

# Ludmila Chistoserdova

## List of Publications by Year in descending order

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107  
papers

6,876  
citations

46918

47  
h-index

69108

77  
g-index

109  
all docs

109  
docs citations

109  
times ranked

5060  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Expanding World of Methylotrophic Metabolism. Annual Review of Microbiology, 2009, 63, 477-499.	2.9	363
2	Modularity of methylotrophy, revisited. Environmental Microbiology, 2011, 13, 2603-2622.	1.8	347
3	C1 Transfer Enzymes and Coenzymes Linking Methylotrophic Bacteria and Methanogenic Archaea. , 1998, 281, 99-102.		295
4	Methylotrophy in Methylobacterium extorquens AM1 from a Genomic Point of View. Journal of Bacteriology, 2003, 185, 2980-2987.	1.0	262
5	High-resolution metagenomics targets specific functional types in complex microbial communities. Nature Biotechnology, 2008, 26, 1029-1034.	9.4	254
6	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
7	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
8	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
9	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
10	Methylotenera mobilis gen. nov., sp. nov., an obligately methylamine-utilizing bacterium within the family Methylophilaceae. International Journal of Systematic and Evolutionary Microbiology, 2006, 56, 2819-2823.	0.8	138
11	<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
12	Distribution of Tetrahydromethanopterin-Dependent Enzymes in Methylotrophic Bacteria and Phylogeny of Methenyl Tetrahydromethanopterin Cyclohydrolases. Journal of Bacteriology, 1999, 181, 5750-5757.	1.0	124
13	The Enigmatic Planctomycetes May Hold a Key to the Origins of Methanogenesis and Methylotrophy. Molecular Biology and Evolution, 2004, 21, 1234-1241.	3.5	123
14	Current Trends in Methylotrophy. Trends in Microbiology, 2018, 26, 703-714.	3.5	119
15	Methane-fed microbial microcosms show differential community dynamics and pinpoint taxa involved in communal response. ISME Journal, 2015, 9, 1119-1129.	4.4	118
16	Methylotrophs in natural habitats: current insights through metagenomics. Applied Microbiology and Biotechnology, 2015, 99, 5763-5779.	1.7	109
17	Plants in the Pink: Cytokinin Production by Methylobacterium. Journal of Bacteriology, 2002, 184, 1818-1818.	1.0	108
18	Genome of Methylobacillus flagellatus , Molecular Basis for Obligate Methylotrophy, and Polyphyletic Origin of Methylotrophy. Journal of Bacteriology, 2007, 189, 4020-4027.	1.0	107

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19	Characterization of a Novel Methanol Dehydrogenase in Representatives of <i>Burkholderiales</i> : Implications for Environmental Detection of Methylophily and Evidence for Convergent Evolution. <i>Journal of Bacteriology</i> , 2008, 190, 3817-3823.	1.0	105
20	<i>Methyloversatilis universalis</i> gen. nov., sp. nov., a novel taxon within the Betaproteobacteria represented by three methylophilyic isolates. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2006, 56, 2517-2522.	0.8	104
21	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
22	A genomic view of methane oxidation by aerobic bacteria and anaerobic archaea. <i>Genome Biology</i> , 2005, 6, 208.	13.9	103
23	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
24	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
25	Complete Genome Sequences of Six Strains of the Genus <i>Methylobacterium</i> . <i>Journal of Bacteriology</i> , 2012, 194, 4746-4748.	1.0	99
26	Insights into Denitrification in <i>Methyloversatilis mobilis</i> from Denitrification Pathway and Methanol Metabolism Mutants. <i>Journal of Bacteriology</i> , 2013, 195, 2207-2211.	1.0	99
27	Molecular and mutational analysis of a DNA region separating two methylophily gene clusters in <i>Methylobacterium extorquens</i> AM1. <i>Microbiology (United Kingdom)</i> , 1997, 143, 1729-1736.	0.7	98
28	Lanthanides: New life metals?. <i>World Journal of Microbiology and Biotechnology</i> , 2016, 32, 138.	1.7	95
29	Real-time detection of actively metabolizing microbes by redox sensing as applied to methylophily populations in Lake Washington. <i>ISME Journal</i> , 2008, 2, 696-706.	4.4	94
30	Glyoxylate Regeneration Pathway in the Methylophily <i>Methylobacterium extorquens</i> AM1. <i>Journal of Bacteriology</i> , 2002, 184, 1750-1758.	1.0	92
31	Multiple Formate Dehydrogenase Enzymes in the Facultative Methylophily <i>Methylobacterium extorquens</i> AM1 Are Dispensable for Growth on Methanol. <i>Journal of Bacteriology</i> , 2004, 186, 22-28.	1.0	90
32	The NADP-Dependent Methylene Tetrahydromethanopterin Dehydrogenase in <i>Methylobacterium extorquens</i> AM1. <i>Journal of Bacteriology</i> , 1998, 180, 5351-5356.	1.0	90
33	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
34	Novel methylophilyic isolates from lake sediment, description of <i>Methyloversatilis versatilis</i> sp. nov. and emended description of the genus <i>Methyloversatilis</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2012, 62, 106-111.	0.8	89
35	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
36	Recent progress and new challenges in metagenomics for biotechnology. <i>Biotechnology Letters</i> , 2010, 32, 1351-1359.	1.1	72

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37	Aerobic Methylophilic Prokaryotes. , 2013, , 267-285.		70
38	Characterization of a second methylene tetrahydromethanopterin dehydrogenase from <i>Methylobacterium extorquens</i> AM1. FEBS Journal, 2000, 267, 3762-3769.	0.2	68
39	Genomes of Three Methylophilic Bacteria from a Single Niche Reveal the Genetic and Metabolic Divergence of the Methylophilaceae. Journal of Bacteriology, 2011, 193, 3757-3764.	1.0	66
40	Multiple Formaldehyde Oxidation/Detoxification Pathways in <i>Burkholderia fungorum</i> LB400. Journal of Bacteriology, 2004, 186, 2173-2178.	1.0	65
41	Identification of a Fourth Formate Dehydrogenase in <i>Methylobacterium extorquens</i> AM1 and Confirmation of the Essential Role of Formate Oxidation in Methylophilicity. Journal of Bacteriology, 2007, 189, 9076-9081.	1.0	64
42	The Expanded Diversity of Methylophilaceae from Lake Washington through Cultivation and Genomic Sequencing of Novel Ecotypes. PLoS ONE, 2014, 9, e102458.	1.1	62
43	Lanthanide-Dependent Methanol Dehydrogenases of XoxF4 and XoxF5 Clades Are Differentially Distributed Among Methylophilic Bacteria and They Reveal Different Biochemical Properties. Frontiers in Microbiology, 2018, 9, 1366.	1.5	57
44	Draft Genome Sequences of Gammaproteobacterial Methanotrophs Isolated from Lake Washington Sediment. Genome Announcements, 2015, 3, .	0.8	55
45	Methylophilicity in a Lake: from Metagenomics to Single-Organism Physiology. Applied and Environmental Microbiology, 2011, 77, 4705-4711.	1.4	54
46	Physiological Effect of XoxG(4) on Lanthanide-Dependent Methanotrophy. MBio, 2018, 9, .	1.8	54
47	Rare earth element alcohol dehydrogenases widely occur among globally distributed, numerically abundant and environmentally important microbes. ISME Journal, 2019, 13, 2005-2017.	4.4	54
48	Poly- $\beta$ -Hydroxybutyrate Biosynthesis in the Facultative Methylophilic <i>Methylobacterium extorquens</i> AM1: Identification and Mutation of <i>gap11</i> , <i>gap20</i> , and <i>phaR</i> . Journal of Bacteriology, 2002, 184, 6174-6181.	1.0	52
49	Methane-Dependent Mineral Reduction by Aerobic Methanotrophs under Hypoxia. Environmental Science and Technology Letters, 2020, 7, 606-612.	3.9	52
50	Natural Selection in Synthetic Communities Highlights the Roles of Methylococcaceae and Methylophilaceae and Suggests Differential Roles for Alternative Methanol Dehydrogenases in Methane Consumption. Frontiers in Microbiology, 2017, 8, 2392.	1.5	51
51	Analysis of two formaldehyde oxidation pathways in <i>Methylobacillus flagellatus</i> KT, a ribulose monophosphate cycle methylophilic bacterium. The GenBank accession numbers for the sequences of 2502 bp containing <i>gndA</i> and part of <i>zwf</i> , and of 2685 bp containing <i>mch</i> , are AF167580 and AF139592, respectively. Microbiology (United Kingdom). 2000, 146, 233-238.	0.7	51
52	<i>Methylosarcina lacus</i> sp. nov., a methanotroph from Lake Washington, Seattle, USA, and emended description of the genus <i>Methylosarcina</i> . International Journal of Systematic and Evolutionary Microbiology, 2005, 55, 2345-2350.	0.8	47
53	Analysis of Gene Islands Involved in Methanopterin-Linked C <sub>1</sub> Transfer Reactions Reveals New Functions and Provides Evolutionary Insights. Journal of Bacteriology, 2005, 187, 4607-4614.	1.0	46
54	Communal Metabolism of Methane and the Rare Earth Element Switch. Journal of Bacteriology, 2017, 199, e00328-17.	1.0	46

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55	Utility of Environmental Primers Targeting Ancient Enzymes: Methylotroph Detection in Lake Washington. <i>Microbial Ecology</i> , 2004, 48, 463-472.	1.4	43
56	Functional Metagenomics: Recent Advances and Future Challenges. <i>Biotechnology and Genetic Engineering Reviews</i> , 2009, 26, 335-352.	2.4	40
57	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
58	Functioning <i>in situ</i> : gene expression in <i>Methylotenera mobilis</i> in its native environment as assessed through transcriptomics. <i>ISME Journal</i> , 2010, 4, 388-398.	4.4	38
59	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
60	Applications of methylotrophs: can single carbon be harnessed for biotechnology?. <i>Current Opinion in Biotechnology</i> , 2018, 50, 189-194.	3.3	34
61	New pieces to the lanthanide puzzle. <i>Molecular Microbiology</i> , 2019, 111, 1127-1131.	1.2	33
62	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
63	<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
64	Is metagenomics resolving identification of functions in microbial communities?. <i>Microbial Biotechnology</i> , 2014, 7, 1-4.	2.0	28
65	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
66	A Synthetic Ecology Perspective: How Well Does Behavior of Model Organisms in the Laboratory Predict Microbial Activities in Natural Habitats?. <i>Frontiers in Microbiology</i> , 2016, 7, 946.	1.5	25
67	Wide Distribution of Genes for Tetrahydromethanopterin/Methanofuran-Linked C1 Transfer Reactions Argues for Their Presence in the Common Ancestor of Bacteria and Archaea. <i>Frontiers in Microbiology</i> , 2016, 7, 1425.	1.5	24
68	Comment on "A Persistent Oxygen Anomaly Reveals the Fate of Spilled Methane in the Deep Gulf of Mexico". <i>Science</i> , 2011, 332, 1033-1033.	6.0	23
69	Highly Divergent Genes for Methanopterin-Linked C1 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
70	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
71	Insights into the physiology of <i>Methylotenera mobilis</i> as revealed by metagenome-based shotgun proteomic analysis. <i>Microbiology (United Kingdom)</i> , 2009, 155, 1103-1110.	0.7	22
72	An Integrated Proteomics/Transcriptomics Approach Points to Oxygen as the Main Electron Sink for Methanol Metabolism in <i>Methylotenera mobilis</i> . <i>Journal of Bacteriology</i> , 2011, 193, 4758-4765.	1.0	22

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73	Identification and mutation of a gene required for glycerate kinase activity from a facultative methylotroph, <i>Methylobacterium extorquens</i> AM1. <i>Journal of Bacteriology</i> , 1997, 179, 4946-4948.	1.0	21
74	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
75	Respiration Response Imaging for Real-Time Detection of Microbial Function at the Single-Cell Level. <i>Applied and Environmental Microbiology</i> , 2011, 77, 67-72.	1.4	21
76	Comparative transcriptomics in three <i>Methylophilaceae</i> species uncover different strategies for environmental adaptation. <i>PeerJ</i> , 2013, 1, e115.	0.9	20
77	Oxidative and assimilative enzyme activities in continuous cultures of the obligate methylotroph <i>Methylobacillus flagellatum</i> . <i>Antonie Van Leeuwenhoek</i> , 1991, 60, 101-107.	0.7	19
78	Genomics of Methylotrophy in Gram-Positive Methylamine-Utilizing Bacteria. <i>Microorganisms</i> , 2015, 3, 94-112.	1.6	19
79	MtdC, a Novel Class of Methylene Tetrahydromethanopterin Dehydrogenases. <i>Journal of Bacteriology</i> , 2005, 187, 6069-6074.	1.0	17
80	Draft Genome Sequences of Five New Strains of <i>Methylophilaceae</i> Isolated from Lake Washington Sediment. <i>Genome Announcements</i> , 2015, 3, .	0.8	17
81	Application of Omics Approaches to Studying Methylotrophs and Methylotroph Communities. <i>Current Issues in Molecular Biology</i> , 2017, 24, 119-142.	1.0	15
82	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
83	Draft Genome of <i>Janthinobacterium</i> sp. RA13 Isolated from Lake Washington Sediment. <i>Genome Announcements</i> , 2015, 3, .	0.8	13
84	A Complex Interplay between Nitric Oxide, Quorum Sensing, and the Unique Secondary Metabolite Tundrenone Constitutes the Hypoxia Response in <i>Methylobacter</i> . <i>MSystems</i> , 2020, 5, .	1.7	13
85	Metabolism of Formaldehyde in <i>M. extorquens</i> AM1. , 1996, , 16-24.		13
86	Fishing for biodiversity: novel methanopterin-linked C1 transfer genes deduced from the Sargasso Sea metagenome. <i>Environmental Microbiology</i> , 2005, 7, 1909-1916.	1.8	12
87	Community-Level Analysis: Genes Encoding Methanopterin-Dependent Enzymes. <i>Methods in Enzymology</i> , 2005, 397, 443-454.	0.4	12
88	Draft Genome of <i>Pseudomonas</i> sp. Strain 11/12A, Isolated from Lake Washington Sediment. <i>Genome Announcements</i> , 2015, 3, .	0.8	10
89	Growth of the obligate methylotroph <i>Methylobacillus flagellatum</i> under stationary and nonstationary conditions during continuous cultivation. <i>Biotechnology and Bioengineering</i> , 1992, 39, 688-695.	1.7	9
90	Functional Metagenomics of Methylotrophs. <i>Methods in Enzymology</i> , 2011, 495, 81-98.	0.4	8

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91	The Distribution and Evolution of C1 Transfer Enzymes and Evolution of the Planctomycetes. , 2013, , 195-209.		7
92	Cycling Single-Carbon Compounds: from Omics to Novel Concepts. Microbe Magazine, 2013, 8, 395-400.	0.4	7
93	Systems Biology Meets Enzymology: Recent Insights into Communal Metabolism of Methane and the Role of Lanthanides. Current Issues in Molecular Biology, 2019, 33, 183-196.	1.0	6
94	Metagenomic Insight into Environmentally Challenged Methane-Fed Microbial Communities. Microorganisms, 2020, 8, 1614.	1.6	5
95	Draft Genomes of Two Strains of Flavobacterium Isolated from Lake Washington Sediment. Genome Announcements, 2015, 3, .	0.8	4
96	Systems Biology Tools for Methyloprophs. Springer Protocols, 2015, , 97-118.	0.1	4
97	Synthetic Methane-Consuming Communities from a Natural Lake Sediment. MBio, 2019, 10, .	1.8	4
98	Effect of formaldehyde on growth of obligate methyloproph Methylobacillus flagellatum in a substrate non-limited continuous culture. Archives of Microbiology, 1992, 158, 145-148.	1.0	2
99	Expression, purification and properties of the enzymes involved in lanthanide-dependent alcohol oxidation: XoxF4, XoxF5, ExaF/PedH, and XoxG4. Methods in Enzymology, 2021, 650, 81-96.	0.4	2
100	Impacts of The Wetland Sedge Carex aquatilis on Microbial Community and Methane Metabolisms. Plant and Soil, 2022, 471, 491.	1.8	2
101	Multi-omics Understanding of Methanotrophs. Microbiology Monographs, 2019, , 121-138.	0.3	1
102	Genetics and Regulation of C1 Metabolism in Methyloprophs. , 1998, , 89-97.		1
103	Methanotrophy: An Evolving Field. , 2018, , 1-15.		0
104	Microbial Cycling of Methane. , 2019, , 115-115.		0
105	To methanotrophy and beyond! New insight into functional and ecological roles for copper chelators. ISME Journal, 2022, 16, 3-4.	4.4	0
106	C1 Microbes And Biotechnological Applications. , 2018, , .		0
107	FUNCTIONAL METAGENOMICS: RECENT ADVANCES AND FUTURE CHALLENGES. , 0, , 335-352.		0