

Paul L Bodelier

List of Publications by Year in descending order

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136
papers

9,279
citations

41344

49
h-index

42399

92
g-index

154
all docs

154
docs citations

154
times ranked

9029
citing authors

#	ARTICLE	IF	CITATIONS
1	Nitrogen as a regulatory factor of methane oxidation in soils and sediments. FEMS Microbiology Ecology, 2004, 47, 265-277.	2.7	639
2	Methane oxidation by an extremely acidophilic bacterium of the phylum Verrucomicrobia. Nature, 2007, 450, 879-882.	27.8	526
3	Stimulation by ammonium-based fertilizers of methane oxidation in soil around rice roots. Nature, 2000, 403, 421-424.	27.8	461
4	Revisiting life strategy concepts in environmental microbial ecology. FEMS Microbiology Ecology, 2017, 93, fix006.	2.7	416
5	Shifting carbon flow from roots into associated microbial communities in response to elevated atmospheric CO ₂ . Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 10938-10942.	7.1	390
6	Trait-based approaches for understanding microbial biodiversity and ecosystem functioning. Frontiers in Microbiology, 2014, 5, 251.	3.5	323
7	The impact of climate change on lakes in the Netherlands: a review. Aquatic Ecology, 2005, 39, 381-400.	1.5	281
8	Conceptualizing functional traits and ecological characteristics of methane-oxidizing bacteria as life strategies. Environmental Microbiology Reports, 2013, 5, 335-345.	2.4	225
9	Differential Effects of Nitrogenous Fertilizers on Methane-Consuming Microbes in Rice Field and Forest Soils. Applied and Environmental Microbiology, 2006, 72, 1346-1354.	3.1	209
10	Conventional methanotrophs are responsible for atmospheric methane oxidation in paddy soils. Nature Communications, 2016, 7, 11728.	12.8	209
11	Dynamics of nitrification and denitrification in root-oxygenated sediments and adaptation of ammonia-oxidizing bacteria to low-oxygen or anoxic habitats. Applied and Environmental Microbiology, 1996, 62, 4100-4107.	3.1	194
12	Interactions between nitrogenous fertilizers and methane cycling in wetland and upland soils. Current Opinion in Environmental Sustainability, 2011, 3, 379-388.	6.3	159
13	Community analysis of ammonia-oxidising bacteria, in relation to oxygen availability in soils and root-oxygenated sediments, using PCR, DGGE and oligonucleotide probe hybridisation. FEMS Microbiology Ecology, 1998, 27, 339-350.	2.7	149
14	Title is missing!. Biogeochemistry, 2000, 51, 225-257.	3.5	127
15	Effect of temperature on composition of the methanotrophic community in rice field and forest soil. FEMS Microbiology Ecology, 2007, 62, 24-31.	2.7	125
16	Oxygen consumption kinetics of Nitrosomonas europaea and Nitrobacter hamburgensis grown in mixed continuous cultures at different oxygen concentrations. Archives of Microbiology, 1994, 161, 156-162.	2.2	124
17	Methylocystis heyeri sp. nov., a novel type II methanotrophic bacterium possessing a "signature" fatty acids of type I methanotrophs. International Journal of Systematic and Evolutionary Microbiology, 2007, 57, 472-479.	1.7	123
18	Effects of Grazing by the Free-Living Soil Amoebae <i>Acanthamoeba castellanii</i> , <i>Acanthamoeba polyphaga</i> , and <i>Hartmannella vermiformis</i> on Various Bacteria. Applied and Environmental Microbiology, 1993, 59, 2317-2319.	3.1	123

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19	Toward Understanding, Managing, and Protecting Microbial Ecosystems. <i>Frontiers in Microbiology</i> , 2011, 2, 80.	3.5	121
20	Interactions between Thaumarchaea, <i>Nitrospira</i> and methanotrophs modulate autotrophic nitrification in volcanic grassland soil. <i>ISME Journal</i> , 2014, 8, 2397-2410.	9.8	121
21	Contribution of Methanotrophic and Nitrifying Bacteria to CH ₄ and NH ₄ ⁺ Oxidation in the Rhizosphere of Rice Plants as Determined by New Methods of Discrimination. <i>Applied and Environmental Microbiology</i> , 1999, 65, 1826-1833.	3.1	118
22	The active methanotrophic community in hydromorphic soils changes in response to changing methane concentration. <i>Environmental Microbiology</i> , 2006, 8, 321-333.	3.8	115
23	<i>Singulisphaera acidiphila</i> gen. nov., sp. nov., a non-filamentous, Isosphaera-like planctomycete from acidic northern wetlands. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2008, 58, 1186-1193.	1.7	110
24	A reanalysis of phospholipid fatty acids as ecological biomarkers for methanotrophic bacteria. <i>ISME Journal</i> , 2009, 3, 606-617.	9.8	110
25	Soil type links microbial colonization of rice roots to methane emission. <i>Global Change Biology</i> , 2008, 14, 657-669.	9.5	109
26	Acetate utilization as a survival strategy of peat-inhabiting <i>Methylocystis</i> spp.. <i>Environmental Microbiology Reports</i> , 2011, 3, 36-46.	2.4	109
27	Biotic Interactions in Microbial Communities as Modulators of Biogeochemical Processes: Methanotrophy as a Model System. <i>Frontiers in Microbiology</i> , 2016, 7, 1285.	3.5	95
28	<i>Schlesneria paludicola</i> gen. nov., sp. nov., the first acidophilic member of the order Planctomycetales, from Sphagnum-dominated boreal wetlands. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2007, 57, 2680-2687.	1.7	93
29	Microbial minorities modulate methane consumption through niche partitioning. <i>ISME Journal</i> , 2013, 7, 2214-2228.	9.8	91
30	Peatland vascular plant functional types affect methane dynamics by altering microbial community structure. <i>Journal of Ecology</i> , 2015, 103, 925-934.	4.0	90
31	Interactions between methane and the nitrogen cycle in light of climate change. <i>Current Opinion in Environmental Sustainability</i> , 2014, 9-10, 26-36.	6.3	89
32	Beyond nitrogen: The importance of phosphorus for CH ₄ oxidation in soils and sediments. <i>Geoderma</i> , 2015, 259-260, 337-346.	5.1	88
33	Community analysis of methanogenic archaea within a riparian flooding gradient. <i>Environmental Microbiology</i> , 2004, 6, 449-461.	3.8	84
34	<i>Zavarzinella formosa</i> gen. nov., sp. nov., a novel stalked, Gemmata-like planctomycete from a Siberian peat bog. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2009, 59, 357-364.	1.7	80
35	Methane-derived carbon flows through methane-oxidizing bacteria to higher trophic levels in aquatic systems. <i>Environmental Microbiology</i> , 2007, 9, 1126-1134.	3.8	76
36	Competitive interactions between methane- and ammonia-oxidizing bacteria modulate carbon and nitrogen cycling in paddy soil. <i>Biogeosciences</i> , 2014, 11, 3353-3368.	3.3	75

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37	<i>Methylocystis bryophila</i> sp. nov., a facultatively methanotrophic bacterium from acidic Sphagnum peat, and emended description of the genus <i>Methylocystis</i> (ex Whittenbury et al. 1970) Bowman et al. 1993. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 1096-1104.	1.7	74
38	Diversity of iron oxidizers in wetland soils revealed by novel 16S rRNA primers targeting <i>Gallionella</i> -related bacteria. <i>ISME Journal</i> , 2009, 3, 715-725.	9.8	73
39	Biphasic kinetics of a methanotrophic community is a combination of growth and increased activity per cell. <i>FEMS Microbiology Ecology</i> , 2010, 71, 12-22.	2.7	72
40	Hydrology is reflected in the functioning and community composition of methanotrophs in the littoral wetland of a boreal lake. <i>FEMS Microbiology Ecology</i> , 2011, 75, 430-445.	2.7	69
41	Combined effects of carbon, nitrogen and phosphorus on CH ₄ production and denitrification in wetland sediments. <i>Geoderma</i> , 2015, 259-260, 354-361.	5.1	64
42	Decomposition of mixtures of cover crop residues increases microbial functional diversity. <i>Geoderma</i> , 2020, 361, 114060.	5.1	64
43	Phosphatases relieve carbon limitation of microbial activity in Baltic Sea sediments along a redox gradient. <i>Limnology and Oceanography</i> , 2011, 56, 2018-2026.	3.1	63
44	<i>Methylomonas paludis</i> sp. nov., the first acid-tolerant member of the genus <i>Methylomonas</i> , from an acidic wetland. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 2282-2289.	1.7	63
45	Microbiology of wetlands. <i>Frontiers in Microbiology</i> , 2013, 4, 79.	3.5	61
46	Living apart together – bacterial volatiles influence methanotrophic growth and activity. <i>ISME Journal</i> , 2018, 12, 1163-1166.	9.8	60
47	Cattle Manure Enhances Methanogens Diversity and Methane Emissions Compared to Swine Manure under Rice Paddy. <i>PLoS ONE</i> , 2014, 9, e113593.	2.5	56
48	Effect of salinity on temporal and spatial dynamics of ammonia-oxidising bacteria from intertidal freshwater sediment. <i>FEMS Microbiology Ecology</i> , 2005, 53, 359-368.	2.7	53
49	<i>Methylovirgula ligni</i> gen. nov., sp. nov., an obligately acidophilic, facultatively methylotrophic bacterium with a highly divergent <i>mxoF</i> gene. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2009, 59, 2538-2545.	1.7	53
50	A nested PCR approach for improved recovery of archaeal 16S rRNA gene fragments from freshwater samples. <i>FEMS Microbiology Letters</i> , 2009, 298, 193-198.	1.8	51
51	Fossil chironomid $\delta^{13}C$ as a proxy for past methanogenic contribution to benthic food webs in lakes?. <i>Journal of Paleolimnology</i> , 2010, 43, 235-245.	1.6	51
52	Title is missing!. <i>Plant and Soil</i> , 1997, 190, 91-103.	3.7	47
53	Improved PCR-DGGE for high resolution diversity screening of complex sulfate-reducing prokaryotic communities in soils and sediments. <i>Journal of Microbiological Methods</i> , 2007, 70, 103-111.	1.6	45
54	Rice straw serves as additional carbon source for rhizosphere microorganisms and reduces root exudate consumption. <i>Soil Biology and Biochemistry</i> , 2019, 135, 235-238.	8.8	44

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55	Organic Residue Amendments to Modulate Greenhouse Gas Emissions From Agricultural Soils. <i>Frontiers in Microbiology</i> , 2018, 9, 3035.	3.5	43
56	<i>Singulisphaera rosea</i> sp. nov., a planctomycete from acidic Sphagnum peat, and emended description of the genus <i>Singulisphaera</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2012, 62, 118-123.	1.7	42
57	Diazotrophic methanotrophs in peatlands: the missing link?. <i>Plant and Soil</i> , 2015, 389, 419-423.	3.7	42
58	Recurrence and Frequency of Disturbance have Cumulative Effect on Methanotrophic Activity, Abundance, and Community Structure. <i>Frontiers in Microbiology</i> , 2015, 6, 1493.	3.5	42
59	Unexpected role of canonical aerobic methanotrophs in upland agricultural soils. <i>Soil Biology and Biochemistry</i> , 2019, 131, 1-8.	8.8	42
60	Interactions between nitrifying and denitrifying bacteria in gnotobiotic microcosms planted with the emergent macrophyte <i>Glyceria maxima</i> . <i>FEMS Microbiology Ecology</i> , 1998, 25, 63-78.	2.7	40
61	Unexpected stimulation of soil methane uptake as emergent property of agricultural soils following bioâ€based residue application. <i>Global Change Biology</i> , 2015, 21, 3864-3879.	9.5	39
62	Impact of Peat Mining and Restoration on Methane Turnover Potential and Methane-Cycling Microorganisms in a Northern Bog. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	39
63	New DGGE strategies for the analyses of methanotrophic microbial communities using different combinations of existing 16S rRNA-based primers. <i>FEMS Microbiology Ecology</i> , 2005, 52, 163-174.	2.7	38
64	Predominance of methanogens over methanotrophs in rewetted fens characterized by high methane emissions. <i>Biogeosciences</i> , 2018, 15, 6519-6536.	3.3	38
65	Impacts of Inter- and Intralaboratory Variations on the Reproducibility of Microbial Community Analyses. <i>Applied and Environmental Microbiology</i> , 2010, 76, 7451-7458.	3.1	37
66	Distribution and Diversity of <i>Gallionella</i> -Like Neutrophilic Iron Oxidizers in a Tidal Freshwater Marsh. <i>Applied and Environmental Microbiology</i> , 2011, 77, 2337-2344.	3.1	37
67	Biogeography of sulfate-reducing prokaryotes in river floodplains. <i>FEMS Microbiology Ecology</i> , 2008, 64, 395-406.	2.7	36
68	Aquatic herbivores facilitate the emission of methane from wetlands. <i>Ecology</i> , 2011, 92, 1166-1173.	3.2	36
69	Archaeal dominated ammonia-oxidizing communities in Icelandic grassland soils are moderately affected by long-term N fertilization and geothermal heating. <i>Frontiers in Microbiology</i> , 2012, 3, 352.	3.5	36
70	Manure-associated stimulation of soil-borne methanogenic activity in agricultural soils. <i>Biology and Fertility of Soils</i> , 2015, 51, 511-516.	4.3	36
71	Characterization of <i>Methylobacterium</i> strains isolated from the phyllosphere and description of <i>Methylobacterium longum</i> sp. nov. <i>Antonie Van Leeuwenhoek</i> , 2012, 101, 169-183.	1.7	35
72	Effects of bioâ€based residue amendments on greenhouse gas emission from agricultural soil are stronger than effects of soil type with different microbial community composition. <i>GCB Bioenergy</i> , 2017, 9, 1707-1720.	5.6	35

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73	Seasonal and vertical distribution of putative ammonia-oxidizing thaumarchaeotal communities in an oligotrophic lake. <i>FEMS Microbiology Ecology</i> , 2013, 83, 515-526.	2.7	33
74	Field-scale tracking of active methane-oxidizing communities in a landfill cover soil reveals spatial and seasonal variability. <i>Environmental Microbiology</i> , 2015, 17, 1721-1737.	3.8	33
75	Animal-plant-microbe interactions: direct and indirect effects of swan foraging behaviour modulate methane cycling in temperate shallow wetlands. <i>Oecologia</i> , 2006, 149, 233-244.	2.0	32
76	Spatial Patterns of Iron- and Methane-Oxidizing Bacterial Communities in an Irregularly Flooded, Riparian Wetland. <i>Frontiers in Microbiology</i> , 2012, 3, 64.	3.5	32
77	Structural and functional response of methane-consuming microbial communities to different flooding regimes in riparian soils. <i>Ecology and Evolution</i> , 2012, 2, 106-127.	1.9	32
78	Positive diversity-functioning relationships in model communities of methanotrophic bacteria. <i>Ecology</i> , 2018, 99, 714-723.	3.2	30
79	Ammonia-limited conditions cause of Thaumarchaeal dominance in volcanic grassland soil. <i>FEMS Microbiology Ecology</i> , 2015, 91, .	2.7	29
80	Temporal and Spatial Coexistence of Archaeal and Bacterial <i>amoA</i> Genes and Gene Transcripts in Lake Lucerne. <i>Archaea</i> , 2013, 2013, 1-11.	2.3	27
81	Spatial patterns of methanotrophic communities along a hydrological gradient in a riparian wetland. <i>FEMS Microbiology Ecology</i> , 2013, 86, 59-70.	2.7	26
82	Resistance and Recovery of Methane-Oxidizing Communities Depends on Stress Regime and History; A Microcosm Study. <i>Frontiers in Microbiology</i> , 2018, 9, 1714.	3.5	26
83	Bypassing the methane cycle. <i>Nature</i> , 2015, 523, 534-535.	27.8	25
84	Quantitative Assessment of Ammonia-Oxidizing Bacterial Communities in the Epiphyton of Submerged Macrophytes in Shallow Lakes. <i>Applied and Environmental Microbiology</i> , 2010, 76, 1813-1821.	3.1	24
85	Soil warming and fertilization altered rates of nitrogen transformation processes and selected for adapted ammonia-oxidizing archaea in sub-arctic grassland soil. <i>Soil Biology and Biochemistry</i> , 2017, 107, 114-124.	8.8	24
86	Trophic state changes can affect the importance of methane-derived carbon in aquatic food webs. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20170278.	2.6	24
87	Modulation of Litter Decomposition by the Soil Microbial Food Web Under Influence of Land Use Change. <i>Frontiers in Microbiology</i> , 2018, 9, 2860.	3.5	23
88	Ethyl tert-butyl ether (EtBE) degradation by an algal-bacterial culture obtained from contaminated groundwater. <i>Water Research</i> , 2019, 148, 314-323.	11.3	23
89	DNA stable-isotope probing highlights the effects of temperature on functionally active methanotrophs in natural wetlands. <i>Soil Biology and Biochemistry</i> , 2020, 149, 107954.	8.8	23
90	Epiphyton as a Niche for Ammonia-Oxidizing Bacteria: Detailed Comparison with Benthic and Pelagic Compartments in Shallow Freshwater Lakes. <i>Applied and Environmental Microbiology</i> , 2008, 74, 1963-1971.	3.1	21

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91	Nitrification in the rhizosphere of a flooding-resistant and a flooding-non-resistant <i>Rumex</i> species under drained and waterlogged conditions. <i>FEMS Microbiology Letters</i> , 1991, 86, 33-42.	1.8	20
92	Remarkable Recovery and Colonization Behaviour of Methane Oxidizing Bacteria in Soil After Disturbance Is Controlled by Methane Source Only. <i>Microbial Ecology</i> , 2014, 68, 259-270.	2.8	20
93	Bacterial Diversity and Geochemical Profiles in Sediments from Eutrophic Azorean Lakes. <i>Geomicrobiology Journal</i> , 2012, 29, 704-715.	2.0	19
94	Response of a methane-driven interaction network to stressor intensification. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	2.7	19
95	Oxygen uptake kinetics of <i>Pseudomonas chlororaphis</i> grown in glucose- or glutamate-limited continuous cultures. <i>Archives of Microbiology</i> , 1997, 167, 392-395.	2.2	18
96	Strain-specific incorporation of methanotrophic biomass into eukaryotic grazers in a rice field soil revealed by PLFA-SIP. <i>FEMS Microbiology Ecology</i> , 2011, 75, 284-290.	2.7	18
97	Weak phylogenetic signal in physiological traits of methane-oxidizing bacteria. <i>Journal of Evolutionary Biology</i> , 2014, 27, 1240-1247.	1.7	18
98	Does microbial stoichiometry modulate eutrophication of aquatic ecosystems?. <i>Environmental Microbiology</i> , 2013, 15, 1572-1579.	3.8	16
99	Whole-community genome amplification (WCGA) leads to compositional bias in methane-oxidizing communities as assessed by <i>pmoA</i> -based microarray analyses and QPCR. <i>Environmental Microbiology Reports</i> , 2009, 1, 434-441.	2.4	15
100	Methane as a carbon source for the food web in raised bog pools. <i>Freshwater Science</i> , 2013, 32, 1260-1272.	1.8	15
101	Niche Differentiation of Host-Associated Pelagic Microbes and Their Potential Contribution to Biogeochemical Cycling in Artificially Warmed Lakes. <i>Frontiers in Microbiology</i> , 2020, 11, 582.	3.5	15
102	<i>Methylothermobacter oryzae</i> Strain C50C1 Is a Novel Type Ib Gammaproteobacterial Methanotroph Adapted to Freshwater Environments. <i>MSphere</i> , 2019, 4, .	2.9	14
103	Trophic and non-trophic effects of fish and macroinvertebrates on carbon emissions. <i>Freshwater Biology</i> , 2021, 66, 1831-1845.	2.4	14
104	Producing organic amendments: Physicochemical changes in biowaste used in anaerobic digestion, composting, and fermentation. <i>Waste Management</i> , 2022, 149, 177-185.	7.4	14
105	Plant community flood resilience in intensively managed grasslands and the role of the plant economic spectrum. <i>Journal of Applied Ecology</i> , 2020, 57, 1524-1534.	4.0	13
106	Steering microbiomes by organic amendments towards climate-smart agricultural soils. <i>Biology and Fertility of Soils</i> , 2021, 57, 1053-1074.	4.3	13
107	Effect of Redox Conditions on Bacterial Community Structure in Baltic Sea Sediments with Contrasting Phosphorus Fluxes. <i>PLoS ONE</i> , 2014, 9, e92401.	2.5	12
108	Environmental legacy contributes to the resilience of methane consumption in a laboratory microcosm system. <i>Scientific Reports</i> , 2018, 8, 8862.	3.3	12

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109	Can flooding-induced greenhouse gas emissions be mitigated by trait-based plant species choice?. <i>Science of the Total Environment</i> , 2020, 727, 138476.	8.0	12
110	Oxygen consumption kinetics of <i>Nitrosomonas europaea</i> and <i>Nitrobacter hamburgensis</i> grown in mixed continuous cultures at different oxygen concentrations. <i>Archives of Microbiology</i> , 1994, 161, 156-162.	2.2	12
111	Greenhouse gas (CO ₂ , CH ₄ , and N ₂ O) emissions after abandonment of agriculture. <i>Biology and Fertility of Soils</i> , 2022, 58, 579-591.	4.3	12
112	Response of the Sulfate-Reducing Community to the Re-establishment of Estuarine Conditions in Two Contrasting Soils: a Mesocosm Approach. <i>Microbial Ecology</i> , 2010, 59, 109-120.	2.8	11
113	USC $\delta^{13}C$ Dominated Community Composition and Cooccurrence Network of Methanotrophs and Bacteria in Subterranean Karst Caves. <i>Microbiology Spectrum</i> , 2021, 9, e0082021.	3.0	11
114	Discrepancy in exchangeable and soluble ammonium-induced effects on aerobic methane oxidation: a microcosm study of a paddy soil. <i>Biology and Fertility of Soils</i> , 2021, 57, 873-880.	4.3	10
115	Ecological Aspects of Microbes and Microbial Communities Inhabiting the Rhizosphere of Wetland Plants. , 2006, , 205-238.		10
116	Validation of the Correct Start Codon of <i>norX/nxrX</i> and Universality of the <i>norAXB/nxrAXB</i> Gene Cluster in <i>Nitrobacter</i> Species. <i>Current Microbiology</i> , 2006, 53, 255-257.	2.2	9
117	Limitations of the use of group-specific primers in real-time PCR as appear from quantitative analyses of closely related ammonia-oxidising species. <i>Water Research</i> , 2008, 42, 1093-1101.	11.3	9
118	Co-occurrence patterns among prokaryotes across an age gradient in pit mud of Chinese strong-flavor liquor. <i>Canadian Journal of Microbiology</i> , 2020, 66, 495-504.	1.7	9
119	Aquatic herbivores facilitate the emission of methane from wetlands. <i>Ecology</i> , 2011, 92, 1166-1173.	3.2	8
120	Preliminary investigations into the background levels of various metals and boron in the aquatic liverwort <i>Scapania uliginosa</i> (Sw.) Dum.. <i>Aquatic Botany</i> , 1991, 39, 345-352.	1.6	7
121	Active methane processing microbes and the disproportionate role of NC10 phylum in methane mitigation in Amazonian floodplains. <i>Biogeochemistry</i> , 2021, 156, 293-317.	3.5	7
122	Compositional and functional stability of aerobic methane consuming communities in drained and rewetted peat meadows. <i>FEMS Microbiology Ecology</i> , 2015, 91, fiv119.	2.7	6
123	Abundance and $\delta^{13}C$ values of fatty acids in lacustrine surface sediments: Relationships with in-lake methane concentrations. <i>Quaternary Science Reviews</i> , 2018, 191, 337-347.	3.0	6
124	Grand Challenges in Terrestrial Microbiology: Moving on From a Decade of Progress in Microbial Biogeochemistry. <i>Frontiers in Microbiology</i> , 2020, 11, 981.	3.5	6
125	Methanotroph Ecology, Environmental Distribution and Functioning. <i>Microbiology Monographs</i> , 2019, , 1-38.	0.6	6
126	Community analysis of ammonia-oxidising bacteria, in relation to oxygen availability in soils and root-oxygenated sediments, using PCR, DGGE and oligonucleotide probe hybridisation. <i>FEMS Microbiology Ecology</i> , 1998, 27, 339-350.	2.7	6

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127	Phylogenetic Characterization of Phosphatase-Expressing Bacterial Communities in Baltic Sea Sediments. <i>Microbes and Environments</i> , 2015, 30, 192-195.	1.6	4
128	Microbial Ecosystem Functions in Wetlands under Disturbance. , 2017, , 227-274.		3
129	Relief of Phosphate Limitation Stimulates Methane Oxidation. <i>Frontiers in Environmental Science</i> , 2022, 10, .	3.3	3
130	Effect of the aerenchymatous helophyte <i>Glyceria maxima</i> on the sulfate-reducing communities in two contrasting riparian grassland soils. <i>Plant and Soil</i> , 2013, 370, 73-87.	3.7	2
131	Methane-Derived Carbon as a Driver for Cyanobacterial Growth. <i>Frontiers in Microbiology</i> , 2022, 13, 837198.	3.5	2
132	PhyloFunDB: A Pipeline to Create and Update Functional Gene Taxonomic Databases. <i>Microorganisms</i> , 2022, 10, 1093.	3.6	1
133	Microbial trait-based approaches for agroecosystems. <i>Advances in Agronomy</i> , 2022, , 259-299.	5.2	1
134	Complete and Draft Genome Sequences of Aerobic Methanotrophs Isolated from a Riparian Wetland. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	0
135	Microbial Ecosystems, Protection of. , 2012, , 1-9.		0
136	Extraction Methods, Variability Encountered in. , 2014, , 1-9.		0