Complete genome sequence of *Desulfotomaculum acetoxidans* type strain (5575T)

Stefan Spring1, Alla Lapidus2, Maren Schröder1, Dorothea Gleim1, David Sims3, Linda Meincke1, Tijana Glavina Del Rio3, Hope Tice2, Alex Copeland1, Jan-Fang Cheng2, Susan Lucas2, Feng Chen2, Matt Nolan2, David Bruce2,3, Lynne Goodwin2,3, Sam Pitluck2, Natalia Ivanova2, Konstantinos Mavromatis2, Natalia Mikhailova2, Amrita Pati1, Amy Chen2, Krishna Palaniappan3, Miriam Land2,3, Loren Hauser4,5, Yun-Juan Chang2,5, Cynthia D. Jeffries2,5, Patrick Chain2,6, Elizabeth Saunders2,3, Thomas Brettin2,3, John C. Detter2,3, Markus Göker1, Jim Bristow2, Jonathan A. Eisen2,7, Victor Markowitz4, Philip Hugenholtz2, Nikos C. Kyrpides2, Hans-Peter Klenk1, and Cliff Han2,3

1 DSMZ - German Collection of Microorganisms and Cell Cultures GmbH, Braunschweig, Germany
2 DOE Joint Genome Institute, Walnut Creek, California, USA
3 Los Alamos National Laboratory, Bioscience Division, Los Alamos, New Mexico, USA
4 Biological Data Management and Technology Center, Lawrence Berkeley National Laboratory, Berkeley, California, USA
5 Oak Ridge National Laboratory, Oak Ridge, Tennessee, USA
6 Lawrence Livermore National Laboratory, Livermore, California, USA
7 University of California Davis Genome Center, Davis, California, USA
*Corresponding author: Hans-Peter Klenk

Keywords: sulfate-reducer, hydrogen sulfide, piggery waste, mesophile, motile, sporulating, obligate anaerobic, Peptococcaceae, Clostridiales, Firmicutes.

*Desulfotomaculum acetoxidans* Widdel and Pfennig 1977 was one of the first sulfate-reducing bacteria known to grow with acetate as sole energy and carbon source. It is able to oxidize substrates completely to carbon dioxide with sulfate as the electron acceptor, which is reduced to hydrogen sulfide. All available data about this species are based on strain 5575T, isolated from piggery waste in Germany. Here we describe the features of this organism, together with the complete genome sequence and annotation. This is the first completed genome sequence of a *Desulfotomaculum* species with validly published name. The 4,545,624 bp long single replicon genome with its 4370 protein-coding and 100 RNA genes is a part of the Genomic Encyclopedia of Bacteria and Archaea project.

Introduction

Strain 5575T, also known as “Göttingen” strain (= DSM 771 = ATCC 49208 = VKM B-1644 = KCTC 5769) is the type strain of the species *Desulfotomaculum acetoxidans* [1]. Strain 5575T is the only strain of the species that is available from public culture collections. It was isolated from piggery waste in Göttingen, Germany. Widdel and Pfennig [2] reported the isolation of additional strains from animal manure, rumen content and dung-contaminated freshwater habitats and concluded that members of *D. acetoxidans* are primarily intestinal bacteria. Unclassified strains with rather high 16S rRNA gene sequence similarity to strain 5575T were reported from rice field soil (AJ012600 and AJ012601, 98%) and from a freshwater sediment in The Netherlands [3]. A complete genome sequence of the strain ‘*Desulfotomaculum reducens*’ MI-1 was recently determined by the DOE Joint Genome Institute (GenBank accession number NC_009253). However, this strain is only distantly related with *D. acetoxidans* 5575T, both sharing a 16S rRNA sequence similarity of only 86%, and has no taxonomic status, because the species epithet was never validly published. Here we present a summary classification and a set of features for *D. acetoxidans* strain 5575T together with the description of the complete genomic sequencing and annotation.
Classification and features

The genus Desulfotomaculum currently represents a rather heterogeneous taxon. The available 16S rRNA gene sequences (GenBank accession numbers AB294139 and NR_026409) of the type strain of Desulfotomaculum guttoideum, DSM 4024, appear to be unrelated to the type species of the genus, but show high similarity to Clostridium sphenoides and C. celerescens, which both belong to cluster XIVa of the clostridia [4]. An investigation of the phenotypic traits of D. guttoideum strain DSM 4024 indicated its affiliation to the species C. sphenoides, which was also confirmed by a DNA-DNA reassociation value above 70% with the type strain of C. sphenoides (unpublished results). This indicates that either the published species description of D. guttoideum is erroneous or the originally described strain is not identical with the culture that was deposited in culture collections. Apart from this species, the genus Desulfotomaculum is paraphyletic and comprises several distinct phenotypic types including mesophilic species, like D. acetoxidans, moderate thermophiles (e.g. D. thermosubterraneeum), halophiles (D. halophilum) and alkaliphiles (D. alkaliophilum). The type species of the genus, D. nigrificans, is a moderate thermophile and shares only 85% 16S rRNA gene sequence similarity with D. acetoxidans, indicating that the latter species might have been misclassified. The members of the genus Desulfotomaculum are affiliated to the family Peptococcaceae of the order Clostridiales, within the phylum Firmicutes.

Figure 1 shows the phylogenetic neighborhood of D. acetoxidans strain 5575T in a 16S rRNA based tree. The ten 16S rRNA gene copies in the genome of strain 5575T differ by up to 41 nucleotides (2.6%) from each other, and by up to 35 nucleotides (2.2%) from the previously published 16S rRNA sequence generated from DSM 771 (Y11566). D. guttoideum, DSM 4024, has not been included in the phylogenetic analysis for reasons given above.
Vegetative cells of *D. acetoxidans* 5575T are straight to slightly curved rods with pointed ends and dimensions of 1.0-1.5 µm × 3.5-9.0 µm (Table 1 and Figure 2). Motility is conferred by a single polar flagellum [1]. Cells were originally described to stain Gram-negative [1], which is a typical trait among *Desulfotomaculum* species, but all *Desulfotomaculum* strains examined so far by electron microscopy have a cell wall structure of the Gram-positive type [20]. Spherical spores of 1.5 µm diameter are located in a sub terminal position and cause a swelling of cells resulting in a typical spindle shaped morphology. Spores are preferentially formed in agar colonies upon prolonged incubation with acetate as substrate. Formation of spores is often accompanied by the production of gas vacuoles that appear as conic refractile areas adjacent to the spores in sporulating mother cells. Growth occurs between 20 and 40°C with an optimum at 36°C. The pH range for growth is 6.6–7.6, with an optimum at 7.1 [1]. The salinity optimum for growth of *D. acetoxidans* is 1 g/l NaCl and growth is inhibited above 7 g/l NaCl, which is typical for strains showing an adaptation to freshwater habitats [2].

Substrates allowing good growth were found to be acetate and butyrate, whereas long chain fatty acids or carbohydrates were not utilized [2]. In addition, ethanol, n-butanol, iso-butyrate and n-valerate were identified as suitable substrates. With acetate as substrate, only sulfate was reported to be used as electron acceptor, but not sulfite, thiosulfate or fumarate [2]. No fermentative growth on organic substrates in media without sulfate was observed [1]. Biotin was identified as sole growth factor in defined media [2].

**Figure 2.** Scanning electron micrograph of vegetative cells of *D. acetoxidans* strain 5575T (Manfred Rohde, Helmholtz Centre for Infection Research, Braunschweig)

### Chemotaxonomy

Redox difference spectra indicate the presence of membrane bound *b*-type cytochromes, whereas no cytochromes *c* or soluble cytochromes were detected. The CO-difference spectrum of the soluble cell fraction revealed presence of a dissimilatory sulfite reductase of the type P582 [1,2]. *D. acetoxidans* contains only menaquinones, mainly of the MK-7 type and small amounts of MK-6 [21]. Dowling *et al.* [22] determined the whole-cell fatty acid pattern of *D. acetoxidans* strain 5575T and found a dominance of straight-chain, even-numbered fatty acids, whereas neither 10-methyl nor cyclopropyl fatty acids were present. The predominant fatty acids this organism were 16:0 (34.0%), 16:1 ω7c (24.4%) and 18:1 ω7c (24.1%), followed by 16:1 ω9 (5.9%) and 16:1 ω5 (4.8%). The abundance of distinct fatty acids in this species apparently depends strongly on the medium composition: It was found that supplementation of the growth medium with volatile fatty acids led to a decreased proportion of even-numbered fatty acids from 99 to 67% [22]; in addition, Londry *et al.* reported that under conditions of autotrophic growth the proportion of 16:1 fatty acids decreased, whereas 18:1 fatty acids increased compared to growth on acetate as carbon source [23].
Table 1. Classification and general features of *D. acetoxidans* strain 5575<sup>T</sup> in accordance with the MIGS recommendations [9]

| MIGS ID | Property | Term | Evidence code |
|---------|----------|------|---------------|
|         | Current classification | Domain *Bacteria* | TAS [10] |
|         |          | Phylum *Firmicutes* | TAS [11] |
|         |          | Class *Clostridia* | TAS [11] |
|         |          | Order *Clostridiales* | TAS [12] |
|         |          | Family *Peptococcaceae* | TAS [13,14] |
|         |          | Genus *Desulfotomaculum* | TAS [14-16] |
|         |          | Species *Desulfotomaculum acetoxidans* | TAS [1] |
|         |          | Type strain 5575 | TAS [1] |
|         | Gram stain | negative | TAS [1] |
|         | Cell shape | rod with pointed ends | TAS [1] |
|         | Motility | motile (single polar flagellum) | TAS [1] |
|         | Sporulation | spherical endospores | TAS [1] |
|         | Temperature range | 20-40°C | TAS [1] |
|         | Optimum temperature | 36°C | TAS [1] |
|         | Salinity | 1-7 g/l | TAS [2] |
| MIGS-22 | Oxygen requirement | obligate anaerobic | TAS [1] |
|         | Carbon source | CO<sub>2</sub>, acetate | TAS [1,17] |
|         | Energy source | H<sub>2</sub>, acetate, n-butyrate, ethanol, n-butanol, animal intestinal microflora, fresh water, mud, sea water sediment, soil | TAS [2,17] |
| MIGS-6  | Habitat | | TAS [2] |
| MIGS-15 | Biotic relationship | free living | |
| MIGS-14 | Pathogenicity | none | TAS [18] |
|         | Biosafety level | 1 | TAS [18] |
|         | Isolation | piggery waste | TAS [1] |
| MIGS-4  | Geographic location | Göttingen, Germany | NAS |
| MIGS-5  | Sample collection time | 1976 | NAS |
| MIGS-4.1 | Latitude – Longitude | +51.54 - +9.93 | NAS |
| MIGS-4.2 | Altitude | 240 m | NAS |
| MIGS-4.3 | Depth | not reported | |

Evidence codes - IDA: Inferred from Direct Assay (first time in publication); TAS: Traceable Author Statement (i.e., a direct report exists in the literature); NAS: Non-traceable Author Statement (i.e., not directly observed for the living, isolated sample, but based on a generally accepted property for the species, or anecdotal evidence). These evidence codes are from the Gene Ontology project [19]. If the evidence code is IDA, then the property was observed for a living isolate by one of the authors or an expert mentioned in the acknowledgments.

**Genome sequencing and annotation**

**Genome project history**

This organism was selected for sequencing on the basis of its phylogenetic position, and is part of the *Genomic Encyclopedia of Bacteria and Archaea* project. The genome project is deposited in the Genomes OnLine Database [8] and the complete genome sequence in GenBank. Sequencing, finishing and annotation were performed by the DOE Joint Genome Institute (JGI). A summary of the project information is shown in Table 2.

**Growth conditions and DNA isolation**

*D. acetoxidans* strain 5575<sup>T</sup>, DSM 771, was grown anaerobically in DSMZ medium 124 [24] at 37°C. DNA was isolated from 1-1.5 g of cell paste using Qia-gen Genomic 500 DNA Kit (Qiagen, Hilden, Germany) following the manufacturer’s instructions, with a modified protocol for cell lysis (modification LALMP), as described in [25].

http://standardsingenomics.org
Desulfitomaculum acetoxidans type strain (5575T)

Table 2. Genome sequencing project information

| MIGS ID | Property                  | Term                                      |
|---------|---------------------------|-------------------------------------------|
| MIGS-31 | Finishing quality         | Finished                                  |
| MIGS-28 | Libraries used            | Two genomic libraries (8 kb pMCL200 and fosmid pcc1Fos) |
| MIGS-29 | Sequencing platforms      | ABI3730                                   |
| MIGS-31.2| Sequencing coverage     | 8.56 x Sanger                            |
| MIGS-30 | Assemblers               | phrap                                     |
| MIGS-32 | Gene calling method       | Prodigal, GenePRIMP                      |
|         | GenBank ID                | CP001720                                  |
|         | GenBank Date of Release   | September 10, 2009                        |
|         | GOLD ID                   | Gc01106                                   |
|         | NCBI project ID           | 27947                                     |
|         | Database: IMG-GEBA        | 2501651223                                |
| MIGS-13 | Source material identifier| DSM 771                                   |
|         | Project relevance         | Tree of Life, GEBA                        |

Genome sequencing and assembly
The genome of *D. acetoxidans* strain 5575T was sequenced using a combination of 8 kb and fosmid genomic libraries on a Sanger sequencing platform. The Phred/Phrap/Consed software package (http://www.phrap.com) was used for sequence assembly and quality assessment. Possible misassemblies were corrected with Dupfinisher or transposon bombing of bridging clones [26]. Gaps between contigs were closed by editing in Consed, custom primer walk or PCR amplification. A total of 3,281 Sanger finishing reads were produced to close gaps, to resolve repetitive regions, and to raise the quality of the finished sequence. The error rate of the completed genome sequence is less than 1 in 100,000. Together all sequence types provided 9.2× coverage of the genome. The completed genome sequences of *D. acetoxidans* contains 46,605 reads.

Genome annotation
Genes were identified using Prodigal [27] as part of the Oak Ridge National Laboratory genome annotation pipeline, followed by a round of manual curation using the JGI GenePRIMP pipeline [28]. The predicted CDSs were translated and used to search the National Center for Biotechnology Information (NCBI) nonredundant database, UniProt, TIGRFam, Pfam, PRIAM, KEGG, COG, and InterPro databases. Additional gene prediction analysis and functional annotation was performed within the Integrated Microbial Genomes Expert Review (IMG-ER) platform [29].

Genome properties
The genome is 4,545,624 bp long with a 41.6% GC content (Table 3 and Figure 3). Of the 4470 genes predicted, 4370 were protein coding genes, and 100 RNAs; 302 pseudogenes were also identified. The majority of the protein-coding genes (65.6%) were assigned with a putative function while the remaining ones were annotated as hypothetical proteins. The distribution of genes into COGs functional categories is presented in Table 4.

Table 3. Genome Statistics

| Attribute             | Value     | % of Total |
|-----------------------|-----------|------------|
| Genome size (bp)      | 4,545,624 | 100.00%    |
| DNA coding region (bp)| 3,870,017 | 85.14%     |
| DNA G+C content (bp)  | 1,888,927 | 41.55%     |
| Number of replicons   | 1         |            |
| Extrachromosomal elements | 0      |            |
| Total genes           | 4470      | 100.00%    |
| RNA genes             | 100       | 2.24%      |
Table 3. Genome Statistics (cont.)

| Attribute                           | Value  | % of Total |
|-------------------------------------|--------|------------|
| rRNA operons                        | 10     |            |
| Protein-coding genes                | 4370   | 97.76%     |
| Pseudo genes                        | 302    | 6.76%      |
| Genes with function prediction      | 2932   | 65.59%     |
| Genes in paralog clusters           | 1045   | 23.38%     |
| Genes assigned to COGs              | 2702   | 60.45%     |
| Genes assigned Pfam domains         | 2814   | 62.95%     |
| Genes with signal peptides          | 701    | 15.68%     |
| Genes with transmembrane helices    | 791    | 17.70%     |
| CRISPR repeats                      | 11     |            |

Figure 3. Graphical circular map of the genome. From outside to the center: Genes on forward strand (color by COG categories), Genes on reverse strand (color by COG categories), RNA genes (tRNAs green, rRNAs red, other RNAs black), GC content, GC skew.
Insights from the genome sequence

Heterotrophic substrate utilization

It has been shown that in *Desulfotomaculum acetoxidans* acetate is oxidized to CO₂ via the acetyl-CoA/carbon monoxide dehydrogenase (CODH) pathway [30] and all necessary genes required for this pathway have been annotated in the finished genome sequence. Interestingly, a core set of genes that is specific for this pathway shows the same arrangement in *D. acetoxidans* (Dtox_1269 to 1276) as in the distantly related homoacetogenic bacterium *Moorella thermoacetica* (*cooC/acsE*) [31]. A cluster of genes (Dtox_1697 to 1703) that is probably required for growth with butyrate as substrate could be also identified. It has been reported that acetate accumulates upon growth on butyrate and that acetate is only further metabolized to CO₂ under conditions of carbon substrate limitation [2]. This could indicate that the acetyl-CoA/CODH pathway in this strain is only induced under conditions of energy limitation. For the utilization of primary alcohols several putative alcohol dehydrogenases may be used that are encoded at various sites in the genome of *D. acetoxidans*.

Strain 5575ᵀ exhibits a prolonged lag phase upon transfer from media with acetate or butyrate as carbon source to media supplied with other organic substrates [2]. Hence, the identification of additional growth substrates might have been hampered by requiring elongated incubation times of several weeks. This could explain why the utilization of lactate is discussed controversially in the literature. According to Widdel and Pfennig [1,2] this strain is unable to use lactate, whereas Pawłowska-Ćwięk and Pado have repeatedly postulated growth on lactate as sole carbon source [32]. The genome here reported encodes a putative D-lactate dehydrogenase gene.
(Dtox_0988), which is however only distantly related to genes encoding enzymes known to be involved in the respiration or fermentation of lactate. Hence, it is unclear if this enzyme could be involved in the utilization of lactate by *D. acetoxidans*. In our experiments strain 5575^T^ did not show any visible growth on lactate after an incubation period of four weeks.

It was also stated that glucose, fructose, maltose and cellobiose are unsuitable electron donors for this species [2]. However, all necessary genes encoding enzymes of the Embden-Meyerhof-Parnas pathway for the conversion of sugars to pyruvate (glycolysis) were identified in the genome sequence. Hence, it is possible that this pathway is used only for the internal metabolism of carbohydrates and that a transport system for the efficient uptake of sugars is not expressed.

**Autotrophic growth**

Londry and Des Marais [17] reported that *D. acetoxidans* can grow autotrophically with H2 as the electron donor and CO2 as carbon source, which is contradictory to the original species description [1,2]. Genes for several subunits of a putative Fe-only hydrogenase (Dtox_0168, Dtox_0169 and Dtox_0172 to 0178) and a [NiFe]-hydrogenase (Dtox_0791 to 0796) were detected in the genome of *D. acetoxidans*, which would confirm the finding of H2 utilization in this species.

The acetyl-CoA/CODH pathway is fully reversible and it was shown that in *D. autotrophicum* it is used for both the cleavage and formation of acetyl-CoA [33]. Hence, Londry and Des Marais [17] proposed that *D. acetoxidans* uses the acetyl-CoA/CODH pathway for the fixation of CO2 under lithoautotrophic growth conditions. They reported that during growth on H2/CO2 and sulfate, small amounts of acetate were excreted, which would confirm that the reductive acetyl-CoA pathway is used as mechanism for CO2 assimilation.

Interestingly, a cluster of nitrogenase genes (Dtox_1023 to 1030) could be detected within the annotated genome sequence, so that *D. acetoxidans* likely has the capacity to use dinitrogen as nitrogen source. However, the fixation of molecular nitrogen has not been analyzed by laboratory experiments in this species so far.

**Electron transport phosphorylation**

The oxidation of carbon sources by dehydrogenases leads to the formation of reduced pyridine nucleotides that are most likely reoxidized in *D. acetoxidans* by a proton-translocating NADH dehydrogenase complex, which reduces menaquinones. The structure of the NADH dehydrogenase seems to be similar to complex I in the electron transport chain of *E. coli* and mitochondria. Most genes for this complex are located in a single operon (Dtox_1205 to 1215), but genes for the subunits E, F, and G are located elsewhere in the genome and often found in close proximity to genes involved in energy metabolism. Several genes encoding heterodisulfide reductases were annotated and also found close to genes involved in electron transport. Hence, it can be assumed that besides the NADH dehydrogenase complex, heterodisulfide reductases play a role in the generation of a proton gradient, as has been previously proposed for the homoacetogenic bacterium *Moorella thermoaceta*ica [31]. An established proton gradient could then be utilized by an ATP synthase of the FOF1-type, which is encoded in a single gene cluster (Dtox_4164 to 4172).

Besides genes involved in sulfate reduction no other genes encoding known enzymes for alternative pathways of anaerobic respiration were detected in the genome, so that in this species the utilization of electron acceptors seems to be restricted to oxidized sulfur species for sulfate reduction and CO2 for the synthesis of acetyl-CoA. So far, no homoacetogenic growth of *D. acetoxidans* with H2 or organic compounds as electron donor could be shown, so that apparently the reduction of CO2 is not coupled to the generation of energy in this species.

**Defense against oxidative stress**

Widdel and Pfennig reported in the original species description of *D. acetoxidans* an inhibition of growth in media that were not fully reduced [1], which would indicate a high sensitivity against oxygen. Most known sulfate-reducers tolerate exposure to oxygen for at least short intervals without any recognizable cellular damage. Aerobic respiration was identified as one principal mechanism for the detoxification of oxygen in cultures of Gram-negative sulfate-reducers [34]. Accordingly, quinol oxidases of the cytochrome *bd* type that are characterized by a high-affinity to oxygen were identified in several Gram-negative sulfate-reducers [35-38] and *D. reducens* (this study). However, no genes encoding a potential terminal oxidase could be identified in the genome of *D. acetoxidans*. Only genes encoding enzymes...
representing a second line of defense against reactive oxygen species were identified, for example superoxide dismutase (Dtox_4195) and catalase (Dtox_1104).

Thus, a peculiarity of the *D. acetoxidans* metabolism could be its strategy against oxidative stress. In this species other reactions may be involved in the scavenging of oxygen, so that highly sensitive compounds within the cytoplasm are protected. A potential mechanism could be the chemical reaction of oxygen with ferrous iron or iron sulfides. It was shown that cells of *D. acetoxidans* produce hydroxamic siderophores (probably deferoxamine) and accumulate large amounts of ferrous sulfide (FeS) or pyrite (FeS₂) in their cell wall [39].

**Acknowledgements**

We would like to gratefully acknowledge the help of Susanne Schneider (DSMZ) for DNA extraction and quality analysis. This work was performed under the auspices of the US Department of Energy’s Office of Science, Biological and Environmental Research Program, and by the University of California, Lawrence Berkeley National Laboratory under contract No. DE-AC02-05CH11231, Lawrence Livermore National Laboratory under Contract No. DE-AC52-07NA27344, and Los Alamos National Laboratory under contract. German Research Foundation (DFG) supported DSMZ under INST 599/1-1.

**References**

1. Widdel F, Pfennig N. A new anaerobic, sporing, acetate-oxidizing, sulfate-reducing bacterium, *Desulfotomaculum* (emend.) acetoxidans. *Arch Microbiol* 1977; 112: 119-122. 
   **PubMed**
   [doi:10.1007/BF00446665](https://doi.org/10.1007/BF00446665)

2. Widdel F, Pfennig N. Sporulation and further nutritional characteristics of *Desulfotomaculum* acetoxidans. *Arch Microbiol* 1981; 129: 401-402.
   **PubMed**
   [doi:10.1007/BF00406471](https://doi.org/10.1007/BF00406471)

3. Scholten JC, Stams AJ. Isolation and characterization of acetate-utilizing anaerobes from a freshwater sediment. *Microb Ecol* 2000; 40: 292-299.
   **PubMed**

4. Stackebrandt E, Spröer C, Rainey FA, Burghardt J, Päuker O, Hippe H. Phylogenetic analysis of the genus *Desulfotomaculum*: evidence for the misclassification of *Desulfotomaculum guttoides* and description of *Desulfotomaculum orientis* as *Desulfovosporinus orientis* gen. nov., comb. nov. *Int J Syst Bacteriol* 1997; 47: 1134-1139.
   **PubMed**

5. Lee C, Grasso C, Sharlow MF. Multiple sequence alignment using partial order graphs. *Bioinformatics* 2002; 18: 452-464.
   **PubMed**
   [doi:10.1093/bioinformatics/18.3.452](https://doi.org/10.1093/bioinformatics/18.3.452)

6. Castresana J. Selection of conserved blocks from multiple alignments for their use in phylogenetic analysis. *Mol Biol Evol* 2000; 17: 540-552.
   **PubMed**

7. Stamatakis A, Hoover P, Rougemont J. A rapid bootstrap algorithm for the RAxML web-servers. *Syst Biol* 2008; 57: 758-771.
   **PubMed**
   [doi:10.1080/10635150802429642](https://doi.org/10.1080/10635150802429642)

8. Liolios K, Mavromatis K, Tavernarakis N, Kyrpides NC. The Genomes OnLine Database (GOLD) in 2007: status of genomic and metagenomic projects and their associated metadata. *Nucleic Acids Res* 2008; 36: D475-D479.
   **PubMed**
   [doi:10.1093/nar/gkm884](https://doi.org/10.1093/nar/gkm884)

9. Field D, Garrity G, Gray T, Morrison N, Selengut J, Sterk P, Tatusova T, Tompson N, Allen MJ, An- giuoli SV, et al. Towards a richer description of our complete collection of genomes and metagenomes: the “Minimum Information about a Genome Sequence” (MIGS) specification. *Nat Biotechnol* 2008; 26: 541-547.
   **PubMed**
   [doi:10.1038/nbt1360](https://doi.org/10.1038/nbt1360)

10. Woese CR, Kandler O, Wheelis ML. Towards a natural system of organisms: proposal for the domains *Archaea*, *Bacteria*, and *Eucarya*. *Proc Natl Acad Sci USA* 1990; 87: 4576-4579.
    **PubMed**
    [doi:10.1073/pnas.87.12.4576](https://doi.org/10.1073/pnas.87.12.4576)

11. Garrity GM, Holt JG. Taxonomic Outline of the *Archaea* and *Bacteria*. *Berger's Manual of Syste-
matic Bacteriology 2nd ed. (D.R. Boone and R.W. Castenholz, eds.), Springer-Verlag, New York 2001; 1:155-166.

12. Prévot AR. Dictionnaire des Bactéries Pathogènes. 2nd ed. Edited by: Hauderoy P, Ehringer G, Guillot G, Magrou J., Prévot AR, Rosset D, Urbain A. Masson et Cie, Paris; 1953; 692 pages.

13. Rogosa M. Peptococaceae, a new family to include the Gram-positive, anaerobic cocci of the genera Peptococcus, Peptostreptococcus and Ruminococcus. Int J Syst Bacteriol 1971; 21: 234-237.

14. Skerman VBD, McGowan V, Sneath PHA. Approved Lists of Bacterial Names. Int J Syst Bacteriol 1980; 30: 225-420.

15. Campbell LL, Singleton R, Jr. Genus IV. Desulfo-tomaculum Campbell and Postgate 1965, 361AL. In: Bergey's Manual of Systematic Bacteriology, vol. 2. 1st ed. Edited by: Holt JG. The Williams and Wilkins Co., Baltimore; 1986; pp 1200-1202.

16. Dowling NJE, Widdel F, White DC. Phospholipid ester-linked fatty acid biomarkers of acetate-oxidizing sulphate-reducers and other sulphide-forming bacteria. J Gen Microbiol 1986; 132: 1815-1825.

17. Londry K, Des Marais DJ. Stable carbon isotope ratios of lipid biomarkers of sulfate-reducing bacteria. Appl Environ Microbiol 2004; 70: 745-751. PubMed:10.1128/AEM.70.2.745-751.2004

18. Anonymous. Biological Agents: Technical rules for biological agents (TRBA 466)

19. Anonymous. Prodigal Prokaryotic Dynamic Programming Genefinding Algorithm. Oak Ridge National Laboratory and University of Tennessee 2009

20. Liu Y, Karnauchow TM, Jarrell KF, Balkwill DL, Drake GR, Ringelberg D, Clarro R, Boone DR. Description of two new thermophilic Desulfitomaculum spp., Desulfitomaculum putei sp. nov., from a deep terrestrial subsurface, and Desulfitomaculum luciae sp. nov., from a hot spring. Int J Syst Bacteriol 1997; 47: 615-621.

21. Collins MD, Widdel F. Respiratory quinones of sulphate-reducing and sulphur-reducing bacteria: a systematic investigation. Syst Appl Microbiol 1986; 8: 8-18.

22. Dowling NJE, Widdel F, White DC. Phospholipid ester-linked fatty acid biomarkers of acetate-oxidizing sulphate-reducers and other sulphide-forming bacteria. J Gen Microbiol 1986; 132: 1815-1825.

23. Londry KL, Jahnke LL, Des Marais DJ. Stable carbon isotope ratios of lipid biomarkers of sulfate-reducing bacteria. Appl Environ Microbiol 2004; 70: 745-751. PubMed:10.1128/AEM.70.2.745-751.2004

24. List of growth media used at DSMZ: http://www.dsmz.de/microorganisms/media_list.php

25. Wu D, Hugenholtz P, Mavromatis K, Pukall R, Dalin E, Ivanova N, Kunin V, Goodwin L, Wu M, Tindall BJ, et al. A phylogeny-driven genomic encyclopedia of Bacteria and Archaea. Nature (In press).

26. Sims D, Brettin T, Detter JC, Han C, Lapidus A, Copeland A, Glavina Del Rio T, Nolan M, Chen F, Lucas S, et al. Complete genome sequence of Kytococcus sedentarius type strain (5412). Stand Genomic Sci 2009; 1: 12-20. doi:10.4056/sigs.761

27. Anonymous. Prodigal Prokaryotic Dynamic Programming Genefinding Algorithm. Oak Ridge National Laboratory and University of Tennessee 2009

28. Pati A, Ivanova N, Mikhailova N, Ochkinova G, Hooper SD, Lykidis A, Kyrpides NC. GenePRIMP: A Gene Prediction Improvement Pipeline for microbial genomes. (Submitted) 2009.

29. Markowitz VM, Szeto E, Palaniappan K, Grechkin Y, Chu K, Chen IM, Dubchak I, Anderson I, Lykidis A, Mavromatis K, et al. The integrated microbial genomes (IMG) system in 2007: data content and analysis tool extensions. Nucleic Acids Res 2008; 36: D528-D533. PubMed:10.1093/nar/gkm846

30. Spormann AM, Thauer RK. Anaerobic acetate oxidation to CO2 in Desulfitomaculum acetoxidans. Demonstration of enzymes required for the operation of an oxidative acetyl-CoA/carbon monoxide dehydrogenase pathway. Arch Microbiol 1988; 150: 374-380. doi:10.1007/BF00408310

31. Pierce E, Xie G, Barabote RD, Saunders E, Han CS, Detter JC, Richardson P, Detter TS, Das A, Ljungdahl LG, Ragsdale SW. The complete genome sequence of Moorella thermoaceticita (f. Clostridium thermoacetaticum). Environ Microbiol 2008; 10: 2550-2573. PubMed:10.1111/j.1462-2920.2008.01679.x

32. Pawłowska-Ćwiąk L, Pado R. Growth and antioxid activity of Desulfitomaculum acetoxidans DSM 771 cultivated in acetate or lactate containing media. Pol J Microbiol 2007; 56: 205-213. PubMed
Desulfotomaculum acetoxidans type strain (5575T)

33. Schauder R, Preuß A, Jetten M, Fuchs G. Oxidative and reductive acetyl CoA/carbon monoxide dehydrogenase pathway in Desulfbacterium autotrophicum. 2. Demonstration of the enzymes of the pathway and comparison of CO dehydrogenase. *Arch Microbiol* 1989; 151: 84-89. doi:10.1007/BF00444674

34. Cypionka H. Oxygen respiration by *Desulfovibrio* species. *Annu Rev Microbiol* 2000; 54: 827-848. PubMed doi:10.1146/annurev.micro.54.1.827

35. Lemos RS, Gomes CM, Santana M, LeGall J, Xavier AV, Teixeira M. The 'strict' anaerobe *Desulfovibrio gigas* contains a membrane-bound oxygen-reducing respiratory chain. *FEBS Lett* 2001; 496: 40-43. PubMed doi:10.1016/S0014-5793(01)02399-7

36. Rabus R, Ruepp A, Frickey T, Rattei T, Fartmann B, Stark M, Bauer M, Zibat A, Lombardot T, Becker I, et al. The genome of *Desulfotalea psychrophila*, a sulfate-reducing bacterium from permanently cold arctic sediments. *Environ Microbiol* 2004; 6: 887-902. PubMed doi:10.1111/j.1462-2920.2004.00665.x

37. Heidelberg JF, Seshadri R, Havemann SA, Hemme CL, Paulson IT, Kolonay JF, Eiden JA, Ward N, Methe B, Brinkac LM, et al. The genome sequence of the anaerobic sulfate-reducing bacterium *Desulfovibrio vulgaris* strain Hildenborough. *Nat Biotechnol* 2004; 22: 554-559. PubMed doi:10.1038/nbt959

38. Strittmatter AW, Liesegang H, Rabus R, Decker I, Amann J, Sönke A, Henna A, Fricke WF, Martinez-Arias R, Bartels D, et al. Genome sequence of *Desulfbacterium autotrophicum* HRM2, a marine sulfate reducer oxidizing organic carbon completely to carbon dioxide. *Environ Microbiol* 2009; 11: 1038-1055. PubMed doi:10.1111/j.1462-2920.2008.01825.x

39. Pado R, Pawłowska-Ćwięk L. The uptake and accumulation of iron by the intestinal bacterium *Desulfotomaculum acetoxidans* DSM 771. [Krakow]. *Folia Biol* 2005; 53: 79-81. doi:10.3409/1734916054663519

40. Brock TD, O’Dea K. Amorphous ferrous sulfide as a reducing agent for culture of anaerobes. *Appl Environ Microbiol* 1977; 33: 254-256. PubMed

41. Widdel F. The genus *Desulfotomaculum*. *The Prokaryotes* 3rd ed. Springer New York 2006; 4:787-794.