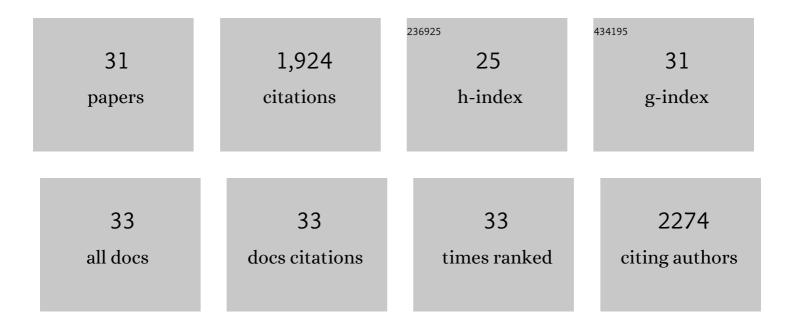
Claudia L

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/10117014/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Conceptualizing functional traits and ecological characteristics of methaneâ€oxidizing bacteria as life strategies. Environmental Microbiology Reports, 2013, 5, 335-345.	2.4	225
2	Nitrate―and nitriteâ€dependent anaerobic oxidation of methane. Environmental Microbiology Reports, 2016, 8, 941-955.	2.4	150
3	Potential of <i>pmoA</i> Amplicon Pyrosequencing for Methanotroph Diversity Studies. Applied and Environmental Microbiology, 2011, 77, 6305-6309.	3.1	131
4	One millimetre makes the difference: high-resolution analysis of methane-oxidizing bacteria and their specific activity at the oxic–anoxic interface in a flooded paddy soil. ISME Journal, 2012, 6, 2128-2139.	9.8	127
5	Classification of pmoA amplicon pyrosequences using BLAST and the lowest common ancestor method in MEGAN. Frontiers in Microbiology, 2012, 5, 34.	3.5	121
6	Enrichment of anaerobic nitrate-dependent methanotrophic â€~Candidatus Methanoperedens nitroreducens' archaea from an Italian paddy field soil. Applied Microbiology and Biotechnology, 2017, 101, 7075-7084.	3.6	110
7	Biogeography of wetland rice methanotrophs. Environmental Microbiology, 2010, 12, 862-872.	3.8	92
8	Metagenomic analysis of nitrogen and methane cycling in the Arabian Sea oxygen minimum zone. PeerJ, 2016, 4, e1924.	2.0	77
9	Recovery of methanotrophs from disturbance: population dynamics, evenness and functioning. ISME Journal, 2011, 5, 750-758.	9.8	71
10	McrA primers for the detection and quantification of the anaerobic archaeal methanotroph â€~Candidatus Methanoperedens nitroreducens'. Applied Microbiology and Biotechnology, 2017, 101, 1631-1641.	3.6	65
11	Stratification of Diversity and Activity of Methanogenic and Methanotrophic Microorganisms in a Nitrogen-Fertilized Italian Paddy Soil. Frontiers in Microbiology, 2017, 8, 2127.	3.5	62
12	Linking Nitrogen Load to the Structure and Function of Wetland Soil and Rhizosphere Microbial Communities. MSystems, 2018, 3, .	3.8	56
13	Aerobic methanotroph diversity in <scp>R</scp> iganqiao peatlands on the <scp>Q</scp> inghai– <scp>T</scp> ibetan <scp>P</scp> lateau. Environmental Microbiology Reports, 2013, 5, 566-574.	2.4	55
14	Succession of methanotrophs in oxygen–methane counter-gradients of flooded rice paddies. ISME Journal, 2010, 4, 1603-1607.	9.8	49
15	Ageing well: methane oxidation and methane oxidizing bacteria along a chronosequence of 2000 years. Environmental Microbiology Reports, 2011, 3, 738-743.	2.4	49
16	Structure and function of methanotrophic communities in a landfill-cover soil. FEMS Microbiology Ecology, 2012, 81, 52-65.	2.7	46
17	Macroecology of methaneâ€oxidizing bacteria: the βâ€diversity of <i>pmoA</i> genotypes in tropical and subtropical rice paddies. Environmental Microbiology, 2014, 16, 72-83.	3.8	45
18	Effects of nitrogen fertilization on diazotrophic activity of microorganisms associated with Sphagnum magellanicum. Plant and Soil, 2016, 406, 83-100.	3.7	44

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19	Metagenomic potential for and diversity of Nâ€cycle driving microorganisms in the Bothnian Sea sediment. MicrobiologyOpen, 2017, 6, e00475.	3.0	43
20	Methane source strength and energy flow shape methanotrophic communities in oxygen–methane counterâ€gradients. Environmental Microbiology Reports, 2012, 4, 203-208.	2.4	41
21	Resilience of (seed bank) aerobic methanotrophs and methanotrophic activity to desiccation and heat stress. Soil Biology and Biochemistry, 2016, 101, 130-138.	8.8	38
22	Impacts of Inter- and Intralaboratory Variations on the Reproducibility of Microbial Community Analyses. Applied and Environmental Microbiology, 2010, 76, 7451-7458.	3.1	37
23	Selective stimulation in a natural community of methane oxidizing bacteria: Effects of copper on pmoA transcription and activity. Soil Biology and Biochemistry, 2013, 65, 211-216.	8.8	35
24	Fieldâ€scale tracking of active methaneâ€oxidizing communities in a landfill cover soil reveals spatial and seasonal variability. Environmental Microbiology, 2015, 17, 1721-1737.	3.8	33
25	Gammaproteobacterial Methanotrophs Dominate Cold Methane Seeps in Floodplains of West Siberian Rivers. Applied and Environmental Microbiology, 2014, 80, 5944-5954.	3.1	27
26	Survey of methanotrophic diversity in various ecosystems by degenerate methane monooxygenase gene primers. AMB Express, 2017, 7, 162.	3.0	24
27	Methanotrophic bacteria associated to rice roots: the cultivar effect assessed by Tâ€RFLP and microarray analysis. Environmental Microbiology Reports, 2011, 3, 518-525.	2.4	21
28	Spatial heterogeneity of methanotrophs: a geostatistical analysis of <i>pmoA</i> â€based Tâ€RFLP patterns in a paddy soil. Environmental Microbiology Reports, 2009, 1, 393-397.	2.4	18
29	<i>Methylotetracoccus oryzae</i> Strain C50C1 Is a Novel Type Ib Gammaproteobacterial Methanotroph Adapted to Freshwater Environments. MSphere, 2019, 4, .	2.9	14
30	Effect of water management on microbial diversity and composition in an Italian rice field system. FEMS Microbiology Ecology, 2022, 98, .	2.7	11
31	Compositional and functional stability of aerobic methane consuming communities in drained and rewetted peat meadows. FEMS Microbiology Ecology, 2015, 91, fiv119.	2.7	6