomic DNA"

/strain="2-40"

/db_xref="taxon:203122"

gene 1..2682

/gene="Mdeg3040"

CDS 1..2682

/gene="Mdeg3040"

/codon_start=1

/transl_table=11

/product="COG1472: Beta-glucosidase-related glycosidases"

/protein_id="ZP_00067626.1"

/db_xref="GI:23029277"

/db_xref="COG:COG1472"

/translation="MNKHFLVGIVITLGVILQGLTACSKSAAPNANQPQDTAASTATYP
FRDASLSVDARVDDLVSRLTTTEKIAQMFNDTPAIERLGIPAYNWWNESLHGVARAGK
ATVYPQAIGLASTFDEDLMLRVATISDEGRAKYHDFLSKDVRTIYGGTLFWSPNINI
FRDPRWGRGQETYGEDPFLTGRMAINFVKGIQGENDNSDYLKAVATIKHYAVHSGPEK
TRHSDDYHPTRKDLFETYLPAFRMAIAETNVQSLMCAYNRVDGAPACGNNELMQEILR
GDMGFNGYVVSDCGAIADFYESRSHHVVDSPAEEAAWAVKSGTDLNCGDSHGNTYTNL
HYALQQGLITEDYIDIAVKRLFKARIKGMFDEQDRVPYSEIGMDVVGSPKHLALTQE
AAEKSIVLLKNNGVLPKAGVKVAVIGPNAVDEDVLVGNYHGVVPKPVLPLEGIVNRV
GEANVFYAPGSAQIADIYSHYEPISAENFYHKDANGNLAAGLKAEEYADYYNAAEIND
DTFSATPALNRIDADINFSWPVSPIDNSLDDEFSAVWTGILKPKKSGSYRFSGTVALA
INGKPVNGAVNLKAGESYNIKAIFGVQKWVNVNAIHPYGKLTWLDESRLDEEEALAAA
RKADVIIFMGGIDAHLEGEEMPLELDGFTHGDRTHINLPKVQTNLLKQLKATGKPVVM
VNFSGSAMALNWESEKLDAILQAFYPGEATGTALANILWGDVSPSGRLPVTFYKGVDD
LPAFNDYHMENRTYKFYRGEPLYAFGHGLGYVDFAYNNLVVANTAEGKALPIAVSVT

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DNGKTQTYTGRVEVTVGSGQKGYVKENAIIVATINVQ"

ORIGIN

1 atgaataaac acttttagt aggtgtaatt acgttagggg taattctgca ggggctaact
61 gcatgtagca aaagcgctgc acctaagcc aatcaaccgc aagataccgc agctagtacg
121 gctacctacc cgtttaggga tgcaagctta agttagatg cccgcgtaga cgacttgga
181 tcgcgtttaa ccacaaccga aaaaattgcc caaatgttta acgatacgcc cgcaatcgag
241 cgattgggta ttccgccta caattgggtg aacgaatcgt tgacgggtg ggcccgtagc
301 ggtaaagcaa cggatatacc gcaggcaata ggcttagcgt ctacattga tgaagactta
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481 ttccgcgacc cgcgttggg cagggggcaa gaaacctacg gtgaagaccc gttctaacg
541 gggcgatgg ccattaattt tgtaagggt attcaaggcg aaaacgacaa cagcgattac
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661 cattcgatg actaccatcc aaccgtaaa gatttattcg aaacctattt gcctgcatt
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901 caccacgtg ttgactcacc tgcagaggct gcagcgtgg ccgttaaatc ggtaccgat
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1801 atacaccgct acgaaaaact tacttgcta gatgagtcgc gcgattaga agaagaggca
1861 tttagctgtg cccgaaaagc cgatgtgatt attttatgg gcggtataga tgcgcacct
1921 gaaggcgaag aaatgccgct agagctagat ggcttactc acggtgatc tacgcacatt
1981 aatttacct aagtaaaaac caatttgctt aaacaattaa aagcaacggg taaacctgtt
2041 gtaatggtta actttagtgg tagtgccatg gctttaaatt gggaaagcga aaagctagac
2101 gcaatactgc aagcgtttaa cccaggtgaa gcaaccgga cagcgttagc taatatttg
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2221 ctaccagcat ttaatgatta ccacatgaa aaccgcacct ataaatttta ccgcggtgag
2281 ccttgtatg cattggcca cggtttaggt tacgttgatt ttgctataa caatttagc
2341 gtacgaaata ctgcagaagc gggcaaacgc ctacctatag ctgtaagcgt aaccaatacc
2401 ggtaaaatgc aagcagaaga cgttgcccaa gtttatataa gtttgcaga tgcgccgca
2461 aacacgcccc tccgcgattt aaaagcgtt aaacgtacca agcttgcgc aggcgaaagc
2521 accgagctg aatttaactt gccggcgaga gtgcttacct atatagacga taatgtaaa
2581 acccaaacct atactggcag ggtagaagt actgtggct ctgggcaaaa gggatagcga
2641 aaagaaaatg cgatagctgt agcgactatt aacgttcagt ag

LOCUS NZ_AABI02000026 954 bp DNA linear BCT 23-SEP-2003
 DEFINITION Microbulbifer degradans 2-40 Mdeg_26, whole genome shotgun
 sequence.

ACCESSION NZ_AABI02000026 REGION: complement(16626..17579)

VERSION NZ_AABI02000026.1 GI:28878276

KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40

ORGANISM Microbulbifer degradans 2-40

Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
 Microbulbifer.

REFERENCE 1 (bases 1 to 954)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
 Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23029482.
 Protein-coding genes were predicted using GeneMark program (kindly
 provided by M. Borodovsky). Functional annotation is based on CDD
 (Conserved Domain Database) and COG (Clusters of Orthologous
 Groups) assignments, it has not yet been subject to manual review.
 DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson

microbes@cuba.jgi-psf.org.

COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

source 1..954

/organism="Microbulbifer degradans 2-40"

/mol_type="genomic DNA"

/strain="2-40"

/db_xref="taxon:203122"

gene 1..954

/gene="Mdeg3244"

CDS 1..954

/gene="Mdeg3244"

/codon_start=1

/transl_table=11

/product="COG3507: Beta-xylosidase"

/protein_id="ZP_00067829.1"

/db_xref="GI:23029495"

/db_xref="COG:COG3507"

/translation="MYTYVSAIALFISASSCCVAQNPLDFGSNIKTADPSGHIWAD

GRMYLYTSHDQECQEDFYMKDWHTFSSDLINWTAHGPSLSVADITWADNYAWAPDAA

YKNGKYLLFFPAGTGKDRVNPEKSTKWMGIGVAVSDSPTGPFKDAIGAPLWTDPYAN

DPSIFIDDDGKGGLYFHGKGADYLVLAEMADDLLSVKGEFHKMDMGGYEPKMEGPWVFK

REGMYFFTMPENNRSLAYYMAKSPFGPWEYKGIFMQEEGGNNHHSIVQFKGKWILFYH

RWLMGEGECKKKQRHTAAEYLHFNADGTIKEVKRTREGLTK"

ORIGIN

1 atgtacacat atgtatccgc catagcacta ttatatattt caattgcctc gtcgtgtgt
 61 gttgccc aaa accgcctcga cttggcagt aatattaaaa ccgcagatcc gtctggccat
 121 atatgggctg atggcagaat gtacctttac acctgcacg accaagaatg ccaagaagat
 181 ttatatga aggattggca tacctttcgc tccagcgact taataaattg gactgcccac
 241 ggcccaagtt tatctgtagc ggatattacg tgggcagata actacgcatg ggcgcccgc
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 361 agagtaaacc ccgaaaaaag cactaagtgg atgggcattg gtgtgcagt aagcgatagc

421 cctacaggcc cctttaaaga tgcgattggc gcccccttgt ggaccgaccc ctatgccaac
481 gaccaagta ttttataga tgaagacggc aagggtact tatatttca cggtaaaggt
541 gcagactacc tagtagccga aatggcagac gatttactga gtgtaaaagg tgagtctac
601 aaaatggata tggcggtta cgagccaaa atggagggcc ctgggttt taagcgcgag
661 ggaatgtatt actttaccat gccagaaaac aatcggtcac ttgcttacta tatggcgaaa
721 tctcccttg ggccgtggga atacaagggc attttatgc aagaagaagg cggtaacaac
781 caccattcta ttgtcaatt taaaggcaag tggatattgt ttatcaccg ctggtaatg
841 ggcgaaggcg agtgtaaaaa gaagcaacgc cacaccgcag cggaatacct tcaattaat
901 gccgacggca caattaaaga agtaaaaaga acgcgcgagg ggtaactaa gtag

LOCUS NZ_AABI02000004 1734 bp DNA linear BCT 23-SEP-2003
DEFINITION Microbulbifer degradans 2-40 Mdeg_4, whole genome shotgun sequence.
ACCESSION NZ_AABI02000004 REGION: complement(182992..184725)
VERSION NZ_AABI02000004.1 GI:28878298
KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40
ORGANISM Microbulbifer degradans 2-40
Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
Microbulbifer.

REFERENCE 1 (bases 1 to 1734)
AUTHORS NCBI Microbial Genomes Annotation Project.
TITLE Direct Submission
JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA
COMMENT On Mar 7, 2003 this sequence version replaced gi:23027141.
Protein-coding genes were predicted using GeneMark program (kindly
provided by M. Borodovsky). Functional annotation is based on CDD
(Conserved Domain Database) and COG (Clusters of Orthologous
Groups) assignments, it has not yet been subject to manual review.
DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.
URL -- <http://www.jgi.doe.gov>
Contact: Paul Richardson
microbes@cuba.jgi-psf.org.
COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

source 1..1734
/organism="Microbulbifer degradans 2-40"
/mol_type="genomic DNA"
/strain="2-40"
/db_xref="taxon:203122"
gene 1..1734
/gene="Mdeg1098"
CDS 1..1734
/gene="Mdeg1098"
/codon_start=1
/transl_table=11
/product="COG3507: Beta-xylosidase"
/protein_id="ZP_00065724.1"
/db_xref="GI:23027269"
/db_xref="COG:COG3507"
/translation="MKIKCLLLAVYAGLLAACALDAPLKTSSKPLAHFSWFEYQGND
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TQ LGNAIHRPEQLSFDGIHLGYNGVYAPAIEYRDGTFYVINTCVACGGNFIVTATNPAGP
WSDPIWLPEVIGIDPSLFFDEDGKTYIVHHRNPPVQKYPAAHTALWVMEVDSKTFAPVS
DDVMLVDGGDEAPWHTYIEGPHIYKIDGTYYLYAPGGGTGYFHGQLVYRSDNVFGPY
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NFATGRETFMLPVTWQNGWPHVLEKGEAVPYRVTKPKLPAGKPAPRAMTGNFTVREEF
TNASLAPHWLFVRTPRSKWWQTGNGELILEARADTIGAVNQPSFIGRRLAHMTASFAT
QLTFNPHTVGDEAGLLAVQNDEHFYAFGLGLNSKGQTVLRVRKKAGKNESIRGDTVAE
QVVKLKHGHPILRVNIGKAELNFAYSTNGKRYTLLNQADANLLTTAKAGGFTGAVV
GMYAESTAQQN"

ORIGIN

1 atgaaaatta agtgcttact ccttgctgtt tacgcgggtc tacttgccgc ttgcgcgctg
61 gacgcgccgc taaaacctc aagtaaaccg ctacgcgatt ttctgtggtt tgaatatcaa
121 ggtaacgacg agatatattaa ggctccactc gcctcaaacc aataccaaaa ccccatatct

181 gccggctacc acccagaccc aagtattgtg cgagtaggcg aagattatta ttggtgaac
241 tccaccttg gcttctacc tggcattcca gtattcaca gccgtgactt agtgaattgg
301 acccaactgg gtaacgctat tcaccgcca gagcaacttt catttgatgg taitcactta
361 ggctacaacg gcgtttatgc accggcaatc gaataccgcg acgggacctt ttacgtaata
421 aatactgcg tagcctgcg aggaaattt atcgttaccg ccaccaatcc cgcgggcccc
481 tggtcagacc caatatggct accagaggta attggcatag acccctcgt attttcgac
541 gaggacggca aaacctatat cgtgcatcat cgtaatccac ctgtgcagaa ataccctgcc
601 cacacagccc tgtgggtaat ggaagttgac tccaaaacat ttgcgcgggt atctgacgat
661 gtaatgcttg tggacggtgg cgacgaagcg ccatggcaca cagaatata tgaaggcgcg
721 catatatata aaattgatgg cacctactac ctctatgccc ctggtggcgg cacgggatac
781 ttccacggcc aattggtgta tagatcigac aatgtattg gaccctacga agccaacccc
841 aataaccctg tgtgactca agttggttta cccgacgaca gagaacaccc tgaacggca
901 acgggtcatg cagatttatt tcaagatacc aacggcgact ggtggacggt atttctgggt
961 actcgcgtt acgatttagc taagccacca caagacccc gcaatttgc caccggacgc
1021 gaaacattta tgttccagt aacatggcaa aacggctggc cacacgtct cgaaaaaggc
1081 gaggctgtg cctaccgagt aaccaaacc aaattacct caggcaaacc cgccccgcg
1141 gcaatgactg gaaactttac tgtgcgcgag gaattacca acgcttcgt tgcctccac
1201 tggctatttg ttgcacacc gcgttccaaa tgggtggcaa caggtaatgg cgaacttatt
1261 ttagaagcg gcgccgatac cattggggca gtaaccagc cgtcgttat tggccgacgg
1321 ctgcctcata tgacggcctc ctgcgcacc caactaacct ttaaccaca caccgtggc
1381 gacgaagcag ggttactcg cgtacaaaac gacgaacact ttacgcctt tggcctaggg
1441 ttaaacagta aaggggcaaac cgtttgcgc gtgcgtaaaa aagcgggtaa aaatgaatcg
1501 ataaggggag atacggttgc cgagcaggtt gtaagctta agcacggcca ccctattac
1561 ctgcgtgtaa atataggtaa agccgaatta aatttcgct atagcaccaa cggcaaacgc
1621 tacaccacct tgtgaacca agccgatgcc aacctacta ccacagctaa agcgggcggg
1681 ttactggcg cagtagtggg tatgtacgcc gaatccacc cacaacaaaa ctaa

LOCUS NZ_AABI02000011 1701 bp DNA linear BCT 23-SEP-2003
DEFINITION Microbulbifer degradans 2-40 Mdeg_9, whole genome shotgun sequence.
ACCESSION NZ_AABI02000011 REGION: 31082..32782
VERSION NZ_AABI02000011.1 GI:28878291
KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40
ORGANISM Microbulbifer degradans 2-40
Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
Microbulbifer.

REFERENCE 1 (bases 1 to 1701)
AUTHORS NCBI Microbial Genomes Annotation Project.
TITLE Direct Submission
JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23028020.
Protein-coding genes were predicted using GeneMark program (kindly
provided by M. Borodovsky). Functional annotation is based on CDD
(Conserved Domain Database) and COG (Clusters of Orthologous
Groups) assignments, it has not yet been subject to manual review.
DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson
microbes@cuba.jgi-psf.org.

COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers
source 1..1701
/organism="Microbulbifer degradans 2-40"
/mol_type="genomic DNA"
/strain="2-40"
/db_xref="taxon:203122"
gene 1..1701
/gene="Mdeg1856"
CDS 1..1701
/gene="Mdeg1856"
/codon_start=1
/transl_table=11
/product="COG3507: Beta-xylosidase"
/protein_id="ZP_00066469.1"
/db_xref="GI:23028051"
/db_xref="COG:COG3507"
/translation="MRLLPILLVSLPLLSSCTSAINGQQNSQTSPVFDWFEYAGSDA
LYNTVAPSKNAYTNPVIKGFYPDPSIVRVGADYYLVNSSFGYFPGVPIFHSTDLVNWW
QIGNILERPSQLQIPSGMGVSRGIFAPTLRHHNGIFYMITTMVDGGGNFIVTAKNPAG
PWSDPWVLPEVGGIDPDLFFDDNGKAYILNNDAPIGEPLYDGHRAIWIREFDLATLKT
VGDAKLIVNGGVDITTKPVWIEGPHLFKNKGAYYLINAEGGTSVNHSQVVFKAQSPWG
PYIPWENNPILTQRHLPADRANPVTSVGHVDLVQTQHGDWWAVFLGCRPYKDNYYNTG
RETFLLPVDWSGEYPVILRGDAEVPYHHQRPQLGASQQPAIALSGNFIERDEFDSALK
LYWRKVRTPTNFTDLTSQKGKLVLTANNTDLSDFGSPAFIARAQQHLTGSATTKLKY
TPPHVGDKAGIAAFQNDYFYALTVTKNNSGLAIQLEKQLGKNKEIVAQYPLQEKTLR
NGLYLKIEFNNDKYDFSYSTNNTKWQSVGETQDGTILSTQSAGGFVGATLGIFAYTAH
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ORIGIN

1 atgcgacttt tacctatctt actcgttagc ttacttcac tgctctcaag ctgcacaagc
61 gccataaacg ggcaacaaaa tagccaaacc tcgctgtat ttgattggtt tgaatacgcg
121 ggaagcgatg cttatacaa cacggttgcg ccaagtaaaa atgcctatac caaccagta

181 ataaaaggg tttatccaga tccaagcatt gtaagagtg gagcagatta ctacctcg
241 aactctcat ttggctactt ccctggcgtg ccgatattc atagcacaga ttagtgaat
301 tgggttcaaa taggtaatat tctcgagcgc ccatcacaat taaaaatacc cagcggcatg
361 ggtgtgtcgc gaggtatatt cgtcccaaca ctgcgccacc acaacggtat ttttacatg
421 attactaca tggtagacgg tggcggcaat ttattgta ctgcaaaaaa cccgcaggc
481 ccttggtcgg acccagtatg gttacctgaa gtgggcggta tagaccaga tttatttt
541 gatgacaacg gcaaagccta cataactaac aacgacgcc ccattggcga gccgcttac
601 gatggccacc gagccatttg gattcgcga ttcgacttag ccacattaaa aaccgtggc
661 gacgccaagt taatagtaaa cggcgggtga gatataacta ccaaaccgt ttgtagaa
721 ggccacacc tttcaaaaa taaaggcgt tactattaa ttaatgcaga aggtggcacc
781 agcgtgaatc acagccaagt tgtattaaa gcgcaaagcc ctggggggcc gtatattcct
841 tgggaaaaca atccaattt aacacagcgc cattaccgg ctgatcgcgc caacccgct
901 acatccgttg gccatgtcga ttagtaca actcaacatg gcgactgtg ggcgtatt
961 ttaggtgca ggcctataa agataactac tacaatccg gccgcgaaac attttatta
1021 ccggtagatt ggtctggcga atacccgct attctcgcg gcgatgccga ggtgccctat
1081 catcaccaac gcccctaatt gggagcatcc caacaaccag ccattgccct tagcggtaac
1141 ttattgagc gcgatgaatt tgactcagca cttaacttt attggcgcaa ggtcgcacc
1201 ccacaaaaca actttacaga ttaacctct caaaaaggca agctgtttt aactgcaaac
1261 aatacagatt taagcgactt tggatcacca gcattattg cgcgcgcaca gcagcaccta
1321 acaggcagcg caacaacca actggttac acacccccc acgtgggcga caaagcggg
1381 attgctgcct tcaaaacga tgagtattt tatgcgcta ccgttacaaa aaataatagc
1441 ggccttgcca tacaactaga aaaacaact ggcaagaaca aagaaatgt tgcgcaatat
1501 ccactacaag aaaaaacgt tcgcaatggc ttatattga aaatagaatt taataacgac
1561 aaatatgatt tcagctattc caaaaataac accaagtggc aatcggtagg cgaaacacaa
1621 gatggaacta tattaagcac gcaaagtga ggcgggttg taggtgccac gctaggata
1681 ttgcatata ccgcgacta a

LOCUS NZ_AABI02000014 960 bp DNA linear BCT 23-SEP-2003

DEFINITION Microbulbifer degradans 2-40 Mdeg_13, whole genome shotgun sequence.

ACCESSION NZ_AABI02000014 REGION: 125907..126866

VERSION NZ_AABI02000014.1 GI:28878288

KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40

ORGANISM Microbulbifer degradans 2-40

Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
Microbulbifer.

REFERENCE 1 (bases 1 to 960)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23028504.
Protein-coding genes were predicted using GeneMark program (kindly
provided by M. Borodovsky). Functional annotation is based on CDD
(Conserved Domain Database) and COG (Clusters of Orthologous
Groups) assignments, it has not yet been subject to manual review.
DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson
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COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

source 1..960

/organism="Microbulbifer degradans 2-40"

/mol_type="genomic DNA"

/strain="2-40"

/db_xref="taxon:203122"

gene 1..960

/gene="Mdeg2391"

CDS 1..960

/gene="Mdeg2391"

/codon_start=1

/transl_table=11

/product="COG3507: Beta-xylosidase"

/protein_id="ZP_00066992.1"

/db_xref="GI:23028599"

/db_xref="COG:COG3507"

/translation="MSMFNKKTLAAGIVAACLTNVSASYAANPAITDHTADPAALVH
GDTVYLYVGNDEAKDNRVFDLKKWLVSCKDMVNWNTNHGSPLAATDFKWASGDAAWAA
HTVEKDGGKFYWYTTVRHATINGFAIGVAVSDSPTGPFKDALGKALISNDMTTDTDIDW
DDIDPAVFIDDDGQAYIFWGNTKPRWAKLKPNIEMLDGPIHAIDIPHFTEALYVHKHG
EYYYLSYATGFPEKTAYAMSKSIEGPWEYKILNELAGNSNTNHQSVIDFKGKSYFIY
HNGGLGQDGGSFRRSVCIDYLNYNADGTIKRIVMTSEGVDPVK"

ORIGIN

1 gtgagtatgt ttaataaaaa aacactagca gccggtattg tagctgcatg ttaactaac
61 gtaagtgaac gctatgctgc caaccccgca attaccgata ctacacggc cgatcccgct
121 gcgtagtgac acggcgatgc cggtattttg tacgtgggta acgatgaagc gaaggataac
181 cgcgtatgtt acgatcttaa aaaaatggtg gtgtattcat caaaagatat ggtgaactgg
241 accaatcacg gtgcgccgtt agctgcaacg gattttaagt gggccagcgg cgatgcgtgg
301 gcggcgacac cggtagaaaa agatggcaag tttatttgtt ataccacggt gcgtcacgca
361 accattaatg gttttgcat tggcgttgca gtaagtata gccctacagg gccattcaaa

421 gatgctttgg gtaaagcact aataagtaat gacatgacca ccgataccga tattgattgg
481 gacgatatag acccagcagt atttattgac gacgatggcc aagcgtatat ttttggggc
541 aacaccaaac cgcgctgggc caagltaaaa cccaatatga ttgaactaga tggacctatt
601 cacgcaatcg atattccaca cttaccgaa gcgctatacg tgcacaaaca cggtgaatat
661 tactacttaa gctatgacgac aggctttcca gaaaaaacag cttacgctat gagcaaactt
721 atagaagggc cgtgggaata caaaggcatt cttaatgaat tggctggtaa ctcaaatact
781 aatcaccaat ctgtcatcga ttttaagggc aagtcatact ttattatca caatggtggc
841 ttgggtcaag atggcggtag cttccgtcgc agtgtatgta tggattattt gaactacaac
901 gcggatggta ctatcaagcg aattgtaatg acatcagaag gtgtagaccc agttaaataa

LOCUS NZ_AABI03000012 1158 bp DNA linear BCT 17-JUN-2004
 DEFINITION Microbulbifer degradans 2-40 Mdeg03_12, whole genome shotgun
 sequence.

ACCESSION NZ_AABI03000012 REGION: complement(71021..72178)

VERSION NZ_AABI03000012.1 GI:48861146

KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40

ORGANISM Microbulbifer degradans 2-40

Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
 Alteromonadaceae; Microbulbifer.

REFERENCE 1 (bases 1 to 1158)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
 Information, NIH, Bethesda, MD 20894, USA

COMMENT Protein-coding genes were predicted using GeneMark program (kindly
 provided by M. Borodovsky). Functional annotation is based on CDD
 (Conserved Domain Database) and COG (Clusters of Orthologous
 Groups) assignments, it has not yet been subject to manual review.
 DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson

microbes@cuba.jgi-psf.org.

FEATURES Location/Qualifiers

source 1..1158

/organism="Microbulbifer degradans 2-40"

/mol_type="genomic DNA"

/strain="2-40"

/db_xref="taxon:203122"

gene 1..1158

/locus_tag="Mdeg02003585"

CDS 1..1158

/locus_tag="Mdeg02003585"

/codon_start=1

/product="COG3507: Beta-xylosidase"

/protein_id="ZP_00315109.1"

/db_xref="GI:48861205"

/db_xref="COG:COG3507"

/translation="MPEHTRKRLSTLGLALSGTAITLTLVGCCKDNPATQTEGSHSA

GHTEVAEEQTHDIGGPGPEGKPINPLVTHIYTADPSAHVFDGKLYIYPSHDVEAGIP

QNDNGDHFDMRDYHVLSEEPGGKVTDHGVALAREDDVAWAGRQLWAPDAAEKDGTYYL

YFPMKDKDDIFRIGVASGSTPYGPFKAPEPMPGSYSIDPSVFQDGDYYMYIGGIWG

GQLQRWTTGEYNPEDVYPADDEPALLPKMAKLSADMKSFAEPLRDIQILDENGELIKA

GDNDRRFFEAAWVHKYNGKYYLSYSTGDTHYVYAIGDNPYGPFTYQGVLNPNVIGWT

NHHSIAEFKKGWYLFYHSSLSGGVTHLRSVKMTELTNPDTGTITINAYK"

ORIGIN

1 atgccagaac atacgcgtaa gcgcttacta tcaaccttag gcctagcttt atcgggcaca
 61 gctataaccc taacgctgt ggggtgcggt aaagacaacc ccgcaactca aacagaaggc
 121 agccacagcg ctggccatac agaagtgcc gcagaacaaa cacacgacat aggcggccca
 181 ggccctgagg gcaagccaat taacgacctg ctgttacctt acatatacac cgcagaccct
 241 tctgcccatt tcttgacgg caaacttat atttacctt cgcacgatgt ggaagcgggt
 301 attccgcaa acgataacgg cgatcacttc gatatgcgag attatcacgt gcttccatg
 361 gaagagcctg gtggcaaagt caccgatcac ggcgtagccc ttgcgcgca agatgtagct
 421 tgggctgtgc gccaaactgt ggcgcccgat gcgctgaaa aagacggcac ttactacctg
 481 tatttcccca tgaaagataa ggtgacatc ttccgattg gtgtcgccag tggcagtagc

541 ccttatggcc catttaaagc cgagccagag ccaatgccg gcagctatag catagacca
601 agcgtatttc aggatggcga cgactactac atgtacatag gtggtatttg gggcggccag
661 ttgcagcggt ggacaaccgg tgagtacaac ccagaagatg tatacccagc ggatgacgag
721 cctgcgctat tacctaaaat ggccaagcta agtcagata tgaaaagctt tgccgagcca
781 ttaagagaca ttcaaatttt ggatgaaaat ggcgagctaa ttaaagctgg cgataacgac
841 cgacgtttct tcgaagccgc gtgggtacac aaatataacg gcaagtatta ctgagctat
901 tcaaccggtg acaccacta tattgtgtat gccattggcg ataaccata cggcccgttt
961 acttaccagg gtgtagtgtc caaccccggt attggttga ctaaccatca ctcaattgct
1021 gaatttaaag gtaagtggta ttgttctac cacgatatgt cgctttccgg tgggtgaaca
1081 catttgcgca gcgtagaaat gacagagcta actcacaacc cagatggcac tatccaaacc
1141 attaatgcct ataagtaa

LOCUS NZ_AABI03000013 2217 bp DNA linear BCT 17-JUN-2004
DEFINITION Microbulbifer degradans 2-40 Mdeg03_13, whole genome shotgun
sequence.

ACCESSION NZ_AABI03000013 REGION: complement(100192..102408)

VERSION NZ_AABI03000013.1 GI:48861059

KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40

ORGANISM Microbulbifer degradans 2-40

Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
Alteromonadaceae; Microbulbifer.

REFERENCE 1 (bases 1 to 2217)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA

COMMENT Protein-coding genes were predicted using GeneMark program (kindly
provided by M. Borodovsky). Functional annotation is based on CDD
(Conserved Domain Database) and COG (Clusters of Orthologous
Groups) assignments, it has not yet been subject to manual review.
DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson

microbes@cuba.jgi-psf.org.

FEATURES Location/Qualifiers

source 1..2217

/organism="Microbulbifer degradans 2-40"

/mol_type="genomic DNA"

/strain="2-40"

/db_xref="taxon:203122"

gene 1..2217

/locus_tag="Mdeg02003703"

CDS 1..2217

/locus_tag="Mdeg02003703"

/codon_start=1

/product="COG3661: Alpha-glucuronidase"

/protein_id="ZP_00315039.1"

/db_xref="GI:48861134"

/db_xref="COG:COG3661"

/translation="MATLGVNAAKFAMFAAICLQFSVAEAAKSRDGYGLWLDYQPITN
TREREGYIKALSPWQVEGEAATADFIRQELTAALGAMLGVEAGPVG DYTHNSLAHPVA
RLLVATPEESAVIRSLALGDALTRVGQEGYLIKTTTRYRDKPITIVTANTHAGLLYGTF
KLLQLLQTGQAVSNLAIESAPATKLRVLNHWDLNDRYVERGYAGESIWNWHKLPHYKS
QRYYYDYARANASIGINGVVLNNVNADPLILTPQYLVKVKALADIFRPYGIKVYLSVKF
SSPNLIGGLPTSDPLDKNVQAWWQAKANEIYSLIPDFGGFLVKANSEGQPGPGDFGRS
HAQGANMLADALAPHGGNVMWRAFYVNVEANVERSKQAYNEFKPLDGTFRQNVLVQVK
NGPIDFQPREPFSPLFGAMPKTPLMMEFQITQEYLG FSTHLVYLGPLYEEVLKADTYA
KGAGSTVAKVVDGSLYGHGITGMAGVANIGSDRNWTGHIFGQANWYVFGQLAWNPEVS
TKQIADDWIRMTLTRDDKAVNTIRAMMMASRETAVNYMTPLGLHHIMGWGHHYGPAPW
IGEQQPDWMREDWTSVYYHSANATGLGKDR TASGSNVIAQYHAPLRQAYS DPKTTTPE
LLLWFHHPWHYELANGNSLWHEL VARYYLGAQAVAEMAKTWDGLEANIPPQLFKQVQ
MALAIQTQEAAWWRDACLVL YFQSYSKQSLPEGFAKPKHSLEYKGLSFP HAPGDGR"

ORIGIN

1 atggctactt tgggggtaaa tgccgctaag ttgcatgt ttgcagctat ttgcttgag

61 tttagtgtcg ccgaagcggc taaaagccgc gatggatatg ggctgtggtt agattaccag

121 ccaattacca ataccgcga acgcgagggc tatataaaag cattaagccc atggcaggta

181 gaaggcgaag ctgcaactgc cgattttatt cggcaagagc ttactgcagc gttgggcgct
 241 atgcttggcg ttgaggctgg tccagtgggt gattacaccc ataactccct cgctcaccct
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 421 gacaagccta tcaccattgt taccggaac acgcatgcag gcctgctgta tggcacattc
 481 aaactactgc agctgctgca aacagggcag gccgtttcta atttagctat tgagtccgcc
 541 ccagcaacca aactgcgtgt gcttaaccac tgggataacc tcgatcgcta tgtggagcgc
 601 ggctatgccg gtgagtctat ttggaactgg cacaagtcgc cgcactacaa atcgagcgc
 661 tactacgatt acgctcgcgc taacgcgtcc attggtatta acggtgtgt actaaacaat
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 781 gatatttta ggccctacgg cattaaagt tatcttcgg tgaagtttag ctgccgaat
 841 ctatttggcg ggcgccaac atccgacccg ttagataaaa atgtgcaagc ttgtggcaa
 901 gcgaaagcga atgaaattta ctgctcatt cccgacttg gtggctttt agtaaaagcg
 961 aattcggaag ggcagcccgg cccaggggac ttggccgca gccatgcaca aggggcaaat
 1021 atgttggccg atgactggc acccatggc ggcaatgtaa tgtggcgcgc gttgtatat
 1081 aacgtagaag ccaatgtga gcatccaag caggcataca acgaattaa gccattagac
 1141 ggtacctta ggcaaacgt attggtgcaa gtaaaaaatg ggccaattga tttagacca
 1201 cgtgaaccgt ttagccgct gttggtgct atgccccaaa cgccgttaat gatggagtt
 1261 caaattactc aggagtactt ggggttagt actcacttg ttacttggg gccgctgtac
 1321 gaagaagtac ttaaggccga tacctatgcg aagggggcag ggtctactgt tgcgaagggtg
 1381 gtcgatggct cgctctacgg gcacggtata acgggtatgg ctggggtagc taatatggc
 1441 agcgatcgca attggaccgg ccatatttc ggccaagcca actggtatgt atttgccaa
 1501 ttggcgtgga acccgaggt aagcactaag caaatagccg atgattggat tcgatgaca
 1561 ctacccgcg acgataaagc ggtaaacacc attcgccaa tgatgatggc cagccgcgaa
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 1681 tacggcccag cgccgtgat agcgagcaa aaaccgatt gcatgctga agattggaca
 1741 tctgttact atcatagcgc aaacgccaca gggctaggca aagatagaac agcttctggc
 1801 agcaatgtca tagcgcaata ccacgccct ttacggcagg cctatagcga cccgaaaacc
 1861 acgcccaccg agttgctatt gtggttcat cattgcctt ggcattatga attagcgaat
 1921 ggcaatagcc tgggcatga actggtagcg cgttactatt taggcgcgca ggctgtggca
 1981 gaaatggcca aaacgtggga tggcctagaa gctaatalcc cccgcagct attcaaaca
 2041 gtacaaatgg cgctggctat tcaaaccaca gaagccgct ggtggcgcga tgcctgcgtg
 2101 ctgtatttc aaagctattc taagcagtcg ctaccgagg gctttgcaa acctaagcac
 2161 tcgctgaat actataaagg gtaagcttc ccgatgcgc cgggtgacgg gcgttaa

LOCUS NZ_AABI02000026 3951 bp DNA linear BCT 23-SEP-2003

DEFINITION Microbulbifer degradans 2-40 Mdeg_26, whole genome shotgun sequence.

ACCESSION NZ_AABI02000026 REGION: complement(19875..23825)

VERSION NZ_AABI02000026.1 GI:28878276

KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40

ORGANISM Microbulbifer degradans 2-40

Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae; Microbulbifer.

REFERENCE 1 (bases 1 to 3951)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23029482.

Protein-coding genes were predicted using GeneMark program (kindly provided by M. Borodovsky). Functional annotation is based on CDD (Conserved Domain Database) and COG (Clusters of Orthologous Groups) assignments, it has not yet been subject to manual review.

DNA sequence and predicted proteins are available for BLAST at

http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson

microbes@cuba.jgi-psf.org.

COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

source 1..3951

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CDS 1..3951

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/transl_table=11

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LOCUS NZ_AABI02000026 1284 bp DNA linear BCT 23-SEP-2003

DEFINITION Microbulbifer degradans 2-40 Mdeg_26, whole genome shotgun sequence.

ACCESSION NZ_AABI02000026 REGION: complement(32631..33914)

VERSION NZ_AABI02000026.1 GI:28878276

KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40

ORGANISM Microbulbifer degradans 2-40

Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae; Microbulbifer.

REFERENCE 1 (bases 1 to 1284)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23029482. Protein-coding genes were predicted using GeneMark program (kindly provided by M. Borodovsky). Functional annotation is based on CDD (Conserved Domain Database) and COG (Clusters of Orthologous Groups) assignments, it has not yet been subject to manual review. DNA sequence and predicted proteins are available for BLAST at http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson
microbes@cuba.jgi-psf.org.

COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

source 1..1284

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CDS 1..1284

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ORIGIN

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LOCUS NZ_AABI02000026 2310 bp DNA linear BCT 23-SEP-2003

DEFINITION Microbulbifer degradans 2-40 Mdeg_26, whole genome shotgun sequence.

ACCESSION NZ_AABI02000026 REGION: complement(24098..26407)

VERSION NZ_AABI02000026.1 GI:28878276

KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40

ORGANISM Microbulbifer degradans 2-40

Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae; Microbulbifer.

REFERENCE 1 (bases 1 to 2310)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23029482. Protein-coding genes were predicted using GeneMark program (kindly provided by M. Borodovsky). Functional annotation is based on CDD (Conserved Domain Database) and COG (Clusters of Orthologous Groups) assignments, it has not yet been subject to manual review. DNA sequence and predicted proteins are available for BLAST at http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson

microbes@cuba.jgi-psf.org.

COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

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ORIGIN

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LOCUS NZ_AABI02000015 1785 bp DNA linear BCT 23-SEP-2003

DEFINITION Microbulbifer degradans 2-40 Mdeg_15, whole genome shotgun sequence.

ACCESSION NZ_AABI02000015 REGION: complement(111927..113711)

VERSION NZ_AABI02000015.1 GI:28878287

KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40

ORGANISM Microbulbifer degradans 2-40

Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae; Microbulbifer.

REFERENCE 1 (bases 1 to 1785)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23028706.

Protein-coding genes were predicted using GeneMark program (kindly provided by M. Borodovsky). Functional annotation is based on CDD (Conserved Domain Database) and COG (Clusters of Orthologous Groups) assignments, it has not yet been subject to manual review.

DNA sequence and predicted proteins are available for BLAST at

http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson

microbes@cuba.jgi-psf.org.

COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

source 1..1785

/organism="Microbulbifer degradans 2-40"

/mol_type="genomic DNA"

/strain="2-40"

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gene 1..1785

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CDS 1..1785

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/transl_table=11

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/db_xref="COG:COG3866"

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ORIGIN

1 atgaaaattt taaattgtt attaattgtt gtactcgccc acaacttagt tgcttggtg

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241 ttgccggcc acaattttaa tcttaccggt gccgaaggcg gcacagccta taccgttaat
301 aacggcaaag atttgcaaac agttttagac aacgccaat cgagtaattc accggtcatt
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661 tacgacggtt taatcgatag taaaagcggc gcgagcaaca ttactatttc ttacaactac
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1381 gtaaccggca cggtggaat taacgcacag caattggata tgactggcg acgcgtatca
1441 attggcaaca caacgccaag tgtaagcaca accggtgcag acaccactac aacgggcgta
1501 ttagatttaa gcgcgcccta caccgtaagc tttaaagtgg taagcgtagg cggcaccccta
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1681 acagtaaccg gctttaccgc caccaacagc tcttcataa cattacgtac cgaaagtagc
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LOCUS NZ_AABI02000001 1278 bp DNA linear BCT 23-SEP-2003
DEFINITION Microbulbifer degradans 2-40 Mdeg_1, whole genome shotgun sequence.
ACCESSION NZ_AABI02000001 REGION: complement(71234..72511)
VERSION NZ_AABI02000001.1 GI:28878301
KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40
ORGANISM Microbulbifer degradans 2-40
Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
Microbulbifer.

REFERENCE 1 (bases 1 to 1278)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23026153.
Protein-coding genes were predicted using GeneMark program (kindly
provided by M. Borodovsky). Functional annotation is based on CDD
(Conserved Domain Database) and COG (Clusters of Orthologous
Groups) assignments, it has not yet been subject to manual review.
DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson
microbes@cuba.jgi-psf.org.

COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

source 1..1278

/organism="Microbulbifer degradans 2-40"

/mol_type="genomic DNA"

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CDS 1..1278

/gene="Mdeg0054"

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ORIGIN

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301 acggcccccac caccgggtat cacccttacc aaggcgccgac taagaataga aaccacaat
361 gtcaaagttt cgcaccttat gattaggcct ggtgacgcag ggtactccaa aggtcaaggt

421 tggaaacccg acggcataac tatatatggc agcaaagcga ggcattgtgt tattgatcat
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781 catatgtctt cgggccgtgc tgatgctagc ctgccaacac tgtcaattac aggaatttg
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961 tcattgactg cgccgccgt acagcaagta ggcataaatt taaccgatac aggtacacia
1021 aacgacttt gccaaacct aagcaacgca ggtgccgcc cgtgggaccc cgaccgatt
1081 gatattagaa taaaacaca acttttgct ggcgaaggac gaattattga tagccagagc
1141 gaggttgag gctaccaat acataacgtc aataaaaag aaaccgctga agcaggctct
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1261 ttagtgga tgatgaa

LOCUS NZ_AABI02000001 2319 bp DNA linear BCT 23-SEP-2003
 DEFINITION Microbulbifer degradans 2-40 Mdeg_1, whole genome shotgun sequence.
 ACCESSION NZ_AABI02000001 REGION: 76773..79091
 VERSION NZ_AABI02000001.1 GI:28878301
 KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40
 ORGANISM Microbulbifer degradans 2-40
 Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
 Microbulbifer.

REFERENCE 1 (bases 1 to 2319)
 AUTHORS NCBI Microbial Genomes Annotation Project.
 TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
 Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23026153.
 Protein-coding genes were predicted using GeneMark program (kindly
 provided by M. Borodovsky). Functional annotation is based on CDD
 (Conserved Domain Database) and COG (Clusters of Orthologous
 Groups) assignments, it has not yet been subject to manual review.
 DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.
 URL -- <http://www.jgi.doe.gov>
 Contact: Paul Richardson
microbes@cuba.jgi-psf.org.
 COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

source 1..2319
 /organism="Microbulbifer degradans 2-40"
 /mol_type="genomic DNA"
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ORIGIN

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LOCUS NZ_AABI02000001 1536 bp DNA linear BCT 23-SEP-2003
 DEFINITION Microbulbifer degradans 2-40 Mdeg_1, whole genome shotgun sequence.
 ACCESSION NZ_AABI02000001 REGION: 73615..75150
 VERSION NZ_AABI02000001.1 GI:28878301
 KEYWORDS WGS.
 SOURCE Microbulbifer degradans 2-40
 ORGANISM Microbulbifer degradans 2-40
 Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
 Microbulbifer.

REFERENCE 1 (bases 1 to 1536)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
 Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23026153.
 Protein-coding genes were predicted using GeneMark program (kindly
 provided by M. Borodovsky). Functional annotation is based on CDD
 (Conserved Domain Database) and COG (Clusters of Orthologous
 Groups) assignments, it has not yet been subject to manual review.
 DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.
 URL -- <http://www.jgi.doe.gov>
 Contact: Paul Richardson
microbes@cuba.jgi-psf.org.
 COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

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 utilization or adhesion"
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ORIGIN

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LOCUS NZ_AABI02000004 1368 bp DNA linear BCT 23-SEP-2003
DEFINITION Microbulbifer degradans 2-40 Mdeg_4, whole genome shotgun sequence.
ACCESSION NZ_AABI02000004 REGION: 203603..204970
VERSION NZ_AABI02000004.1 GI:28878298
KEYWORDS WGS.
SOURCE Microbulbifer degradans 2-40
ORGANISM Microbulbifer degradans 2-40
Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
Microbulbifer.
REFERENCE 1 (bases 1 to 1368)
AUTHORS NCBI Microbial Genomes Annotation Project.
TITLE Direct Submission
JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA
COMMENT On Mar 7, 2003 this sequence version replaced gi:23027141.
Protein-coding genes were predicted using GeneMark program (kindly
provided by M. Borodovsky). Functional annotation is based on CDD
(Conserved Domain Database) and COG (Clusters of Orthologous
Groups) assignments, it has not yet been subject to manual review.
DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.
URL -- <http://www.jgi.doe.gov>
Contact: Paul Richardson
microbes@cuba.jgi-psf.org.
COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers
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/organism="Microbulbifer degradans 2-40"
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gene 1..1368
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CDS 1..1368
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ORIGIN

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121  tgtctgttaa gctcgtctac caacgttgcg ttcggcgctg ctggttaagt tgtttacaaa
181  gtaattaacg gtacctttac ttgtaataca tctactttg gcagcgatcc taaccctgct
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361  ggcggcgcaa ctgtatgttt aagtgcaggt ggcggcagta acgatatcga ttaacttgg
421  acagtatctg gttctatttc tagcgctcag gttaccgcg acacagattc taaccctagt
481  ggtcgcacac gtattgtcca attagtggtc gatgcaagaa gctatagcga tacgaatgtt
541  agtgcgtgta agcagtacta ctactggatt aagtttggcg ccaacggctc taactacaat
601  tcgaatgcgg ctctgctac ctatagtggg tcaagtagct catcgagttc ttcaagctct
661  tctagttcct catctggcgg ctcggtgaa tgtaaagctg gcgctactat ttctggtaaa
721  accgtagatt gcggtggtaa agaaattggc ttgtcgtgct cgggtgatag tgaaactcaa
781  ccaccagtat taacgcttaa aaatgccacc attaaaaact tggtaatttc tgctaaaggt
841  gggccgacg gtattcactg tactggcaac tgcaccatgg aaaatgttgt ttggaaagat
901  atctgtgaag atgctgctac caacaaaacc gacgtatta ccatgaccat tattgtgtgt
961  agtgcgtata actctacaag cggttacggc ggcaagccag ataaggtttt ccaacataac
1021  tctaaaaaca gtactactgt aattaaaggc ggcttacct taacaggtga gcacggcaaa
1081  ttgtggcgtt catgtggtaa ctgtactaat aacggcggcc cagctaatgt gactatcgac
1141  aacgttaaag tagacgcgaa aataggcagt attgttggcg ttaaccgcaa ctatggcgat
1201  aaggcaacaa tcaaaaactt aaagattaaa gactacaaat ctggtagccc caaagtgtgt
1261  gaagaataca aggggtgaca aaagggtagt ggcgagtcct ctaagtatgg cgaatactgg
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LOCUS NZ_AABI02000010 1275 bp DNA linear BCT 23-SEP-2003
DEFINITION Microbulbifer degradans 2-40 Mdeg_14, whole genome shotgun
sequence.

ACCESSION NZ_AABI02000010 REGION: complement(30476..31750)

VERSION NZ_AABI02000010.1 GI:28878292

KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40

ORGANISM Microbulbifer degradans 2-40

Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
Microbulbifer.

REFERENCE 1 (bases 1 to 1275)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23028613.
Protein-coding genes were predicted using GeneMark program (kindly
provided by M. Borodovsky). Functional annotation is based on CDD
(Conserved Domain Database) and COG (Clusters of Orthologous
Groups) assignments, it has not yet been subject to manual review.
DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson
microbes@cuba.jgi-psf.org.

COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

source 1..1275

/organism="Microbulbifer degradans 2-40"

/mol_type="genomic DNA"

/strain="2-40"

/db_xref="taxon:203122"

gene 1..1275

/gene="Mdeg2416"

CDS 1..1275

/gene="Mdeg2416"

/codon_start=1

/transl_table=11

/product="COG5295: Autotransporter adhesin"

/protein_id="ZP_00067017.1"

/db_xref="GI:23028629"

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/translation="MFNKILVAVGLLAASLSVHAATNRPSGYTTICKVGETCSVSQST
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SSGSSSGGGCGSGGGSTVCLSASGSSNGINLSWSVSGSISSVQLYRDTDSNPGRTRI
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ORIGIN

1 atgtttaaca agatactcgt tgcagtagga ttacttcgcg ctacgcttcc tgtcacgcc
61 gcaacaaacc gccaagtgg ttatacaaca atttgaagg ttggtgaaac atgctcggt
121 agtcagtcta cgaatgtagc cttggcgcg tctgggcagt ttgtgtataa agtattaaac
181 ggtagctttt cttgtagtg ttctacgttt ggtagtgacc ctattccttc taaatctgta
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301 agcagctctt ccggtagctc ttctgggtgt ggctgtggca gcggtgggtg ttctacggtg
361 tgcttatcgg cctcgggttc tagcaatggt atcaatttaa gtgggtctgt atctggttct
421 atatcttccg tgcagcttta tcgcgatacc gattcaaacc caagcggtcg cacgcgtatt
481 gctagtgtat ctagctctac tactagcttt agtgataccg gcgcggcatc gggcaccact
541 tattactact gggtaaata ttatgaaat ggtactgctt acaactcggg tgttgcttct
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661 ggtggaaaag gttctagttg tagctctact ggtagccaat ctgtgtcttc tactattaag
721 gtaaccagcg gtacttacga tgggtggtgt aaaacattta accctaccag tgctttgggt
781 gatgtagcc aatctgaaag ccaaaaacct gctttccgtg tagaaaacgg tgcaacgtta
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LOCUS NZ_AABI02000027 1179 bp DNA linear BCT 23-SEP-2003
DEFINITION Microbulbifer degradans 2-40 Mdeg_27, whole genome shotgun
sequence.

ACCESSION NZ_AABI02000027 REGION: complement(32448..33626)

VERSION NZ_AABI02000027.1 GI:28878275

KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40

ORGANISM Microbulbifer degradans 2-40

Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
Microbulbifer.

REFERENCE 1 (bases 1 to 1179)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23029524.
Protein-coding genes were predicted using GeneMark program (kindly
provided by M. Borodovsky). Functional annotation is based on CDD
(Conserved Domain Database) and COG (Clusters of Orthologous
Groups) assignments, it has not yet been subject to manual review.
DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson

microbes@cuba.jgi-psf.org.

COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

source 1..1179

/organism="Microbulbifer degradans 2-40"

/mol_type="genomic DNA"

/strain="2-40"

/db_xref="taxon:203122"

gene 1..1179

/gene="Mdeg3302"

CDS 1..1179

/gene="Mdeg3302"

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ORIGIN

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181 cagcagtttg acgtggcagt gcttagcgat gccagttact ccatacgacc agtgcacagc
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301 gcatacacag gcgcagataa ccaacgttgg tatatcgata atcaaagtgg cgattactat

361 tcaattacgt ctaaatttag cgggcgcgca ttggatgtat ggggtatgag tatgtacacc
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481 aaggtaggta gctcaagtga gtgttacgca ggtgctacgt taacaaaccg ctttgtggat
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601 ctaaccotta aaaactcgtc cattcgcaat gttaagtgg ctgcaaaccg tggtcggat
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REFERENCE 1 (bases 1 to 2202)
AUTHORS NCBI Microbial Genomes Annotation Project.
TITLE Direct Submission
JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA
COMMENT On Mar 7, 2003 this sequence version replaced gi:23027577.
Protein-coding genes were predicted using GeneMark program (kindly
provided by M. Borodovsky). Functional annotation is based on CDD
(Conserved Domain Database) and COG (Clusters of Orthologous
Groups) assignments, it has not yet been subject to manual review.
DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.
URL -- <http://www.jgi.doe.gov>
Contact: Paul Richardson
microbes@cuba.jgi-psf.org.
COG assignment was automatically updated on Sep 23, 2003.

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FEATURES             Location/Qualifiers
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     gene              1..2202
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     CDS               1..2202
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                        /transl_table=11
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                        /protein_id="ZP_00066061.1"
                        /db_xref="GI:23027623"
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131

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 1921 caacactact tccgcaataa tgtttctgta tctggcgtg tgaatattag caatgccgac
 1981 aacaaataca attcgtggaa cggcggagta acagcatcca cggcagattt tgaaaacgta
 2041 gatttatcca aagccaccgc tgcacgtaac atagatggca gcctgcaaa caacggccta
 2101 ttccgttaa aaagcggcag cgatttaata gacgccggg tagaggtagg ttaccaagt
 2161 aacggcagcg cgcccgatat gggagcgttc gaagctaact ag

LOCUS NZ_AABI02000042 2103 bp DNA linear BCT 23-SEP-2003
DEFINITION Microbulbifer degradans 2-40 Mdeg_42, whole genome shotgun
sequence.

ACCESSION NZ_AABI02000042 REGION: 7251..9353

VERSION NZ_AABI02000042.1 GI:28878260

KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40

ORGANISM Microbulbifer degradans 2-40

Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
Microbulbifer.

REFERENCE 1 (bases 1 to 2103)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23029937.
Protein-coding genes were predicted using GeneMark program (kindly
provided by M. Borodovsky). Functional annotation is based on CDD
(Conserved Domain Database) and COG (Clusters of Orthologous
Groups) assignments, it has not yet been subject to manual review.
DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson

microbes@cuba.jgi-psf.org.

COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

source 1..2103

/organism="Microbulbifer degradans 2-40"

/mol_type="genomic DNA"

/strain="2-40"

/db_xref="taxon:203122"

gene 1..2103

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CDS 1..2103

/gene="Mdeg3649"

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/transl_table=11

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IVLDKAKQGVAPLNGDLLTSNQRARLSSAVNKGVDYILKSQWRQNGTLTVWCAQH GKD
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gene complement(405..623)

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CDS complement(405..623)
 /gene="Mdeg3650"
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ORIGIN

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 1981 gatagagata gcagaaaagt ttacgatatt ttagatatt ctacagagcg taaagatggc
 2041 tatcgtggg gcggtgatta tggctcggc atcattagt acgcggaaag cgttggttac
 2101 taa

135

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 EFLTMQYSTGGWPQVYPARTGTSYSNHVTFNDNAMARVLILLDKAARLEAPLDGDI
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 ESVLVVAFLMTRPQSEAIENAVKAALAWYRNPVQVANTEYVKRTNDDNYPNQTKA
 GSTMWYRFYDLQDVGFFSGRSASDNPAAGNGKQYDIMLIEPERRYGYEWGGNYGKKII
 DYANSVGY"

ORIGIN

1 atgaatttc tacgccttat tacactcgca ctgcccga cactattaag tgccctgcgt
 61 ggaggtagtt ctggcccagc caaagagata aacgcttcca ccagttcctc tagctctagc
 121 agctccacga gttctagcag ctcatccagc tctagtagtt cgtctagctc aagcagctcg
 181 tcttccagtt ccagcagctc atcctctagc tctagcagct ctcttggtgg tagcgccggc
 241 acactcacta ttcaggaaag cgaaaaaggc tttgcactg ttaacggtga gattgtgaat
 301 aatcacgagg ggtatagcgg tacaggtttt gtagacaccg ccaatgccga aggcgccagc
 361 attacttggg aggtagatgt cgtggcggc aattatgatg taagtgtgcg attcgcaaac
 421 ggttcactg cagcgccgcg aacgcttagc agtaacgaaa taaataccac ctatggtttt
 481 gctaccactg gcgactgggc cacatgggca gacgaaacc acaccgttc gttagccgca
 541 ggcgaaaaca ccatccagct aagtgcactt accgcgggtg gcttaccacaa ttagacgct
 601 attactattg caggtgcagg tgtactcgca gcagactgcg ccacagagca tactggcca
 661 atgctttcgc aaacaggcaa cctatttat accgagttaa ataattacaa gtctggcta
 721 acgggtagcg gcacaacagc agccaaatta gccgcagata aaacaattgc cgacaatatg
 781 attacctggc aatgcctca cgggtgtttt tataaatacg gcgtatctaa atacagctcg
 841 gcttgaacg gtagcgatgc ccgctctggc tggactggg ccaacggcgt tgagctggc
 901 acaattgata atgatgaac cgttagcgaa ttattttt tagcggacgt atataaacgc
 961 agcggtgaaa ctaaataatag agatgccgca agaagcgcgt tgaattttt acttaccatg
 1021 caatattcca ctggcgggtg gccacaggtt taccctgcgc gcactggcac cagttactcc
 1081 aatcacgtta cgtttaacga taacgccatg gctcgtgtac ttattttt ggataaagcc
 1141 gcgcgattag aagcaccact cgtggcgac attttacca cagaccagca cagcggtatt
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 1261 gtgaaaaccg tttggtgtgc gcaacacgac cttatacct acgaggcaaa agcagctcgc
 1321 tcttatgagt tggcctctaa aagcggtaaa gaatctgtat tgggtgtagc gttttaatg
 1381 acacgcccgc aaagcgaagc catagaaaat gccgtgaaag cagcccttgc ttggtaccgc
 1441 aacccaaatg ttcaagtgc caacaccgag tatgtaaaac gcacaaataa cgatgacaac
 1501 tacaaccgga tacaacgaa agcaggtagc actatgtgt accgcttta cgatttagac
 1561 caagacgttg gattctttag cggccgctct gcaagtgaca acccagcagg taacggtaag
 1621 caatacgaca ttatgcttat tgaacccgag cgcaggtatg gctatgaatg ggggtgcaat
 1681 tacggcaaaa aaataatcga ttacgctaatt cggtagggt attaa

LOCUS NZ_AABI02000026 1392 bp DNA linear BCT 23-SEP-2003
 DEFINITION Microbulbifer degradans 2-40 Mdeg_26, whole genome shotgun
 sequence.

ACCESSION NZ_AABI02000026 REGION: 5430..6821

VERSION NZ_AABI02000026.1 GI:28878276

KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40

ORGANISM Microbulbifer degradans 2-40

Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
 Microbulbifer.

REFERENCE 1 (bases 1 to 1392)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
 Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23029482.
 Protein-coding genes were predicted using GeneMark program (kindly
 provided by M. Borodovsky). Functional annotation is based on CDD
 (Conserved Domain Database) and COG (Clusters of Orthologous
 Groups) assignments, it has not yet been subject to manual review.
 DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson

microbes@cuba.jgi-psf.org.

COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

source 1..1392

/organism="Microbulbifer degradans 2-40"

/mol_type="genomic DNA"

/strain="2-40"

/db_xref="taxon:203122"

gene 1..1392

/gene="Mdeg3237"

CDS 1..1392

/gene="Mdeg3237"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/protein_id="ZP_00067822.1"

/db_xref="GI:23029488"

/translation="MYKISRRTTLKGLGLTCLAGCTTSLPTLEQDPWAFQAQNIADNTT
 IPTFPNKEFNLLFEGGKEGSDNTLAFKKAIAACSKAGGGKVVVPAGRFETGAIHLESN
 VNLHISEGATIAFFTDPKYYLPAVFTRWEGMECMGYSPLIYAYGKTNIAITGKGTLDG

QADPTHWWAWKGNKEWGVGYPSQKESRNQLFAQAEAGDPVRERVYADGHYLRPSFVQ
 PYKCENVLIEDITIINAPFWLLHPTLSQNVTVRGVHLES LGPNSDGC DPESCKNVVIE
 NCCFNTGDDCIAIKSGRNNDGRRLATPTENVIRNCKMEAGHGGVIGSEISGGVRNV
 FAENNVMS SPDLKGIRIKTNSVRGGLLENIYVRNCTIGEVQQAIVINFQYEEGDAGK
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ORIGIN

1 atgtataaaa ttacgccc cacaacactc aaaggcttag gcctaactg cctagccggc
 61 tgcaccacca gctaccac actagagcaa gacccatggg ctttgcaca aaacatagcg
 121 gacaacacca ccatccccc attcccaaac aaagaattta attactcga attcgccggc
 181 aaagaaggga gcgacaacac cctgccttc aaaaaagcga ttgcagcatg cagcaaagca

241 ggtggcggca aggtggtagt acccgagga cgattgaga caggcgccat ccacttagag
301 tcgaacgta accitcatat tagcgaaggc gctaccatcg cctttttac cgaccccaaa
361 tattacctgc ctgcggtttt cactcgctgg gaaggcatgg agtgcattgg ctactaccc
421 cttatatacg cctacggcaa aaccaacata gccattaccg gtaaaggcac cctcgacggt
481 caagccgacc caacgcactg gtgggcatgg aaaggcaaca aagaatgggg cgtagagggc
541 tacccaagcc aaaaggaaag ccgcaaccaa ctattgccc aagcagaagc tggcgacccc
601 gttagagagc gcgtgtatgc agacggccac tacctgcgcc cctcgttgt gcaaccctac
661 aagtgcgaaa acgtgctgat agaagacata actattatca acgctccctt ctggttgcta
721 caccacccc ttacacaaa cgtcactgta cgcggtgttc acctagaaag cctaggcccc
781 aactcggatg gctgcgatcc tgaaagctgt aagaatgtag ttatcgaaaa ctgcttttt
841 aataccggtg acgactgtat cgctattaaa tctggccgca acaacgatgg ccgcaggctt
901 gccacaccta ccgagaacgt gattattcgc aactgtaaaa tggaagcggg tcacggtggc
961 gtagttatag gtcagaaat ttctggcggc gtgcgcaatg tgttgccga aaataacgta
1021 atgagcagcc ccgatttaga gaaaggcatt cgcattaaaa ccaactctgt gcgcggcgga
1081 ctgctagaga acatctatgt gcgcaactgc accataggcg aagtacaaca agccattgtt
1141 attacttcc aatacgaaga aggcgatgcg ggtaaattg accccaccgt gcgcaatgta
1201 gaaatacgca atttggtctg ccagcacgcc ttacaagtgt ttaacatccg cggttttgag
1261 cgcgccccca ttcaaaactt taggataatc gacagcacct ttgtgcgtgg tgacaacca
1321 ggcgtaattg aacataccac agggtagtt atcgacaacg tccaagtcaa cggcaaagcg
1381 ttaacatct ag

LOCUS NZ_AABI02000015 3255 bp DNA linear BCT 23-SEP-2003
DEFINITION Microbulbifer degradans 2-40 Mdeg_15, whole genome shotgun
sequence.

ACCESSION NZ_AABI02000015 REGION: complement(113840..117094)

VERSION NZ_AABI02000015.1 GI:28878287

KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40

ORGANISM Microbulbifer degradans 2-40

Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
Microbulbifer.

REFERENCE 1 (bases 1 to 3255)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23028706.
Protein-coding genes were predicted using GeneMark program (kindly
provided by M. Borodovsky). Functional annotation is based on CDD
(Conserved Domain Database) and COG (Clusters of Orthologous
Groups) assignments, it has not yet been subject to manual review.
DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

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COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

source 1..3255

/organism="Microbulbifer degradans 2-40"

/mol_type="genomic DNA"

/strain="2-40"

/db_xref="taxon:203122"

gene 1..3255

/gene="Mdeg2590"

CDS 1..3255

/gene="Mdeg2590"

/codon_start=1

/transl_table=11

/product="COG4677: Pectin methylesterase"

/protein_id="ZP_00067183.1"

/db_xref="GI:23028801"

/db_xref="COG:COG4677"

/translation="MLDMTKRTLSALLALCATLTACGGGDITSGGDAIPAVNQAPVQ
EPEPEPEPQPEPEPEPEPEPEPEGAWTCPETGFYFCDDFEDGTFDDKWDDLATYDLP
SPGVFDILD EASGKSLRFTAGTRGGDLADGELIVVKDTAFENVNADYSLEYRIRPRN
NGNTGNKYLHAMSRYEGPKKEYFGGLSMQGSTASTQVEAGFVLPENTTSISNRLVQAK
YPLELGTGMSDGYWYEVRFDMIGNTGTIYLDGEPQGSFTDADGLYPLTGKIGFMTYN
RSFEIDWVRVGDPAIKPVQLSLDYASPLWEAAADQDPLNVTVTAIQSDGVTADTFTAV
SSDTNVVTTSIANNVVTITPVAQGSATVTFTAGSDANRVKTIDVEIARAFVMSTTDYG
DIASKVTPTVGMTDANPD AHL SITFDSAPTLSGVGSIRIYNAADDSEVDVIRLTDES
ALGYAGQANKRELNTTPVYLDGNTLHVSPHSNALAYGQDYVAIGDNVLTGATLNTIA
FDGLGKNAGWTFSTKASAPTGNVTVD D DASADFSTVQGALNYAMANTTDD SITINIA
NGNYEPLYLAERNNVTLKGESRDGVVIHYNHHEAMNGGSTGRANFYVANS DMLTLET
LTLKNGHQRTGGGDQAETIYFNSSSNTDRLIAKGA AFISEQDTLLLKGYNWFYNSLVV
GNVDFIWGYSAVTLFEETEIRSIADSKPGAGDSGGYILQARTPLETDLGFVFLNSEL
T KATGVNGNEIGDGKTYLARSGGSTGYFDNISFINTKMGSHIADIGFAYADINGQPAPN

PAVATADAGWREFGSMDSAGTALDVSARCGDSGSCIQLTQAQVDAQYCNRAQIFASWN
 DWTGWDPEDTSDDACADPVIPGAVTWTGIAMSLGGSTTSVSGNITEQTDNITFTA
 DGGKFESSKLSTYFAYQELTGDFVISAKAKTIGLLRENGSYQFPTGILMCVCDAAAT
 TGLMGHASLNDITVDTTVNLVATYGHQTTAGSWNKTGTTDVTAGDNLYIQLERAGNS
 YTARYSTDGGATYSNIGGSSFTDLPDTLKVGFATPNNTGEQTFVYEDIQITQ"

ORIGIN

1 atgctcgata tgacaaaacg aactctatct gcgttgtag ccctgtgcgc aacattaacg
 61 gcttgccgtg gtggcgatat aaccagcggc ggcgatgcta taccggcagt aaaccaaccc
 121 gccccagtac aagagcctga acctgaacct gaaccacaac cggaaccgga acccgaaccc
 181 gagcccgagc cagaaccaga gggcgcgtgg acctgcccag aaacaggctt ctactctgt
 241 gacgacttg aagacggcac gttgatgac aagtgggacg atctattgc cacatagcag
 301 ctaccaagcc ctggtgtatt cgacatatta gacgaagcaa gcggcaaate ttgcgcttt
 361 acagcaggca cccgtggcgg tgacttagca gatggcgaac ttattgtgt aaaagataca
 421 gcattcgaaa atgtaacca cgcagattac tccttagagt accgtattcg cccgcgcaac
 481 aacggcaaca caggcaacaa gtacctgcac gctatgtgc gctacgaagg ccctaaagaa
 541 tattactttg gcggttaag catgcaaggc tctactgcaa gtacgcaagt agaagcagg
 601 ttctattgc cagaaaacac cactagcatt agcaaccgt tggcgcaggc caagtacccg
 661 ttagagctag gtacaacagg catgagcgac ggctactggt acgaagtacg ctctgatag
 721 ataggcaata caggcaccat ttacctagat ggcaaccac aaggcagctt taccgatgcc
 781 gatggcctt acccataac aggtaaaatt ggcttatga ctacaaccg ctactcgaa
 841 attgattggg tgcgagtagg cgaccagct attagcctg tacaacttc actggattac
 901 gccagcccg cttgggaagc agcggcagac caagaccgc taaacgtaac agttactgcc
 961 atacaaagcg atggcgtaac agcagatacc ttaccgcag ttacgagca taccaatgta
 1021 gtaaccacaa gtattgcaaa taacgtagta accattacc ctgtagctca aggtatgcc
 1081 accgtgacct ttaccgctg ttcatgct aatcgctta aaacaattga ttagaaaatt
 1141 gcacgcgct ttgtatgtc tactaccgac tacggcgata tagctctaa ggtaacacca
 1201 actgttgga tgaactgac caaccagac gcacattaa gcattacatt cgatagcgca
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 1441 agtaacgcac ttgcctacg ccaagactac tacgttgcca ttggcgataa cgtacttacc
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 1561 tctaccaaag cctctgccc taccggcaac accgtaactg tagacgacga tgcaagtga
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 1681 atcaccatta acattgctaa cggcaactac tacgagccgc tatatctagc agagcgcaac
 1741 aacgtaacgc taaaaggta aagccgcgac gggttggtta ttcatataa caaccacgaa
 1801 gccatgaac gtggcagcac tggccgcgca aacttctatg ttccaactc agacatgta
 1861 accctagaaa cgtaaacct taaaacggg catcagcgca ctggtggtg cgaccaagca
 1921 gaaactatct acttcaatag cagcagcaat accgatcgt taattgcaa aggcgctgt
 1981 ttatttagt aacaagatac gctgttact aaaggctaca actggttcta caactcgtt
 2041 tggtaggta acgtagactt tattggggc tacagcgag taacctgtt tgaagaaca
 2101 gaaattcgat ctattgccga ctctaaacca ggtgcggcg actcggttg ctatattctg
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 2701 aacattaccg agcaaacaga cagcaatatt acattcactg cagacggcg taagttaga
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 2821 gccaaagcta aaaccattg ctactgcgc gaaaacggca gctaccagt ccctacaggc
 2881 atattgatg gtgttgca tgcgcgagc gcaacaactg gctaatggg ccacgccagc
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3001 accacagctg gtagctggaa taaaactgga acgactgacg taaccgctgg cgacaacctg
3061 tatatacagc tagagcgcg aggtaatagt tataccgcac gctactcgac tgatggcgg
3121 gccacctata gcaacattgg tggcagctca ttacagaca ccctccaga cacacttaa
3181 gtgggtttct tcgctacgcc taacaacacc ggtgagcaaa cttcgttta cgaagatata
3241 caaatcactc agtaa

LOCUS NZ_AABI02000026 1176 bp DNA linear BCT 23-SEP-2003
DEFINITION Microbulbifer degradans 2-40 Mdeg_26, whole genome shotgun
sequence.

ACCESSION NZ_AABI02000026 REGION: complement(18555..19730)

VERSION NZ_AABI02000026.1 GI:28878276

KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40

ORGANISM Microbulbifer degradans 2-40

Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
Microbulbifer.

REFERENCE 1 (bases 1 to 1176)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23029482.
Protein-coding genes were predicted using GeneMark program (kindly
provided by M. Borodovsky). Functional annotation is based on CDD
(Conserved Domain Database) and COG (Clusters of Orthologous
Groups) assignments, it has not yet been subject to manual review.
DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson
microbes@cuba.jgi-psf.org.

COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

source 1..1176

/organism="Microbulbifer degradans 2-40"

/mol_type="genomic DNA"

/strain="2-40"

/db_xref="taxon:203122"

gene 1..1176

/gene="Mdeg3246"

CDS 1..1176

/gene="Mdeg3246"

/codon_start=1

/transl_table=11

/product="COG4677: Pectin methylesterase"

/protein_id="ZP_00067831.1"

/db_xref="GI:23029497"

/db_xref="COG:COG4677"

/translation="MGMGTKINFLLLGFILSACSLSGCADKIKRNTPLTETALPSKKI

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DIVGAGKNKTYVQYNLNAEQGKAYHRDVGWGTGPSATFTINASEVNVSDLTIENTFDL

RNDSKDKTDPSKVRASQGVALLLDEHSDKVALYRVGLYGYQDTLFGANGKRAFIYQSDI

AGNVDFIFGAGQVVIENSRRVISRPRGKAIASNEIAGYITAPSTNITDAFGLVFINSRL

EREQGVADASVTLGRPWHPTTNFSDGRYADPNAIGHALFFNCFMDAHIHPARWSSMKG

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ORIGIN

1 gtgggtatgg gtacaaaaat taatttttg ctattaggtt ttatttgc tgcatgtca
61 ttaagtggct gcgccgacaa aataaagcgc aatacgctt taaccgaaac ggcattgccg
121 agtaaaaaaa tactctatgt acaaaccgaa gtatgtgacc cgccttcgca attaacgggt
181 agttgtaca acagcttgca gcgagctatt gacgtggcgc acacagtgcc gtctgctacc
241 catgtaacca ttgaaatggc tgcggggcat taccacgaac gcattgtgct tagccgtggc
301 aatatcgata ttgttggtgc aggtaaaaat aaaacctatg ttcaatacaa cctgaatgcc

361 gagcagggt aagcttatca cgcgcacggt tggggtactc ctggctcagc tacatttacc
421 attaatgcca gtgaagtaaa tgtagcgat ttaactatcg aaaatacttt cgacttttta
481 agaaatgatt caaaagataa aaccgaccct tcaaaagtga gggcatcgca aggcgttgca
541 ttattattgg atgaacacag cgataagggt gcgctgtatc gagtaggcct atacggatac
601 caagacaccc tatttgcaaa tggaaagcgt gcaattatct accaatcaga tattgcaggc
661 aatgttgatt ttatttttg cgctggccaa gtgggtatag aaaatagtcg tgttatttct
721 aggccgcgcg gcaaagccat tgctccaat gaaattgccg gctatatcac agcgccatcc
781 accaatatta cggacgcctt tggctgggt ttattaata gtcgattaga acgtgagcaa
841 ggcgtggcag atgcgtcggc cacctgggt cgccctggc accctacaac caatttcagc
901 gatggccgat atgccgaccc aaacgcgatt ggccatgcgc tattttttaa ctgctttatg
961 gatgcgcata ttcacccgcg gagatggct agcatgaaag gcaccgctaa agacggcagt
1021 aaaacgctag tgtttacgcc cgagcaatcg cgttttttg aagttcagtc ctttgcccc
1081 agcggcaacg atgaagtaac cacctcgat caticgttaa gcgccgactc attacgcgaa
1141 caagcgctcg gcgattggaa tgtatcaatt aactaa

LOCUS NZ_AABI02000011 2745 bp DNA linear BCT 23-SEP-2003
 DEFINITION Microbulbifer degradans 2-40 Mdeg_9, whole genome shotgun sequence.
 ACCESSION NZ_AABI02000011 REGION: 36905..39649
 VERSION NZ_AABI02000011.1 GI:28878291
 KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40
 ORGANISM Microbulbifer degradans 2-40
 Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
 Microbulbifer.

REFERENCE 1 (bases 1 to 2745)
 AUTHORS NCBI Microbial Genomes Annotation Project.
 TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
 Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23028020.
 Protein-coding genes were predicted using GeneMark program (kindly
 provided by M. Borodovsky). Functional annotation is based on CDD
 (Conserved Domain Database) and COG (Clusters of Orthologous
 Groups) assignments, it has not yet been subject to manual review.
 DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.
 URL -- <http://www.jgi.doe.gov>
 Contact: Paul Richardson
microbes@cuba.jgi-psf.org.
 COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

source 1..2745
 /organism="Microbulbifer degradans 2-40"
 /mol_type="genomic DNA"
 /strain="2-40"
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 gene 1..2745
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 CDS 1..2745
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 /transl_table=11
 /product="hypothetical protein"
 /protein_id="ZP_00066475.1"
 /db_xref="GI:23028057"
 /translation="MSALTRPKFGAHTKLFHAIKHALTPVIFLGAAAFPLAAHSQYNM
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 DLDGDGGYELIVKWDPSNAKDNSQSGYTGNNVYLDAYEISGEFMWRIDLGRNIRAGAHY
 TQFLAFDFDSDGKAEVAVKTADATKDSQGVVIGDSNADYRNSAGYVLSGPEYLTMFEG
 QTGRALNTVNYVPARGSVSSWGDNYGNRVDRFLGGVAYLDGQNPSLMSRGYYTRTVV
 AAWDWNRNGQLSQRWVFDSNTSGNSSYAGQGAHSLTIGDVEDADGKQEIFGAMTIDDNG
 TGLNNTLRLGHGDALHLSMDPSNPGLEVFVMECPSCYGEHGIEMHDAATGQILWSHP
 GDYIDIGRGVAMDIDPRYAGYEAWASRGGLYSAGKETISSTRPSQINFAAWWDGDLR
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          /db_xref="GI:23028058"
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ORIGIN

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1 atgtcgccac tcaactgtcc caaatttggg gcacacacca aactgttcca cgctataaag
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121 caatacaaca tggaaaacct cgaccgctgg ttggtggcca tagatcgcaa agacggcagc
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601 gagtttatgt ggcgataga cctaggccgc aatattcgag caggcgccca ctacacgcaa
661 ttttagcat tcgatttga tagcgatggc aaagcagaag ttgcagttaa aaccgcagac
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1801 aacgtgggct acaaccaacc acctacccc tcttacttti tgggtgcggg tatgactacc
1861 cccaaccaac cacacataac catagtggc gaaggcacag tgcagcctcc agcccctaca
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2401 agttccagta gtatctcgag cagcagctca tccggcggtt caacagcagg cctagcttgc
2461 gccaacggca gtacagatac atggggaacg gggtttgtgt taaacggctt ccaagtagaa
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2581 aacataacca acgcatgggg tgtaaacgta gaaacaacag gcacaaccgt ttagcaaca
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2701 acatcggcaa cggcggtaag caaccgcta tgcagtgcc agtaa

LOCUS NZ_AABI02000009 2370 bp DNA linear BCT 23-SEP-2003
 DEFINITION *Microbulbifer degradans* 2-40 Mdeg_10, whole genome shotgun
 sequence.

ACCESSION NZ_AABI02000009 REGION: 151580..153949

VERSION NZ_AABI02000009.1 GI:28878293

KEYWORDS WGS.

SOURCE *Microbulbifer degradans* 2-40

ORGANISM *Microbulbifer degradans* 2-40

Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
Microbulbifer.

REFERENCE 1 (bases 1 to 2370)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
 Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23028157.

Protein-coding genes were predicted using GeneMark program (kindly
 provided by M. Borodovsky). Functional annotation is based on CDD
 (Conserved Domain Database) and COG (Clusters of Orthologous
 Groups) assignments, it has not yet been subject to manual review.

DNA sequence and predicted proteins are available for BLAST at

http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson

microbes@cuba.jgi-psf.org.

COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

source 1..2370

/organism="Microbulbifer degradans 2-40"

/mol_type="genomic DNA"

/strain="2-40"

/db_xref="taxon:203122"

gene 1..2370

/gene="Mdeg2067"

CDS 1..2370

/gene="Mdeg2067"

/codon_start=1

/transl_table=11

/product="COG3507: Beta-xylosidase"

/protein_id="ZP_00066674.1"

/db_xref="GI:23028263"

/db_xref="COG:COG3507"

/translation="MRSLAPIKIREKIRETLMFNIRAWQLDLPLALLAFSSTSIAIDN

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PSFTNIAVHDPSVIEANHQYYVFGSHLSVAKTPDLKNWSRVADGVTNNPLFNDVTSE

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ORIGIN

1 gtgcgcagtc tagccccc at aaaaataaga gagaaaataa gagagacact catgtttaat
 61 atacgcgctt ggcaactga ctggccctg gcgtattgg cggttctgct tacaagttac
 121 gctatcgata acggcactta cacaattcaa tctaaacaca gtggcaaggt ttagaagtg
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 961 ggcaactgca gcggcgcaat tgaacctatc acttttgcca caccaagctt taccaatata
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LOCUS NZ_AABI02000014 1089 bp DNA linear BCT 23-SEP-2003
 DEFINITION Microbulbifer degradans 2-40 Mdeg_13, whole genome shotgun
 sequence.

ACCESSION NZ_AABI02000014 REGION: 123595..124683

VERSION NZ_AABI02000014.1 GI:28878288

KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40

ORGANISM Microbulbifer degradans 2-40

Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
 Microbulbifer.

REFERENCE 1 (bases 1 to 1089)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
 Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23028504.
 Protein-coding genes were predicted using GeneMark program (kindly
 provided by M. Borodovsky). Functional annotation is based on CDD
 (Conserved Domain Database) and COG (Clusters of Orthologous
 Groups) assignments, it has not yet been subject to manual review.
 DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson
microbes@cuba.jgi-psf.org.

COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

source 1..1089

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/mol_type="genomic DNA"

/strain="2-40"

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gene 1..1089

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CDS 1..1089

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/transl_table=11

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/protein_id="ZP_00066990.1"

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/db_xref="COG:COG3940"

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 GPIVTLSEPTLPWEIIGHKVNEGA AVIKHGKRIFISYASATDHNYAMGLLWADENAD
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 DPNRHTRVRKVYWDEQGMPDFRQHEADL"

ORIGIN

1 atgagtagct tcataatgga taaaagccag ctacaaagtg gttttgcgtt taaaacaagt
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 121 agcagcgcca agctcgacc cgtcgctct cctagttac cgcagccatt agtggcccaa
 181 cgggcagacc cttgggtgca caagcacagc gatgggtatt actactttat agcaacggt
 241 ccagcatatg accgcttaga aatgcgtagg gccacaacca tagcaggctt acgtagcgcg
 301 cccgctgtag tggataggca gcgcaatact attggaggta tgagcgcgaa tatttggg

361 cccgagctgc atttattga tggtaaattg tacatctatg tagcggctgc caccgatcac
421 aacaagccgt ggacaattcg tatgcacacg cttccaatg catcggccaa ccctatgcaa
481 ggtgagtggc aagaagaggg gcgctttcat acaccgctag atactttctc gctagatgcc
541 acaaccttg agcacagggg taaacgctat ttagtatggg cgcaacagaa tgaagcccg
601 acttataact cggcgttact tatagcgcaa atggatagcc ctacaagtat tactggcccc
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781 gatcataact atgcgatggg ttgttatgg gcagacgaaa acgctgattt gctcgacgca
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901 ggccctggcc ataattgtt ttgtaaagct gaagatggg ttaccgattt aatgggtgac
961 cacgcgcgtg attataaaga gatagatggg gagccattgc gagacccaaa ccgccacacg
1021 cgggtgcgca aagtgtattg ggatgaacag ggcattgccg atttcgtca acatgaagca
1081 gacctatag

LOCUS NZ_AABI02000014 945 bp DNA linear BCT 23-SEP-2003
 DEFINITION Microbulbifer degradans 2-40 Mdeg_13, whole genome shotgun
 sequence.

ACCESSION NZ_AABI02000014 REGION: 109190..110134

VERSION NZ_AABI02000014.1 GI:28878288

KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40

ORGANISM Microbulbifer degradans 2-40

Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
 Microbulbifer.

REFERENCE 1 (bases 1 to 945)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
 Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23028504.
 Protein-coding genes were predicted using GeneMark program (kindly
 provided by M. Borodovsky). Functional annotation is based on CDD
 (Conserved Domain Database) and COG (Clusters of Orthologous
 Groups) assignments, it has not yet been subject to manual review.
 DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson
microbes@cuba.jgi-psf.org.

COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

source 1..945
 /organism="Microbulbifer degradans 2-40"
 /mol_type="genomic DNA"
 /strain="2-40"
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 CDS 1..945
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 /db_xref="COG:COG3940"
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 AISCSDANPLTGEWIFEGKIDSGIDAFCLDATTFTHSNELYYVWAQKELDV RGNSNLM
 IAKMETPTKLATKPVRLSKPEYDWEIQGFVWNEGPSIVKHGSRIFISYSGSATDERYA
 MGILWAEQSADLLDPASWTKSVEPVLVSEPSEKVFPGPHNSFTVDEEGNDMLVYHARN
 YTEIEGDPLWDPNRHTYVKKLRWDETGMPIFGSPA FEE"

ORIGIN

1 gtgaaaaaat tatcgctct tatagagcaa cgtgcagacc cttatat tta taaacacacc
 61 gacggctact attattttac ggcttcgggt cccgcctatg atggcataga actgcgtcgc
 121 gcaaaaacta tacaagcgtt agccaccgca gaaaccgtta tgggtggcg caagccaago
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 361 aaaatagata gcggcataga tgcattctgt ttatagcca ccacctttac tcacagcaat

421 gagctctact atgtttgggc gcaaaaagaa ttagatgttc gcggcaactc taatttgatg
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541 gaatacgact gggagattca gggtttttgg gtaacgaag gcccatccat tgtaagcac
601 ggctcacgta tttttatttc ttattctggc tctgctaccg atgagcgcta cgcaatgggt
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721 gagcctgtat tagtttctga accctctgaa aaagtatttg gccaggcca caatagttt
781 actgtggatg aagagggtaa cgatagttg gtgtatcatg ctgcgaatta taccgaaatt
841 gaaggcgacc cgctgtggga cccaaatcgt catacttacg ttaaaaaatt gcgctgggat
901 gaaacaggca tgcctatttt tggcagccct gcgtttgaag agtag

LOCUS NZ_AABI02000038 1053 bp DNA linear BCT 23-SEP-2003
DEFINITION Microbulbifer degradans 2-40 Mdeg_38, whole genome shotgun
sequence.

ACCESSION NZ_AABI02000038 REGION: <3..1055

VERSION NZ_AABI02000038.1 GI:28878264

KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40

ORGANISM Microbulbifer degradans 2-40

Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
Microbulbifer.

REFERENCE 1 (bases 1 to 1053)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23029863.
Protein-coding genes were predicted using GeneMark program (kindly
provided by M. Borodovsky). Functional annotation is based on CDD
(Conserved Domain Database) and COG (Clusters of Orthologous
Groups) assignments, it has not yet been subject to manual review.
DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson

microbes@cuba.jgi-psf.org.

COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

source 1..1053

/organism="Microbulbifer degradans 2-40"

/mol_type="genomic DNA"

/strain="2-40"

/db_xref="taxon:203122"

gene <1..1053

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CDS <1..1053

/gene="Mdeg3581"

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/transl_table=11

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/protein_id="ZP_00068164.1"

/db_xref="GI:23029864"

/db_xref="COG:COG3507"

/translation="NGYYAVLNKHSKGKALDLYGFDTSNGANIAQWAFWGGDPQQWQFT
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GLAWDGLPSVFPNGLSWWKTYVPGQSNNDVWAPDVRTYNGRVLYYSISTFGSRVSAI
GLASASSLAASDWQDHGLVINTTSSSDWNAIDPDLVVDEHGNPWLTMGSWNSGIKVMR
LNPITMKPIGTLYSIAQKGGGIEAPSIVYRRGYLYFVSIGKCCAGVDSTYQIAYGRS
TSITGPYLDKNGNDMMSSGGGSILDAGNNVWVPGGQDIINTDVIVRHAYDATDAGTPK
MIISTLNWDANGWPKY"

ORIGIN

1 aatggctatt atgccgtgct aaataaacac agcggcaaag cgtagattt gtatggttt
61 gatacgtcta acggcgcgaa tattgcgcaa tgggcctttt gggcgggga cccgcagcag
121 tggcaattta ccaaaatcgc caatgtaggt gcgcccag tagatacatc taccaccaac
181 ggtgcaacca accactggtc ctaaccgtt aatctagtga ctcacgaccc cacaatggcc
241 tacgaaaacg gctcatggtg gttgtatcaa accggcgagg gaatttacg taagtattca
301 gccaatgggt tggcgaggga tggcttacct tctgtgttc ccaatggtt aagtggtgg

361 aagacctatg taccggcca gtcgaacaac gatgatggg cgcctgatgt acgcactat
421 aatgggcggg ttatttga ctattccatc tctactttg gctcgcgtgt atctgccatt
481 ggtttggcgt cggcatcgag ttggctgcg agtgattggc aggaccacgg cttagtaatt
541 aataccacct catctagcga ttggaatgcg atcgaccag atttagtggc cgatgagcat
601 ggcaaccctt ggtaacaat gggaagtgg aacagcggta ttaaagtgat gcgctgaac
661 cccattacca tgaagccaat tggcacactt tattctattg cgaaaaggg cggcggatt
721 gaagcgcctt ctattgtgta tcgccgtggg tattactatt tattgtttc tatcgcaaa
781 tgctgtcggg gcgtagatag cacctatcaa attgcttacg ggcgctctac aagtattacc
841 ggcccttatt tggataagaa cggcaacgat atgatgagtg gtggtggcag tattttagat
901 gcgggcaaca acgtgtgggt tggccctggg gggcaagata ttattaacac cgatgtcatt
961 gtgcgccacg cgtacgatgc cacagatgca ggcacaccta agatgattat tagtaccttg
1021 aattgggatg ctaatggatg gccgaaatac tag

LOCUS NZ_AABI02000014 1041 bp DNA linear BCT 23-SEP-2003
 DEFINITION Microbulbifer degradans 2-40 Mdeg_13, whole genome shotgun
 sequence.

ACCESSION NZ_AABI02000014 REGION: complement(121237..122277)

VERSION NZ_AABI02000014.1 GI:28878288

KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40

ORGANISM Microbulbifer degradans 2-40

Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
 Microbulbifer.

REFERENCE 1 (bases 1 to 1041)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
 Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23028504.
 Protein-coding genes were predicted using GeneMark program (kindly
 provided by M. Borodovsky). Functional annotation is based on CDD
 (Conserved Domain Database) and COG (Clusters of Orthologous
 Groups) assignments, it has not yet been subject to manual review.
 DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson

microbes@cuba.jgi-psf.org.

COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

source 1..1041

/organism="Microbulbifer degradans 2-40"

/mol_type="genomic DNA"

/strain="2-40"

/db_xref="taxon:203122"

gene 1..1041

/gene="Mdeg2388"

CDS 1..1041

/gene="Mdeg2388"

/codon_start=1

/transl_table=11

/product="COG3507: Beta-xylosidase"

/protein_id="ZP_00066989.1"

/db_xref="GI:23028596"

/db_xref="COG:COG3507"

/translation="MLNKNKRPITFALVVSLLALLALAGCSEAKQVSIHDPVMIKEGD
 TYYLFSTGPGITMYSSSDMKNWRRGEVFNQAPSWASNAVYPYFKGHLWAPDIEKDGL
 FYLYYSVSAFGKNTSGIGVTVSPTLNPRAPNYGWQDKGMVLRVPERDEWNAIDPNIV
 VDNINGTAWMAFGSFWQSLKMVALDSSWTKIAEPQQWHTIAALPKGSMPTGDAVKDGEI
 EAPFIFKKNDYFLFVSWGKCCRKDESTYRLAMGRSKNTTGPFLDKNGKDLAQGGGTL
 LISGNKNWPGLGHNSAYTFDGKDWLVHAYESADNGLQKLKILEINWDKDGWPTVDTK
 ELDEFVSIELTQ"

ORIGIN

1 atgcttaaca aaaacaaacg cccaattaca ttcgcttag tcgttagcct ctagccctg
 61 ctgcccctg caggctcgag cgaggcaaaa caagtaagca tccacgaccc agtaatgatt
 121 aaagaagggt acacctacta ctgttttagc actggcccg gcataacaat gtagctct
 181 agcgatatga aaaactggcg ccggaaggc gaagtattta atcaagcccc tagtggggc
 241 tccaacgcg taccctatit taaaggccac ctgtgggcac ccgacatcat tgaaaaagat
 301 ggtctgtt accttacta ttctgtgtct gctttggaa agaacacatc cggcattggc

361 gttaccgtat cgccacgct taaccacgc gcgccaatt acggttgga agataaaggc
421 atggtattgc gcagcgtgcc tgagcgcgac gagggaacg ctatcgacc caatattgtg
481 gtagataaca acggcaccgc atggatggct ttggctcct ttggcaaag cttaaaaatg
541 gtggcactag acagcagctg gacaaaaata gctgagcctc aacagtggca taccatagca
601 gccttacca aaggcagtat gccacaggc gacgcagtaa aggacggcga aatagaagct
661 ccttttatt ttaaaaagaa cgacgattac ttttgttg taagtgggg taaatgctgc
721 cgcaaagatg aaagcaccta cgcctagca atgggcccga gaaaaatac taccggtcca
781 ttcttagata aaaacggcaa agacctgcc caaggtggg gcacctatt aataagtggc
841 aacaaaaact ggcccggctt aggccacaac agcgcctaca cctcgacgg caaagattgg
901 cttgtgctac acgctatga atctgcagat aacggttac aaaaactaaa aatattagaa
961 ataaactggg ataaagacgg ctggccaact gtagatacca aagaactgga tgagttgtt
1021 agtattgaat taactcaata a

LOCUS NZ_AABI02000014 1860 bp DNA linear BCT 23-SEP-2003
DEFINITION Microbulbifer degradans 2-40 Mdeg_13, whole genome shotgun
sequence.

ACCESSION NZ_AABI02000014 REGION: 129042..130901

VERSION NZ_AABI02000014.1 GI:28878288

KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40

ORGANISM Microbulbifer degradans 2-40

Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
Microbulbifer.

REFERENCE 1 (bases 1 to 1860)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23028504.
Protein-coding genes were predicted using GeneMark program (kindly
provided by M. Borodovsky). Functional annotation is based on CDD
(Conserved Domain Database) and COG (Clusters of Orthologous
Groups) assignments, it has not yet been subject to manual review.
DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson
microbes@cuba.jgi-psf.org.

COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

source 1..1860

/organism="Microbulbifer degradans 2-40"

/mol_type="genomic DNA"

/strain="2-40"

/db_xref="taxon:203122"

gene <1

/gene="Mdeg2392"

CDS <1

/gene="Mdeg2392"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/protein_id="ZP_00066993.1"

/db_xref="GI:23028600"

/translation="MDNIMKMIKLALAVTLAVVWAGCTNQAGLNAENKNIERQTINS
PDKSLKVRLSLDESGKVFYSISRNGEQVMLPSQLGVELNSQAFTDGLTITDVGKVN
DSYTLHGGKQRDITYNANEKIYSLKNKQGDKLIIFRVSNMGVAFQYRFPNTAKQLLA
VKKEITSFAFEHTTKAWLQPIAVAQGTWANTNPSYEEHYQMNIPVDTVSPSPAGWVFP
ALFKANKHWLLITEAGMNGDYHASRLHAESPNGEYSLGIPMAAEVFEQDGNKGALLAQ
SNTAFHSPWRVILVGGLDTIIASTLGTDLADPAIAKMDVFKPGTASWSWALLKDESVN
YETSLEFIDYAAEMGWDTLVADWDRRIGYERTAQLAAYAQSKNVGLLVWYNSSGDW
NTTEYSPKSALLDRDKRRAEFARLQNMGVKGVKIDFFPGDGKSVMAYYNDLAKDAADY
NLLVNYHGSSLPRGLHRTYPNIMTMESVHGFEMITFMQPSADKAATHMAILPFTRNAF
DPMDFPTTFSDIPNIERRTSNGFELALPVLFLSGLQHIAETAQGMATNAPDYVKAYM
RDIPVLWDESKLIDGMPGEHVVIARKHGERWVAGINATNEAINLEMNFDALGKQGT
LITDSNINTKGVESFTSHTITATKNNALTVKANGGFVIVFN"

gene 1..1860

/gene="Mdeg2393"

CDS 1..1860

/gene="Mdeg2393"
 /codon_start=1
 /transl_table=11
 /product="COG3940: Predicted beta-xylosidase"
 /protein_id="ZP_00066994.1"
 /db_xref="GI:23028601"
 /db_xref="COG:COG3940"
 /translation="MAAGQIISLEVVKVKKIEIMKHTARTIALGATGAALLTGLIACN
 GTNVNTNGDTQQASIKKAPEGMFANPLFANGADPWLEYYDGNYYLTTTTWTSQVLVMRK
 SPTLDGLSTALPVNVWSDSDLTRCCNFWAFEFHRLNGPNGWRWYLMYTSQGHGTLDHQ
 HLSVLESVGDDPMGPYTYKGEMMPNTWNIDGSYLEHNGQLYLLWSEWVGDEQQNFISK
 MTTTPWSIEGPRALLTRPEAEWEKSGRKVNEGPEILKKDGRFTLIYSASYCDTPDYKLA
 MKELTGDDPMNSEHWTKYDKPVFERGNGVFAPGHNGFFKSPDGTEDWIVYHGSKEEH
 GCGATRSVRAQKFTWNTDGTNPFGEPIEGQFLPLPSGENGPLVTALQGARIQLRNGE
 SCLLAEGKELKQGSCQAEASLWVMDNTADNHYRFGNVASNLFLTADEGLSQSAWVNTA
 SQRWALNAGEGNFVAFTNKYTGDALMQNNWQILPVGKVAISSIQSGRVLQACDKNSAN
 VNQGGWQGRACQAWQFNPASEGHVQIKTGNQCLTVENKSIVPGTNVIAGECESTSSQW
 LYQLDKEGRATFTNRESKQRLDLANGLADGTNFAQAPALDTICQAFQVRYLP"

ORIGIN

1 gtggccgcag gccaaataat ttcactggag gttaaagtga aaaagataga agaaataatg
 61 aaacacacag cgcgactat agcgctaggt gcaacagggt ccgccttgct aacgggggta
 121 atgcctgta acggtacca tgtgaataca aacgggggata cccaacaagc aagcattaaa
 181 aaagcgccag aaggcatgtt tgccaaccgg ttgttcgcca atggcgcgaga cccttggtta
 241 gagtattacg atggcaatta ctacctcact accaccacat ggacatcgca acttggtatg
 301 cgtaaatcac ccacgttga tggttgtct actgcgctgc cggtgatgt atggtccgat
 361 tcagatttaa ccgcgtctg taactttgg gcgttgaat tccatcgctt aaacggccct
 421 aacggctggc gttgtattt aatgtacacc tcgggccagc acggcacttt agatcaccaa
 481 cacttaagcg tattagaaag tgtgggtgac gaccctatgg ggccatacac ctacaaaggt
 541 gaaatgatgc ccaatacatg gaatatagac ggcagttatt tagagcataa tggcaatta
 601 tattgtgtg ggtctgaatg ggtaggtgac gaggcagaaa actttataic taaatgacc
 661 acccatgga gcattgaagg ccgcgagca ctgttaactc ggccggaagc agagtgggaa
 721 aaaagcggtc gcaaagttaa cgaaggccca gagattctaa aaaaagatgg tcgtacctt
 781 ttgatttact cggcgagcta ttgcgatacg ccagattata aactggcaat gaaagagcta
 841 acggcgagc acccaatgaa ctccgagcac tggactaaat acgataagcc cgtgtttgaa
 901 agaggggaac gtgtgtttgc ccaggccac aatggtttct tcaaatcgcc cgtggcaca
 961 gaagattgga ttgtgtacca cggaaattcg aaagaagagc acggctgcgg tgcaacgcgc
 1021 tctgtgcgcg cacagaaatt tacttggaac acagacggca ccccaaattt tggtagcca
 1081 ataccagaag gccaaatttt gcccttacct tctggcgaaa acggtccttt agtgactgca
 1141 ctgcaagggt cacgtattca gtgcgcaat ggcgaaagct gtttattagc cgaaggtaaa
 1201 gagctgaagc agggcagttg ccaagcagaa gccagttat gggtaattga taacacggca
 1261 gataatcact accgctttgg caatgtagcc agcaatttat ttttaacggc agacgaaggc
 1321 cttagtcaga gtgcctgggt taatactgca agccagcgct gggcacttaa tgcaggcgaa
 1381 ggtaactttg ttgcgtttac aaacaagtac accggcgatg cgcttatgca aaataattgg
 1441 caaatactac cggttgcaaa agtggcaatt agcagcattc aaagtggccg cgtattacag
 1501 gcgtgcgata aaaacagcgc gaatgtaaac caaggcggct ggcagggtag ggctgtcaa
 1561 gcattggcaat ttaaccagc aagtgaaggc catgtgcaaa ttaaaccggg caaccaatgt
 1621 ttaaccgttg agaataaatt catagtgcct ggcaccaatg ttattgccg cgagtgtgaa
 1681 tcaactagca gccaatggct ttatcaatta gataaagaag gccgcgcaac cttcacaac
 1741 cgcgaaagca aacagcggtt agatttagca aactgcggcc tagccgacgg caccaacttc
 1801 gcacaagccc ctgcgttaga tactatttgc caagcattcc aagtgcgtta ttaccgtaa

LOCUS NZ_AABI03000006 1605 bp DNA linear BCT 17-JUN-2004
DEFINITION Microbulbifer degradans 2-40 Mdeg03_6, whole genome shotgun
sequence.

ACCESSION NZ_AABI03000006 REGION: 149813..151417

VERSION NZ_AABI03000006.1 GI:48861946

KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40

ORGANISM Microbulbifer degradans 2-40

Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
Alteromonadaceae; Microbulbifer.

REFERENCE 1 (bases 1 to 1605)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA

COMMENT Protein-coding genes were predicted using GeneMark program (kindly
provided by M. Borodovsky). Functional annotation is based on CDD
(Conserved Domain Database) and COG (Clusters of Orthologous
Groups) assignments, it has not yet been subject to manual review.
DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson

microbes@cuba.jgi-psf.org.

FEATURES Location/Qualifiers

source 1..1605

/organism="Microbulbifer degradans 2-40"

/mol_type="genomic DNA"

/strain="2-40"

/db_xref="taxon:203122"

gene 1..1605

/locus_tag="Mdeg02002711"

CDS 1..1605

/locus_tag="Mdeg02002711"

/codon_start=1

/product="COG3534: Alpha-L-arabinofuranosidase"

/protein_id="ZP_00315975.1"

/db_xref="GI:48862077"

/db_xref="COG:COG3534"

/translation="MNPASTLSVKTTNKTTHLKKVALTVAIVAPLTSWADV KVS LN
PQNTGETISKYIYGQFAEHLGSGIYGGIWWGEDSPIPNKNGFRNDVIKALQELQVPVI
RWPGGCFADEYRWRD GIGPREQRP IRV NTHWGGVEEPNTFGTHEFFELVELLNTEAYV
AGNLGTGSPQEMA EWLEYIVSNSNSTVVAERKKNGREEPW E VAFWGVGNESWGCGGNL
TPEYYTNLYRHFSTFVKATGAKRPKLVASGSYDDDETWTTPLSKLKNNIDGISHHYT
LPTSDWSIKGAATGFDEKEWILT LERTLKIDSYLATQTGILKKNPEGNIGLYLDEWG
TWYDAEPGTNPGFLYQQNTVRDAIVA AVNLNIFHNYADRLHMANIAQMVNVLQAMILT
DNEKM L LTPTYHVF KMYIPFQDATHIPLDIKGQRDYS AHKTTVPGFSA SAAKTPNGNI
V VSLVNLNPNEAE E VSIALQG I KVTITGELLTSQKMDAHNTFDKPNNVQPRALNQSD
YSISKNGKTLTVKLPAKAVVVLQLNK"

ORIGIN

1 atgaaccag cttaaccct aagtgtaaa acaactaata aaacaacaaa ccacctcaaa
61 aaagttgcc ttaccgtagc cgctatagtt gccccgctaa caagctgggc cgatgtgaaa
121 gttagcctaa acccacaaaa cacaggcgaa accataagta aatatatcta cggccaattc
181 gcagagcacc ttggcagcgg catatacggc ggcatatggg tggcggaaga ctccccaata
241 cccaacaaaa acggtcttcg taacgatgta atcaaagccc tgcaagagct acaagtacct
301 gttataagat ggccccgttg ctgcttgcc gacgaatac gctggcgtga tggcattggc

361 ccacgtgagc aacgccctat ccgcgtaaat acccactggg gcggtgtgga agaacccaat
421 acctttgta ctacgaatt ctgcgaatta gttgagctac ttaataccga agcctatgtg
481 gcaggtaacc taggcactgg ctaccacaa gaaatggccg aatggctgga atatattgtt
541 tccaactcca actctactgt agtggcagag cgcaaaaaaa atggccgca agagccttg
601 gaagtggcct ttgggggtgt gggtaatgaa tctgggggt gcggtggcaa ctaacgccc
661 gagtactaca ccaattata tgcctatctt tccactttg ttaaagccac tggcgctaag
721 cgccgaagt tagttgcaag cggctcgtat gatgatgacg aaacttgac aacgccacta
781 agtaagctca aaaataatat agatgtata agccaccact actacacct acccaccagc
841 gactggagca taaaagggtc ggctacaggc ttgatgaaa aagaatggat tctaccctt
901 gagcgacat tgaaaataga cagctacctt gcaactcaaa cgggtattct taaaaagaat
961 aacccgaag gcaatatagg gttgtattta gatgaatggg gtacgtgga cgatgcagag
1021 cccggtacaa acccggctt ttataccaa caaaataccg tgcgcgacgc catagtagca
1081 gcagtaaact taaatatatt ccacaactat gccgaccgt tacacatggc gaacatcgcc
1141 caaatgtaa acgtactaca ggcaatgata ctgaccgaca acgaaaaaat gttgctaca
1201 cccacgtatc acgtttta gatgtacata ccattcaag atgctacca tataccgtta
1261 gatataaaag gccagcgca ctacagcga cataaaacta ccgtaccagg gttctggcc
1321 tcggcagcta aaaccccaa tggcaatatt gtagttcac ttgtaacct taacccaaac
1381 gaagcgaag aagttagcat tgcactaaa ggcatcaagg taaaaacat tactggtgaa
1441 ttactacca gccaaaaat ggatgcgat aacacctcg acaagccaaa caatgtgcag
1501 ccacgcgcac ttaacaaag cgactacagc attagcaaaa acggcaaac cctaccgtt
1561 aagctaccg ctaaagccgt agttgttta cagctaata aataa

LOCUS NZ_AABI02000036 1194 bp DNA linear BCT 23-SEP-2003
DEFINITION Microbulbifer degradans 2-40 Mdeg_35, whole genome shotgun
sequence.

ACCESSION NZ_AABI02000036 REGION: 4764..5957

VERSION NZ_AABI02000036.1 GI:28878266

KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40

ORGANISM Microbulbifer degradans 2-40

Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
Microbulbifer.

REFERENCE 1 (bases 1 to 1194)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23029800.
Protein-coding genes were predicted using GeneMark program (kindly
provided by M. Borodovsky). Functional annotation is based on CDD
(Conserved Domain Database) and COG (Clusters of Orthologous
Groups) assignments, it has not yet been subject to manual review.
DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson
microbes@cuba.jgi-psf.org.

COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

source 1..1194

/organism="Microbulbifer degradans 2-40"

/mol_type="genomic DNA"

/strain="2-40"

/db_xref="taxon:203122"

gene 1..1194

/gene="Mdeg3529"

CDS 1..1194

/gene="Mdeg3529"

/codon_start=1

/transl_table=11

/product="COG3867: Arabinogalactan
endo-1,4-beta-galactosidase"

/protein_id="ZP_00068112.1"

/db_xref="GI:23029804"

/db_xref="COG:COG3867"

/translation="MLLAQLPVKKYFVLLAIFSFMLGCNSAGVQQSAKSIQVAGTHSK
PARFFAGADLSYVNEMEDCGATYRVNGVTTDPYQAFADAGANLVRVRLWHNPTWTEYS
DFADVKKTKIRKAKQNNQTVLLDFHYSDTWADPEKQFVPAAWEHMVDDTPALAQALAQY
TTDVLEKLQAENLLPDMVQVGNETNAEVLQLEAHMKHGEIDWQRNAALLNSGLAAVAE
FNQNNNTYIERVLHIAQPENALWWFDDAAQAGITDFEIIIGLSYYAKWSTYKLDISGEA
IRALRTAFNKDVLVVETSYPWMTMQNFDQANNVLDATSLQQGYPATAEQGKKYMMDLAK
QIMYAGGIGIAYWEPAAVWSTPCKTLWGTGSHWENAVFFDSGNNNEALPALSFYTDIMA
LFKQD"

ORIGIN

1 atgttattag ctcaattgcc agttaaaaaa tattttgtct tattagctat ttctcggtt

61 atgctggggt gtaatagtgc tggcgtacaa caaagtgcta aatcaattca gggtgctggc

121 acgcacagta aaccgcctcg ttttttgct ggtgccgacc ttcttacgt aaacgaaatg

181 gaagattgcg gagcaacata ccgcgtaaac ggtgtaacta ccgaccctta ccaagccttt

241 gccgatgccg gcgcaaattt agtgcgctg cgcttatggc acaaccctac ttggacagaa
301 tattccgact ttgccgacgt taaaaaaact atccgcaaag ccaaacaaaa taatcaaacg
361 gtattgttag attttcatta ttcagatacc tgggccgacc cagaaaaaca atttgtcca
421 gccgctggg aacatatggt gcatgacacc ccagcactag cgcaagcctt agcgcaatac
481 acaaccgatg tattagaaaa gctgcaagca gaaaacctat tgccagatat ggtgcaagta
541 ggtaacgaaa caaacgcaga agtcttacag ctagaagcgc acatgaaaca cggcgaaata
601 gattggcagc gcaatgcagc gctactaaac agtgggtag cagccgttc tgaattaac
661 caaaacaaca acacctatat tgaacgcgta ttacatatcg cccagccaga aaatgcttg
721 tgggtggttg acgatgccgc gcaggctggc ataaccgatt ttgaaattat aggtcttagc
781 tactatgcca aatggtaac gtataaatta gattccatcg gcgaagctat acgcgccttg
841 cgaaccgcat tcaataaaga tgtgttggtg gtagaaacct catacccctg gactatgcaa
901 aatttcgatc aagccaataa cgtgctcgat gctaccagct tgcagcaggg ctaccctgca
961 acggccgaag gccaaaaaaa atacatgatg gatttagcta aacaaattat gtacgccggt
1021 ggaattgga ttgcctactg ggaaccagct tgggtaagca cccctgcaa aactctatgg
1081 ggtacaggtt ctactggga aaatgccgtg tttttgact ctggcaaca caacgaagcg
1141 ctaccgcgc ttagtttcta cacagacata atggctctt ttaagcaaga ttaa

LOCUS NZ_AABI02000005 1263 bp DNA linear BCT 23-SEP-2003
DEFINITION Microbulbifer degradans 2-40 Mdeg_5, whole genome shotgun sequence.
ACCESSION NZ_AABI02000005 REGION: complement(76912..78174)
VERSION NZ_AABI02000005.1 GI:28878297
KEYWORDS WGS.
SOURCE Microbulbifer degradans 2-40
ORGANISM Microbulbifer degradans 2-40
Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
Microbulbifer.
REFERENCE 1 (bases 1 to 1263)
AUTHORS NCBI Microbial Genomes Annotation Project.
TITLE Direct Submission
JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA
COMMENT On Mar 7, 2003 this sequence version replaced gi:23027361.
Protein-coding genes were predicted using GeneMark program (kindly
provided by M. Borodovsky). Functional annotation is based on CDD
(Conserved Domain Database) and COG (Clusters of Orthologous
Groups) assignments, it has not yet been subject to manual review.
DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.
URL -- <http://www.jgi.doe.gov>
• Contact: Paul Richardson
microbes@cuba.jgi-psf.org.
COG assignment was automatically updated on Sep 23, 2003.
FEATURES Location/Qualifiers
source 1..1263
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CDS 1..1263
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endo-1,4-beta-galactosidase"
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1 gtgctgcaaa ttctaaaaga tcacggtatg gattccatcc gtctgcgcgt gtgggtaaac
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LOCUS NZ_AABI02000044 1770 bp DNA linear BCT 23-SEP-2003
DEFINITION Microbulbifer degradans 2-40 Mdeg_43, whole genome shotgun
sequence.

ACCESSION NZ_AABI02000044 REGION: <2..1771

VERSION NZ_AABI02000044.1 GI:28878258

KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40

ORGANISM Microbulbifer degradans 2-40

Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
Microbulbifer.

REFERENCE 1 (bases 1 to 1770)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23029947.

Protein-coding genes were predicted using GeneMark program (kindly
provided by M. Borodovsky). Functional annotation is based on CDD
(Conserved Domain Database) and COG (Clusters of Orthologous
Groups) assignments, it has not yet been subject to manual review.

DNA sequence and predicted proteins are available for BLAST at

http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson

microbes@cuba.jgi-psf.org.

COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

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CDS <1..1770

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/transl_table=11

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endo-1,4-beta-galactosidase"

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ORIGIN

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LOCUS NZ_AABI02000005 1020 bp DNA linear BCT 23-SEP-2003
DEFINITION Microbulbifer degradans 2-40 Mdeg_5, whole genome shotgun sequence.
ACCESSION NZ_AABI02000005 REGION: 56447..57466
VERSION NZ_AABI02000005.1 GI:28878297
KEYWORDS WGS.
SOURCE Microbulbifer degradans 2-40
ORGANISM Microbulbifer degradans 2-40
Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
Microbulbifer.
REFERENCE 1 (bases 1 to 1020)
AUTHORS NCBI Microbial Genomes Annotation Project.
TITLE Direct Submission
JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA
COMMENT On Mar 7, 2003 this sequence version replaced gi:23027361.
Protein-coding genes were predicted using GeneMark program (kindly
provided by M. Borodovsky). Functional annotation is based on CDD
(Conserved Domain Database) and COG (Clusters of Orthologous
Groups) assignments, it has not yet been subject to manual review.
DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.
URL -- <http://www.jgi.doe.gov>
Contact: Paul Richardson
microbes@cuba.jgi-psf.org.
COG assignment was automatically updated on Sep 23, 2003.
FEATURES Location/Qualifiers
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CDS 1..1020
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LOCUS NZ_AABI02000003 1686 bp DNA linear BCT 23-SEP-2003
 DEFINITION Microbulbifer degradans 2-40 Mdeg_3, whole genome shotgun sequence.
 ACCESSION NZ_AABI02000003 REGION: 276126..277811
 VERSION NZ_AABI02000003.1 GI:28878299
 KEYWORDS WGS.
 SOURCE Microbulbifer degradans 2-40
 ORGANISM Microbulbifer degradans 2-40
 Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
 Microbulbifer.
 REFERENCE 1 (bases 1 to 1686)
 AUTHORS NCBI Microbial Genomes Annotation Project.
 TITLE Direct Submission
 JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
 Information, NIH, Bethesda, MD 20894, USA
 COMMENT On Mar 7, 2003 this sequence version replaced gi:23026886.
 Protein-coding genes were predicted using GeneMark program (kindly
 provided by M. Borodovsky). Functional annotation is based on CDD
 (Conserved Domain Database) and COG (Clusters of Orthologous
 Groups) assignments, it has not yet been subject to manual review.
 DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.
 URL -- <http://www.jgi.doe.gov>
 Contact: Paul Richardson
microbes@cuba.jgi-psf.org.
 COG assignment was automatically updated on Sep 23, 2003.
 FEATURES Location/Qualifiers
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LOCUS NZ_AABI02000004 1545 bp DNA linear BCT 23-SEP-2003
DEFINITION Microbulbifer degradans 2-40 Mdeg_4, whole genome shotgun sequence.
ACCESSION NZ_AABI02000004 REGION: 268515..270059
VERSION NZ_AABI02000004.1 GI:28878298
KEYWORDS WGS.
SOURCE Microbulbifer degradans 2-40
ORGANISM Microbulbifer degradans 2-40
Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
Microbulbifer.
REFERENCE 1 (bases 1 to 1545)
AUTHORS NCBI Microbial Genomes Annotation Project.
TITLE Direct Submission
JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA
COMMENT On Mar 7, 2003 this sequence version replaced gi:23027141.
Protein-coding genes were predicted using GeneMark program (kindly
provided by M. Borodovsky). Functional annotation is based on CDD
(Conserved Domain Database) and COG (Clusters of Orthologous
Groups) assignments, it has not yet been subject to manual review.
DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.
URL -- <http://www.jgi.doe.gov>
Contact: Paul Richardson
microbes@cuba.jgi-psf.org.
COG assignment was automatically updated on Sep 23, 2003.
FEATURES Location/Qualifiers
source 1..1545
/organism="Microbulbifer degradans 2-40"
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IKRLPQVV"

ORIGIN

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LOCUS NZ_AABI02000004 1374 bp DNA linear BCT 23-SEP-2003
DEFINITION Microbulbifer degradans 2-40 Mdeg_4, whole genome shotgun sequence.
ACCESSION NZ_AABI02000004 REGION: 56484..57857
VERSION NZ_AABI02000004.1 GI:28878298
KEYWORDS WGS.
SOURCE Microbulbifer degradans 2-40
ORGANISM Microbulbifer degradans 2-40
Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
Microbulbifer.
REFERENCE 1 (bases 1 to 1374)
AUTHORS NCBI Microbial Genomes Annotation Project.
TITLE Direct Submission
JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA
COMMENT On Mar 7, 2003 this sequence version replaced gi:23027141.
Protein-coding genes were predicted using GeneMark program (kindly
provided by M. Borodovsky). Functional annotation is based on CDD
(Conserved Domain Database) and COG (Clusters of Orthologous
Groups) assignments, it has not yet been subject to manual review.
DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.
URL -- <http://www.jgi.doe.gov>
Contact: Paul Richardson
microbes@cuba.jgi-psf.org.
COG assignment was automatically updated on Sep 23, 2003.
FEATURES Location/Qualifiers
source 1..1374
/organism="Microbulbifer degradans 2-40"
/mol_type="genomic DNA"
/strain="2-40"
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gene 1..1374
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CDS 1..1374
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ORIGIN
1 atggtgaact acttaaagcg cgctgccctg tgcctgcttg cgctcgttgc tgtggcttgc
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121 gccggtgtgg cagcgacaga gttgtgcaa gtaaagtg ggcgctttac attgcgctgg
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541 atggcagacc ccaccaaacc atggccagct ttgcactff ttcagcggg gttttactct
601 aatgaagagg cgaaacaact attcaataat taccttaca aagtgtgaag ccgccgcaat
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LOCUS NZ_AABI02000001 2553 bp DNA linear BCT 23-SEP-2003
DEFINITION Microbulbifer degradans 2-40 Mdeg_1, whole genome shotgun sequence.
ACCESSION NZ_AABI02000001 REGION: complement(355661..358213)
VERSION NZ_AABI02000001.1 GI:28878301
KEYWORDS WGS.
SOURCE Microbulbifer degradans 2-40
ORGANISM Microbulbifer degradans 2-40
Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
Microbulbifer.
REFERENCE 1 (bases 1 to 2553)
AUTHORS NCBI Microbial Genomes Annotation Project.
TITLE Direct Submission
JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA
COMMENT On Mar 7, 2003 this sequence version replaced gi:23026153.
Protein-coding genes were predicted using GeneMark program (kindly
provided by M. Borodovsky). Functional annotation is based on CDD
(Conserved Domain Database) and COG (Clusters of Orthologous
Groups) assignments, it has not yet been subject to manual review.
DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.
URL -- <http://www.jgi.doe.gov>
Contact: Paul Richardson
microbes@cuba.jgi-psf.org.
COG assignment was automatically updated on Sep 23, 2003.
FEATURES Location/Qualifiers
source 1..2553
/organism="Microbulbifer degradans 2-40"
/mol_type="genomic DNA"
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/db_xref="taxon:203122"
gene 1..2553
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CDS 1..2553
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/product="hypothetical protein"
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ORIGIN

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LOCUS NZ_AABI02000011 1227 bp DNA linear BCT 23-SEP-2003
DEFINITION Microbulbifer degradans 2-40 Mdeg_9, whole genome shotgun sequence.
ACCESSION NZ_AABI02000011 REGION: complement(88053..89279)
VERSION NZ_AABI02000011.1 GI:28878291
KEYWORDS WGS.
SOURCE Microbulbifer degradans 2-40
ORGANISM Microbulbifer degradans 2-40
Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
Microbulbifer.
REFERENCE 1 (bases 1 to 1227)
AUTHORS NCBI Microbial Genomes Annotation Project.
TITLE Direct Submission
JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA
COMMENT On Mar 7, 2003 this sequence version replaced gi:23028020.
Protein-coding genes were predicted using GeneMark program (kindly
provided by M. Borodovsky). Functional annotation is based on CDD
(Conserved Domain Database) and COG (Clusters of Orthologous
Groups) assignments, it has not yet been subject to manual review.
DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.
URL -- <http://www.jgi.doe.gov>
Contact: Paul Richardson
microbes@cuba.jgi-psf.org.
COG assignment was automatically updated on Sep 23, 2003.
FEATURES Location/Qualifiers
source 1..1227
/organism="Microbulbifer degradans 2-40"
/mol_type="genomic DNA"
/strain="2-40"
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gene 1..1227
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CDS 1..1227
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LOCUS NZ_AABI02000013 5202 bp DNA linear BCT 23-SEP-2003
DEFINITION Microbulbifer degradans 2-40 Mdeg_12, whole genome shotgun
sequence.
ACCESSION NZ_AABI02000013 REGION: complement(66951..72152)
VERSION NZ_AABI02000013.1 GI:28878289
KEYWORDS WGS.
SOURCE Microbulbifer degradans 2-40
ORGANISM Microbulbifer degradans 2-40
Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
Microbulbifer.
REFERENCE 1 (bases 1 to 5202)
AUTHORS NCBI Microbial Genomes Annotation Project.
TITLE Direct Submission
JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA
COMMENT On Mar 7, 2003 this sequence version replaced gi:23028387.
Protein-coding genes were predicted using GeneMark program (kindly
provided by M. Borodovsky). Functional annotation is based on CDD
(Conserved Domain Database) and COG (Clusters of Orthologous
Groups) assignments, it has not yet been subject to manual review.
DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.
URL -- <http://www.jgi.doe.gov>
Contact: Paul Richardson
microbes@cuba.jgi-psf.org.
COG assignment was automatically updated on Sep 23, 2003.
FEATURES Location/Qualifiers
source 1..5202
/organism="Microbulbifer degradans 2-40"
/mol_type="genomic DNA"
/strain="2-40"
/db_xref="taxon:203122"
gene 1..5202
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CDS 1..5202
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 LAFLNSL"

ORIGIN

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LOCUS NZ_AABI02000006 4326 bp DNA linear BCT 23-SEP-2003
DEFINITION Microbulbifer degradans 2-40 Mdeg_6, whole genome shotgun sequence.
ACCESSION NZ_AABI02000006 REGION: 86580..90905
VERSION NZ_AABI02000006.1 GI:28878296
KEYWORDS WGS.
SOURCE Microbulbifer degradans 2-40
ORGANISM Microbulbifer degradans 2-40
Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
Microbulbifer.
REFERENCE 1 (bases 1 to 4326)
AUTHORS NCBI Microbial Genomes Annotation Project.
TITLE Direct Submission
JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA
COMMENT On Mar 7, 2003 this sequence version replaced gi:23027577.
Protein-coding genes were predicted using GeneMark program (kindly
provided by M. Borodovsky). Functional annotation is based on CDD
(Conserved Domain Database) and COG (Clusters of Orthologous
Groups) assignments, it has not yet been subject to manual review.
DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.
URL -- <http://www.jgi.doe.gov>
Contact: Paul Richardson
microbes@cuba.jgi-psf.org.
COG assignment was automatically updated on Sep 23, 2003.
FEATURES Location/Qualifiers
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LOCUS NZ_AABI02000013 3624 bp DNA linear BCT 23-SEP-2003
DEFINITION Microbulbifer degradans 2-40 Mdeg_12, whole genome shotgun
sequence.

ACCESSION NZ_AABI02000013 REGION: complement(2677..6300)

VERSION NZ_AABI02000013.1 GI:28878289

KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40

ORGANISM Microbulbifer degradans 2-40

Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
Microbulbifer.

REFERENCE 1 (bases 1 to 3624)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23028387.

Protein-coding genes were predicted using GeneMark program (kindly
provided by M. Borodovsky). Functional annotation is based on CDD
(Conserved Domain Database) and COG (Clusters of Orthologous
Groups) assignments, it has not yet been subject to manual review.

DNA sequence and predicted proteins are available for BLAST at

http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson

microbes@cuba.jgi-psf.org.

COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

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LOCUS NZ_AABI02000010 2124 bp DNA linear BCT 23-SEP-2003
 DEFINITION Microbulbifer degradans 2-40 Mdeg_14, whole genome shotgun
 sequence.

ACCESSION NZ_AABI02000010 REGION: complement(50649..52772)

VERSION NZ_AABI02000010.1 GI:28878292

KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40

ORGANISM Microbulbifer degradans 2-40

Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
 Microbulbifer.

REFERENCE 1 (bases 1 to 2124)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
 Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23028613.

Protein-coding genes were predicted using GeneMark program (kindly
 provided by M. Borodovsky). Functional annotation is based on CDD
 (Conserved Domain Database) and COG (Clusters of Orthologous
 Groups) assignments, it has not yet been subject to manual review.

DNA sequence and predicted proteins are available for BLAST at

http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson

microbes@cuba.jgi-psf.org.

COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

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/organism="Microbulbifer degradans 2-40"

/mol_type="genomic DNA"

/strain="2-40"

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CDS 1..>98

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/transl_table=11

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ORIGIN

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LOCUS NZ_AABI02000004 1722 bp DNA linear BCT 23-SEP-2003
 DEFINITION Microbulbifer degradans 2-40 Mdeg_4, whole genome shotgun sequence.
 ACCESSION NZ_AABI02000004 REGION: complement(261777..263498)
 VERSION NZ_AABI02000004.1 GI:28878298
 KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40
 ORGANISM Microbulbifer degradans 2-40
 Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
 Microbulbifer.

REFERENCE 1 (bases 1 to 1722)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
 Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23027141.
 Protein-coding genes were predicted using GeneMark program (kindly
 provided by M. Borodovsky). Functional annotation is based on CDD
 (Conserved Domain Database) and COG (Clusters of Orthologous
 Groups) assignments, it has not yet been subject to manual review.
 DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.igi.doe.gov>

Contact: Paul Richardson

microbes@cuba.igi-psf.org.

COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

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 CDS 1..1722
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ORIGIN

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LOCUS NZ_AABI02000008 2229 bp DNA linear BCT 23-SEP-2003
DEFINITION Microbulbifer degradans 2-40 Mdeg_7, whole genome shotgun sequence.
ACCESSION NZ_AABI02000008 REGION: 137194..139422
VERSION NZ_AABI02000008.1 GI:28878294
KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40
ORGANISM Microbulbifer degradans 2-40
Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
Microbulbifer.

REFERENCE 1 (bases 1 to 2229)
AUTHORS NCBI Microbial Genomes Annotation Project.
TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23027735.
Protein-coding genes were predicted using GeneMark program (kindly
provided by M. Borodovsky). Functional annotation is based on CDD
(Conserved Domain Database) and COG (Clusters of Orthologous
Groups) assignments, it has not yet been subject to manual review.
DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.
URL -- <http://www.jgi.doe.gov>
Contact: Paul Richardson
microbes@cuba.jgi-psf.org.
COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

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gene 1..2229
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CDS 1..2229
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AN"

ORIGIN

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LOCUS NZ_AABI02000048 2646 bp DNA linear BCT 23-SEP-2003

DEFINITION Microbulbifer degradans 2-40 Mdeg_49, whole genome shotgun sequence.

ACCESSION NZ_AABI02000048 REGION: 1591..4236

VERSION NZ_AABI02000048.1 GI:28878254

KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40

ORGANISM Microbulbifer degradans 2-40

Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae; Microbulbifer.

REFERENCE 1 (bases 1 to 2646)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23030011.

Protein-coding genes were predicted using GeneMark program (kindly provided by M. Borodovsky). Functional annotation is based on CDD (Conserved Domain Database) and COG (Clusters of Orthologous Groups) assignments, it has not yet been subject to manual review.

DNA sequence and predicted proteins are available for BLAST at

http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson

microbes@cuba.jgi-psf.org.

COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

source 1..2646

/organism="Microbulbifer degradans 2-40"

/mol_type="genomic DNA"

/strain="2-40"

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gene 1..2646

/gene="Mdeg3707"

CDS 1..2646

/gene="Mdeg3707"

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/db_xref="GI:23030013"

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FNFAGGMNFWFAIVPPPIAIFIEAEDYSSMAGVQLEDTADEGGGQNVGYIDAGDFLQ
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ORIGIN

1 atgggggttaa caatgggttaa gaataaattg tatctagcgc tatctatagc ggctgctaca
 61 agcctaacgg catgtgtgtg tggcggggat gcggctgatg acactgttaa acgcaacgta
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 2581 caaacacttc gtttcgactt tatcgttggg gccattaact ttaactggat caatgtcacc
 2641 aactaa

LOCUS NZ_AABI02000054 3558 bp DNA linear BCT 23-SEP-2003

DEFINITION Microbulbifer degradans 2-40 Mdeg_54, whole genome shotgun sequence.

ACCESSION NZ_AABI02000054 REGION: complement(<2..3559)

VERSION NZ_AABI02000054.1 GI:28878248

KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40

ORGANISM Microbulbifer degradans 2-40

Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae; Microbulbifer.

REFERENCE 1 (bases 1 to 3558)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23030054.

Protein-coding genes were predicted using GeneMark program (kindly provided by M. Borodovsky). Functional annotation is based on CDD (Conserved Domain Database) and COG (Clusters of Orthologous Groups) assignments, it has not yet been subject to manual review.

DNA sequence and predicted proteins are available for BLAST at

http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson

microbes@cuba.jgi-psf.org.

COG assignment was automatically updated on Sep 23, 2003.

FEATURES . Location/Qualifiers

source 1..3558

/organism="Microbulbifer degradans 2-40"

/mol_type="genomic DNA"

/strain="2-40"

/db_xref="taxon:203122"

gene <1..3558

/gene="Mdeg3739"

CDS <1..3558

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/codon_start=1

/transl_table=11

/product="COG3979: Uncharacterized protein contain chitin-binding domain type 3"

/protein_id="ZP_00068322.1"

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/translation="MILRLIRAAIYIVAFVSLIACGGSSSTSKPAQPDIPDPTDLPDTGT

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ORIGIN

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ORIGIN
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LOCUS NZ_AABI02000023 3129 bp DNA linear BCT 23-SEP-2003

DEFINITION Microbulbifer degradans 2-40 Mdeg_24, whole genome shotgun sequence.

ACCESSION NZ_AABI02000023 REGION: complement(46057..49185)

VERSION NZ_AABI02000023.1 GI:28878279

KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40

ORGANISM Microbulbifer degradans 2-40

Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae; Microbulbifer.

REFERENCE 1 (bases 1 to 3129)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23029379.

Protein-coding genes were predicted using GeneMark program (kindly provided by M. Borodovsky). Functional annotation is based on CDD (Conserved Domain Database) and COG (Clusters of Orthologous Groups) assignments, it has not yet been subject to manual review. DNA sequence and predicted proteins are available for BLAST at http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson

microbes@cuba.jgi-psf.org.

COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

source 1..3129

/organism="Microbulbifer degradans 2-40"

/mol_type="genomic DNA"

/strain="2-40"

/db_xref="taxon:203122"

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CDS 1..3129

/gene="Mdeg3180"

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/protein_id="ZP_00067765.1"

/db_xref="GI:23029424"

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ORIGIN

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LOCUS NZ_AABI02000007 2802 bp DNA linear BCT 23-SEP-2003
DEFINITION Microbulbifer degradans 2-40 Mdeg_8, whole genome shotgun sequence.
ACCESSION NZ_AABI02000007 REGION: 111940..114741
VERSION NZ_AABI02000007.1 GI:28878295
KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40
ORGANISM Microbulbifer degradans 2-40
Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
Microbulbifer.

REFERENCE 1 (bases 1 to 2802)
AUTHORS NCBI Microbial Genomes Annotation Project.
TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23027895.
Protein-coding genes were predicted using GeneMark program (kindly
provided by M. Borodovsky). Functional annotation is based on CDD
(Conserved Domain Database) and COG (Clusters of Orthologous
Groups) assignments, it has not yet been subject to manual review.
DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson
microbes@cuba.jgi-psf.org.

COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

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CDS 1..2802

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LOCUS NZ_AABI02000004 1755 bp DNA linear BCT 23-SEP-2003
 DEFINITION Microbulbifer degradans 2-40 Mdeg_4, whole genome shotgun sequence.
 ACCESSION NZ_AABI02000004 REGION: 257640..259394
 VERSION NZ_AABI02000004.1 GI:28878298
 KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40
 ORGANISM Microbulbifer degradans 2-40
 Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
 Microbulbifer.

REFERENCE 1 (bases 1 to 1755)
 AUTHORS NCBI Microbial Genomes Annotation Project.
 TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
 Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23027141.
 Protein-coding genes were predicted using GeneMark program (kindly
 provided by M. Borodovsky). Functional annotation is based on CDD
 (Conserved Domain Database) and COG (Clusters of Orthologous
 Groups) assignments, it has not yet been subject to manual review.
 DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson
microbes@cuba.jgi-psf.org.

COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

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LOCUS NZ_AABI02000004 2367 bp DNA linear BCT 23-SEP-2003
DEFINITION Microbulbifer degradans 2-40 Mdeg_4, whole genome shotgun sequence.
ACCESSION NZ_AABI02000004 REGION: complement(138007..140373)
VERSION NZ_AABI02000004.1 GI:28878298
KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40
ORGANISM Microbulbifer degradans 2-40
Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
Microbulbifer.

REFERENCE 1 (bases 1 to 2367)
AUTHORS NCBI Microbial Genomes Annotation Project.
TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23027141.
Protein-coding genes were predicted using GeneMark program (kindly
provided by M. Borodovsky). Functional annotation is based on CDD
(Conserved Domain Database) and COG (Clusters of Orthologous
Groups) assignments, it has not yet been subject to manual review.
DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson
microbes@cuba.jgi-psf.org.

COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

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ORIGIN

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LOCUS NZ_AABI02000006 2364 bp DNA linear BCT 23-SEP-2003
DEFINITION Microbulbifer degradans 2-40 Mdeg_6, whole genome shotgun sequence.
ACCESSION NZ_AABI02000006 REGION: 67047..69410
VERSION NZ_AABI02000006.1 GI:28878296
KEYWORDS WGS.
SOURCE Microbulbifer degradans 2-40
ORGANISM Microbulbifer degradans 2-40
Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
Microbulbifer.
REFERENCE 1 (bases 1 to 2364)
AUTHORS NCBI Microbial Genomes Annotation Project.
TITLE Direct Submission
JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA
COMMENT On Mar 7, 2003 this sequence version replaced gi:23027577.
Protein-coding genes were predicted using GeneMark program (kindly
provided by M. Borodovsky). Functional annotation is based on CDD
(Conserved Domain Database) and COG (Clusters of Orthologous
Groups) assignments, it has not yet been subject to manual review.
DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.
URL -- <http://www.jgi.doe.gov>
Contact: Paul Richardson
microbes@cuba.jgi-psf.org.
COG assignment was automatically updated on Sep 23, 2003.
FEATURES Location/Qualifiers
source 1..2364
/organism="Microbulbifer degradans 2-40"
/mol_type="genomic DNA"
/strain="2-40"
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gene 1..2364
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CDS 1..2364
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beta-propeller domain distantly related to WD-40 repeats"
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ORIGIN

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LOCUS NZ_AABI02000040 2046 bp DNA linear BCT 23-SEP-2003
DEFINITION Microbulbifer degradans 2-40 Mdeg_40, whole genome shotgun
sequence.

ACCESSION NZ_AABI02000040 REGION: 9019..11064

VERSION NZ_AABI02000040.1 GI:28878262

KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40

ORGANISM Microbulbifer degradans 2-40

Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
Microbulbifer.

REFERENCE 1 (bases 1 to 2046)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23029901.
Protein-coding genes were predicted using GeneMark program (kindly
provided by M. Borodovsky). Functional annotation is based on CDD
(Conserved Domain Database) and COG (Clusters of Orthologous
Groups) assignments, it has not yet been subject to manual review.
DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson
microbes@cuba.jgi-psf.org.

COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

source 1..2046

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/mol_type="genomic DNA"

/strain="2-40"

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gene 1..2046

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CDS 1..2046

/gene="Mdeg3624"

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gene complement(24..224)

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CDS complement(24..224)

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LOCUS NZ_AABI02000007 1965 bp. DNA linear BCT 23-SEP-2003
 DEFINITION Microbulbifer degradans 2-40 Mdeg_8, whole genome shotgun sequence.
 ACCESSION NZ_AABI02000007 REGION: 160746..162710
 VERSION NZ_AABI02000007.1 GI:28878295
 KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40
 ORGANISM Microbulbifer degradans 2-40
 Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
 Microbulbifer.

REFERENCE 1 (bases 1 to 1965)
 AUTHORS NCBI Microbial Genomes Annotation Project.
 TITLE Direct Submission
 JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
 Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23027895.
 Protein-coding genes were predicted using GeneMark program (kindly
 provided by M. Borodovsky). Functional annotation is based on CDD
 (Conserved Domain Database) and COG (Clusters of Orthologous
 Groups) assignments, it has not yet been subject to manual review.
 DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.
 URL -- <http://www.jgi.doe.gov>
 Contact: Paul Richardson
microbes@cuba.jgi-psf.org.
 COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

source 1..1965
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ORIGIN

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1921 ccatctgata accctggctt ggatgcgtca ctactacca actag

LOCUS NZ_AABI02000003 1653 bp DNA linear BCT 23-SEP-2003
DEFINITION Microbulbifer degradans 2-40 Mdeg_3, whole genome shotgun sequence.
ACCESSION NZ_AABI02000003 REGION: 51474..53126
VERSION NZ_AABI02000003.1 GI:28878299
KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40
ORGANISM Microbulbifer degradans 2-40
Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
Microbulbifer.

REFERENCE 1 (bases 1 to 1653)
AUTHORS NCBI Microbial Genomes Annotation Project.
TITLE Direct Submission
JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23026886.
Protein-coding genes were predicted using GeneMark program (kindly
provided by M. Borodovsky). Functional annotation is based on CDD
(Conserved Domain Database) and COG (Clusters of Orthologous
Groups) assignments, it has not yet been subject to manual review.
DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.
URL -- <http://www.jgi.doe.gov>
Contact: Paul Richardson
microbes@cuba.jgi-psf.org.
COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

source 1..1653
/organism="Microbulbifer degradans 2-40"
/mol_type="genomic DNA"
/strain="2-40"
/db_xref="taxon:203122"
gene 1..1653
/gene="Mdeg0757"
CDS 1..1653
/gene="Mdeg0757"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="ZP_00065386.1"
/db_xref="GI:23026923"
/translation="MKSCCIKFFTTLCTAVYVLGCGALAHAAQTGPAGYNYAAAENETV
YLN GTTNVAYGANGSFYYAYNQ TGSVNC SNQTFGDP IFGVRKACYTQQVASNNPPSVS
FASPTGNLTVDEGYALSVTVNASDS DGSIASVELFINNQLVRQELYAPYEWGAAAEPD
ELNGLPVGHTHIKAVATDNDGDTKQASFKLTVRGAADV PGLVQAEDYTG FYD TTNGN
TGGAYRNDNV DVETTS DSNGGYDVGWFAANEWLEYPINVTEAGNYVLEARVASAVGGG
MFTAEINGNNSSTFSIGN TGGWQNWQTLNNNIGNLSTGKKTLRIQAQSGNFNLNWLRL
KRATTSVCTLNTPAENIPTPFNLFTVIDTDLNRYEFCKASKWFEESNGKQVFKLFTGD
NLADNVPGARVHARTEAGQGLKFKAGSTWHTFEARMKPSKKLDYTYTIAQLFAGCCGP
QLRIEVKSNGR IHMGSRGN GNIRISDDQDYANGSR SFKIKIR TNGDQQFEVYFNSSKKF
SGRTDEAKNGNTSALYHFRWGVYSNEVMSEDL SNTVTEIIRN"

ORIGIN

1 atgaaatcat gttgtatcaa gtttttacc acactctgta ctgctgttta tgtactgggt
61 tgtggcgcgt tagcgcgcatgc gcaaactggc ccggcgggtt ataactacgc tgcgccgaa
121 aacgaaacgg tgtatttaaa cggaaccacc aacgttcct acggcgcgaa tggctcggtt
181 tattacgctt acaatcaaac cggttcgggt aattgtctta atcaaacctt tggcgaccct
241 atttttgggg tgcgcaaagc gtgttacacc cagcaagtgg cgagcaataa cccgccgtcg

301 gtttcgttg ctatcccaac gggcaacctt acagtcgacg aagggtatgc tctttctgta
361 accgtgaacg ccagcgatag cgacggcagc attgccagtg tagagctgtt tattaacaac
421 caattagtag gacaagagct ttacgcacct tacgagtggg gcgcagctgc tgagccagac
481 gaattaaatg gcctaccctg tggtagacac acaataaaaag cggtagccac cgataacgac
541 ggcgacacca aacaagctag cttaagcta acggtacgcg gtgcggcggg agatgttcct
601 ggcttggtac aagcggagga ttacacaggc tttagcaca caaccaatgg caacactggt
661 ggtgcgtatc gcaacgacaa ttagacgta gaaaccacaa gcgatagtaa cgggtggtac
721 gacgtagggt gggttcggc aaacgaatgg ctggaatacc ccattaacgt taccgaagcg
781 ggcaattatg tattagaagc acgcgtcgca tctgctgtag gcgggtggtat gttaccgca
841 gaaataaatg gcaacaacag cagtacattt agcataggca ataccggcgg ctggcaaaat
901 tggcaaaccg tgaataacaa tattggcaat ttaagcaccg gtaaaaaaac gttagcatt
961 caagcgcaaa gcggaaactt taattaaac tgctgcgcc tcaagcgtgc cacaacctct
1021 gtgtgcacac ttaatactcc tgccgaaaac attccaacgc catttaattt atttaccgtt
1081 atcgatacag atttaaaccg ctacgaatc tgaagagct ctaaaggtt tgaggaatct
1141 aacggtaaac aagtgtttaa attatttacc ggcgacaacc tagcagataa cgtacctggc
1201 gcccgctac atgctcgac agaagctggc caagggctta agtttaaagc aggtccaca
1261 tggcacacct tgaagccag aatgaaacc agcaaaaagt tagactacac ttacaccatt
1321 gctcaattgt ttgccggctg ttgcgggccc cagttgcgca ttgaagtaaa atctaacgga
1381 cgcatccaca tggggtcgcg cggtaacggc aatattcgt ttagtgacga ccaagattac
1441 gccaacggct ctagatcgtt caaaattaaa attcgacca atggcgatca gttcgaagt
1501 tattttaaca gcagcaaaaa gttcagcggc cgcacagacg aagccaagaa cggcaatacc
1561 agtgcgctt accacttccg ctggggtgta tattccaacg aagtaatgag cgaagattta
1621 tctaactctg ttacagaaat tattcgaaat taa

LOCUS NZ_AABI02000037 1503 bp DNA linear BCT 23-SEP-2003
 DEFINITION Microbulbifer degradans 2-40 Mdeg_37, whole genome shotgun
 sequence.

ACCESSION NZ_AABI02000037 REGION: complement(7812..9314)

VERSION NZ_AABI02000037.1 GI:28878265

KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40

ORGANISM Microbulbifer degradans 2-40

Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
 Microbulbifer.

REFERENCE 1 (bases 1 to 1503)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
 Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23029842.
 Protein-coding genes were predicted using GeneMark program (kindly
 provided by M. Borodovsky). Functional annotation is based on CDD
 (Conserved Domain Database) and COG (Clusters of Orthologous
 Groups) assignments, it has not yet been subject to manual review.
 DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson
microbes@cuba.jgi-psf.org.

COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

source 1..1503

/organism="Microbulbifer degradans 2-40"

/mol_type="genomic DNA"

/strain="2-40"

/db_xref="taxon:203122"

gene 1..1503

/gene="Mdeg3569"

CDS 1..1503

/gene="Mdeg3569"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/protein_id="ZP_00068152.1"

/db_xref="GI:23029850"

/translation="MFASNLEDPTYIYIKYKGVYMNTRKQVNQNLIALLGLMLLMFLT

PHGYAQDQCNTTLECKILHGDATDCKNSRSDNSICMCGSTECVDNPQPEPSNSAAV

PGLIQAEDFTDYDVTAAANHGGAYRSTGVDIQVTTDTNGGYNVGVIAANEWLEYNINV

LQAGNYTANIRVASNNGVGMYS LAVDGVTVSGTNTVNGTGGWQVWITQTANLGYLTQG

EHTLRIAVQAGNFNINWLELLLAGTQQPDM LGVFNKSRDLLANFDSRPDPDDIHSVA

ALATMLKDSRFSNVQYHAVSGAYGIQGGDYIEATHLFNLAFGAGNWSNAHTNRDVALT

TVYNKVAATLTNGGDIWVQEAGQSDFSADLVRRIKQQLPAINTQTRIHIVQHSNWNQD

KTPPADLTYVKNQTDYKKIADGNSTGNGTPGFNSSSSANWNRALNHAQVGAIWQEAKR

IADNAIANHQGWQNPNI RDGGMDFSDA VEDCWIFGFNSLTNINSFFDEFL"

ORIGIN

1 atgtttgcta gcaacctga agacctact tactatataa aatataaagg tgtttacatg

61 aatactaata ggaacaagt caacaaaac ctatcgcg cgtattggcgt aatgttgcta

121 atgctattta cacctcatgg ctatcgcaa gaccaatgca acaccacgct tgagtgc aaa

181 atactccacg gcgatacagc caggattgt aaaaatagtc gctcagataa cagtatttgc

241 atgtgtggaa gtactgaatg tgcagtagat aatccacaac ccgaacctag caattccgcc

301 gcagtaccgg gcctaataca agcagaagac ttaccgatt actacgatgt aacggcggct
361 aatcacggcg gcgcttaccg ctccacaggc gtagacattc aagttaccac agacaccaat
421 ggcggttaca acgtaggctg gatagccgct aatgaatggc tagagtacaa cataaacgta
481 ctgcaagctg gtaactacac cgcgaaatatt cgtgtgcat ctaataatgg tgttgcatg
541 tatagcttgg cggtagatgg tgtaacggtg agtggcacca acaccgttaa tggcacgggt
601 ggctggcaag ttggattac ccaaaccgca aacctggct acttaacca aggcgagcat
661 acgttgcgtg tagcagtaca ggctggcaat tttaataata actggttaga gctgctgcta
721 gcgggtactc agcaaccaga tatgcttggg gtatttaata aaagccgcga cctgttgta
781 gcaaatttcg atagccgccc agaccagac gatattcatt cagtagcggc cctggcaaca
841 atgctaaaag attcccgtt tagcaatgtg caataccacg cagtacggg tgcttacggt
901 atacaagggtg gtgattacat tgaagctaca cattgttta acttagcctt tggcgccgtt
961 aattggtcca acgcgcacac caatagagat gtggcgctta caactgtta caacaaagt
1021 gccgcaacgt taaccaatgg tggatgatt tgggtcaag aggccggtca atccgactt
1081 agcgccgatt tggtagcag aatcaaaaca cagttaccg ctattaatac gcaaaccgca
1141 attcatatag tgcagcatag taactggaac caagacaaa cactccagc cgatttaacc
1201 tatgtaaaaa accaaaccga ctacaaaaa attgctgatg gcaattccac aggcaacggc
1261 acgcctgggt ttaactatc cagcagcgc aactggaacc gcgcactaaa ccacgcgcaa
1321 gtaggcgcaa ttggcaaga agcaaacgc atagccgaca atgccatgc caaccacaa
1381 ggctggcaaa accccaatat tcgagacggc ggtatggact tctcgatgc agtogaagac
1441 tgctggatat tcggctcaa ctactcaca aatataaaca gcttttga tgagtttta
1501 tag

221

301 gaaaacgacc tcaaagctat gcagggtaaa gtgaagtggg ggtacaactg ggatacccaa
361 gcggacgcga acgtaaaaga gaattacgcc agttatggct acgatittgt tcctatggcg
421 tgggacgaaa actttaacga agaagcgctg cgcagctttt tagataatca ccccgatgtg
481 aaatacctgc tgggctggaa tgaaccaaac tcatggaac aggccaacct cacaccagcg
541 gaagccgcag cccattggcc cgtgctagag gccatcgcg aggattacaa cctaaaatta
601 gtgccccctg cggtgaacta cagccccggg aatgttgata ttccaggtag cgatgatgat
661 tacgacctt ggctatacct cgaatgcctt ttgaagcgt gtgaagggtg ccaagtagat
721 tacattgccg tgcattgcta tatgaaatac gaaagcgctt tcagtggta tggggtgaa
781 ttgagcgct acaacaaacc tatttggta accgagtggg cagggtgga cgatggcggc
841 ccagcgaata tgggtgagca aatgaactt ttgtccgata ctgtcgctg gatggagagc
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961 ttccataacc tagatgttt actggccgat ggcgaactaa caccgttgg tagtgtgtat
1021 acctctattc cgtccaacga tttcgctac aaaatacccg cgctattga ggccgaaggc
1081 gccatagct taacgggctt caaacactta gccacaaccg atactacagg tttagctaag
1141 ttaatagccg cgtctaacga agtagcagag taaaaattaa acgtggaaga gggggcgat
1201 tacaccttag cttacgttt ggctcatct gcaaacagt atattgcat ccgtgtgat
1261 ggcttattg gtacacctt cgaagatatt aataccggcg gtgtgaggc gtggatgacc
1321 tttagtcaa cccctattag ttaaccgcg ggtgatcaca tattacgtgt agagtctaaa
1381 tcgtcgctt ttggcttaa ttggttagag ctactaatt ag

LOCUS NZ_AABI02000003 1398 bp DNA linear BCT 23-SEP-2003
DEFINITION Microbulbifer degradans 2-40 Mdeg_3, whole genome shotgun sequence.
ACCESSION NZ_AABI02000003 REGION: 85570..86967
VERSION NZ_AABI02000003.1 GI:28878299
KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40
ORGANISM Microbulbifer degradans 2-40
Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
Microbulbifer.

REFERENCE 1 (bases 1 to 1398)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23026886.
Protein-coding genes were predicted using GeneMark program (kindly
provided by M. Borodovsky). Functional annotation is based on CDD
(Conserved Domain Database) and COG (Clusters of Orthologous
Groups) assignments, it has not yet been subject to manual review.
DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson

microbes@cuba.jgi-psf.org.

COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

source 1..1398
/organism="Microbulbifer degradans 2-40"
/mol_type="genomic DNA"
/strain="2-40"
/db_xref="taxon:203122"
gene 1..1398
/gene="Mdeg0792"
CDS 1..1398
/gene="Mdeg0792"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="ZP_00065421.1"
/db_xref="GI:23026958"
/translation="MKLLSITHLTKRAIASAVFVASAATASIANAVTVDILVLYDNYS
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THSRKQGDQGGTRYRYGVGYGVQDVFDIMAYEGVFNTSRVNVFSNPNLNCRGLPCGK
PVG DSEEAHASLAIHNVRNELANFRNTVNSGGPVRLFEHCYYTG YTVGLGEGSYRLAD
LMNRGLVNDDLSSLQVDAGYRVEMFQHDNFTGNVVRTGSDDCLVDEGMNDDISSLRI
TRVSGGFSQTIQAENFFANNGVQLENTTDSGGGQNVGWIDANDWMAFSNITIPTTGNY
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NAPGWNINWFRIVQL"

ORIGIN

1 atgaaattac tctcaatcac tcacacacta aagcggggcaa ttgcgagcgc agttttgtc
61 gcgtccgctg ctaccgcctc tatagccaat gcagtaacgg tagatattct tgtgcttac
121 gataattatt cggcaaat ta tttggcggc gacccgcaga cggccatgaa cgttgggct
181 aacgatatga actctgcgtt aaaagccagc caaattgata tgaagtccg cattgttgg
241 gtgcgtcatc acgaagaaga tggcgcgggc atggcgacg tacttggtaa ttgcgcgtt
301 gacggtggcg caatagccct gcgcgatcaa cttggtgcag atatggtgtc acaactccac

361 gaaaaggggtg cctgtggcgt ggggtatgtt gccgtagata aaaattacac atggaacgtt
421 actcaccag gctgcgggcc aatggtaatg ctgcatgaat ttggccataa catgggggtt
481 actcactcgc gtaaacaggg tgatcaagggt ggtacccgct atcgctatgg cgtagggtat
541 ggtgtgcagg atgtttcgt cgatatcatg gcttacgaag gcgttttaa caccagccgc
601 gtaatgtat ttctaacc taacctcaat tgcagaggcc ttccgtgtgg taaaccgtt
661 ggcgattccg aagaagccca cgcttcactc gctattcaca atgtgcgtaa cgaactgcc
721 aattttcgca ataccgtaaa ttctgggtga ccggttcgat tgtttgaaca ctgtattac
781 acgggttata cagttggctt aggcgaagggt agctatcgct tagccgattt gatgaaccgc
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961 gtcgatgaag gcatgaacga cgatataagt tcaactcgta taacacgagt aagtggcggg
1021 tttagtcaaa ctatccaagc agagaatttt ttcgctaaca acggcgtgca actagagaat
1081 acaaccgata gcggtggcgg ccaaaacgta ggttggaattg atgctaacga ttgatggct
1141 ttacgaaca ttaccattcc aaccaccggt aactaccgta tcgaataccg cgttcaggt
1201 ttggtggca cgcttcgct cgacttaaat ggcggcgcta tagtgctagg ccaaattaat
1261 ttaccaata ccaatggctg gcagaattgg caaaccgcat cgcacactgt acacattaat
1321 gctggcactt ataatttcgg tattttgct aacgcaccg gctggaatat caattggtc
1381 cgtatagtac agctttaa

LOCUS NZ_AABI02000007 3075 bp DNA linear BCT 23-SEP-2003
DEFINITION Microbulbifer degradans 2-40 Mdeg_8, whole genome shotgun sequence.
ACCESSION NZ_AABI02000007 REGION: 24366..27440
VERSION NZ_AABI02000007.1 GI:28878295
KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40
ORGANISM Microbulbifer degradans 2-40
Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
Microbulbifer.

REFERENCE 1 (bases 1 to 3075)
AUTHORS NCBI Microbial Genomes Annotation Project.
TITLE Direct Submission
JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23027895.
Protein-coding genes were predicted using GeneMark program (kindly
provided by M. Borodovsky). Functional annotation is based on CDD
(Conserved Domain Database) and COG (Clusters of Orthologous
Groups) assignments, it has not yet been subject to manual review.
DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson
microbes@cuba.jgi-psf.org.

COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

source 1..3075
/organism="Microbulbifer degradans 2-40"
/mol_type="genomic DNA"
/strain="2-40"
/db_xref="taxon:203122"
gene 1..3075
/gene="Mdeg1720"
CDS 1..3075
/gene="Mdeg1720"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="ZP_00066336.1"
/db_xref="GI:23027911"
/translation="MKKPPSRYSTLAITLCMSLSQAAIAKDIYVAPTGDDAGAGSFSS
PYQTLAKAAQTAQAGDVVYLREGTYQETLRPANSGTASHPIVFQSYQNEKVIISAMEA
LSGWQQDTSNIYKTTVNWDLGQENFVMHKSTALDLARWPNNTDADPFTLNSKRNTGGS
GPEVGQGAYIEYAAGLPNINWTGGTVFYYGDKPGGGWLAWRETIVSHTQTTRINIDLK
KNPAWVRTAHDPASGGEFYLMGVKGALDYQNEWYFDSNTRELFVQLPNGARPQNGDIQ
FRKRLQTINLANRSHIHKNIIVFGGAIEITNNANSNLLSGVSSFYGNATLGVHTGFS
APSYSVKIQGSDNRIENSEIAYGSGTGIYDSGTRSQIVNNYIHDFNTLGDYNAPVNAR
GGSNTLVKNNRISRGGRTIQAFNRDSEWSYNDVSHSNLIADDCGLFYTVGGPHNVEI
HHNWFHDAYSHGNKKNKAAGIYLDNDARGFKVHHNVVWNTTEWTGIQINWNGTDIDVFNN

TLWNNSAAMGAWHKAGTAFSDVRVWNNLSNSNKWEEQANKQNNLTGTGDPFVNSQAGD
FRLKANTAPIDYGRTIAGTTEGHSGANPDAGAYEYGATAWKAGVTWDITKGAANRCYQ
LPGEVCFDDTDTGGDIGELPGKVEAENYAHYYDTTPGNIGGAYRNQDVIDQPTTDTLG
GYNVGWINAGEWLEYDIDVTQAGRYDAELRVASKLGAGQVAIAIDGVARGEALTIQST
GDWQNWATLTTQLGYLEAGLHLRVSAMSGGFNLNWNFTKQVSFGETAVGFTNTPTPT
RIPATRHQSFSVDYVANEPRELFLLFFNPDWSWVASTKTTVEPGKASTTLQLNLFPVP

TAVQAFNVKLENRPIGANWDNPNNVEAHA AVTTQAAPLQHNGGFENG GTSGWNGYGS
 ALSTEAHSGSYAGKVTGGPSAFSQTIPNLTPNTTYSLSAFVKARAGHTGFLGVKEYGG
 QETSLIVNSTHYQKKTITFTTGP NASSAKIYLYVRDNNH VAFIDELVIVKVY"

ORIGIN

1 atgaaaaaac cacctagccg ttacagtacg ctggccataa cccgtgtat gagttatcg
 61 caggccgcta tagcaaagga tatctacgtc gccctacag gagatgacgc tggagccgga
 121 tcgtttagca gccctatca aacgctggcg aaagcggcac aaaccgcaca agctggtgat
 181 gtctgttacc tgcgcgaagg cacctatcag gaaacgctc gccagcgaa ttcaggcaca
 241 gccagtcacc ccattgtgt tcaatcctat cagaatgaaa aagtgtatcat cagtgaatg
 301 gaagccttaa gcggctggca gcaagacacc tcaaatatt ataaaaccac ggtgaactgg
 361 gatctaggcc aagaaaatt tgtgatgat aaatctacag cactggattt agcccgctgg
 421 ccaacaata ccgatgcaga cccctcacg ttaaattcta aaagaaacac agggggaagt
 481 ggccccgagg taggccaagg tgcttatata gaatacgcag caggattgcc caatattaat
 541 tggactgggg gtaccgtatt ttattatggc gataaaccg gtggcggttg gctagcgtgg
 601 cgcgagacga ttgtaagcca cactcaaacc cgtataaata tagaccttc taaaagaat
 661 cccgctgggg tacgcaccgc acacgaccg gcaagcggcg gagaattcta ttaatggcg
 721 gtaaaagggt ctttagatta tcagaacgaa tggactctg attcaatac gcgagagctt
 781 ttgtccaac tgccaacgg cgcgcgccca caaatggcg atattcaatt tagaaaacgc
 841 ctgcagacca ttaacttggc aatagaagc cacatacaca taaaaacat tgctgtttt
 901 ggtggcgcta tagaaatac caataacgct aattctaacc tgctttctg ggtatccagt
 961 tttatggca atgtacgct cgggtacac accggattt cgcgccaag ctacagcgta
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 1081 gggatatacg acagcggcac ccgagccaa attgtgaata actacattca cgattttaat
 1141 acccttggcg actacaacgc gccgttaac gcgcgcgcg gaagtaatac gtagtaaaa
 1201 aataatcgaa tctcccgcg aggcgcgac accatacaag ctttaatcg agacagcgaa
 1261 tggctgtata acgatgttc ccacagta ttaatagccg atgactgcg ctgttttac
 1321 accgttggcg gaccacaca tgtggaaatc catcacaact ggtttcaga cgcattatca
 1381 cacggcaaca aaaacaaagc cgctgtatt tatttagata acgatgccc aggttttaa
 1441 gtacaccaca acgtggtgtg gaacaccgag tggacaggca tcaataaaa ttgaacggc
 1501 acggacatag acgtatttaa caacacatta tgaacaaca gtccgctat gggagcatg
 1561 cacaagccg ggactcggt ttcggatgtt cgagtttga acaaccttc caacagtaat
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 1861 cgtgctatc aactcccg tgaggttgc ttgatgaca ccgataccg cgagagacat
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 1981 ggtaatattg gcggcgcta ccgcaacca gatgtagata ttacgccac caccgataca
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 2101 gtcactcagg cggggcgcta tgatgccgag cttagagtag cctctaaact gggtcgggc
 2161 caagtagcca tagccataga tggggtcgt agaggcgaag cgtaacgat tcagtgcag
 2221 ggcgattggc aaaattggc aaccctaaca actcaactag ggtatttaga agcagggcta
 2281 catacgtgc gggatccgc tatgagcgtt ggcttcaat taaattggta taacttact
 2341 aaacaagtaa gcttgggga aaccgcccga ggcttacca acactctcc tacacgtata
 2401 ccagctacaa ggcacagag ctttctgtg gattatgtt ccaacgagc gcgagaactg
 2461 ttctattat tttcaacc cgactggagt tggtagcct cgacaaaaac aaccgtagag
 2521 cccggtaaag cttctaccac gtgcaatta aacctccct ttgtccaac cgtgtgcaa
 2581 gcatttaacg ttaaattaga aaatcgcccc ataggcgcca actgggataa cccgaacaat
 2641 gtcgaagcg acgtgccgt taccacgcaa gcagaccgc tacaacataa cgttggttc
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 2881 cacacggggt tttaggcgt taaagaatat ggaggccaag aaacgagcct gatagtaaac
 2941 agcaccact atcaaaagaa aaccatcacc ttaccaccg gcccaacgc cagctcgga
 3001 aaaatttatt tatagttag ggataacaac catgtggcgt ttattgatga gtagtcatt
 3061 gtgaaagtgt actag

LOCUS NZ_AABI02000009 2739 bp DNA linear BCT 23-SEP-2003
DEFINITION Microbulbifer degradans 2-40 Mdeg_10, whole genome shotgun
sequence.

ACCESSION NZ_AABI02000009 REGION: complement(131625..134363)

VERSION NZ_AABI02000009.1 GI:28878293

KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40

ORGANISM Microbulbifer degradans 2-40

Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
Microbulbifer.

REFERENCE 1 (bases 1 to 2739)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23028157.
Protein-coding genes were predicted using GeneMark program (kindly
provided by M. Borodovsky). Functional annotation is based on CDD
(Conserved Domain Database) and COG (Clusters of Orthologous
Groups) assignments, it has not yet been subject to manual review.
DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson
microbes@cuba.jgi-psf.org.

COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

source 1..2739

/organism="Microbulbifer degradans 2-40"

/mol_type="genomic DNA"

/strain="2-40"

/db_xref="taxon:203122"

gene 1..2739

/gene="Mdeg2055"

CDS 1..2739

/gene="Mdeg2055"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/protein_id="ZP_00066663.1"

/db_xref="GI:23028252"

/translation="MKKILFLALGLLISQASFAQQTISSLAEFIALQDGSNQNIKMAP

GTYHISSSSKSLFPGGDWRANVEGNWPGLFKFSGNNNTFDLTGVTFTFDSTILLEMPN

LVHANLMEFGGSGNVWKGLNIQEKPNKGEYGAFIHTSGGTIAVFTGDNHKVSDFTLK

TRFSRPYGLGSLYGKGTGNSSSTLPGVRLSKKTAMFLISLDDSYFENVLIDHSGFGHTL

AFNGVDNVVFNTVEIIAESRSTDDLYANGIGGTDRNGVPFNVLFNGDELIGTNFADAD

YFLNLFDTDNFNQCQNMMSGGVQYSPIRKGYQYSLTEDSFRGYYAGSLGNIEIYNATV

TGSRAGVMEYASEGMIVDGMTVRGIAGHGVPACDGAWNSANGGEGDASAYGPPPSNSV

LKRAKADAAYSTVLEIPNFVDNVTADIEVLDPLNGYNRPSASNALALIKGDDHDIRLW

KRDNQALTRDLVVKVSDADNLLCNMTKQGVTVASSVTNSTIYVSGSISNSSGSSNTV

VKLSSAADEPAICKALETNEVITDCGDFDAFAGIQAEAYCDMAGVEIESSDDGGEQV

GYINNNEWIAFNDVDFGNGASGFEARVSSATSGGNIELRLDSQTGALIGTCSVNGTGS

WTTYETVSCDIGGVSGVQDLYLVTGNSGYLMNVNWFNFTQAATNCSLPWSDSDSFVE

KEIVNYSSGAIDISCASNVEISMNLEGVGAMEDADYLNYYRVDGGAQQVISENVNAF

SEKTVSVSGINGSSLEIIANVYTSYGAEIYTISDMSVKADSQTAYSLEVVSVLASADD

GNVPANTRDGLGTRWSANGDSQWITYDLGSSKTVTDVGIAFFRGDQRTAFISIETST

NNSTWQTVYSDEQSSSTTEIQNFDVTDNARYVRIIGYGNSVNNWNSFTEVEIIGR"

ORIGIN

1 atgaaaaaaa tctgtttt ggccttaggc ctttaataa gtcaggcttc gttgcccag
 61 cagacgattt caagccttgc cgagtttatt gctcttcaag atggcagcaa tcaaaacata
 121 aaaatggccc ccggcaccta tcatatatca tcatcgtcta aatcactgtt ccccggtggg
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 241 aatacgtttg acctgaccgg cgttacctic acctcgact ccacgatctt gtagaaatg
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 361 ctgaatatlc aggagaagcc caacagtaag ggcgagtacg gcgctttat tcatacctct
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 481 acacgtttt ctggcccta tggtttaggt tctctctatg gaaaaacggg taactcgtct
 541 agcacgtgc ccggcgttcg cctgtccaag aaaacggcca tgttcttat tagtttagat
 601 gatagtact ttgaaaatgt tctgattgat cacagtggct ttggtcatal gctgccttt
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 901 cccatccgaa aaggttacca atatagcctg actgaagatt cgtttcgcg gtactacagt
 961 gctgttccc ttggcaatat cgagatttat aacgccaccg ttacgggttc aagagcgggc
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 1081 gccgggcgtg gcgtgccagc gtgcgacggc gcgtggaatt cagctaaccg ttgtgaaggc
 1141 gatgcttcg cctatgttc tccatcaaac agtgtactta agcgtgcgaa agccgatgcc
 1201 gcctattcca ctgtttaga aatcccaat ttgtcgata acgtgacggc cgatattgaa
 1261 gtgttgacc cgtaaacgg ttacaaccgt ccttcggcat caaacgctt ggcgcttatt
 1321 aaaggtgatg atcacgatat tcgactttg aaacgtgata accaagcctt aaccgtgac
 1381 ttgttggtta aggtgagtga tgcggataat ctattgctt gtaacatgac aaaacaaggc
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 1861 ggaacgggca gttggacgac ctatgaaacg gttcttgcg atatcggtgg cgtcagcggc
 1921 gtgcaggatt tgtacctcgt gttaccgga aatagtggtt attaatgaa tgttaattgg
 1981 ttaacttca cgcaagctgc aacgaattgt tctctgcctt ggagtacag tgacttcagc
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 2161 gtttattacc gcgtgatgg cggtgcccc caagtatat ctgaaaatgt gaatgcgtt
 2221 tctgaaaaaa ccgtatcgtt atcaggtatc aatggcagta gcttagaaat tatcgccaat
 2281 gtttatacca gctatggcgc agagatttat acgatttctg atatgagtgt taaagctgat
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 2641 gtgaccgata gcaatgctcg ctatgtaaga attattggct acggaaatag cgtaaataac
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LOCUS NZ_AABI02000051 1626 bp DNA linear BCT 23-SEP-2003
DEFINITION Microbulbifer degradans 2-40 Mdeg_51, whole genome shotgun
sequence.

ACCESSION NZ_AABI02000051 REGION: complement(8184..>9809)

VERSION NZ_AABI02000051.1 GI:28878251

KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40

ORGANISM Microbulbifer degradans 2-40

Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
Microbulbifer.

REFERENCE 1 (bases 1 to 1626)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23030027.
Protein-coding genes were predicted using GeneMark program (kindly
provided by M. Borodovsky). Functional annotation is based on CDD
(Conserved Domain Database) and COG (Clusters of Orthologous
Groups) assignments, it has not yet been subject to manual review.
DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson
microbes@cuba.jgi-psf.org.

COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

source 1..1626

/organism="Microbulbifer degradans 2-40"

/mol_type="genomic DNA"

/strain="2-40"

/db_xref="taxon:203122"

gene 1..>1626

/gene="Mdeg3723"

CDS 1..>1626

/gene="Mdeg3723"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/protein_id="ZP_00068306.1"

/db_xref="GI:23030033"

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KITGSAGRVDQDVAVTPNTNYQLTAYVLGSGRVGVTGTAVYDEAVNTSSWSKVTVNF
NSGSANSVEVFGKYNSGTGRFDDFSLVETGTPTPTPTPTPTPTPTPAGCNLSNTIDIS
SATDDGSHDGHGPHLAVDGDLSADSRWSSKGDGKAITLDLGAEATVRQLKTAWYKGDS
RTAYFDVETSTDKSNWSTALSNVQSQGSGTGLKSNSIDDVARTARYVRIVGHGNSNTWNS
LIEAQLVLCAGTVTPTPTPTPTPTPTPTPTPTPTPTPSGSKIPESITNSDVWDLEGENPH
PLVDPYTLFVPLEARVTTPNGNGWRHEYKIASSERTAMTATYEDFSATIKVDLSTGG
KTIVAQHHAGDTGTIMKLYVSDTSESGFFDSVAANGIFDVYVRIRNTSGVEEKKPLGT
IRSGDSFSFHVLLNNGVVKVSAFGKNLETEVEDDSASYLKFGNYLQSQYPQGSKDCGS
HGSDSDSFRACYEDIGITEAKITMTNVSYTRITK"

ORIGIN

1 ctgcgcctta gtgcacatc aacacaggct gcgaccattt ctaactcagg ctgcgaaagt
61 ggctttgacg gttggacaga cactgacctt tcggcacttt ctacgcatgc aaataacggc
121 agccgatctg ccaaaattac tggctccgcc gcccgtag atcaagacgt tgcgtaacc
181 ccaaacacca actaccagtt aactgcatat gtactggca gtggacgcgt ggggttaac

241 accggcactg cagtttatga cgaagccgta aacacaagca gctggagcaa agtaactgtt
301 aactttaact ctggctctgc aaactctgta gaagtgttg gtaagtacaa tagtggtact
361 ggccgcttg acgatttcag cttagttgag acgggaacac cgactcctac gccaacacct
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721 gtgcagtcac aaggtagcac tggccttaa tcaaacagca ttgacgacgt aacagcgct
781 tacgtacgta ttgtggta cggtaactcg tcgaatactt ggaacagctt gattgaagca
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961 acaaacagcg atgtttgga ttggaaggc gagaaccac acccattggt agacccttac
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1501 caaggtagca aagattgtg ttacatggc gactccgatt cgttccgtgc ctgtacgaa
1561 gatataggca ttaccgaagc gaaaatcacc atgactaacg tttcttacac gcgtatcact
1621 aagtaa

LOCUS NZ_AABI02000004 3102 bp DNA linear BCT 23-SEP-2003
 DEFINITION Microbulbifer degradans 2-40 Mdeg_4, whole genome shotgun sequence.
 ACCESSION NZ_AABI02000004 REGION: 20681..23782
 VERSION NZ_AABI02000004.1 GI:28878298
 KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40
 ORGANISM Microbulbifer degradans 2-40
 Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
 Microbulbifer.

REFERENCE 1 (bases 1 to 3102)
 AUTHORS NCBI Microbial Genomes Annotation Project.
 TITLE Direct Submission
 JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
 Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23027141.
 Protein-coding genes were predicted using GeneMark program (kindly
 provided by M. Borodovsky). Functional annotation is based on CDD
 (Conserved Domain Database) and COG (Clusters of Orthologous
 Groups) assignments, it has not yet been subject to manual review.
 DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.
 URL -- <http://www.jgi.doe.gov>
 Contact: Paul Richardson
microbes@cuba.jgi-psf.org.
 COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers
 source 1..3102
 /organism="Microbulbifer degradans 2-40"
 /mol_type="genomic DNA"
 /strain="2-40"
 /db_xref="taxon:203122"
 gene 1..3102
 /gene="Mdeg0984"
 CDS 1..3102
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 /codon_start=1
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 /product="COG3488: Predicted thiol oxidoreductase"
 /protein_id="ZP_00065611.1"
 /db_xref="GI:23027156"
 /db_xref="COG:COG3488"
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 AANAASYTIEGSDNGVNWTQIGTYTGGTFGNRTDTNVVDGNYRHVRLNGTQRSDGNAW
 GYSIWELEVHGTEVTEPPVVEPPTEPGENLAIYGTATASSGNADVAIDNNAGTRWESD
 HGIDPSSFTLDLGATYSLNQVVIDWEAANAKVYAIQGSNDGTNFTTLANYSGGEFGTR
 TDTLNIAGDYRYVRLLGTERSDGNAWGYSIWEFKVYGGGKTEPPVTEPPVTEPPVVEP
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 TDTYRFLKGQPGIYVIGDEAMEEKIRAGGRATAPYVKGGDSVPVNEISVNGDNTLT
 KVMANGKWTQKDNPNGTVVTFPIRDGIEVDNYVVASGVADWTTYFREALNIQWDTHN
 AFMQGRRVHFTRMDTGVHEEVGNPDFPELANIADGLMVKNCLGCHVNNGRGIAPQNG
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GAQQTACIQNSGQGVELSDLRLNELVYVLQALGAPSRRPETVDQPMVVAGEQRFTDIG
CASCHRPEMNTGHKHDLAELRGNVIRPYTDMLLHDMGPGGLADSLTQAPELNREWRTAP
LWGLGMNLAVNGHDNLLHDGRARSIEEAILWHGGEAQASNNAYKALSAQQRAELIAFL
RSL"

ORIGIN

1 gtgggagaag cacctgtgaa aaaacaagct tatacaacta caccagttaa accaaatgcg
61 ttaggttag ccattgcac actggccctt ggtggcctag ctgcgggact tgtaaactga
121 gcgcatgcag atttattgtc ggtaaataaa actgctacgg ccagcagtga aatgcaagct
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241 ccaaccagca taagtgtaga ctgggcgaa acctacgatt tagatagcat tgcgttcac
301 tgggaagctg ccaacgctgc aagctacacc atagagggtc ccgataacgg tgtaactgg
361 acgcaaatag gcacctatac cgtgtgtacc ttggcaata gaaccgatac cgtaaactga
421 gatgtaatt accgtcacgt gcgattaaat ggtactcagc gcagcgatgg caatgcattg
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541 gaacctccta cagagcctgg cgagaatttg gcaatatatg gcacggcaac cgccagctct
601 ggtaacgccg atgtgtctat tgataataac gctgttacgc gctgggagag tgaccacggc
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721 atagattggg agggcgcaa cgccaagggt tatgtctacc aaggctctaa cgatggcact
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2881 gcgccagagc taaatcgca atggcgta ggcgcgtgt gggcgttgg catgaactg
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LOCUS NZ_AABI02000005 1674 bp DNA linear BCT 23-SEP-2003
DEFINITION Microbulbifer degradans 2-40 Mdeg_5, whole genome shotgun sequence.
ACCESSION NZ_AABI02000005 REGION: complement(228218..229891)
VERSION NZ_AABI02000005.1 GI:28878297
KEYWORDS WGS.
SOURCE Microbulbifer degradans 2-40
ORGANISM Microbulbifer degradans 2-40
Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
Microbulbifer.
REFERENCE 1 (bases 1 to 1674)
AUTHORS NCBI Microbial Genomes Annotation Project.
TITLE Direct Submission
JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA
COMMENT On Mar 7, 2003 this sequence version replaced gi:23027361.
Protein-coding genes were predicted using GeneMark program (kindly
provided by M. Borodovsky). Functional annotation is based on CDD
(Conserved Domain Database) and COG (Clusters of Orthologous
Groups) assignments, it has not yet been subject to manual review.
DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.
URL -- <http://www.jgi.doe.gov>
Contact: Paul Richardson
microbes@cuba.jgi-psf.org.
COG assignment was automatically updated on Sep 23, 2003.
FEATURES Location/Qualifiers
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301 tgtggtaacg ggcccgccaa cgatgctgcc gatgaagcgg ggtgccagg ccgagtggat
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421 ccatggccag atggcgggct taatagggat gcttgggaag tgagtgcctc aaacggttct
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541 caatcgccag gtcagtattt tgatattgat ttcaagacg cgctaacttt cgattcaata
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661 tcaaatggca gcgactggg agtaccagt gtgacgggag ccggtaacgg ctccactaca
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961 caacgagcag ggcagagttt tgaggtagat ttaggagaac tcaacacgct agcggccatt
1021 gagctggatt cagcaggcag tgccaatgac tatccgcggg gttacgccgt ttatgtatcg
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LOCUS NZ_AABI02000025 2025 bp DNA linear BCT 23-SEP-2003

DEFINITION Microbulbifer degradans 2-40 Mdeg_25, whole genome shotgun sequence.

ACCESSION NZ_AABI02000025 REGION: complement(50063..52087)

VERSION NZ_AABI02000025.1 GI:28878277

KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40

ORGANISM Microbulbifer degradans 2-40

Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae; Microbulbifer.

REFERENCE 1 (bases 1 to 2025)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23029437. Protein-coding genes were predicted using GeneMark program (kindly provided by M. Borodovsky). Functional annotation is based on CDD (Conserved Domain Database) and COG (Clusters of Orthologous Groups) assignments, it has not yet been subject to manual review. DNA sequence and predicted proteins are available for BLAST at http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

URL -- <http://www.jgi.doe.gov>

Contact: Paul Richardson
microbes@cuba.jgi-psf.org.

COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers

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gene 1..2025

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CDS 1..2025

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NEPVAICSVSASSSDGNIAENTLDGDYATRWSANGDGEWQFNLCSQVADRVELAWY

KGDTRSSTFSIEYITTDGYVWYTPVRRYSSGASLGLESASFTAAEIQSLRITGYGNS

SNTWNSITEAVIYTPSAGLDYPNLVAPTDAATVTGQSQITISWADTNSEESYFVEA

RIGGNDFFAIGLTEANATSYHTDLIAEGLYEYRVTAVSGIIRSNFAAASVYFQPAGG

SQANLVRPENFTVTANAQQQIALSWVDVSEGEEGYTLEYKLSSEAEFTVIELAANADS

AIVSDLAAGSYFRVSSYFGNNASEYSELLVTVFASEATIVPVDVYASSDDGNVASNV

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ORIGIN

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181 gtaagaaaag cggttgagcg tacitgggag caggagtcac tagtccgctt caccgggttg
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841 cgctcaagta ccttctctat tgagtatata actaccgatg gttacgtttg gtataccacg
901 cctgttcgct gatattcttc cgggtcctcg ctaggcttgg aatctgcgct attactgca
961 gctgaaattc agtccttgcg tattactggc tacggcaact cgtctaacac ttggaatagt
1021 attaccgaag cggtaattta tactccaagc gctgggctag attaccctaa cttagtgcga
1081 cctacagatg tggcggctac ggtaacaggg caatcgcaaa ttactattc atgggcagat
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WO 2008/033330

PCT/US2007/019708

LOCUS NZ_AABI02000005 2457 bp DNA linear BCT 23-SEP-2003
 DEFINITION Microbulbifer degradans 2-40 Mdeg_5, whole genome shotgun sequence.
 ACCESSION NZ_AABI02000005 REGION: complement(73784..76240)
 VERSION NZ_AABI02000005.1 GI:28878297
 KEYWORDS WGS.

SOURCE Microbulbifer degradans 2-40
 ORGANISM Microbulbifer degradans 2-40
 Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
 Microbulbifer.

REFERENCE 1 (bases 1 to 2457)
 AUTHORS NCBI Microbial Genomes Annotation Project.
 TITLE Direct Submission
 JOURNAL Submitted (17-JUN-2004) National Center for Biotechnology
 Information, NIH, Bethesda, MD 20894, USA

COMMENT On Mar 7, 2003 this sequence version replaced gi:23027361.
 Protein-coding genes were predicted using GeneMark program (kindly
 provided by M. Borodovsky). Functional annotation is based on CDD
 (Conserved Domain Database) and COG (Clusters of Orthologous
 Groups) assignments, it has not yet been subject to manual review.
 DNA sequence and predicted proteins are available for BLAST at
http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.
 URL -- <http://www.jgi.doe.gov>
 Contact: Paul Richardson
microbes@cuba.jgi-psf.org.
 COG assignment was automatically updated on Sep 23, 2003.

FEATURES Location/Qualifiers
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ORIGIN

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2401 actggtgaaa gtgtgggtga ggtgactgat aatgggacgg gaaatagctt gaaatag

We claim:

1. A method for producing ethanol from lignocellulosic material, comprising treating lignocellulosic material with an effective saccharifying amount of one or more compounds listed in Figures 4-11 to obtain saccharides and converting the saccharides to produce ethanol.
2. The method of claim 1, wherein the at least one of the compounds listed in Figures 4-11 are from *Microbulbifer degradans* 2-40.
3. The method of claim 1, wherein the lignocellulosic material is treated with an effective saccharifying amount of all of the compounds listed in Figures 4-11.
4. The method of claim 1, wherein the one or more compounds listed in Figures 4-11 are present in dry form, in a buffer, or in the form of a paste, paint, or micelle.
5. The method of claim 1, wherein the one or more compounds listed in Figures 4-11 are in a system consisting essentially of one or more compounds listed in Figures 4-11.
6. The method of claim 1, wherein the one or more compounds listed in Figures 4-11 are present in a system further comprising metal ions, chelators, detergents, organic ions, inorganic ions, or one or more additional proteins.
7. The method of claim 6, where the one or more additional proteins are biotin and/or albumin.
8. The method of claim 1, wherein the treating is conducted in a marine environment.
9. The method of claim 8, wherein the treating is conducted under water.

10. The method of claim 1, wherein the one or more compounds listed in Figures 4-11 is cellulase cel5A listed in Figure 4.
11. A method for producing ethanol from lignocellulosic material, comprising contacting lignocellulosic material with a microorganism expressing an effective saccharifying amount of one or more compounds listed in Figures 4-11 to obtain saccharides and converting the saccharides to produce ethanol.
12. The method according to claim 11, wherein the microorganism is *Microbulbifer degradans* 2-40.
13. The method of claim 11, wherein the microorganism is a recombinant microorganism containing a chimeric gene comprising at least one polynucleotide encoding a polypeptide comprising an amino acid sequence of at least one of the compounds listed in Figures 4-11; wherein the gene is operably linked to regulatory sequences that allow expression of the amino acid sequence by the microorganism.
14. The method of claim 13, wherein the recombinant microorganism is a bacteria or yeast.
15. The method of claim 13, wherein the recombinant microorganism is *Escherichia coli*.
16. The method of claim 14, wherein the bacteria or yeast is ethanologenic.
17. The method of claim 11, wherein the contacting is conducted in a marine environment.
18. The method of claim 17, wherein the contacting is conducted under water.
19. The method of claim 11, wherein the one or more compounds listed in Figures 4-11 is cellulase cel5A listed in Figure 4.

20. A method for producing ethanol from lignocellulosic material, comprising contacting lignocellulosic material with an ethanologenic microorganism expressing an effective saccharifying amount of one or more compounds listed in Figures 4-11 to produce ethanol.
21. Use of one or more compounds listed in Figures 4-11 for the production of ethanol from lignocellulosic material.
22. Use of a microorganism expressing an effective saccharifying amount of one or more compounds listed in Figures 4-11 to produce ethanol from lignocellulosic material.
23. Use of an ethanologenic microorganism expressing an effective saccharifying amount of one or more compounds listed in Figures 4-11 to produce ethanol from lignocellulosic material.

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FIG. 1A

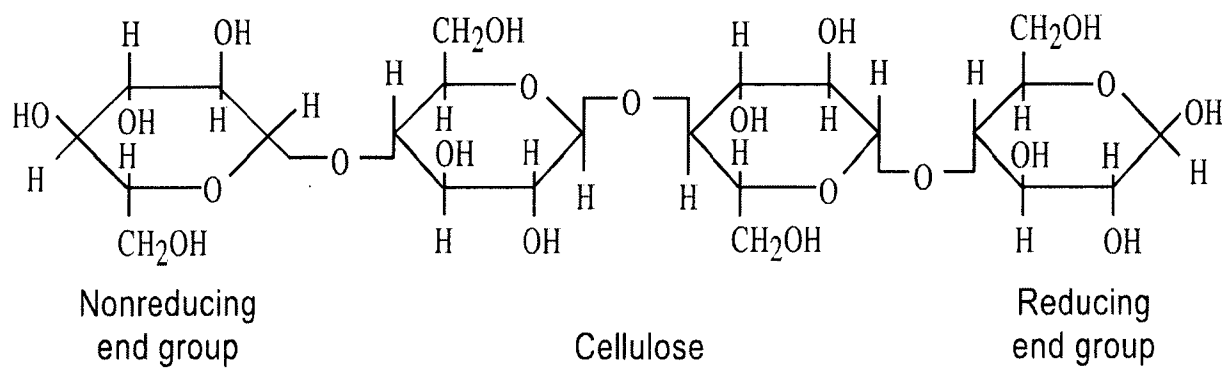
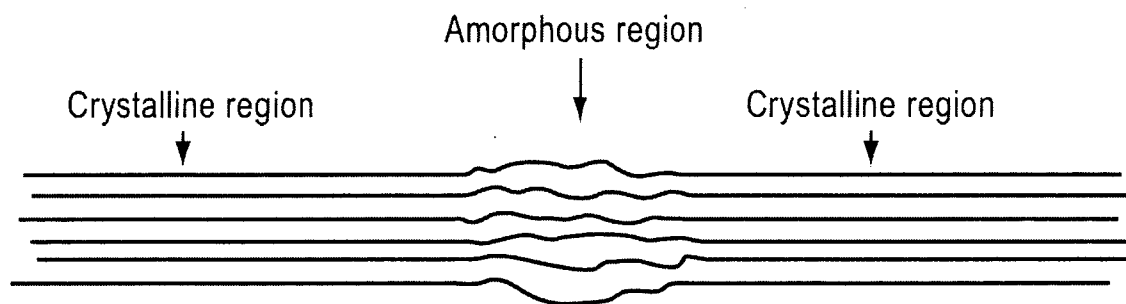


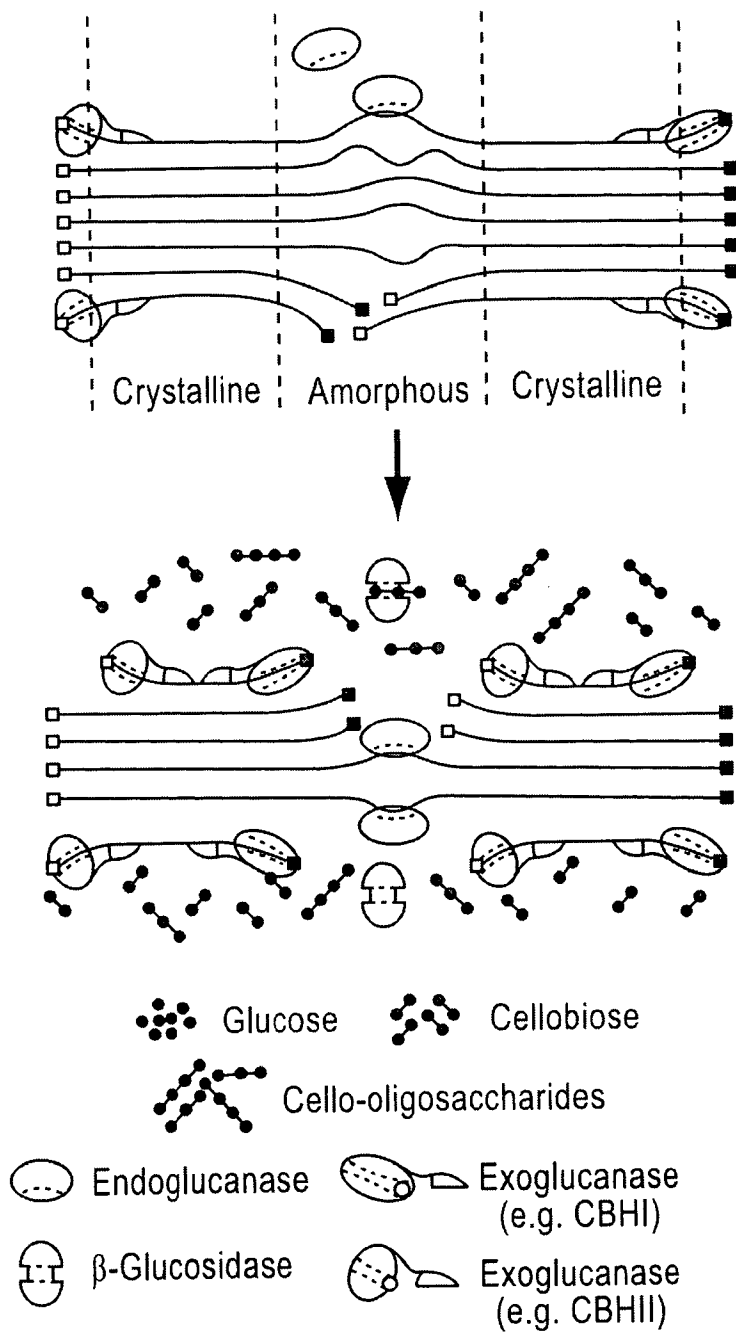
FIG. 1B



Panel B from Beguin and Aubert, 1994.

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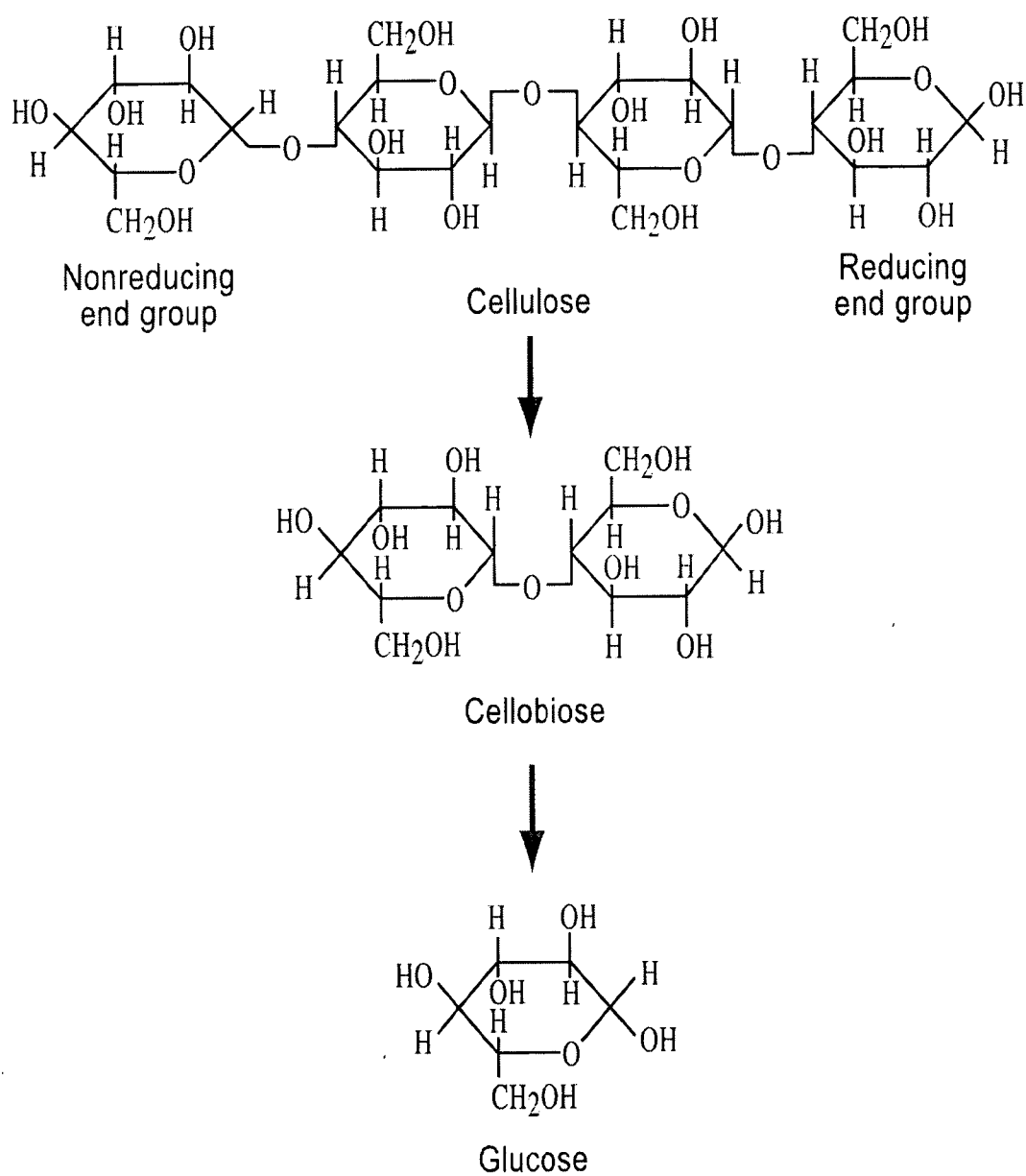
FIG. 2A



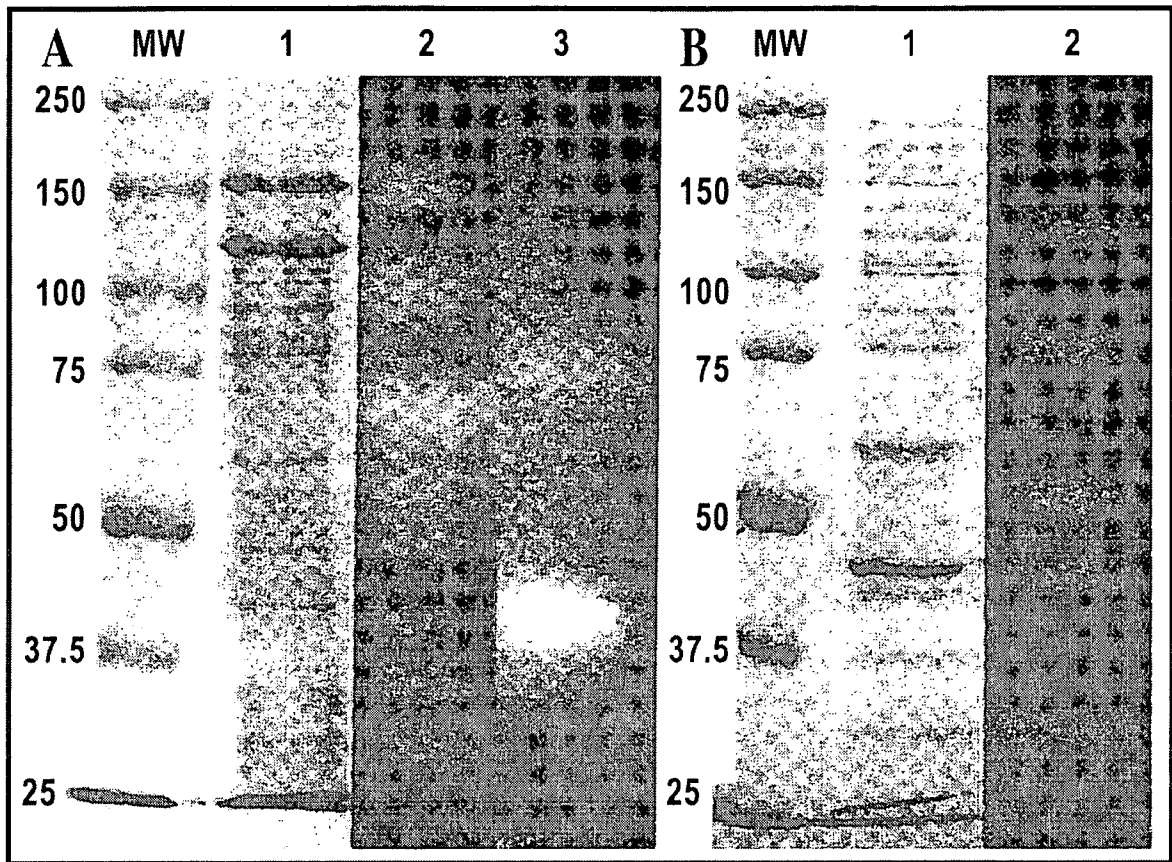
From Lynd, Weimer et al., 2002.

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FIG.2B



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SDS-PAGE and Zymogram analysis is of 2-40 culture supernatants.

FIG.3

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Predicted cellulases of *M. degradans* 2-40. Cellulase depolymerases and accessories as predicted by CAZyme analysis and sequence-based functional predictions as described in the text.

Name	MS	amino acids	MW	Predicted function	Modules	Refseq accession
cel5A		1,167	127.2	endo 1,4-glucanase	GH5/CBM6/CBM6/CBM6/GH5	ZP_00067013.1
cel5B		566	60.8	endo 1,4-glucanase	LPB/PSL(47)/CBM6/GH5	ZP_00064853.1
cel5C		451	49.1	endo 1,4-glucanase	LPB/PSL(47)/GH5	ZP_00067454.1
cel5D		621	65.9	endo 1,4-glucanase	CBM2/PSL(58)/CBM10/PSL(36)/GH5	ZP_00064986.1
cel5E		673	72.6	endo 1,4-glucanase	CBM6/CBM6/GH5	ZP_00066079.1
cel5F		365	42.0	endo 1,4-glucanase	GH5	ZP_00066536.1
cel5G		638	67.9	endo 1,4-glucanase	GH5/PSL(21)/CBM6/PSL(32)/Y95	ZP_00066178.1
cel5H	av	630	66.9	endo 1,4-glucanase	GH5/PSL(32)/CBM6/EPR(16)	ZP_00068260.1
cel5I	av	725	77.2	endo 1,4-glucanase	CBM2/PSL(33)/CBM10/PSL(58)/GH5	ZP_00067367.1
cel5J		610	65.2	endo 1,4-glucanase	GH5/CBM6/CBM6	ZP_00064857.1
cel6A		791	81.9	non-reducing end cellobiohydrolase	CBM2/PSL(43)/CBM2/PSL(85)/GH6	ZP_00064659.1
cel9A		578	62.7	endo-1,4-glucanase	GH9	ZP_00065765.1
cel9B	av	867	89.5	endo-1,4-glucanase	GH9/PSL(54)/CBM10/PSL(50)/CBM2	ZP_00065776.1
ced3A	av, cm, xn	1,072	116.0	cellodextrinase	LPB/GH3/PLP	ZP_00064860.1
ced3B	xn	862	92.9	cellodextrinase	LPB/GH3	ZP_00068210.1
bgl1A		461	52.8	cellobiase	[†] GH1	ZP_00067238.1
bgl1B		444	49.8	cellobiase	[†] GH1	ZP_00066838.1
bgl3C	av, cm, xn	866	95.4	β -glucosidase	LPB/GH3/UNK(511)	ZP_00066570.1
cep94A		811	91.7	cellobiose phosphorylase	[†] GH94	ZP_00067911.1
cep94B	cm	788	88.7	cellodextrin phosphorylase	[†] GH94	ZP_00068287.1

FIG.4

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Predicted xylansases, xylosidases and related accessories.

Name	MS	amino acids	MW	Predicted function	Modules	Refseq accession
xyn10A		574	61.7	β -1,4-xylanase	GH10/PSR(29)/Y94/PSL(21)/CBM5	ZP_00066395.1
xyn10B		619	65.0	β -1,4-xylanase	CBM2/PSL(42)/CBM10/PSL(48)/GH10	ZP_00066073.1
xyn10C		374	42.3	β -1,4-xylanase	GH10	ZP_00064983.1
xyl/arb43G-		1,186	129.6	β -xylosidase/ α -L-arabino furanosidase/ β -1,4-xylanase	GH43/CBM6/Y94/PSL(24)/CBM2/PSL(22)/CBM22/GH10	ZP_00067229.1
xyn10D						
xyn10E	xn	670	75.2	β -1,4-xylanase	LPB/EPR(47)/GH10	ZP_00067456.1
xyn11A		275	30.4	β -1,4-xylanase	GH11	ZP_00066908.1
xyn11B-		767	80.8	bifunctional β -1,4-xylanase/acetylxylnesterase	GH11/PSL(10)/PSL(19)/CE4/CBM10	ZP_00067071.1
axe4A						
axe2A		360	40.9	acetylxyln esterase	CE2	ZP_00064735.1
xyl31A	xn	973	110.2	α -xylosidase for xyloglucans	LPB/GH31	ZP_00064863.1
xyl3A	av,cm,xn	893	97.6	β -xylosidase	LPB/GH3	ZP_00067626.1
xyl43L		317	36.1	α -xylosidase	GH43	ZP_00067829.1
xyl/arb43H		577	63.8	bifunctional β -xylosidase/ α -L-arabinofuranosidase	LPB/GH43	ZP_00065724.1
xyl/arb43I		566	62.6	bifunctional β -xylosidase/ α -L-arabinofuranosidase	LPB/GH43	ZP_00066469.1
xyl/arb43J		317	35.1	bifunctional β -xylosidase/ α -L-arabinofuranosidase	LPB/GH43	ZP_00066992.1
xyl/arb43K		385	42.6	bifunctional β -xylosidase/ α -L-arabinofuranosidase	LPB/GH43	ZP_00315109.1
agu67A		738	82.0	α -1,2-glucuronidase	GH67	ZP_00315039.1

FIG.5

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Predicted pectinases and accessories.

Name	amino acids	MW	Predicted function	Modules	Refseq accession
pel1A	1,316	136.4	pectate lyase	PL1/PSL(35)/PSL(29)/FN3/PSL(65)/PL1	ZP_00067832.1
pel1B	427	46.1	pectate lyase	PL1	ZP_00067840.1
pel1C	769	78.9	pectate lyase	PL1/PSL(33)/PSL(23)/FN3	ZP_00067834.1
pel1D	772	63.3	pectate lyase	LPB/EPR(24)/PL1	ZP_00067182.1
pel1E	511	45.4	pectate lyase	LPB/PL1	ZP_00064693.1
pel1F	452	81.5	polysaccharide lyase (pectate?)	CBM2/PSL(45)/PSL(31)/PL1	ZP_00064697.1
pel3A	424	52.3	pectate lyase	CBM2/PSL(30)/PSL(20)/PL3	ZP_00064694.1
pel3B	392	46.1	pectate lyase	PSL(24)/FN3/PSL(20)/PL3	ZP_00065735.1
pel3C	733	42.9	pectate lyase	PSL(19)/FN3/PSL(18)/PL3	ZP_00067017.1
pel3D	700	41.6	pectate lyase	CBM13/PL3	ZP_00067887.1
pel9A	574	75.6	pectate lyase	PSL(47)/FN3/FN3/PL9	ZP_00066061.1
pel10A	463	73.3	pectate lyase	CBM2/PSL(54)/PSL(28)/PL10	ZP_00068232.1
pel10B	1,081	60.8	pectate lyase	LPB/PSL(46)/PL10	ZP_00066059.1
pgl28A	389	50.9	polygalacturonanase	LPB/GH28	ZP_00067822.1
pes8A	914	115.1	pectin methylesterase	LPB/EPR(23)/CE8	ZP_00067183.1
pes8B		42.4	pectin methylesterase	LPB/CE8	ZP_00067831.1
rgl11A		97.6	rhamnogalacturonan lyase	PL11/PSL(33)/CBM2	ZP_00066475.1

FIG.6

Predicted arabinanases and arabinogalactanases of 2-40. The bifunctional xylosidase/arabinanases in table 2 are also expected to function as accessories to these enzymes

Name	amino acids	MW	Predicted function	Modules	Refseq accession
arb43A	789	85.0	endo-1,5-a-L-arabinanase	CBM13/GH43	ZP_00066674.1
arb43B	362	40.7	exo-1,5-a-L-arabinofuranosidase	LPB/GH43	ZP_00066990.1
arb43C	314	35.9	exo-1,5-a-L-arabinofuranosidase	*GH43	ZP_00066981.1
arb43D	472	51.1	endo-1,5-a-L-arabinanase	CBM13/GH43	ZP_00068164.1
arb43E	346	38.6	endo-1,5-a-L-arabinanase	LPB/GH43	ZP_00066989.1
arb43F	607	67.2	exo-1,5-a-L-arabinofuranosidase	GH43	ZP_00066994.1
arb51A	534	59.4	exo-1,5-a-L-arabinofuranosidase	GH51	ZP_00315975.1
arg53A	397	44.5	arabinogalactanase	GH53	ZP_00068112.1
arg53B	476	52.6	arabinogalactanase	GH53/CBM13	ZP_00065874.1
arg53C	650	71.1	arabinogalactanase	GH53	ZP_00068237.1

FIG.7

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Predicted mannanases of 2-40.

Name	MS	amino acids	MW	Predicted function	Modules	Refseq accession
man26A		506	54.9	mannanase	LPB/PSL(52)/CBM10/GH26	ZP_00065857.1
man5N		561	57.6	mannanase	GH5/PSL(32)/CBM10/PSR(44)/CBM2	ZP_00065570.1
man5O		507	52.6	mannanase	GH5/PSL(23)/CBM10/CBM10	ZP_00065784.1
man5P	cm	457	50.9	mannanase	GH5	ZP_00065642.1
man5Q	ag	850	92.3	mannanase	LQAC/GH5	ZP_00064894.1
ag127A		408	46.5	α -galactosidase	GH27	ZP_00066516.1

FIG.8

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Predicted laminarinases of 2-40.

Name	amino acids	MW	Predicted function	Modules	Refseq accession
lam16A	1,707	163.3	B-1,3-glucanase	GH16/CBM6/CBM6/TSP3/TSP3/COG3488	ZP_00066839.1
lam16B	1,441	158.6	B-1,3-glucanase	GH16/CBM6/CBM6/EPR(56)/CBM32/CBM32	ZP_00066081.1
lam16C	1,184	129.1	B-1,3-glucanase	GH16/CBM4/CBM32/CBM32	ZP_00066789.1
lam16D	722	77.7	B-1,3-glucanase	GH16/CBM32/PSR(48)/TMR	ZP_00067027.1
lam16E	569	61.4	B-1,3-glucanase	CBM6/CBM6/GH16	ZP_00065780.1
lam16F	742	80.2	B-1,3-glucanase	LPB/GH16	ZP_00066288.1
lam16G	877	94.2	catalytic residues missing	LPB/GH16/CBM6/CBM6	ZP_00068290.1
lam81A	1,238	133.1	B-1,3-glucanase	LPB/CADG/GH81/FN3/FN3	ZP_00068322.1

FIG.9

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Selected carbohydrate-binding module (CBM) proteins. Function is unknown for containing CBM domains but lacking another well-characterized domain.

Name	MS	amino acids	MW	Predicted function	Modules	Refseq accession
cbm2A		354	37.9	cbm2a binds crystalline cellulose	CBM2/EPH(48)/UNK(174)	ZP_00067766.1
cbm2B	av	1,042	112.1	cbm2a	CBM2/UNK(914)	ZP_00067765.1
cbm2C	xn	933	97.5	cbm2a	CBM2/PSL(58)/Y94/PSL(25)/UNK(577)	ZP_000666396.1
cbm2D-cbm10A		558	56.3	cbm2a	CBM2/PSL(43)/CBM10/PSL(101)/UNK(231)	ZP_00065777.1
cbm2E		781	85.0	cbm2a	CBM2/PSL(18)/PSL(18)/UNK(471)	ZP_00065695.1
cbm2F		787	84.8	cbm2a	CBM2/PSL(33)/PSL(17)/UNK(544)	ZP_00066068.1
cbm6A		681	72.5	cbm6 binds glycan chains	LPB/PSL(28)/CBM6/UNK(476)	ZP_00068207.1
cbm6B		630	67.2	cbm6	CBM6/CBM6/UNK(217)	ZP_00066418.1
cbm6C		550	59.8	cbm6	CBM6/UNK(216)	ZP_00065386.1
cbm6D		500	54.6	cbm6	CBM6/UNK(262)	ZP_00068152.1
cbm6E		473	53.0	cbm6	LPB/UNK(~300)/CBM6	ZP_00066788.1
cbm6F		465	50.4	cbm6	UNK(~300)/CBM6	ZP_00065421.1
cbm6G-cbm16B		1,024	111.4	cbm6; cbm16 unknown	CBM6/CBM16/UNK(704)	ZP_00066336.1
cbm6H-cbm32F		912	97.5	cbm6; cbm32 binds monos/oligos (1-3)	UNK(~500)CBM6/CBM32	ZP_00066663.1
cbm16A-cbm32E		552	58.456	cbm16; cbm32	CBM16/PTR/CBM32/PTR/UNK(232)	ZP_00068306.1
cbm32A	xn	1,028	111.9	cbm32; COG3488 thiol-oxidoreductase	CBM32/CBM32/UNK(251)/COG3488	ZP_00065611.1
cbm32B		557	59.5	cbm32	UNK(~100)/CBM32/CBM32/CBM32	ZP_00066007.1
cbm32C		674	73.6	Zn-protease; Cbm32; FN3 unknown	ZDP/CBM32/FN3/CBM32	ZP_00067813.1
cbm32D		818	88.8	Cbm32; FCL eel fucosyltransferase-like domain	CBM32/FCL/UNK(521)	ZP_00065873.1

FIG.10

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Recombinant proteins and comparison of predicted vs. observed molecular weights. Proteins cloned and expressed for functional characterization as described in text.

Name	amino acids	MW (kDa)	PAGE MW	Predicted function	Modules
rLam16A	1,738	186.9	~240	β -1,3-glucanase	GH16/CBM6/CBM6/TSP3/TSP3/TSP3/COG3488
rLam16D	761	82.2	~90	β -1,3-glucanase	GH16/CBM32/PSL(48)/TMR
rCel5A	1,117	121.9	~130	β -1,4-endoglucanase	GH5/CBM6/CBM6/CBM6/GH5
rGly3D	1,591	174.3	~180	β -glycosidase	CBM32/CBM32/CBM32/GH3/CBM32
rGly5K	892	97.8	~115	(1,3 or 1,4) endoglucanase	GH5/CBM6/CBM6/CBM13
rGly5M	885	96.5	~125	(1,3 or 1,4) endoglucanase	LPB/EPR(34)/GH5/FN3/CBM6
rGly9C	663	72.9	~70	glycanase <25% ID to cellulases	GH9
rGly43M	1,198	130.3	~135	β -glycosidase	LPB/GH43/LGL/LGL
rCbm2A	340	36.6	~45	binds crystalline cellulose	CBM2/EPR(48)/UNKNOWN(174)
rCbm2B	1,031	110.9	~125	binds crystalline cellulose	CBM2/UNKNOWN(914)
rCbm2C	950	99.3	~140	binds crystalline cellulose	CBM2/PSL(58)/Y94/PSL(25)/UNKNOWN(577)
rCbm2D-cbm10A	578	58.7	15-25 [†]	binds crystalline cellulose	CBM2/PSL(43)/CBM10/PSL(101)UNKNOWN(231)

FIG.11