

# 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	To methanotrophy and beyond! New insight into functional and ecological roles for copper chelators. <i>ISME Journal</i> , 2022, 16, 3-4.	4.4	0
2	Impacts of The Wetland Sedge <i>Carex aquatilis</i> on Microbial Community and Methane Metabolisms. <i>Plant and Soil</i> , 2022, 471, 491.	1.8	2
3	Expression, purification and properties of the enzymes involved in lanthanide-dependent alcohol oxidation: XoxF4, XoxF5, ExaF/PedH, and XoxG4. <i>Methods in Enzymology</i> , 2021, 650, 81-96.	0.4	2
4	Metagenomic Insight into Environmentally Challenged Methane-Fed Microbial Communities. <i>Microorganisms</i> , 2020, 8, 1614.	1.6	5
5	Methane-Dependent Mineral Reduction by Aerobic Methanotrophs under Hypoxia. <i>Environmental Science and Technology Letters</i> , 2020, 7, 606-612.	3.9	52
6	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
7	Synthetic Methane-Consuming Communities from a Natural Lake Sediment. <i>MBio</i> , 2019, 10, .	1.8	4
8	New pieces to the lanthanide puzzle. <i>Molecular Microbiology</i> , 2019, 111, 1127-1131.	1.2	33
9	Rare earth element alcohol dehydrogenases widely occur among globally distributed, numerically abundant and environmentally important microbes. <i>ISME Journal</i> , 2019, 13, 2005-2017.	4.4	54
10	Microbial Cycling of Methane. , 2019, , 115-115.		0
11	Multi-omics Understanding of Methanotrophs. <i>Microbiology Monographs</i> , 2019, , 121-138.	0.3	1
12	Systems Biology Meets Enzymology: Recent Insights into Communal Metabolism of Methane and the Role of Lanthanides. <i>Current Issues in Molecular Biology</i> , 2019, 33, 183-196.	1.0	6
13	Current Trends in Methylotrophy. <i>Trends in Microbiology</i> , 2018, 26, 703-714.	3.5	119
14	Physiological Effect of XoxG(4) on Lanthanide-Dependent Methanotrophy. <i>MBio</i> , 2018, 9, .	1.8	54
15	Applications of methylotrophs: can single carbon be harnessed for biotechnology?. <i>Current Opinion in Biotechnology</i> , 2018, 50, 189-194.	3.3	34
16	Methanotrophy: An Evolving Field. , 2018, , 1-15.		0
17	Lanthanide-Dependent Methanol Dehydrogenases of XoxF4 and XoxF5 Clades Are Differentially Distributed Among Methylotrophic Bacteria and They Reveal Different Biochemical Properties. <i>Frontiers in Microbiology</i> , 2018, 9, 1366.	1.5	57
18	C1 Microbes And Biotechnological Applications. , 2018, , .		0

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19	Communal Metabolism of Methane and the Rare Earth Element Switch. <i>Journal of Bacteriology</i> , 2017, 199, e00328-17.	1.0	46
20	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
21	Natural Selection in Synthetic Communities Highlights the Roles of Methylococcaceae and Methylophilaceae and Suggests Differential Roles for Alternative Methanol Dehydrogenases in Methane Consumption. <i>Frontiers in Microbiology</i> , 2017, 8, 2392.	1.5	51
22	Application of Omics Approaches to Studying Methylophils and Methylophil Communities. <i>Current Issues in Molecular Biology</i> , 2017, 24, 119-142.	1.0	15
23	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
24	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
25	Lanthanides: New life metals?. <i>World Journal of Microbiology and Biotechnology</i> , 2016, 32, 138.	1.7	95
26	Multiphyletic origins of methylophilicity in <i>Alphaproteobacteria</i> , exemplified by comparative genomics of <i>Leptothrix</i> and <i>Wickettsiella</i> isolates. <i>Environmental Microbiology</i> , 2015, 17, 547-554.	1.8	38
27	Draft Genome of <i>Pseudomonas</i> sp. Strain 11/12A, Isolated from Lake Washington Sediment. <i>Genome Announcements</i> , 2015, 3, .	0.8	10
28	Genomics of Methylophilicity in Gram-Positive Methylamine-Utilizing Bacteria. <i>Microorganisms</i> , 2015, 3, 94-112.	1.6	19
29	Draft Genome Sequences of Gammaproteobacterial Methanotrophs Isolated from Lake Washington Sediment. <i>Genome Announcements</i> , 2015, 3, .	0.8	55
30	Draft Genome Sequences of Five New Strains of Methylophilaceae Isolated from Lake Washington Sediment. <i>Genome Announcements</i> , 2015, 3, .	0.8	17
31	Draft Genome of <i>Janthinobacterium</i> sp. RA13 Isolated from Lake Washington Sediment. <i>Genome Announcements</i> , 2015, 3, .	0.8	13
32	Draft Genomes of Two Strains of <i>Flavobacterium</i> Isolated from Lake Washington Sediment. <i>Genome Announcements</i> , 2015, 3, .	0.8	4
33	Methylophilicity in natural habitats: current insights through metagenomics. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 5763-5779.	1.7	109
34	Systems Biology Tools for Methylophilicity. <i>Springer Protocols</i> , 2015, , 97-118.	0.1	4
35	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
36	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

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37	The Expanded Diversity of Methylophilaceae from Lake Washington through Cultivation and Genomic Sequencing of Novel Ecotypes. PLoS ONE, 2014, 9, e102458.	1.1	62
38	Is metagenomics resolving identification of functions in microbial communities?. Microbial Biotechnology, 2014, 7, 1-4.	2.0	28
39	Aerobic Methylophilic Prokaryotes. , 2013, , 267-285.		70
40	Insights into Denitrification in Methylophilaceae mobilis from Denitrification Pathway and Methanol Metabolism Mutants. Journal of Bacteriology, 2013, 195, 2207-2211.	1.0	99
41	The Distribution and Evolution of C1 Transfer Enzymes and Evolution of the Planctomycetes. , 2013, , 195-209.		7
42	Cycling Single-Carbon Compounds: from Omics to Novel Concepts. Microbe Magazine, 2013, 8, 395-400.	0.4	7
43	Comparative transcriptomics in three <i>Methylophilaceae</i> species uncover different strategies for environmental adaptation. PeerJ, 2013, 1, e115.	0.9	20
44	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
45	Complete Genome Sequences of Six Strains of the Genus Methylobacterium. Journal of Bacteriology, 2012, 194, 4746-4748.	1.0	99
46	Novel methylophilic isolates from lake sediment, description of Methylophilaceae versatilis sp. nov. and emended description of the genus Methylophilaceae. International Journal of Systematic and Evolutionary Microbiology, 2012, 62, 106-111.	0.8	89
47	Functional Metagenomics of Methylophilic. Methods in Enzymology, 2011, 495, 81-98.	0.4	8
48	Modularity of methylophilic, revisited. Environmental Microbiology, 2011, 13, 2603-2622.	1.8	347
49	Genomes of Three Methylophilic from a Single Niche Reveal the Genetic and Metabolic Divergence of the Methylophilaceae. Journal of Bacteriology, 2011, 193, 3757-3764.	1.0	66
50	An Integrated Proteomics/Transcriptomics Approach Points to Oxygen as the Main Electron Sink for Methanol Metabolism in Methylophilaceae mobilis. Journal of Bacteriology, 2011, 193, 4758-4765.	1.0	22
51	Respiration Response Imaging for Real-Time Detection of Microbial Function at the Single-Cell Level. Applied and Environmental Microbiology, 2011, 77, 67-72.	1.4	21
52	Methylophilic in a Lake: from Metagenomics to Single-Organism Physiology. Applied and Environmental Microbiology, 2011, 77, 4705-4711.	1.4	54
53	Comment on "A Persistent Oxygen Anomaly Reveals the Fate of Spilled Methane in the Deep Gulf of Mexico" Science, 2011, 332, 1033-1033.	6.0	23
54	Recent progress and new challenges in metagenomics for biotechnology. Biotechnology Letters, 2010, 32, 1351-1359.	1.1	72

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55	Expressed Genome of <i>Methylobacillus flagellatus</i> as Defined through Comprehensive Proteomics and New Insights into Methylo-trophy. <i>Journal of Bacteriology</i> , 2010, 192, 4859-4867.	1.0	31
56	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
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	<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
59	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
60	Functional Metagenomics: Recent Advances and Future Challenges. <i>Biotechnology and Genetic Engineering Reviews</i> , 2009, 26, 335-352.	2.4	40
61	The Expanding World of Methylo-trophic Metabolism. <i>Annual Review of Microbiology</i> , 2009, 63, 477-499.	2.9	363
62	<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
63	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
64	High-resolution metagenomics targets specific functional types in complex microbial communities. <i>Nature Biotechnology</i> , 2008, 26, 1029-1034.	9.4	254
65	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
66	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
67	Identification of a Fourth Formate Dehydrogenase in <i>Methylobacterium extorquens</i> AM1 and Confirmation of the Essential Role of Formate Oxidation in Methylo-trophy. <i>Journal of Bacteriology</i> , 2007, 189, 9076-9081.	1.0	64
68	<i>Methylotenera mobilis</i> gen. nov., sp. nov., an obligately methylamine-utilizing bacterium within the family <i>Methylophilaceae</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2006, 56, 2819-2823.	0.8	138
69	<i>Methyloversatilis universalis</i> gen. nov., sp. nov., a novel taxon within the <i>Betaproteobacteria</i> represented by three methylo-trophic isolates. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2006, 56, 2517-2522.	0.8	104
70	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
71	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
72	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

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73	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
74	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
75	<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
76	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
77	Community-Level Analysis: Genes Encoding Methanopterin-Dependent Enzymes. <i>Methods in Enzymology</i> , 2005, 397, 443-454.	0.4	12
78	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
79	<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
80	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
81	MtdC, a Novel Class of Methylene Tetrahydromethanopterin Dehydrogenases. <i>Journal of Bacteriology</i> , 2005, 187, 6069-6074.	1.0	17
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	A genomic view of methane oxidation by aerobic bacteria and anaerobic archaea. <i>Genome Biology</i> , 2005, 6, 208.	13.9	103
84	The Enigmatic Planctomycetes May Hold a Key to the Origins of Methanogenesis and Methylotrophy. <i>Molecular Biology and Evolution</i> , 2004, 21, 1234-1241.	3.5	123
85	Multiple Formaldehyde Oxidation/Detoxification Pathways in <i>Burkholderia fungorum</i> LB400. <i>Journal of Bacteriology</i> , 2004, 186, 2173-2178.	1.0	65
86	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
87	Utility of Environmental Primers Targeting Ancient Enzymes: Methylotroph Detection in Lake Washington. <i>Microbial Ecology</i> , 2004, 48, 463-472.	1.4	43
88	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
89	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
90	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

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91	Poly- <sup>12</sup> -Hydroxybutyrate Biosynthesis in the Facultative Methylophile Methylobacterium extorquens AM1: Identification and Mutation of gap11 , gap20 , and phaR. Journal of Bacteriology, 2002, 184, 6174-6181.	1.0	52
92	Glyoxylate Regeneration Pathway in the Methylophile Methylobacterium extorquens AM1. Journal of Bacteriology, 2002, 184, 1750-1758.	1.0	92
93	Plants in the Pink: Cytokinin Production by Methylobacterium. Journal of Bacteriology, 2002, 184, 1818-1818.	1.0	108
94	Characterization of a second methylene tetrahydromethanopterin dehydrogenase from Methylobacterium extorquens AM1. FEBS Journal, 2000, 267, 3762-3769.	0.2	68
95	Analysis of two formaldehyde oxidation pathways in Methylobacillus flagellatus KT, a ribulose monophosphate cycle methylophile The GenBank accession numbers for the sequences of 2502Ånt containing gndA and part of zwf, and of 2685Ånt containing mch, are AF167580 and AF139592, respectively. Microbiology (United Kingdom). 2000. 146. 233-238.	0.7	51
96	A methenyl tetrahydromethanopterin cyclohydrolase and a methenyl tetrahydrofolate cyclohydrolase in Methylobacterium extorquens AM1. FEBS Journal, 1999, 261, 475-480.	0.2	80
97	Distribution of Tetrahydromethanopterin-Dependent Enzymes in Methylophile Bacteria and Phylogeny of Methenyl Tetrahydromethanopterin Cyclohydrolases. Journal of Bacteriology, 1999, 181, 5750-5757.	1.0	124
98	C1 Transfer Enzymes and Coenzymes Linking Methylophile Bacteria and Methanogenic Archaea. , 1998, 281, 99-102.		295
99	Genetics and Regulation of C1 Metabolism in Methylophiles. , 1998, , 89-97.		1
100	The NADP-Dependent Methylene Tetrahydromethanopterin Dehydrogenase in <i>Methylobacterium extorquens</i> AM1. Journal of Bacteriology, 1998, 180, 5351-5356.	1.0	90
101	Molecular and mutational analysis of a DNA region separating two methylophile gene clusters in Methylobacterium extorquens AM1. Microbiology (United Kingdom), 1997, 143, 1729-1736.	0.7	98
102	Identification and mutation of a gene required for glycerate kinase activity from a facultative methylophile, Methylobacterium extorquens AM1. Journal of Bacteriology, 1997, 179, 4946-4948.	1.0	21
103	Metabolism of Formaldehyde in M. extorquens AM1. , 1996, , 16-24.		13
104	Effect of formaldehyde on growth of obligate methylophile Methylobacillus flagellatum in a substrate non-limited continuous culture. Archives of Microbiology, 1992, 158, 145-148.	1.0	2
105	Growth of the obligate methylophile Methylobacillus flagellatum under stationary and nonstationary conditions during continuous cultivation. Biotechnology and Bioengineering, 1992, 39, 688-695.	1.7	9
106	Oxidative and assimilative enzyme activities in continuous cultures of the obligate methylophile Methylobacillus flagellatum. Antonie Van Leeuwenhoek, 1991, 60, 101-107.	0.7	19
107	FUNCTIONAL METAGENOMICS: RECENT ADVANCES AND FUTURE CHALLENGES. , 0, , 335-352.		0