

Mary E Lidstrom

List of Publications by Year in descending order

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184
papers

14,595
citations

11608

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23472

111
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188
all docs

188
docs citations

188
times ranked

9432
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Evidence that participate methane monooxygenase and ammonia monooxygenase may be evolutionarily related. FEMS Microbiology Letters, 1995, 132, 203-208. | 0.7 | 776 |
| 2 | Molecular Characterization of Functional and Phylogenetic Genes from Natural Populations of Methanotrophs in Lake Sediments. Applied and Environmental Microbiology, 1999, 65, 5066-5074. | 1.4 | 495 |
| 3 | The Expanding World of Methylophilic Metabolism. Annual Review of Microbiology, 2009, 63, 477-499. | 2.9 | 363 |
| 4 | Trichloroethylene Biodegradation by a Methane-Oxidizing Bacterium. Applied and Environmental Microbiology, 1988, 54, 951-956. | 1.4 | 356 |
| 5 | Evidence that particulate methane monooxygenase and ammonia monooxygenase may be evolutionarily related. FEMS Microbiology Letters, 1995, 132, 203-8. | 0.7 | 353 |
| 6 | Development of improved versatile broad-host-range vectors for use in methylophilic and other Gram-negative bacteria The GenBank accession numbers for the sequences reported in this paper are AF327711, AF327712, AF327713, AF327714, AF327715, AF327716, AF327717, AF327718, AF327719 and AF327720.. Microbiology (United Kingdom), 2001, 147, 2065-2075. | 0.7 | 316 |
| 7 | Broad-Host-Range <i>cre-lox</i> System for Antibiotic Marker Recycling in Gram-Negative Bacteria. BioTechniques, 2002, 33, 1062-1067. | 0.8 | 305 |
| 8 | C1 Transfer Enzymes and Coenzymes Linking Methylophilic Bacteria and Methanogenic Archaea. , 1998, 281, 99-102. | | 295 |
| 9 | The role of physiological heterogeneity in microbial population behavior. Nature Chemical Biology, 2010, 6, 705-712. | 3.9 | 287 |
| 10 | Computational protein design enables a novel one-carbon assimilation pathway. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 3704-3709. | 3.3 | 286 |
| 11 | Metabolic engineering in methanotrophic bacteria. Metabolic Engineering, 2015, 29, 142-152. | 3.6 | 274 |
| 12 | Methylophilicity in Methylobacterium extorquens AM1 from a Genomic Point of View. Journal of Bacteriology, 2003, 185, 2980-2987. | 1.0 | 262 |
| 13 | High-resolution metagenomics targets specific functional types in complex microbial communities. Nature Biotechnology, 2008, 26, 1029-1034. | 9.4 | 254 |
| 14 | Symbiosis of methylophilic bacteria and deep-sea mussels. Nature, 1987, 325, 346-348. | 13.7 | 216 |
| 15 | Molecular Characterization of Methanotrophic Isolates from Freshwater Lake Sediment. Applied and Environmental Microbiology, 2000, 66, 5259-5266. | 1.4 | 204 |
| 16 | Methylobacterium Genome Sequences: A Reference Blueprint to Investigate Microbial Metabolism of C1 Compounds from Natural and Industrial Sources. PLoS ONE, 2009, 4, e5584. | 1.1 | 204 |
| 17 | Bacterial Populations Active in Metabolism of C 1 Compounds in the Sediment of Lake Washington, a Freshwater Lake. Applied and Environmental Microbiology, 2005, 71, 6885-6899. | 1.4 | 198 |
| 18 | Novel Formaldehyde-Activating Enzyme inMethylobacterium extorquens AM1 Required for Growth on Methanol. Journal of Bacteriology, 2000, 182, 6645-6650. | 1.0 | 173 |

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 19 | nifH Sequences and Nitrogen Fixation in Type I and Type II Methanotrophs. Applied and Environmental Microbiology, 2001, 67, 4009-4016. | 1.4 | 161 |
| 20 | Lanthanide-dependent cross-feeding of methane-derived carbon is linked by microbial community interactions. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 358-363. | 3.3 | 156 |
| 21 | Life-on-a-chip. Nature Reviews Microbiology, 2003, 1, 158-164. | 13.6 | 154 |
| 22 | Formate as the Main Branch Point for Methylotrophic Metabolism in <i>Methylobacterium extorquens</i> AM1. Journal of Bacteriology, 2008, 190, 5057-5062. | 1.0 | 146 |
| 23 | Genetic Tools for the Industrially Promising Methanotroph <i>Methylomicrobium buryatense</i> . Applied and Environmental Microbiology, 2015, 81, 1775-1781. | 1.4 | 144 |
| 24 | XoxF Acts as the Predominant Methanol Dehydrogenase in the Type I Methanotroph <i>Methylomicrobium buryatense</i> . Journal of Bacteriology, 2016, 198, 1317-1325. | 1.0 | 142 |
| 25 | A metagenomic insight into freshwater methane-utilizing communities and evidence for cooperation between the <i>Methylococcaceae</i> and the <i>Methylophilaceae</i> . PeerJ, 2013, 1, e23. | 0.9 | 139 |
| 26 | <i>Methylotenera mobilis</i> gen. nov., sp. nov., an obligately methylamine-utilizing bacterium within the family <i>Methylophilaceae</i> . International Journal of Systematic and Evolutionary Microbiology, 2006, 56, 2819-2823. | 0.8 | 138 |
| 27 | A pathway for biological methane production using bacterial iron-only nitrogenase. Nature Microbiology, 2018, 3, 281-286. | 5.9 | 131 |
| 28 | <i>Methylophilaceae</i> link methanol oxidation to denitrification in freshwater lake sediment as suggested by stable isotope probing and pure culture analysis. Environmental Microbiology Reports, 2009, 1, 385-392. | 1.0 | 129 |
| 29 | Seasonal Study of Methane Oxidation in Lake Washington. Applied and Environmental Microbiology, 1984, 47, 1255-1260. | 1.4 | 129 |
| 30 | Distribution of Tetrahydromethanopterin-Dependent Enzymes in Methylotrophic Bacteria and Phylogeny of Methenyl Tetrahydromethanopterin Cyclohydrolases. Journal of Bacteriology, 1999, 181, 5750-5757. | 1.0 | 124 |
| 31 | The first methane-oxidizing bacterium from the upper mixing layer of the deep ocean: <i>Methylomonas pelagica</i> sp. nov.. Current Microbiology, 1987, 14, 285-293. | 1.0 | 121 |
| 32 | X-ray Absorption and EPR Studies on the Copper Ions Associated with the Particulate Methane Monooxygenase from <i>Methylococcus capsulatus</i> (Bath). Cu(I) Ions and Their Implications. Journal of the American Chemical Society, 1996, 118, 12766-12776. | 6.6 | 120 |
| 33 | Methane-fed microbial microcosms show differential community dynamics and pinpoint taxa involved in communal response. ISME Journal, 2015, 9, 1119-1129. | 4.4 | 118 |
| 34 | Genome-scale metabolic reconstructions and theoretical investigation of methane conversion in <i>Methylomicrobium buryatense</i> strain 5G(B1). Microbial Cell Factories, 2015, 14, 188. | 1.9 | 117 |
| 35 | Stoichiometric model for evaluating the metabolic capabilities of the facultative methylotroph <i>Methylobacterium extorquens</i> AM1, with application to reconstruction of C3 and C4 metabolism. Biotechnology and Bioengineering, 2002, 78, 296-312. | 1.7 | 111 |
| 36 | Plants in the Pink: Cytokinin Production by <i>Methylobacterium</i> . Journal of Bacteriology, 2002, 184, 1818-1818. | 1.0 | 108 |

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|----|---|-----|-----------|
| 37 | Genome of <i>Methylobacillus flagellatus</i> , Molecular Basis for Obligate Methylo-trophy, and Polyphyletic Origin of Methylo-trophy. <i>Journal of Bacteriology</i> , 2007, 189, 4020-4027. | 1.0 | 107 |
| 38 | Isolation and characterization of marine methanotrophs. <i>Antonie Van Leeuwenhoek</i> , 1988, 54, 189-199. | 0.7 | 106 |
| 39 | Refined crystal structure of methylamine dehydrogenase from <i>Paracoccus denitrificans</i> at 1.75 Å resolution. <i>Journal of Molecular Biology</i> , 1998, 276, 131-149. | 2.0 | 106 |
| 40 | Characterization of a Novel Methanol Dehydrogenase in Representatives of <i>Burkholderiales</i> : Implications for Environmental Detection of Methylo-trophy and Evidence for Convergent Evolution. <i>Journal of Bacteriology</i> , 2008, 190, 3817-3823. | 1.0 | 105 |
| 41 | <i>Methyloversatilis universalis</i> gen. nov., sp. nov., a novel taxon within the Betaproteobacteria represented by three methylo-trophic isolates. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2006, 56, 2517-2522. | 0.8 | 104 |
| 42 | Oxygen availability is a major factor in determining the composition of microbial communities involved in methane oxidation. <i>PeerJ</i> , 2015, 3, e801. | 0.9 | 104 |
| 43 | Formaldehyde-Detoxifying Role of the Tetrahydromethanopterin-Linked Pathway in <i>Methylobacterium extorquens</i> AM1. <i>Journal of Bacteriology</i> , 2003, 185, 7160-7168. | 1.0 | 101 |
| 44 | Fluorescence In Situ Hybridization-Flow Cytometry-Cell Sorting-Based Method for Separation and Enrichment of Type I and Type II Methanotroph Populations. <i>Applied and Environmental Microbiology</i> , 2006, 72, 4293-4301. | 1.4 | 100 |
| 45 | Insights into Denitrification in <i>Methylo-tenera mobilis</i> from Denitrification Pathway and Methanol Metabolism Mutants. <i>Journal of Bacteriology</i> , 2013, 195, 2207-2211. | 1.0 | 99 |
| 46 | Molecular and mutational analysis of a DNA region separating two methylo-trophy gene clusters in <i>Methylobacterium extorquens</i> AM1. <i>Microbiology (United Kingdom)</i> , 1997, 143, 1729-1736. | 0.7 | 98 |
| 47 | Methylo-trophs: Genetics and Commercial Applications. <i>Annual Review of Microbiology</i> , 1990, 44, 27-58. | 2.9 | 97 |
| 48 | Characterization of the Minimal Replicon of a Cryptic <i>Deinococcus radiodurans</i> SARK Plasmid and Development of Versatile <i>Escherichia coli</i> -D. <i>radiodurans</i> Shuttle Vectors. <i>Applied and Environmental Microbiology</i> , 2000, 66, 3856-3867. | 1.4 | 96 |
| 49 | Real-time detection of actively metabolizing microbes by redox sensing as applied to methylo-troph populations in Lake Washington. <i>ISME Journal</i> , 2008, 2, 696-706. | 4.4 | 94 |
| 50 | Glyoxylate Regeneration Pathway in the Methylo-troph <i>Methylobacterium extorquens</i> AM1. <i>Journal of Bacteriology</i> , 2002, 184, 1750-1758. | 1.0 | 92 |
| 51 | Construction of insertion and deletion <i>mx</i> A mutants of <i>Methylobacterium extorquens</i> AM1 by electroporation. <i>FEMS Microbiology Letters</i> , 1998, 166, 1-7. | 0.7 | 90 |
| 52 | Multiple Formate Dehydrogenase Enzymes in the Facultative Methylo-troph <i>Methylobacterium extorquens</i> AM1 Are Dispensable for Growth on Methanol. <i>Journal of Bacteriology</i> , 2004, 186, 22-28. | 1.0 | 90 |
| 53 | The NADP-Dependent Methylene Tetrahydromethanopterin Dehydrogenase in <i>Methylobacterium extorquens</i> AM1. <i>Journal of Bacteriology</i> , 1998, 180, 5351-5356. | 1.0 | 90 |
| 54 | Estimation of methanotroph abundance in a freshwater lake sediment. <i>Environmental Microbiology</i> , 2002, 4, 443-450. | 1.8 | 89 |

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|----|--|-----|-----------|
| 55 | The tungsten-containing formate dehydrogenase from <i>Methylobacterium extorquens</i> AM1: Purification and properties. <i>FEBS Journal</i> , 2003, 270, 325-333. | 0.2 | 89 |
| 56 | Novel methylotrophic isolates from lake sediment, description of <i>Methylotenera versatilis</i> sp. nov. and emended description of the genus <i>Methylotenera</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2012, 62, 106-111. | 0.8 | 89 |
| 57 | XoxF Is Required for Expression of Methanol Dehydrogenase in <i>Methylobacterium extorquens</i> AM1. <i>Journal of Bacteriology</i> , 2011, 193, 6032-6038. | 1.0 | 87 |
| 58 | Bioreactor performance parameters for an industrially-promising methanotroph <i>Methylomicrobium buryatense</i> 5GB1. <i>Microbial Cell Factories</i> , 2015, 14, 182. | 1.9 | 85 |
| 59 | Electroporation-Based Genetic Manipulation in Type I Methanotrophs. <i>Applied and Environmental Microbiology</i> , 2016, 82, 2062-2069. | 1.4 | 85 |
| 60 | Identification and organization of carbon dioxide fixation genes in <i>Xanthobacter flavus</i> H4-14. <i>Molecular Genetics and Genomics</i> , 1991, 225, 320-330. | 2.4 | 81 |
| 61 | The genetic organization of the mau gene cluster of the facultative autotroph <i>Paracoccus denitrificans</i> . <i>Biochemical and Biophysical Research Communications</i> , 1992, 184, 1181-1189. | 1.0 | 81 |
| 62 | Oxygen-limited metabolism in the methanotroph <i>Methylomicrobium buryatense</i> 5GB1C. <i>PeerJ</i> , 2017, 5, e3945. | 0.9 | 81 |
| 63 | A methenyl tetrahydromethanopterin cyclohydrolase and a methenyl tetrahydrofolate cyclohydrolase in <i>Methylobacterium extorquens</i> AM1. <i>FEBS Journal</i> , 1999, 261, 475-480. | 0.2 | 80 |
| 64 | MeaB Is a Component of the Methylmalonyl-CoA Mutase Complex Required for Protection of the Enzyme from Inactivation. <i>Journal of Biological Chemistry</i> , 2004, 279, 13652-13658. | 1.6 | 80 |
| 65 | Comprehensive two-dimensional gas chromatography with time-of-flight mass spectrometry detection: analysis of amino acid and organic acid trimethylsilyl derivatives, with application to the analysis of metabolites in rye grass samples. <i>Talanta</i> , 2005, 65, 380-388. | 2.9 | 80 |
| 66 | Promoter Cloning in the Radioresistant Bacterium <i>Deinococcus radiodurans</i> . <i>Journal of Bacteriology</i> , 2001, 183, 3169-3175. | 1.0 | 78 |
| 67 | Nucleotide sequence of the <i>Methylobacterium extorquens</i> AM1 <i>moxF</i> and <i>moxJ</i> genes involved in methanol oxidation. <i>Gene</i> , 1990, 90, 173-176. | 1.0 | 77 |
| 68 | Connection between Poly- β -Hydroxybutyrate Biosynthesis and Growth on C 1 and C 2 Compounds in the Methylotroph <i>Methylobacterium extorquens</i> AM1. <i>Journal of Bacteriology</i> , 2001, 183, 1038-1046. | 1.0 | 76 |
| 69 | Liquid chromatography-tandem quadrupole mass spectrometry and comprehensive two-dimensional gas chromatography-time-of-flight mass spectrometry measurement of targeted metabolites of <i>Methylobacterium extorquens</i> AM1 grown on two different carbon sources. <i>Journal of Chromatography A</i> , 2009, 1216, 3280-3289. | 1.8 | 75 |
| 70 | Involvement of the S-layer proteins Hpi and SlpA in the maintenance of cell envelope integrity in <i>Deinococcus radiodurans</i> R1. <i>Microbiology (United Kingdom)</i> , 2006, 152, 2779-2787. | 0.7 | 74 |
| 71 | A microwell array device capable of measuring single-cell oxygen consumption rates. <i>Sensors and Actuators B: Chemical</i> , 2009, 135, 678-686. | 4.0 | 74 |
| 72 | Streamlined pentafluorophenylpropyl column liquid chromatography-tandem quadrupole mass spectrometry and global ^{13}C -labeled internal standards improve performance for quantitative metabolomics in bacteria. <i>Journal of Chromatography A</i> , 2010, 1217, 7401-7410. | 1.8 | 74 |

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|----|--|-----|-----------|
| 73 | Purification of the Formate-Tetrahydrofolate Ligase from <i>Methylobacterium extorquens</i> AM1 and Demonstration of Its Requirement for Methylotrophic Growth. <i>Journal of Bacteriology</i> , 2003, 185, 7169-7175. | 1.0 | 73 |
| 74 | Flux Analysis Uncovers Key Role of Functional Redundancy in Formaldehyde Metabolism. <i>PLoS Biology</i> , 2005, 3, e16. | 2.6 | 72 |
| 75 | Production of bromoform and dibromomethane by Giant Kelp: Factors affecting release and comparison to anthropogenic bromine sources. <i>Limnology and Oceanography</i> , 1997, 42, 1725-1734. | 1.6 | 71 |
| 76 | Kinetic analysis of virus adsorption and inactivation in batch experiments. <i>Water Resources Research</i> , 1993, 29, 2067-2085. | 1.7 | 69 |
| 77 | Characterization of a second methylene tetrahydromethanopterin dehydrogenase from <i>Methylobacterium extorquens</i> AM1. <i>FEBS Journal</i> , 2000, 267, 3762-3769. | 0.2 | 68 |
| 78 | Genomes of Three Methylotrophs from a Single Niche Reveal the Genetic and Metabolic Divergence of the Methylophilaceae. <i>Journal of Bacteriology</i> , 2011, 193, 3757-3764. | 1.0 | 66 |
| 79 | Multiple Formaldehyde Oxidation/Detoxification Pathways in <i>Burkholderia fungorum</i> LB400. <i>Journal of Bacteriology</i> , 2004, 186, 2173-2178. | 1.0 | 65 |
| 80 | Identification of a Fourth Formate Dehydrogenase in <i>Methylobacterium extorquens</i> AM1 and Confirmation of the Essential Role of Formate Oxidation in Methylotrophy. <i>Journal of Bacteriology</i> , 2007, 189, 9076-9081. | 1.0 | 64 |
| 81 | Comprehensive proteomics of <i>Methylobacterium extorquens</i> AM1 metabolism under single carbon and nonmethylotrophic conditions. <i>Proteomics</i> , 2008, 8, 3494-3505. | 1.3 | 62 |
| 82 | The Expanded Diversity of Methylophilaceae from Lake Washington through Cultivation and Genomic Sequencing of Novel Ecotypes. <i>PLoS ONE</i> , 2014, 9, e102458. | 1.1 | 62 |
| 83 | Metabolic engineering of <i>Methylobacterium extorquens</i> AM1 for 1-butanol production. <i>Biotechnology for Biofuels</i> , 2014, 7, 156. | 6.2 | 61 |
| 84 | Cloning and sequencing of the structural gene for the small subunit of methylamine dehydrogenase from <i>Methylobacterium extorquens</i> AM1: Evidence for two tryptophan residues involved in the active center. <i>Biochemical and Biophysical Research Communications</i> , 1990, 172, 211-216. | 1.0 | 60 |
| 85 | MxaY regulates the lanthanide-mediated methanol dehydrogenase switch in <i>Methylomicrobium buryatense</i> . <i>PeerJ</i> , 2016, 4, e2435. | 0.9 | 59 |
| 86 | New unified nomenclature for genes involved in the oxidation of methanol in Gram-negative bacteria. <i>FEMS Microbiology Letters</i> , 1994, 117, 103-106. | 0.7 | 58 |
| 87 | Strain IMB-1, a Novel Bacterium for the Removal of Methyl Bromide in Fumigated Agricultural Soils. <i>Applied and Environmental Microbiology</i> , 1998, 64, 2899-2905. | 1.4 | 58 |
| 88 | Reconstruction of C3 and C4 metabolism in <i>Methylobacterium extorquens</i> AM1 using transposon mutagenesis. <i>Microbiology (United Kingdom)</i> , 2003, 149, 601-609. | 0.7 | 55 |
| 89 | Development of an insertional expression vector system for <i>Methylobacterium extorquens</i> AM1 and generation of null mutants lacking <i>mtdA</i> and/or <i>fch</i> . <i>Microbiology (United Kingdom)</i> , 2004, 150, 9-19. | 0.7 | 55 |
| 90 | Promoters and transcripts for genes involved in methanol oxidation in <i>Methylobacterium extorquens</i> AM1. <i>Microbiology (United Kingdom)</i> , 2003, 149, 1033-1040. | 0.7 | 54 |

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|-----|---|-----|-----------|
| 91 | Implementation of Microarrays for <i>Methylobacterium extorquens</i> AM1. <i>OMICS A Journal of Integrative Biology</i> , 2007, 11, 325-340. | 1.0 | 54 |
| 92 | Metabolite profiling analysis of <i>Methylobacterium extorquens</i> AM1 by comprehensive two-dimensional gas chromatography coupled with time-of-flight mass spectrometry. <i>Biotechnology and Bioengineering</i> , 2008, 99, 929-940. | 1.7 | 53 |
| 93 | Poly- ¹² -Hydroxybutyrate Biosynthesis in the Facultative Methylophile <i>Methylobacterium extorquens</i> AM1: Identification and Mutation of <i>gap11</i> , <i>gap20</i> , and <i>phaR</i> . <i>Journal of Bacteriology</i> , 2002, 184, 6174-6181. | 1.0 | 52 |
| 94 | Analysis of sMMO-containing Type I methanotrophs in Lake Washington sediment. <i>Environmental Microbiology</i> , 2002, 4, 517-524. | 1.8 | 52 |
| 95 | Cell-to-Cell Heterogeneity in Growth Rate and Gene Expression in <i>Methylobacterium extorquens</i> AM1. <i>Journal of Bacteriology</i> , 2007, 189, 7127-7133. | 1.0 | 52 |
| 96 | Quantification of central metabolic fluxes in the facultative methylophile <i>Methylobacterium extorquens</i> AM1 using ¹³ C-label tracing and mass spectrometry. <i>Biotechnology and Bioengineering</i> , 2003, 84, 45-55. | 1.7 | 50 |
| 97 | A Systems Biology Approach Uncovers Cellular Strategies Used by <i>Methylobacterium extorquens</i> AM1 During the Switch from Multi- to Single-Carbon Growth. <i>PLoS ONE</i> , 2010, 5, e14091. | 1.1 | 50 |
| 98 | Genetic Characterization of the Carotenoid Biosynthetic Pathway in <i>Methylobacterium extorquens</i> AM1 and Isolation of a Colorless Mutant. <i>Applied and Environmental Microbiology</i> , 2003, 69, 7563-7566. | 1.4 | 49 |
| 99 | The oxidative TCA cycle operates during methanotrophic growth of the Type I methanotroph <i>Methylobacterium buryatense</i> 5GB1. <i>Metabolic Engineering</i> , 2017, 42, 43-51. | 3.6 | 49 |
| 100 | <i>Methylosarcina lacus</i> sp. nov., a methanotroph from Lake Washington, Seattle, USA, and emended description of the genus <i>Methylosarcina</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2005, 55, 2345-2350. | 0.8 | 47 |
| 101 | Marine Bacterial Degradation of Brominated Methanes. <i>Environmental Science & Technology</i> , 1997, 31, 3188-3192. | 4.6 | 46 |
| 102 | Novel Methylophily Genes of <i>Methylobacterium extorquens</i> AM1 Identified by using Transposon Mutagenesis Including a Putative Dihydropyridin Reductase. <i>Journal of Bacteriology</i> , 2003, 185, 669-673. | 1.0 | 46 |
| 103 | Analysis of Gene Islands Involved in Methanopterin-Linked C ₁ Transfer Reactions Reveals New Functions and Provides Evolutionary Insights. <i>Journal of Bacteriology</i> , 2005, 187, 4607-4614. | 1.0 | 46 |
| 104 | Diversity and phylogeny of the ectoine biosynthesis genes in aerobic, moderately halophilic methylophile bacteria. <i>Extremophiles</i> , 2011, 15, 653-663. | 0.9 | 45 |
| 105 | Comprehensive molecular characterization of <i>Methylobacterium extorquens</i> AM1 adapted for 1-butanol tolerance. <i>Biotechnology for Biofuels</i> , 2016, 9, 84. | 6.2 | 42 |
| 106 | Expression of Individual Copies of <i>Methylococcus capsulatus</i> Bath Particulate Methane Monooxygenase Genes. <i>Journal of Bacteriology</i> , 2001, 183, 1810-1812. | 1.0 | 41 |
| 107 | Alternative Route for Glyoxylate Consumption during Growth on Two-Carbon Compounds by <i>Methylobacterium extorquens</i> AM1. <i>Journal of Bacteriology</i> , 2010, 192, 1813-1823. | 1.0 | 39 |
| 108 | Methane consumption in Framvaren, an anoxic marine fjord. <i>Limnology and Oceanography</i> , 1983, 28, 1247-1251. | 1.6 | 38 |

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|-----|---|-----|-----------|
| 109 | Functioning <i>in situ</i> : gene expression in <i>Methylothermobacter mobilis</i> in its native environment as assessed through transcriptomics. <i>ISME Journal</i> , 2010, 4, 388-398. | 4.4 | 38 |
| 110 | Multiphyletic origins of methylotrophy in <i>Alphaproteobacteria</i> , exemplified by comparative genomics of <i>Lake Washington</i> isolates. <i>Environmental Microbiology</i> , 2015, 17, 547-554. | 1.8 | 38 |
| 111 | Molecular analysis of mxbD and mxbM, a putative sensor-regulator pair required for oxidation of methanol in <i>Methylobacterium extorquens</i> AM1. <i>Microbiology (United Kingdom)</i> , 1997, 143, 1737-1744. | 0.7 | 37 |
| 112 | Dissimilative Iron Reduction by the Marine Eubacterium <i>Alteromonas putrefaciens</i> Strain 200. <i>Water Science and Technology</i> , 1988, 20, 69-79. | 1.2 | 33 |
| 113 | pqqA is not required for biosynthesis of pyrroloquinoline quinone in <i>Methylobacterium extorquens</i> AM1. <i>Microbiology (United Kingdom)</i> , 1998, 144, 183-191. | 0.7 | 32 |
| 114 | QscR, a LysR-Type Transcriptional Regulator and CbbR Homolog, Is Involved in Regulation of the Serine Cycle Genes in <i>Methylobacterium extorquens</i> AM1. <i>Journal of Bacteriology</i> , 2003, 185, 1229-1235. | 1.0 | 32 |
| 115 | A Mutagenic Screen Identifies a TonB-Dependent Receptor Required for the Lanthanide Metal Switch in the Type I Methanotroph <i>Methylothermobacter buryatense</i> 5GB1C. <i>Journal of Bacteriology</i> , 2019, 201, . | 1.0 | 32 |
| 116 | Expressed Genome of <i>Methylobacillus flagellatus</i> as Defined through Comprehensive Proteomics and New Insights into Methylotrophy. <i>Journal of Bacteriology</i> , 2010, 192, 4859-4867. | 1.0 | 31 |
| 117 | Core Metabolism Shifts during Growth on Methanol versus Methane in the Methanotroph <i>Methylothermobacter buryatense</i> 5GB1. <i>MBio</i> , 2019, 10, . | 1.8 | 31 |
| 118 | Plasmids in methanotrophic bacteria: isolation, characterization and DNA hybridization analysis. <i>Archives of Microbiology</i> , 1984, 140, 27-33. | 1.0 | 30 |
| 119 | MALDI-TOF Analysis of Polymerase Chain Reaction Products from Methanotrophic Bacteria. <i>Analytical Chemistry</i> , 1998, 70, 2693-2698. | 3.2 | 30 |
| 120 | <i>Labrys methylaminiphilus</i> sp. nov., a novel facultatively methylotrophic bacterium from a freshwater lake sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2005, 55, 1247-1253. | 0.8 | 30 |
| 121 | Global Whole-Cell FTICR Mass Spectrometric Proteomics Analysis of the Heat Shock Response in the Radioresistant Bacterium <i>Deinococcus radiodurans</i> . <i>Journal of Proteome Research</i> , 2005, 4, 709-718. | 1.8 | 30 |
| 122 | QscR-Mediated Transcriptional Activation of Serine Cycle Genes in <i>Methylobacterium extorquens</i> AM1. <i>Journal of Bacteriology</i> , 2005, 187, 7511-7517. | 1.0 | 29 |
| 123 | Quorum Sensing in a Methane-Oxidizing Bacterium. <i>Journal of Bacteriology</i> , 2017, 199, . | 1.0 | 29 |
| 124 | Cloning and characterization of corA, a gene encoding a copper-repressible polypeptide in the type I methanotroph, <i>Methylothermobacter albus</i> BG8. <i>FEMS Microbiology Letters</i> , 2006, 148, 169-174. | 0.7 | 28 |
| 125 | Methanotrophic populations in estuarine sediment from Newport Bay, California. <i>FEMS Microbiology Letters</i> , 2005, 250, 287-293. | 0.7 | 27 |
| 126 | HspR is a global negative regulator of heat shock gene expression in <i>Deinococcus radiodurans</i> . <i>Molecular Microbiology</i> , 2005, 55, 1579-1590. | 1.2 | 27 |

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