

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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188
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188
docs citations

188
times ranked

9432
citing authors

#	ARTICLE	IF	CITATIONS
1	The Entner-Doudoroff Pathway Is an Essential Metabolic Route for <i>Methylotheobacterium buryatense</i> 5GB1C. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	10
2	Cultivation techniques to study lanthanide metal interactions in the haloalkaliphilic Type I methanotroph <i>Methylotheobacterium buryatense</i> 5GB1C. <i>Methods in Enzymology</i> , 2021, 650, 237-259.	0.4	1
3	A Computational Framework for Identifying Promoter Sequences in Nonmodel Organisms Using RNA-seq Data Sets. <i>ACS Synthetic Biology</i> , 2021, 10, 1394-1405.	1.9	15
4	Enzyme engineering and <i>in vivo</i> testing of a formate reduction pathway. <i>Synthetic Biology</i> , 2021, 6, ysab020.	1.2	7
5	Giving <i>E. coli</i> a newfound appetite for formate. <i>Nature Metabolism</i> , 2020, 2, 219-220.	5.1	1
6	The Role of Synthetic Biology in Atmospheric Greenhouse Gas Reduction: Prospects and Challenges. <i>BioDesign Research</i> , 2020, 2020, .	0.8	24
7	Interspecies Chemical Signaling in a Methane-Oxidizing Bacterial Community. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	10
8	A Mutagenic Screen Identifies a TonB-Dependent Receptor Required for the Lanthanide Metal Switch in the Type I Methanotroph <i>Methylotheobacterium buryatense</i> 5GB1C. <i>Journal of Bacteriology</i> , 2019, 201, .	1.0	32
9	Core Metabolism Shifts during Growth on Methanol versus Methane in the Methanotroph <i>Methylotheobacterium buryatense</i> 5GB1. <i>MBio</i> , 2019, 10, .	1.8	31
10	Quantifying Methane and Methanol Metabolism of <i>Methylotheobacterium buryatense</i> 5GB1C under Substrate Limitation. <i>MSystems</i> , 2019, 4, .	1.7	16
11	Tundrenone: An Atypical Secondary Metabolite from Bacteria with Highly Restricted Primary Metabolism. <i>Journal of the American Chemical Society</i> , 2018, 140, 2002-2006.	6.6	23
12	A pathway for biological methane production using bacterial iron-only nitrogenase. <i>Nature Microbiology</i> , 2018, 3, 281-286.	5.9	131
13	The oxidative TCA cycle operates during methanotrophic growth of the Type I methanotroph <i>Methylotheobacterium buryatense</i> 5GB1. <i>Metabolic Engineering</i> , 2017, 42, 43-51.	3.6	49
14	Quorum Sensing in a Methane-Oxidizing Bacterium. <i>Journal of Bacteriology</i> , 2017, 199, .	1.0	29
15	Lanthanide-dependent cross-feeding of methane-derived carbon is linked by microbial community interactions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 358-363.	3.3	156
16	Oxygen-limited metabolism in the methanotroph <i>Methylotheobacterium buryatense</i> 5GB1C. <i>PeerJ</i> , 2017, 5, e3945.	0.9	81
17	Difference in C3-C4 metabolism underlies tradeoff between growth rate and biomass yield in <i>Methylobacterium extorquens</i> AM1. <i>BMC Microbiology</i> , 2016, 16, 156.	1.3	10
18	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

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19	Non-targeted determination of ¹³ C-labeling in the <i>Methylobacterium extorquens</i> AM1 metabolome using the two-dimensional mass cluster method and principal component analysis. <i>Journal of Chromatography A</i> , 2016, 1432, 111-121.	1.8	8
20	Electroporation-Based Genetic Manipulation in Type I Methanotrophs. <i>Applied and Environmental Microbiology</i> , 2016, 82, 2062-2069.	1.4	85
21	XoxF Acts as the Predominant Methanol Dehydrogenase in the Type I Methanotroph <i>Methylomicrobium buryatense</i> . <i>Journal of Bacteriology</i> , 2016, 198, 1317-1325.	1.0	142
22	MxaY regulates the lanthanide-mediated methanol dehydrogenase switch in <i>Methylomicrobium buryatense</i> . <i>PeerJ</i> , 2016, 4, e2435.	0.9	59
23	Bioreactor performance parameters for an industrially-promising methanotroph <i>Methylomicrobium buryatense</i> 5GB1. <i>Microbial Cell Factories</i> , 2015, 14, 182.	1.9	85
24	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
25	Genome-scale metabolic reconstructions and theoretical investigation of methane conversion in <i>Methylomicrobium buryatense</i> strain 5G(B1). <i>Microbial Cell Factories</i> , 2015, 14, 188.	1.9	117
26	Genomics of Methylotrophy in Gram-Positive Methylamine-Utilizing Bacteria. <i>Microorganisms</i> , 2015, 3, 94-112.	1.6	19
27	Ethylmalonyl Coenzyme A Mutase Operates as a Metabolic Control Point in <i>Methylobacterium extorquens</i> AM1. <i>Journal of Bacteriology</i> , 2015, 197, 727-735.	1.0	15
28	Genetic Tools for the Industrially Promising Methanotroph <i>Methylomicrobium buryatense</i> . <i>Applied and Environmental Microbiology</i> , 2015, 81, 1775-1781.	1.4	144
29	Computational protein design enables a novel one-carbon assimilation pathway. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 3704-3709.	3.3	286
30	Metabolic engineering in methanotrophic bacteria. <i>Metabolic Engineering</i> , 2015, 29, 142-152.	3.6	274
31	Methenyl-Dephosphotetrahydromethanopterin Is a Regulatory Signal for Acclimation to Changes in Substrate Availability in <i>Methylobacterium extorquens</i> AM1. <i>Journal of Bacteriology</i> , 2015, 197, 2020-2026.	1.0	14
32	Methane-fed microbial microcosms show differential community dynamics and pinpoint taxa involved in communal response. <i>ISME Journal</i> , 2015, 9, 1119-1129.	4.4	118
33	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
34	The Expanded Diversity of <i>Methylphilaceae</i> from Lake Washington through Cultivation and Genomic Sequencing of Novel Ecotypes. <i>PLoS ONE</i> , 2014, 9, e102458.	1.1	62
35	Metabolic engineering of <i>Methylobacterium extorquens</i> AM1 for 1-butanol production. <i>Biotechnology for Biofuels</i> , 2014, 7, 156.	6.2	61
36	Comprehensive discovery of ¹³ C labeled metabolites in the bacterium <i>Methylobacterium extorquens</i> AM1 using gas chromatography-mass spectrometry. <i>Journal of Chromatography A</i> , 2013, 1317, 175-185.	1.8	7

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37	Elucidation of the Role of the Methylene-Tetrahydromethanopterin Dehydrogenase MtdA in the Tetrahydromethanopterin-Dependent Oxidation Pathway in <i>Methylobacterium extorquens</i> AM1. <i>Journal of Bacteriology</i> , 2013, 195, 2359-2367.	1.0	20
38	Insights into Denitrification in <i>Methylothera mobilis</i> from Denitrification Pathway and Methanol Metabolism Mutants. <i>Journal of Bacteriology</i> , 2013, 195, 2207-2211.	1.0	99
39	Cycling Single-Carbon Compounds: from Omics to Novel Concepts. <i>Microbe Magazine</i> , 2013, 8, 395-400.	0.4	7
40	Comparative transcriptomics in three <i>Methylophilaceae</i> species uncover different strategies for environmental adaptation. <i>PeerJ</i> , 2013, 1, e115.	0.9	20
41	A metagenomic insight into freshwater methane-utilizing communities and evidence for cooperation between the <i>Methylococcaceae</i> and the <i>Methylophilaceae</i> . <i>PeerJ</i> , 2013, 1, e23.	0.9	139
42	CcrR, a TetR Family Transcriptional Regulator, Activates the Transcription of a Gene of the Ethylmalonyl Coenzyme A Pathway in <i>Methylobacterium extorquens</i> AM1. <i>Journal of Bacteriology</i> , 2012, 194, 2802-2808.	1.0	25
43	Novel methylophilic isolates from lake sediment, description of <i>Methylothera versatilis</i> sp. nov. and emended description of the genus <i>Methylothera</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2012, 62, 106-111.	0.8	89
44	Gas chromatography–mass spectrometry with chemometric analysis for determining ¹² C and ¹³ C labeled contributions in metabolomics and ¹³ C flux analysis. <i>Journal of Chromatography A</i> , 2012, 1240, 156-164.	1.8	25
45	Diversity and phylogeny of the ectoine biosynthesis genes in aerobic, moderately halophilic methylophilic bacteria. <i>Extremophiles</i> , 2011, 15, 653-663.	0.9	45
46	Single Cell Methods for Methane Oxidation Analysis. <i>Methods in Enzymology</i> , 2011, 495, 149-166.	0.4	2
47	Genomes of Three Methylophilic Bacteria from a Single Niche Reveal the Genetic and Metabolic Divergence of the <i>Methylophilaceae</i> . <i>Journal of Bacteriology</i> , 2011, 193, 3757-3764.	1.0	66
48	An Integrated Proteomics/Transcriptomics Approach Points to Oxygen as the Main Electron Sink for Methanol Metabolism in <i>Methylothera mobilis</i> . <i>Journal of Bacteriology</i> , 2011, 193, 4758-4765.	1.0	22
49	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
50	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
51	The role of physiological heterogeneity in microbial population behavior. <i>Nature Chemical Biology</i> , 2010, 6, 705-712.	3.9	287
52	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
53	Expressed Genome of <i>Methylobacillus flagellatus</i> as Defined through Comprehensive Proteomics and New Insights into Methylophilicity. <i>Journal of Bacteriology</i> , 2010, 192, 4859-4867.	1.0	31
54	Functioning <i>in situ</i> : gene expression in <i>Methylothera mobilis</i> in its native environment as assessed through transcriptomics. <i>ISME Journal</i> , 2010, 4, 388-398.	4.4	38

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55	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
56	Direct measurement of oxygen consumption rates from attached and unattached cells in a reversibly sealed, diffusively isolated sample chamber. <i>Advances in Bioscience and Biotechnology (Print)</i> , 2010, 01, 398-408.	0.3	18
57	<i>Methylobacterium</i> Genome Sequences: A Reference Blueprint to Investigate Microbial Metabolism of C1 Compounds from Natural and Industrial Sources. <i>PLoS ONE</i> , 2009, 4, e5584.	1.1	204
58	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
59	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
60	The Expanding World of Methylotrophic Metabolism. <i>Annual Review of Microbiology</i> , 2009, 63, 477-499.	2.9	363
61	<i>Methylophilaceae</i> link methanol oxidation to denitrification in freshwater lake sediment as suggested by stable isotope probing and pure culture analysis. <i>Environmental Microbiology Reports</i> , 2009, 1, 385-392.	1.0	129
62	Population heterogeneity in <i>Methylobacterium extorquens</i> AM1. <i>Microbiology (United Kingdom)</i> , 2009, 155, 2040-2048.	0.7	16
63	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
64	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
65	Real-time detection of actively metabolizing microbes by redox sensing as applied to methylotroph populations in Lake Washington. <i>ISME Journal</i> , 2008, 2, 696-706.	4.4	94
66	High-resolution metagenomics targets specific functional types in complex microbial communities. <i>Nature Biotechnology</i> , 2008, 26, 1029-1034.	9.4	254
67	Interface of an Array of Five Capillaries with an Array of One-Nanoliter Wells for High-Resolution Electrophoretic Analysis as an Approach to High-Throughput Chemical Cytometry. <i>Analytical Chemistry</i> , 2008, 80, 7631-7634.	3.2	16
68	Formate as the Main Branch Point for Methylotrophic Metabolism in <i>Methylobacterium extorquens</i> AM1. <i>Journal of Bacteriology</i> , 2008, 190, 5057-5062.	1.0	146
69	Characterization of a Novel Methanol Dehydrogenase in Representatives of <i>Burkholderiales</i> : Implications for Environmental Detection of Methylotrophy and Evidence for Convergent Evolution. <i>Journal of Bacteriology</i> , 2008, 190, 3817-3823.	1.0	105
70	Two-Photon Lithography of Platinum-Porphyrin Oxygen Sensors. <i>IEEE Sensors Journal</i> , 2007, 7, 931-936.	2.4	4
71	Genome of <i>Methylobacillus flagellatus</i> , Molecular Basis for Obligate Methylotrophy, and Polyphyletic Origin of Methylotrophy. <i>Journal of Bacteriology</i> , 2007, 189, 4020-4027.	1.0	107
72	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

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73	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
74	Automated Classification of Macrophage Membrane Integrity using a Fluorescent Live/Dead Stain. , 2007, , .		2
75	Algorithm Advancements for the Measurement of Single Cell Oxygen Consumption Rates. , 2007, , .		3
76	Implementation of Microarrays for <i>Methylobacterium extorquens</i> AM1. <i>OMICS A Journal of Integrative Biology</i> , 2007, 11, 325-340.	1.0	54
77	Microorganisms for MEMS. <i>Journal of Microelectromechanical Systems</i> , 2007, 16, 429-444.	1.7	21
78	<i>Methylotenera mobilis</i> gen. nov., sp. nov., an obligately methylamine-utilizing bacterium within the family Methylophilaceae. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2006, 56, 2819-2823.	0.8	138
79	Cloning and characterization of <i>corA</i> , a gene encoding a copper-repressible polypeptide in the type I methanotroph, <i>Methylomicrobium albus</i> BG8. <i>FEMS Microbiology Letters</i> , 2006, 148, 169-174.	0.7	28
80	Development of a defined medium supporting rapid growth for <i>Deinococcus radiodurans</i> and analysis of metabolic capacities. <i>Applied Microbiology and Biotechnology</i> , 2006, 72, 1074-1082.	1.7	18
81	Physiological analysis of <i>Methylobacterium extorquens</i> AM1 grown in continuous and batch cultures. <i>Archives of Microbiology</i> , 2006, 186, 139-149.	1.0	26
82	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
83	<i>Methyloversatilis universalis</i> gen. nov., sp. nov., a novel taxon within the Betaproteobacteria represented by three methylophilic isolates. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2006, 56, 2517-2522.	0.8	104
84	Measurement of Respiration Rates of <i>Methylobacterium extorquens</i> AM1 Cultures by Use of a Phosphorescence-Based Sensor. <i>Applied and Environmental Microbiology</i> , 2006, 72, 1692-1695.	1.4	18
85	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
86	Methanotrophic populations in estuarine sediment from Newport Bay, California. <i>FEMS Microbiology Letters</i> , 2005, 250, 287-293.	0.7	27
87	Development and application of polymerase chain reaction primers based on <i>fhcD</i> for environmental detection of methanopterin-linked C1-metabolism in bacteria. <i>Environmental Microbiology</i> , 2005, 7, 1269-1274.	1.8	21
88	Flux Analysis Uncovers Key Role of Functional Redundancy in Formaldehyde Metabolism. <i>PLoS Biology</i> , 2005, 3, e16.	2.6	72
89	Identification of an upstream regulatory sequence that mediates the transcription of <i>mox</i> genes in <i>Methylobacterium extorquens</i> AM1. <i>Microbiology (United Kingdom)</i> , 2005, 151, 3723-3728.	0.7	11
90	Identification of Genes Involved in the Glyoxylate Regeneration Cycle in <i>Methylobacterium extorquens</i> AM1, Including Two New Genes, <i>meaC</i> and <i>meaD</i> . <i>Journal of Bacteriology</i> , 2005, 187, 1523-1526.	1.0	25

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91	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
92	Global Transcriptional and Proteomic Analysis of the Sig1 Heat Shock Regulon of <i>Deinococcus radiodurans</i> . <i>Journal of Bacteriology</i> , 2005, 187, 3339-3351.	1.0	23
93	<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
94	Bacterial Populations Active in Metabolism of C 1 Compounds in the Sediment of Lake Washington, a Freshwater Lake. <i>Applied and Environmental Microbiology</i> , 2005, 71, 6885-6899.	1.4	198
95	Highly Divergent Genes for Methanopterin-Linked C 1 Transfer Reactions in Lake Washington, Assessed via Metagenomic Analysis and mRNA Detection. <i>Applied and Environmental Microbiology</i> , 2005, 71, 8846-8854.	1.4	22
96	<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
97	Novel Dephosphotetrahydromethanopterin Biosynthesis Genes Discovered via Mutagenesis in <i>Methylobacterium extorquens</i> AM1. <i>Journal of Bacteriology</i> , 2005, 187, 2508-2512.	1.0	22
98	MtdC, a Novel Class of Methylene Tetrahydromethanopterin Dehydrogenases. <i>Journal of Bacteriology</i> , 2005, 187, 6069-6074.	1.0	17
99	Analysis of <i>fae</i> and <i>fhcD</i> Genes in Mono Lake, California. <i>Applied and Environmental Microbiology</i> , 2005, 71, 8949-8953.	1.4	14
100	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
101	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
102	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
103	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
104	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
105	Multiple Formaldehyde Oxidation/Detoxification Pathways in <i>Burkholderia fungorum</i> LB400. <i>Journal of Bacteriology</i> , 2004, 186, 2173-2178.	1.0	65
106	Multiple Formate Dehydrogenase Enzymes in the Facultative Methylotroph <i>Methylobacterium extorquens</i> AM1 Are Dispensable for Growth on Methanol. <i>Journal of Bacteriology</i> , 2004, 186, 22-28.	1.0	90
107	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
108	Overexpression of a heterologous protein, haloalkane dehalogenase, in a poly- γ -hydroxybutyrate-deficient strain of the facultative methylotroph <i>Methylobacterium extorquens</i> AM1. <i>Biotechnology and Bioengineering</i> , 2003, 81, 263-268.	1.7	22

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109	Quantification of central metabolic fluxes in the facultative methylotroph <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
110	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
111	Life-on-a-chip. <i>Nature Reviews Microbiology</i> , 2003, 1, 158-164.	13.6	154
112	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
113	Novel Methylotrophy Genes of <i>Methylobacterium extorquens</i> AM1 Identified by using Transposon Mutagenesis Including a Putative Dihydropyrimidinase. <i>Journal of Bacteriology</i> , 2003, 185, 669-673.	1.0	46
114	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
115	Methylotrophy in <i>Methylobacterium extorquens</i> AM1 from a Genomic Point of View. <i>Journal of Bacteriology</i> , 2003, 185, 2980-2987.	1.0	262
116	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
117	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
118	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
119	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
120	Poly- ¹² -Hydroxybutyrate Biosynthesis in the Facultative Methylotroph <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
121	Glyoxylate Regeneration Pathway in the Methylotroph <i>Methylobacterium extorquens</i> AM1. <i>Journal of Bacteriology</i> , 2002, 184, 1750-1758.	1.0	92
122	Involvement of Two Putative Alternative Sigma Factors in Stress Response of the Radioresistant Bacterium <i>Deinococcus radiodurans</i> . <i>Journal of Bacteriology</i> , 2002, 184, 6182-6189.	1.0	24
123	Plants in the Pink: Cytokinin Production by <i>Methylobacterium</i> . <i>Journal of Bacteriology</i> , 2002, 184, 1818-1818.	1.0	108
124	PqqC/D, which converts a biosynthetic intermediate to pyrroloquinoline quinone. <i>Biochemical and Biophysical Research Communications</i> , 2002, 299, 268-272.	1.0	23
125	Broad-Host-Range <i>cre-lox</i> System for Antibiotic Marker Recycling in Gram-Negative Bacteria. <i>BioTechniques</i> , 2002, 33, 1062-1067.	0.8	305
126	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. <i>Biotechnology and Bioengineering</i> , 2002, 78, 296-312.	1.7	111

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127	Estimation of methanotroph abundance in a freshwater lake sediment. <i>Environmental Microbiology</i> , 2002, 4, 443-450.	1.8	89
128	Analysis of sMMO-containing Type I methanotrophs in Lake Washington sediment. <i>Environmental Microbiology</i> , 2002, 4, 517-524.	1.8	52
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