Azoarcus sp. strain PA01\textsuperscript{T} belongs to the genus Azoarcus, of the family Rhodocyclaceae within the class Betaproteobacteria. It is a facultatively anaerobic, mesophilic, non-motile, Gram-stain negative, non-spore-forming, short rod-shaped bacterium that was isolated from a wastewater treatment plant in Constance, Germany. It is of interest because of its ability to degrade o-phthalate and a wide variety of aromatic compounds with nitrate as an electron acceptor. Elucidation of the o-phthalate degradation pathway may help to improve the treatment of phthalate-containing wastes in the future.

Here, we describe the features of this organism, together with the draft genome sequence information and annotation. The draft genome consists of 4 contigs with 3,908,301 bp and an overall G + C content of 66.08 %.

Keywords: Azoarcus sp. strain PA01\textsuperscript{T}, o-phthalate degradation, Rhodocyclaceae, Betaproteobacteria, anaerobic degradation, wastewater treatment plant, pollutant

Introduction
Phthalic acid consists of a benzene ring to which two carboxylic groups are attached. There are three isomers of phthalic acid (o-phthalic acid, m-phthalic acid and p-phthalic acid). Phthalic acid esters are widely used as additives in plastic resins such as polyvinyl resin, cellulose and polyurethane polymers for the manufacture of building materials, home furnishings, transportation apparatus, clothing, and to a limited extent in food packaging materials and medical products [1, 2].

Due to the widespread use of phthalates there has been great concern about their release into the environment [3, 4]. In addition, phthalates and their metabolic intermediates have been found to be potentially harmful to humans due to their hepatotoxic, teratogenic and carcinogenic characteristics [5, 6]. Phthalic acid is also an intermediate in the bacterial degradation of phthalic acid esters [7] as well as in degradation of certain fused-ring polycyclic aromatic compounds found in fossil fuel [8], such as phenanthrene [9], fluorene [10] and fluoranthene [11].

Azoarcus sp. strain PA01\textsuperscript{T} (=KCTC 15483) is a mesophilic, Gram-negative, nitrate-reducing bacterium that was isolated from a wastewater treatment plant in Constance, Germany, for its ability to completely degrade o-phthalate and a wide range of aromatic compounds. Strain PA01\textsuperscript{T} is also able to grow with a variety of organic substrates including short-chain fatty acids, alcohols, selected sugars and amino acids. These substrates are degraded completely to carbon dioxide coupled to nitrate reduction. The genus Azoarcus is comprised of nitrogen-fixing bacteria [12] and known for degradation of aromatic compounds. Currently, this genus consists of nine species with validly published names [13]. These species have been isolated from a wide range of environments, including anoxic wastewater sludge and grass root soil [12]. On the basis of 16S rRNA gene sequence similarity search, the closest relatives of strain PA01\textsuperscript{T} are Azoarcus buckelii DSM 14744\textsuperscript{T} (99 % gene similarity) [14, 15] and Azoarcus anaerobius (98 %) [16]. A. buckelii DSM 14744\textsuperscript{T} was also isolated from a sewage treatment plant for its ability to degrade a wide...
range of aromatic compounds. But the biochemistry and genetics of anaerobic \(o\)-phthalate degradation had not been elucidated in detail. Here, we present a summary of the features for \textit{Azoarcus} sp. strain PA01\(^T\) and its classification, together with the description of the genomic information and annotation.

**Organism information**

**Classification and features**

\textit{Azoarcus} sp. strain PA01\(^T\) is a member of the family \textit{Rhodocyclaceae} in the phylum \textit{Proteobacteria}. It was isolated from an activated sewage sludge sample collected (in 2012) from a wastewater treatment plant in Constance, Germany. Enrichment, isolation, purification and growth experiments were performed in anoxic, bicarbonate-buffered, non-reduced freshwater medium containing (g/l); \(\text{NaCl}, 1.0; \text{MgCl}_2 \times 6\text{H}_2\text{O}, 0.4; \text{KH}_2\text{PO}_4, 0.2; \text{NH}_4\text{Cl}, 0.25; \text{KCl}, 0.5; \text{CaCl}_2 \times 2\text{H}_2\text{O}, 0.15; \text{NaHCO}_3, 2.5; \text{Na}_2\text{SO}_4, 1\text{mM}.\) The medium was autoclaved at 121 °C for 25 min and cooled under an oxygen-free mixture of \(\text{N}_2\) : \(\text{CO}_2\) (80/20) gas phase. Further, 1 ml trace element solution SL-10 [17], 1 ml selenate-tungstate solution [18] and 1 ml seven-vitamin solution [19] were added. The initial pH of the medium was adjusted to 7.3 ± 0.2 with sterile 1 N \(\text{NaOH}\) or 1 N \(\text{HCl}\). Cultivations and transfer of the strain were performed under \(\text{N}_2\) : \(\text{CO}_2\) (80:20) gas atmosphere. The strain was cultivated in the dark at 30 °C. Enrichment cultures were started by inoculating approximately 2 ml of sludge sample in 50 ml freshwater medium (described above) containing 2 mM neutralized \(o\)-phthalic acid as sole carbon source and 10–12 mM \(\text{NaNO}_3\) as an electron acceptor. Growth was observed after 3–4 weeks of incubation. Enrichment cultures were sub-cultured for several passages with \(o\)-phthalate as sole carbon source. Pure cultures were obtained in repeated agar (1 %) shake dilutions [20]. Single colonies obtained were retrieved by means of finely-drawn sterile Pasteur pipettes and transferred to fresh liquid medium. The strain was routinely examined for purity by light microscopy (Axiophot, Zeiss, Germany) also after growing the culture with 2 mM phthalate plus 1 % (w/v) yeast extract. For genetic and chemotaxonomic analysis, it was cultivated in the described medium containing 8 mM acetate as a carbon source.

\textit{Azoarcus} sp. strain PA01\(^T\) is a mesophilic, non-motile, Gram-negative, short rod-shaped bacterium measuring 0.5–0.7 \(\mu\)m (wide), 1.6–1.8 \(\mu\)m (length) (Fig. 1a and b) and divides by binary fission. Growth was observed from 25 °C to 37 °C with an optimum at 30 °C and optimal pH of 7.3 ± 0.2 (Table 1). Strain PA01\(^T\) grows anaerobically with nitrate on a wide variety of substrates, including \(o\)-phthalate, benzoate, 3,4-dihydroxy-benzoate, 3-hydroxy-benzoate, 4-hydroxy-benzoate, malate, fructose, glucose, gluconate, ethanol, 1-butanol, 1-propanol, glycerol, arginine, alanine, malate, pyruvate, succinate, crotonate, propionate, valerate and butyrate. No growth was observed with \(iso\)-phthalate, \(tere\)-phthalate, 4-amino-benzoate, resorcinol, methanol, threonine, choline, betaine, formate, citrate, 2-oxoglutarate and oxaloacetate.

Initial identification and validation of strain PA01\(^T\) was performed by 16S rRNA gene amplification using a set of universal bacterial primers; 27 F (5′- AGA GTT TGA TCM TGG CTC AG-3′) and 1492R (5′- TAC GGY TAC CTT GTT ACG ACT T-3′) as described [21]. A phylogenetic tree was constructed from the 16S rRNA gene sequence together with the other representatives of the genus \textit{Azoarcus} (Fig. 2) using the MEGA 4 software package [22]. Phylogenetic analysis indicated that strain PA01\(^T\) belongs to the genus \textit{Azoarcus} and is closely related to \textit{Azoarcus buckelii} (99 %) and \textit{Azoarcus anaerobius} (98 %). Currently, 30 genome sequences are available for the members of the order \textit{Rhodocyclales}. The closest neighbors of strain PA01\(^T\) whose genome sequence is available are \textit{Azoarcus} sp. strain KH32C [23] and \textit{Azoarcus} sp. strain BH72 [24] and \textit{Azoarcus toluclasticus} ATCC.
700605 [25]. The exact phylogenetic position of strain PA01T within the genus Azoarcus is shown in Fig. 2 and the 16S rRNA gene sequence of the strain has been deposited to NCBI under accession number KR025921.

**Chemotaxonomy**
Whole-cell fatty acid methyl esters [26] were analyzed by the Identification Service of the Deutsche Sammlung von Mikroorganismen und Zellkulturen (DSMZ, Braunschweig, Germany). The cellular fatty acid pattern of Azoarcus sp. strain PA01T is dominated by the presence of an un-saturated branched-chain fatty acid C_{16:1}ω7c/15 iso-2OH (49.6 %) and saturated straight-chain fatty acid C_{16:0} (25.2 %), which have also been reported to be common fatty acids among recently described other species of the genus Azoarcus [27, 28]. Other fatty acids include C_{18:1}ω7c (8.8 %), C_{17:1}cyclo (0.82 %), C_{16:1}ω5c (0.68 %), C_{14:0} (0.73 %), C_{12:0} (7.19 %), C_{10:0} 3OH (6.27 %), and C_{10:0} (0.74 %).

**Genome sequencing information**

**Genome project history**
Strain PA01T was selected for genome sequencing on the basis of its phylogenetic position and its ability to grow on o-phthalate together with numerous aromatic compounds under nitrate-reducing conditions. Genome sequencing was performed at GATC Biotech AG, Konstanz (Germany). High-quality genome draft sequence of Azoarcus sp. strain PA01T is listed in the Genomes Online Database of the Joint Genome Institute under project ID Gp0109270 [25]. The Azoarcus sp. PA01T whole genome shotgun (WGS) project has been deposited at DDBJ/EMBL/GenBank under the project accession LARU00000000.

The version described in this paper has the accession...
number LARU01000000, and consists of sequences LARU01000001-LARU01000004. The draft genome sequence was released on August 26, 2015. Annotation of the Azoarcus sp. strain PA01T genome, was performed by the DOE Joint Genome Institute using microbial genome annotation pipeline state of the art technology [29, 30]. Table 2 presents the project information and its association with MIGS version 2.0 compliance [31].

Growth conditions and genomic DNA preparation
For the isolation of genomic DNA, cells were grown in one liter medium with 8 mM acetate plus 10–12 mM nitrate. Cells were harvested in the late stationary phase and cell pellet was stored frozen (−20 °C) until DNA preparation. High-molecular-weight genomic DNA was prepared using modified CTAB DNA extraction protocol [32] with some modifications. Chloroform-isooamyl alcohol (24:1) and phenol:chloroform-isooamyl alcohol (25:24:1) steps were repeated twice and RNase treatment was performed for 2 h. Finally, the DNA was dissolved in RNase and DNase-free molecular grade water. Purity, quality and size of the genomic DNA preparation were analyzed by using nanodrop (639 ng/μl, A260/280 = 1.84, A260/230 = 2.10) and agarose gel electrophoresis (1 % w/v) (see Fig. 1c).

Genome sequencing and assembly
The genome of Azoarcus sp. strain PA01T was sequenced using a library size of 8–12 kb. Library construction, quantification and sequencing (Pacific Bioscience RS) were performed at GATC Biotech AG (Konstanz, Germany). The final high-quality draft assembly was based on 95,883 reads. The combined libraries provided the 97.42 mean coverage of sequencing depth. Final de novo assembly of the genome from the total reads was performed using the PacBio HGAP3 assembly pipeline with default filter parameters. Minimum read length and polymerase read quality was 500 bp and 0.80, respectively. The minimum seed read length was computed automatically and resulted in 5181 bp (length cutoff). The final polished assembly of the sequencing reads yielded 4 linear contigs generating a draft genome size of 3.9 Mb.

Genome annotation
Annotation was carried out using the DOE-JGI annotation pipeline [30] and genes were identified using Prodigal [33]. The predicted CDSs were translated and used to search the NCBI non-redundant database, UniProt, TIGRFam, Pfam, PRIAM, KEGG, COG and InterPro databases. The tRNAScanSE tool [34] was used to find tRNA genes, whereas ribosomal RNA genes were found by searches against models of the ribosomal RNA genes built from SILVA [35]. Other non-coding RNAs such as the RNA components of the protein secretion complex and the RNase P were identified by searching the genome for the corresponding Rfam profiles using INFERNAL [36]. Additional gene prediction analysis and manual functional annotation was performed within the IMG-ER Platform [37].

Genome properties
The draft genome of Azoarcus sp. PA01T is 3,908,301 bp long (with 4 linear contigs, see Fig. 3) with an overall GC content of 66.08 % (Table 3). Of a total 3,712 genes predicted, 3,625 were protein-coding genes, and 87 were RNA genes (15 rRNA genes and 59 tRNA genes); 525 genes without function were identified (pseudogenes). The majority of the protein-coding genes (83.51 %) were assigned a putative function while those remaining were
annotated as hypothetical proteins. The properties and the statistics of the genome are summarized in Table 3, the distribution of genes into COGs functional categories is presented in Table 4. One CRISPR region was found in the genome of strain PA01 which is located in proximity to the CRISPR-associated endonucleases (Cas1 and Cas 2) proteins.

**Insight from the genome sequence**  
*Azoarcus* sp. strain PA01 \(^{T}\) grows on a wide variety of aromatic compounds (Table 1) linked to nitrate reduction like other bacteria capable of growth via anaerobic degradation of aromatic compounds [38]. In the degradation pathway of most aromatic compounds (including *o*-phthalate), benzoate is a central intermediate and has
also been used routinely as the model compound to study the anaerobic degradation of aromatic compounds via the benzoyl-CoA degradation pathway [39]. Annotation of the genome indicated that strain PA01T has key enzymes for the degradation of aromatic compounds such as benzoate. In the past decade, degradation of benzoate through the benzoyl-CoA pathway has been detailed at the molecular level in facultative anaerobes and the phototrophic strictly anaerobic bacteria, i.e. in the denitrifying bacteria *Thauera aromatica* and *Rhodopseudomonas palustris* respectively [40, 41].

Unlike other benzoate and/or aromatic compound degrading bacteria, strain PA01T has the genes for benzoate degradation, which involves a one-step reaction that activates benzoate to benzoyl-CoA by an ATP-dependent benzoate-CoA ligase. The genome of PA01T contains in total two copies of the benzoate-CoA ligase, i.e., benzoate-CoA ligase (EC 6.2.1.25) and benzoate-CoA ligase (EC 6.2.1.25) (locus tag PA01_01819, PA01_03223) which are supposed to be involved in the initial activation of benzoate to benzoyl-CoA. They are located in different positions. These two genes show 68.11 % identity to each other and are also found to be present in the genomes of the other bacteria [23]. The subsequent enzyme of benzoate degradation, benzoyl-CoA reductase is present in one copy with all its four subunits (locus tags PA01_00623, PA01_00625, PA01_00624, PA01_00626) in the genome of strain PA01. The presence of these gene clusters in the genome of *Azoarcus sp. strain PA01T* provides evidence for the capacity of strain PA01T to degrade aromatic compounds.

Most of the novel biochemistry of the anaerobic metabolism of aromatic compounds has been discovered with nitrate-reducing bacteria in the past two decades [42, 43] and little is known about the biochemistry of phthalate degradation in nitrate-reducing and strictly anaerobic (fermenting and sulfate-reducing) bacteria. We are currently exploring the genome of strain PA01T and the enzymes responsible for o-phthalate degradation by using differential proteomics and measuring enzyme activities (unpublished). Thus, the draft genome sequence of strain PA01T provides an opportunity to study the biochemistry of o-phthalate degradation into depth.

**Conclusions**

*Azoarcus* sp. strain PA01T harbors various genes required for degradation of aromatic compounds (which are normally found in the other aromatic degrading bacteria), e.g., genes for benzoate degradation in the genome of strain PA01. Further, the genome of *Azoarcus sp. strain PA01T*
will expands our view to understand the biochemistry of anaerobic degradation of various aromatic compounds, including o-phthalate, a priority pollutant. The genome sequence of strain PA01T will provide insight into the putative genes involved in the degradation of all these compounds, mainly o-phthalate.

**Abbreviations**

PA: Phthalic acid; PAEs: Phthalic acid esters; CoA: Coenzyme A; – 407. Pseudomonas sp. – 1005. – – Mycobacterium sp

**Competing interests**

The authors have declared that they have no competing interests.

**Authors’ contributions**

MJ initiated and BS supervised the study throughout. MJ drafted the manuscript, conducted wet lab work and performed electron microscopy. YP conducted a screening of carbon sources for growth and substrate utilization experiments. MJ, YP and BS discussed, analyzed the data and revised the manuscript. All authors read and approved the final manuscript.

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**References**

1. Vamsee-Krishna C, Mohan Y, Phale PS. Biodegradation of phthalate isomers by Pseudomonas aeruginosa PP4, Pseudomonas sp. PPD and Acinetobacter Iwofii ISP4. Appl Microbiol Biotechnol. 2006;72:263–9.
2. Chen JA, Li X, Li J, Gu Q, Zhu Q, Zhao Q, et al. Degradation of environmental endocrine disruptor di-2-ethylhexyl phthalate by a newly discovered bacterium, Microbacterium sp. strain CQ0110r. Appl Microbiol Biotechnol. 2007;74:676–82.
3. Staples CA, Peterson DR, Parkerton TF, Adams WJ. The environmental fate of phthalate esters: a literature review. Chemosphere. 2002;55:667–749.
4. Giam CS, Chan HS, Neff GS, Atlas E. Phthalate ester plasticizers: A new class of marine pollutant. Science. 1978;199:419–21.
5. Matsumoto M, Hsita-Koizumi M, Ema M. Potential adverse effects of phthalic acid esters on human health: a review of recent studies on reproduction. Regul Toxicol Pharm. 2008;50:37–49.
6. Woodward KN. Phthalate esters, cystic kidney disease in mammals and possible effects on human health. A review. Hum Exp Toxicol. 1990;9:397–401.
7. Ribbons DW, Keyser P, Kunz DA, Taylor BF. Microbial degradation of phthalates. In: Gibson DT, editor. Microbial Degradation of Organic Compounds. New York: Marcel Dekker; 1984.
8. Ribbons DW, Eaton RW. Chemical transformations of aromatic hydrocarbons that support the growth of microorganisms. In: Chakrabarty AM, editor. Biodegradation and detoxification of environmental pollutants. Boca Raton: CRC Press; 1982. p. 59–84.
9. Kyihar A, Niiya K. The catalolism of phenanthrene and anthracene by bacteria. J Gen Microbiol. 1978;105:69–75.
10. Grillo M, Selitron SA, Chapman PJ. Evidence for a novel pathway in the degradation of fluorene by Pseudomonas sp. strain F274, Appl Environ Microbiol. 1994;60:2438–49.
11. Sepic E, Bricelj M, Leskovec H. Degradation of fluoranthene by Pasteurella sp. IFA and Microbacterium sp. PPR-1, Isolation and identification of metabolites. J Appl Microbiol. 1998;85:746–54.
12. Reinhold HB, Hurek T, Gillis M, Hoste B, Vancanneyt M, Kersters K, et al. Azoarcus gen. nov, nitrogen-fixing Proteobacteria associated with roots of kellar grass (Leptochloa fusca (L.) Kunth), and description of two species, Azoarcus indigens sp. nov. and Azoarcus communis sp. nov. Int J Syst Bacteriol. 1993;43:574–84.
13. Parte AC. LPSN-list of prokaryotic names with standing in nomenclature. Nucleic Acids Res. 2014;42(D1):D613–616.
14. Mechichi T, Stackerbrandt E, Gad'om N, Fuchs G. Phylogenetic and metabolic diversity of bacteria degrading aromatic compounds under denitrifying conditions, and description of Thauera phenylacetica sp. nov., Thauera aminooxidatica sp. nov. and Azozcurc buckelli sp. nov. Arch Microbiol. 2002;178(1):26–35.
15. Validation List No. 87. Validation of publication of new names and new combinations previously effectively published outside the IJSEM. Int J Syst Evol Microbiol. 2002;52:1437–8.
16. Springer N, Ludwig W, Philipp B, Schink B. Azoarcus aneurabius sp. nov., a resorcinol-degrading, strictly anaerobic, denitrifying bacterium. Int J Syst Bacteriol. 1998;48:953–6.
17. Widdel F. Kehnert GW, Mayer F. Studies on dissimilatory sulfate-reducing bacteria that decompose fatty acids. Characterization of the filamentous gliding Desulfonema limicola. Arch Microbiol. 1983;134:286–94.
18. Tschech A, Pfennig N. Growth yield increase linked to cafffeate reduction in Acetobacterium woodii. Arch Microbiol. 1984;137:176–7.
19. Pfennig N. Rhodococcus purpurgenes sp. nov. sp. nov. a ring-shaped, vitamin B_{12}-requiring member of the family Rhodopseudomonaceae. Int J Syst Bacteriol. 1978;28:283–8.
20. Widdel F, Bak F. Gram negative mesophilic sulfur reducing bacteria. In: Balbos H, Truper HG, Dworin M, Harder W, Schlefer KE, editors. The Prokaryotes Vol IV, vol. 183. New York/Berlin, Heidelberg: Springer; 1992. p. 3532–78.
21. Patil Y, Junghare M, Pester M, Muller N, Schink B. Characterization and phylogeny of A aerobicum acetethlycicum gen. nov. sp. nov. a strictly anaerobic glutonate-fermenting bacterium isolated from a methanogenic bioreactor. Int J Syst Evol Microbiol 2015, in press.
22. Tamura K, Dudley J, Nei M, Kumar S. MEGA4: molecular evolutionary genetics analysis (MEGA) software version 4.0. Mol Biol Evol. 2007;24:1596–9.
23. Tomoyasu N, Kanako T, Kershiro O, Masahira H, Satoshi I, Shigeto O, et al. Complete Genome Sequence of the Denitrifying and NO2-Reducing Bacterium Azozcurc sp. strain KH15C. J Bacteriol. 2012;194(5):1255.
24. Krause A, Ramakumar A, Bartels D, Battistoni F, Bekel T, Boch J, et al. Complete genome of the mutualistic, N2-fixing grass endophyte Azozcurc sp. strain BH72. Nat Biotechnol. 2006;24(11):1385–91.
25. Lolios K, Mavromatis K, Tavernarakis N, Kyprides NC, The Genomes On Line Database (GOLD) in 2007: status of genomic and metagenomic projects and their associated metadata. Nucleic Acids Res. 2008;36:D475–9.
26. Kämpfer P, Kroppenstedt RM. Numerical analysis of fatty acid patterns of coryneform bacteria and related taxa. Can J Microbiol. 1996;42:10989–1005.
27. Lee DJ, Wong BT, Adav SS. Azozcurc taiwanensis sp. nov., a denitrifying bacterium isolated from a hot spring. Appl Microbiol Biotechnol. 2014;89(3):1301–407.
28. Chen MH, Sheu SJ, James EK, Young CC, Chen WM. Azozcurc oleinicus sp. nov., a nitrogen-fixing bacterium isolated from oil-contaminated soil. Int J Syst Evol Microbiol. 2013;63:3756–61.
29. Mavromatis K, Land ML, Brettin TS, Quest DJ, Copeland A, Clum A, et al. The fast changing landscape of sequencing technologies and their impact on microbial genome assemblies and annotation. PLoS One. 2012;7:48837.
30. Mavromatis K, Ivanova NN, Chen IM, Searl E, Markowitz VM, Kyprides NC. The DOE-JGI Standard operating procedure for the annotations of microbial genomes. Stand Genomic Sci. 2009;1(1):63–7.
31. Field D, Garrity G, Gray T, Morrison N, Selengut J, Sterk P, et al. The minimum information about a genome sequence (MIGS) specification. Nat Biotechnol. 2008;26:541–7.
32. Porebski S, Bailey L, Baum B. Modification of a CTAB DNA extraction protocol for plants containing high polysaccharide and polyphenol components. Plant Mol Biol Rep. 1997;15:18–5.
33. Hyatt D, Chen GL, Locascio PF, Land ML, Lar-imer FW, Hauser LJ. Prodigal: prokaryotic gene recognition and translation initiation site identification. BMC Bioinform. 2010;11:119.
34. Lowe TM, Eddy SR. tRNAscan-SE: a program for improved detection of transfer RNA genes in genomic sequence. Nucleic Acids Res. 1997;25:555–64.
35. Puente E, Quast C, Knittel K, Fuchs BM, Ludwig W, Pepiess J, et al. SILVA: a comprenhensive online resource for quality checked and aligned ribosomal RNA sequence data compatible with ARB. Nucleic Acids Res. 2007;35:7188–96.
36. Nawrocki EP, Eddy SR. Infernal 1.1: 100-fold faster RNA homology searches. Bioinformatics. 2013;29:2933–5.
37. Markowitz VM, Mavromatis K, Ivanova NN, Chen IM, Chu K, Kyprides NC. MG ER: a system for microbial genome annotation expert review and curation. Bioinformatics. 2009;25:2271–8.
38. Evans WC, Fuchs G. Anaerobic degradation of aromatic compounds. Annu Rev Microbiol. 1988;42:289–317.
39. Carmona M, Zamarro MT, Blazquez B, Rubante-Rodriguez G, Juarez JF, Valderrama JA, et al. Anaerobic catabolism of aromatic compounds: a genetic and genomic view. Microbiol Mol Biol Rev. 2009;73(1):71–133.
40. Breese K, Boll M, Alt-Moerne J, Schaeffer H, Fuchs G. Genes coding for the benzoyl-CoA pathway of anaerobic aromatic metabolism in the bacterium Thauera aromatica. Eur J Biochem. 1998;256(1):148–54.
41. Harwood CS, Burchhardt G, Herrmann H, Fuchs G. Anaerobic metabolism of aromatic compounds via the benzoyl-CoA pathway. FEMS Microbiol Rev. 1999;22(5):439–58.
42. Hedder J, Fuchs G. Anaerobic metabolism of aromatic compounds. Eur J Biochem. 1997;243:577–96.
43. Phillip B, Schink B. Different strategies in anaerobic biodegradation of aromatic compounds: nitrate reducers versus strict anaerobes. Environ Microbiol Rep. 2012;4:469–78.
44. Woese CR, Kandler O, Wheelis ML. Towards a natural system of organisms: proposal for the do-mains Bacteria, Archaea and Eucarya. Proc Natl Acad Sci U S A. 1990;87:4576–9.
45. Garrity GM, Bell JA, Lilburn T. Phylum XIV. Proteobacteria phy. nov. In: Garrity GM, Brenner DJ, Krieg NR, Staley JT, editors. Bergey’s Manual of Systematic Bacteriology, Second Edition, Volume 2, Part B. 2nd ed. New York: Springer; 2005.
46. Validation List No. 107. List of new names and new combinations previously effectively, but not validly, published. Int J Syst Evol Microbiol. 2006;56:1–6.
47. Garrity GM, Bell JA, Lilburn T. Class II. Betaproteobacteria class. nov. In: Garrity GM, Brenner DJ, Krieg NR, Staley JT, editors. Bergey’s Manual of Systematic Bacteriology, Second Edition, Volume 2, Part C. New York: Springer; 2005. p. 575.
48. Garrity GM, Bell JA, Lilburn T. Order VI. Rhodocyclales ord. nov. In: Garrity GM, Brenner DJ, Krieg NR, Staley JT, editors. Bergey’s Manual of Systematic Bacteriology, Second Edition, Volume 2, Part C. New York: Springer; 2005. p. 887.
49. Garrity GM, Bell JA, Lilburn T. Family I. Rhodocyclusaceae fam. nov. In: Brenner DJ, Krieg NR, Staley JT, G G, editors. Bergey’s Manual of Systematic Bacteriology, Second Edition, Volume 2, Part C. New York: Springer; 2005. p. 887.
50. Ashburner M, Ball CA, Blake JA, Botstein D, Butler H, Cherry JM, et al. Gene ontology: tool for the unification of biology. The Gene Ontology Consortium. Nat Genet. 2000;25:25–9.

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