## Paul L Bodelier

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Relief of Phosphate Limitation Stimulates Methane Oxidation. Frontiers in Environmental Science, 2022, 10, .	3.3	3
2	Methane-Derived Carbon as a Driver for Cyanobacterial Growth. Frontiers in Microbiology, 2022, 13, 837198.	3.5	2
3	Greenhouse gas (CO2, CH4, and N2O) emissions after abandonment of agriculture. Biology and Fertility of Soils, 2022, 58, 579-591.	4.3	12
4	PhyloFunDB: A Pipeline to Create and Update Functional Gene Taxonomic Databases. Microorganisms, 2022, 10, 1093.	3.6	1
5	Microbial trait-based approaches for agroecosystems. Advances in Agronomy, 2022, , 259-299.	5.2	1
6	Producing organic amendments: Physicochemical changes in biowaste used in anaerobic digestion, composting, and fermentation. Waste Management, 2022, 149, 177-185.	7.4	14
7	Complete and Draft Genome Sequences of Aerobic Methanotrophs Isolated from a Riparian Wetland. Microbiology Resource Announcements, 2021, 10, .	0.6	0
8	Discrepancy in exchangeable and soluble ammonium-induced effects on aerobic methane oxidation: a microcosm study of a paddy soil. Biology and Fertility of Soils, 2021, 57, 873-880.	4.3	10
9	Trophic and nonâ€trophic effects of fish and macroinvertebrates on carbon emissions. Freshwater Biology, 2021, 66, 1831-1845.	2.4	14
10	USC <i>γ</i> Dominated Community Composition and Cooccurrence Network of Methanotrophs and Bacteria in Subterranean Karst Caves. Microbiology Spectrum, 2021, 9, e0082021.	3.0	11
11	Steering microbiomes by organic amendments towards climate-smart agricultural soils. Biology and Fertility of Soils, 2021, 57, 1053-1074.	4.3	13
12	Active methane processing microbes and the disproportionate role of NC10 phylum in methane mitigation in Amazonian floodplains. Biogeochemistry, 2021, 156, 293-317.	3.5	7
13	Decomposition of mixtures of cover crop residues increases microbial functional diversity. Geoderma, 2020, 361, 114060.	5.1	64
14	DNA stable-isotope probing highlights the effects of temperature on functionally active methanotrophs in natural wetlands. Soil Biology and Biochemistry, 2020, 149, 107954.	8.8	23
15	Response of a methane-driven interaction network to stressor intensification. FEMS Microbiology Ecology, 2020, 96, .	2.7	19
16	Plant community flood resilience in intensively managed grasslands and the role of the plant economic spectrum. Journal of Applied Ecology, 2020, 57, 1524-1534.	4.0	13
17	Grand Challenges in Terrestrial Microbiology: Moving on From a Decade of Progress in Microbial Biogeochemistry. Frontiers in Microbiology, 2020, 11, 981.	3.5	6
18	Niche Differentiation of Host-Associated Pelagic Microbes and Their Potential Contribution to Biogeochemical Cycling in Artificially Warmed Lakes. Frontiers in Microbiology, 2020, 11, 582.	3.5	15

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19	Co-occurrence patterns among prokaryotes across an age gradient in pit mud of Chinese strong-flavor liquor. Canadian Journal of Microbiology, 2020, 66, 495-504.	1.7	9
20	Can flooding-induced greenhouse gas emissions be mitigated by trait-based plant species choice?. Science of the Total Environment, 2020, 727, 138476.	8.0	12
21	<i>Methylotetracoccus oryzae</i> Strain C50C1 Is a Novel Type Ib Gammaproteobacterial Methanotroph Adapted to Freshwater Environments. MSphere, 2019, 4, .	2.9	14
22	Rice straw serves as additional carbon source for rhizosphere microorganisms and reduces root exudate consumption. Soil Biology and Biochemistry, 2019, 135, 235-238.	8.8	44
23	Unexpected role of canonical aerobic methanotrophs in upland agricultural soils. Soil Biology and Biochemistry, 2019, 131, 1-8.	8.8	42
24	Ethyl tert-butyl ether (EtBE) degradation by an algal-bacterial culture obtained from contaminated groundwater. Water Research, 2019, 148, 314-323.	11.3	23
25	Methanotroph Ecology, Environmental Distribution and Functioning. Microbiology Monographs, 2019, , 1-38.	0.6	6
26	Living apart together—bacterial volatiles influence methanotrophic growth and activity. ISME Journal, 2018, 12, 1163-1166.	9.8	60
27	Positive diversityâ€functioning relationships in model communities of methanotrophic bacteria. Ecology, 2018, 99, 714-723.	3.2	30
28	Impact of Peat Mining and Restoration on Methane Turnover Potential and Methane-Cycling Microorganisms in a Northern Bog. Applied and Environmental Microbiology, 2018, 84, .	3.1	39
29	Predominance of methanogens over methanotrophs in rewetted fens characterized by high methane emissions. Biogeosciences, 2018, 15, 6519-6536.	3.3	38
30	Modulation of Litter Decomposition by the Soil Microbial Food Web Under Influence of Land Use Change. Frontiers in Microbiology, 2018, 9, 2860.	3.5	23
31	Organic Residue Amendments to Modulate Greenhouse Gas Emissions From Agricultural Soils. Frontiers in Microbiology, 2018, 9, 3035.	3.5	43
32	Resistance and Recovery of Methane-Oxidizing Communities Depends on Stress Regime and History; A Microcosm Study. Frontiers in Microbiology, 2018, 9, 1714.	3.5	26
33	Abundance and δ13C values of fatty acids in lacustrine surface sediments: Relationships with in-lake methane concentrations. Quaternary Science Reviews, 2018, 191, 337-347.	3.0	6
34	Environmental legacy contributes to the resilience of methane consumption in a laboratory microcosm system. Scientific Reports, 2018, 8, 8862.	3.3	12
35	Soil warming and fertilization altered rates of nitrogen transformation processes and selected for adapted ammonia-oxidizing archaea in sub-arctic grassland soil. Soil Biology and Biochemistry, 2017, 107, 114-124.	8.8	24
36	Trophic state changes can affect the importance of methane-derived carbon in aquatic food webs. Proceedings of the Royal Society B: Biological Sciences, 2017, 284, 20170278.	2.6	24

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37	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. GCB Bioenergy, 2017, 9, 1707-1720.	5.6	35
38	Microbial Ecosystem Functions in Wetlands under Disturbance. , 2017, , 227-274.		3
39	Revisiting life strategy concepts in environmental microbial ecology. FEMS Microbiology Ecology, 2017, 93, fix006.	2.7	416
40	Biotic Interactions in Microbial Communities as Modulators of Biogeochemical Processes: Methanotrophy as a Model System. Frontiers in Microbiology, 2016, 7, 1285.	3.5	95
41	Conventional methanotrophs are responsible for atmospheric methane oxidation in paddy soils. Nature Communications, 2016, 7, 11728.	12.8	209
42	Phylogenetic Characterization of Phosphatase-Expressing Bacterial Communities in Baltic Sea Sediments. Microbes and Environments, 2015, 30, 192-195.	1.6	4
43	Peatland vascular plant functional types affect methane dynamics by altering microbial community structure. Journal of Ecology, 2015, 103, 925-934.	4.0	90
44	Unexpected stimulation of soil methane uptake as emergent property of agricultural soils following bioâ€based residue application. Global Change Biology, 2015, 21, 3864-3879.	9.5	39
45	Diazotrophic methanotrophs in peatlands: the missing link?. Plant and Soil, 2015, 389, 419-423.	3.7	42
46	Manure-associated stimulation of soil-borne methanogenic activity in agricultural soils. Biology and Fertility of Soils, 2015, 51, 511-516.	4.3	36
47	Bypassing the methane cycle. Nature, 2015, 523, 534-535.	27.8	25
48	Combined effects of carbon, nitrogen and phosphorus on CH 4 production and denitrification in wetland sediments. Geoderma, 2015, 259-260, 354-361.	5.1	64
49	Beyond nitrogen: The importance of phosphorus for CH 4 oxidation in soils and sediments. Geoderma, 2015, 259-260, 337-346.	5.1	88
50	Ammonia-limited conditions cause of Thaumarchaeal dominance in volcanic grassland soil. FEMS Microbiology Ecology, 2015, 91, .	2.7	29
51	Compositional and functional stability of aerobic methane consuming communities in drained and rewetted peat meadows. FEMS Microbiology Ecology, 2015, 91, fiv119.	2.7	6
52	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
53	Recurrence and Frequency of Disturbance have Cumulative Effect on Methanotrophic Activity, Abundance, and Community Structure. Frontiers in Microbiology, 2015, 6, 1493.	3.5	42
54	Effect of Redox Conditions on Bacterial Community Structure in Baltic Sea Sediments with Contrasting Phosphorus Fluxes. PLoS ONE, 2014, 9, e92401.	2.5	12

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55	Cattle Manure Enhances Methanogens Diversity and Methane Emissions Compared to Swine Manure under Rice Paddy. PLoS ONE, 2014, 9, e113593.	2.5	56
56	Trait-based approaches for understanding microbial biodiversity and ecosystem functioning. Frontiers in Microbiology, 2014, 5, 251.	3.5	323
57	Competitive interactions between methane- and ammonia-oxidizing bacteria modulate carbon and nitrogen cycling in paddy soil. Biogeosciences, 2014, 11, 3353-3368.	3.3	75
58	Weak phylogenetic signal in physiological traits of methaneâ€oxidizing bacteria. Journal of Evolutionary Biology, 2014, 27, 1240-1247.	1.7	18
59	Interactions between Thaumarchaea, <i>Nitrospira</i> and methanotrophs modulate autotrophic nitrification in volcanic grassland soil. ISME Journal, 2014, 8, 2397-2410.	9.8	121
60	Interactions between methane and the nitrogen cycle in light of climate change. Current Opinion in Environmental Sustainability, 2014, 9-10, 26-36.	6.3	89
61	Remarkable Recovery and Colonization Behaviour of Methane Oxidizing Bacteria in Soil After Disturbance Is Controlled by Methane Source Only. Microbial Ecology, 2014, 68, 259-270.	2.8	20
62	Extraction Methods, Variability Encountered in. , 2014, , 1-9.		0
63	Methylocystis bryophila sp. nov., a facultatively methanotrophic bacterium from acidic Sphagnum peat, and emended description of the genus Methylocystis (ex Whittenbury et al. 1970) Bowman et al. 1993. International Journal of Systematic and Evolutionary Microbiology, 2013, 63, 1096-1104.	1.7	74
64	Effect of the aerenchymatous helophyte Glyceria maxima on the sulfate-reducing communities in two contrasting riparian grassland soils. Plant and Soil, 2013, 370, 73-87.	3.7	2
65	Does microbial stoichiometry modulate eutrophication of aquatic ecosystems?. Environmental Microbiology, 2013, 15, 1572-1579.	3.8	16
66	Seasonal and vertical distribution of putative ammonia-oxidizing thaumarchaeotal communities in an oligotrophic lake. FEMS Microbiology Ecology, 2013, 83, 515-526.	2.7	33
67	Conceptualizing functional traits and ecological characteristics of methaneâ€oxidizing bacteria as life strategies. Environmental Microbiology Reports, 2013, 5, 335-345.	2.4	225
68	Methylomonas paludis sp. nov., the first acid-tolerant member of the genus Methylomonas , from an acidic wetland. International Journal of Systematic and Evolutionary Microbiology, 2013, 63, 2282-2289.	1.7	63
69	Microbial minorities modulate methane consumption through niche partitioning. ISME Journal, 2013, 7, 2214-2228.	9.8	91
70	Methane as a carbon source for the food web in raised bog pools. Freshwater Science, 2013, 32, 1260-1272.	1.8	15
71	Spatial patterns of methanotrophic communities along a hydrological gradient in a riparian wetland. FEMS Microbiology Ecology, 2013, 86, 59-70.	2.7	26
72	Temporal and Spatial Coexistence of Archaeal and Bacterial <i>amoA</i> Genes and Gene Transcripts in Lake Lucerne. Archaea, 2013, 2013, 1-11.	2.3	27

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73	Microbiology of wetlands. Frontiers in Microbiology, 2013, 4, 79.	3.5	61
74	Archaeal dominated ammonia-oxidizing communities in Icelandic grassland soils are moderately affected by long-term N fertilization and geothermal heating. Frontiers in Microbiology, 2012, 3, 352.	3.5	36
75	Bacterial Diversity and Geochemical Profiles in Sediments from Eutrophic Azorean Lakes. Geomicrobiology Journal, 2012, 29, 704-715.	2.0	19
76	Singulisphaera rosea sp. nov., a planctomycete from acidic Sphagnum peat, and emended description of the genus Singulisphaera. International Journal of Systematic and Evolutionary Microbiology, 2012, 62, 118-123.	1.7	42
77	Spatial Patterns of Iron- and Methane-Oxidizing Bacterial Communities in an Irregularly Flooded, Riparian Wetland. Frontiers in Microbiology, 2012, 3, 64.	3.5	32
78	Structural and functional response of methaneâ€consuming microbial communities to different flooding regimes in riparian soils. Ecology and Evolution, 2012, 2, 106-127.	1.9	32
79	Characterization of Methylobacterium strains isolated from the phyllosphere and description of Methylobacterium longum sp. nov. Antonie Van Leeuwenhoek, 2012, 101, 169-183.	1.7	35
80	Microbial Ecosystems, Protection of. , 2012, , 1-9.		0
81	Interactions between nitrogenous fertilizers and methane cycling in wetland and upland soils. Current Opinion in Environmental Sustainability, 2011, 3, 379-388.	6.3	159
82	Acetate utilization as a survival strategy of peatâ€inhabiting <i>Methylocystis</i> spp Environmental Microbiology Reports, 2011, 3, 36-46.	2.4	109
83	Toward Understanding, Managing, and Protecting Microbial Ecosystems. Frontiers in Microbiology, 2011, 2, 80.	3.5	121
84	Aquatic herbivores facilitate the emission of methane from wetlands. Ecology, 2011, 92, 1166-1173.	3.2	36
85	Strain-specific incorporation of methanotrophic biomass into eukaryotic grazers in a rice field soil revealed by PLFA-SIP. FEMS Microbiology Ecology, 2011, 75, 284-290.	2.7	18
86	Hydrology is reflected in the functioning and community composition of methanotrophs in the littoral wetland of a boreal lake. FEMS Microbiology Ecology, 2011, 75, 430-445.	2.7	69
87	Distribution and Diversity of <i>Gallionella</i> -Like Neutrophilic Iron Oxidizers in a Tidal Freshwater Marsh. Applied and Environmental Microbiology, 2011, 77, 2337-2344.	3.1	37
88	Phosphatases relieve carbon limitation of microbial activity in Baltic Sea sediments along a redoxâ€gradient. Limnology and Oceanography, 2011, 56, 2018-2026.	3.1	63
89	Aquatic herbivores facilitate the emission of methane from wetlands. Ecology, 2011, 92, 1166-1173.	3.2	8
90	Response of the Sulfate-Reducing Community to the Re-establishment of Estuarine Conditions in Two Contrasting Soils: a Mesocosm Approach. Microbial Ecology, 2010, 59, 109-120.	2.8	11

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91	Fossil chironomid δ13C as a proxy for past methanogenic contribution to benthic food webs in lakes?. Journal of Paleolimnology, 2010, 43, 235-245.	1.6	51
92	Biphasic kinetics of  a methanotrophic community is a combination of growth and increased activity per cell. FEMS Microbiology Ecology, 2010, 71, 12-22.	2.7	72
93	Quantitative Assessment of Ammonia-Oxidizing Bacterial Communities in the Epiphyton of Submerged Macrophytes in Shallow Lakes. Applied and Environmental Microbiology, 2010, 76, 1813-1821.	3.1	24
94	Impacts of Inter- and Intralaboratory Variations on the Reproducibility of Microbial Community Analyses. Applied and Environmental Microbiology, 2010, 76, 7451-7458.	3.1	37
95	Shifting carbon flow from roots into associated microbial communities in response to elevated atmospheric CO <sub>2</sub> . Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 10938-10942.	7.1	390
96	Methylovirgula ligni gen. nov., sp. nov., an obligately acidophilic, facultatively methylotrophic bacterium with a highly divergent mxaF gene. International Journal of Systematic and Evolutionary Microbiology, 2009, 59, 2538-2545.	1.7	53
97	Zavarzinella formosa gen. nov., sp. nov., a novel stalked, Gemmata-like planctomycete from a Siberian peat bog. International Journal of Systematic and Evolutionary Microbiology, 2009, 59, 357-364.	1.7	80
98	A reanalysis of phospholipid fatty acids as ecological biomarkers for methanotrophic bacteria. ISME Journal, 2009, 3, 606-617.	9.8	110
99	Diversity of iron oxidizers in wetland soils revealed by novel 16S rRNA primers targeting <i>Gallionella-</i> related bacteria. ISME Journal, 2009, 3, 715-725.	9.8	73
100	A nested PCR approach for improved recovery of archaeal 16S rRNA gene fragments from freshwater samples. FEMS Microbiology Letters, 2009, 298, 193-198.	1.8	51
101	Wholeâ€community genome amplification (WCGA) leads to compositional bias in methaneâ€oxidizing communities as assessed by <i>pmoA</i> â€based microarray analyses and QPCR. Environmental Microbiology Reports, 2009, 1, 434-441.	2.4	15
102	Biogeography of sulfate-reducing prokaryotes in river floodplains. FEMS Microbiology Ecology, 2008, 64, 395-406.	2.7	36
103	Soil type links microbial colonization of rice roots to methane emission. Clobal Change Biology, 2008, 14, 657-669.	9.5	109
104	Limitations of the use of group-specific primers in real-time PCR as appear from quantitative analyses of closely related ammonia-oxidising species. Water Research, 2008, 42, 1093-1101.	11.3	9
105	Singulisphaera acidiphila gen. nov., sp. nov., a non-filamentous, Isosphaera-like planctomycete from acidic northern wetlands. International Journal of Systematic and Evolutionary Microbiology, 2008, 58, 1186-1193.	1.7	110
106	Epiphyton as a Niche for Ammonia-Oxidizing Bacteria: Detailed Comparison with Benthic and Pelagic Compartments in Shallow Freshwater Lakes. Applied and Environmental Microbiology, 2008, 74, 1963-1971.	3.1	21
107	Methylocystis heyeri sp. nov., a novel type II methanotrophic bacterium possessing â€~signature' fatty acids of type I methanotrophs. International Journal of Systematic and Evolutionary Microbiology, 2007, 57, 472-479.	1.7	123
108	Schlesneria paludicola gen. nov., sp. nov., the first acidophilic member of the order Planctomycetales, from Sphagnum-dominated boreal wetlands. International Journal of Systematic and Evolutionary Microbiology, 2007, 57, 2680-2687.	1.7	93

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109	Improved PCR-DGGE for high resolution diversity screening of complex sulfate-reducing prokaryotic communities in soils and sediments. Journal of Microbiological Methods, 2007, 70, 103-111.	1.6	45
110	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
111	Methane oxidation by an extremely acidophilic bacterium of the phylum Verrucomicrobia. Nature, 2007, 450, 879-882.	27.8	526
112	Methane-derived carbon flows through methane-oxidizing bacteria to higher trophic levels in aquatic systems. Environmental Microbiology, 2007, 9, 1126-1134.	3.8	76
113	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
114	The active methanotrophic community in hydromorphic soils changes in response to changing methane concentration. Environmental Microbiology, 2006, 8, 321-333.	3.8	115
115	Animal–plant–microbe interactions: direct and indirect effects of swan foraging behaviour modulate methane cycling in temperate shallow wetlands. Oecologia, 2006, 149, 233-244.	2.0	32
116	Validation of the Correct Start Codon of norX/nxrX and Universality of the norAXB/nxrAXB Gene Cluster in Nitrobacter Species. Current Microbiology, 2006, 53, 255-257.	2.2	9
117	Ecological Aspects of Microbes and Microbial Communities Inhabiting the Rhizosphere of Wetland Plants. , 2006, , 205-238.		10
118	New DGGE strategies for the analyses of methanotrophic microbial communities using different combinations of existing 16S rRNA-based primers. FEMS Microbiology Ecology, 2005, 52, 163-174.	2.7	38
119	Effect of salinity on temporal and spatial dynamics of ammonia-oxidising bacteria from intertidal freshwater sediment. FEMS Microbiology Ecology, 2005, 53, 359-368.	2.7	53
120	The impact of climate change on lakes in the Netherlands: a review. Aquatic Ecology, 2005, 39, 381-400.	1.5	281
121	Community analysis of methanogenic archaea within a riparian flooding gradient. Environmental Microbiology, 2004, 6, 449-461.	3.8	84
122	Nitrogen as a regulatory factor of methane oxidation in soils and sediments. FEMS Microbiology Ecology, 2004, 47, 265-277.	2.7	639
123	Stimulation by ammonium-based fertilizers of methane oxidation in soil around rice roots. Nature, 2000, 403, 421-424.	27.8	461
124	Title is missing!. Biogeochemistry, 2000, 51, 225-257.	3.5	127
125	Contribution of Methanotrophic and Nitrifying Bacteria to CH <sub>4</sub> and NH <sub>4</sub> <sup>+</sup> Oxidation in the Rhizosphere of Rice Plants as Determined by New Methods of Discrimination. Applied and Environmental Microbiology, 1999, 65, 1826-1833.	3.1	118
126	Interactions between nitrifying and denitrifying bacteria in gnotobiotic microcosms planted with the emergent macrophyte Glyceria maxima. FEMS Microbiology Ecology, 1998, 25, 63-78.	2.7	40

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127	Community analysis of ammonia-oxidising bacteria, in relation to oxygen availability in soils and root-oxygenated sediments, using PCR, DGCE and oligonucleotide probe hybridisation. FEMS Microbiology Ecology, 1998, 27, 339-350.	2.7	149
128	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	6
129	Title is missing!. Plant and Soil, 1997, 190, 91-103.	3.7	47
130	Oxygen uptake kinetics of Pseudomonas chlororaphis grown in glucose- or glutamate-limited continuous cultures. Archives of Microbiology, 1997, 167, 392-395.	2.2	18
131	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
132	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
133	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	12
134	Effects of Grazing by the Free-Living Soil Amoebae <i>Acanthamoeba castellanii, Acanthamoeba polyphaga</i> , and <i>Hartmannella vermiformis</i> on Various Bacteria. Applied and Environmental Microbiology, 1993, 59, 2317-2319.	3.1	123
135	Preliminary investigations into the background levels of various metals and boron in the aquatic liverwort Scapania uliginosa (Sw.) Dum Aquatic Botany, 1991, 39, 345-352.	1.6	7
136	Nitrification in the rhizosphere of a flooding-resistant and a flooding-non-resistantRumexspecies under drained and waterlogged conditions. FEMS Microbiology Letters, 1991, 86, 33-42.	1.8	20