

# Katherine D McMahon

## List of Publications by Year in descending order

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Version: 2024-02-01

149  
papers

15,219  
citations

18482

62  
h-index

20961

115  
g-index

183  
all docs

183  
docs citations

183  
times ranked

13888  
citing authors

#	ARTICLE	IF	CITATIONS
1	Minimum information about a single amplified genome (MISAG) and a metagenome-assembled genome (MIMAG) of bacteria and archaea. <i>Nature Biotechnology</i> , 2017, 35, 725-731.	17.5	1,512
2	A Guide to the Natural History of Freshwater Lake Bacteria. <i>Microbiology and Molecular Biology Reviews</i> , 2011, 75, 14-49.	6.6	1,356
3	Metagenomic analysis of two enhanced biological phosphorus removal (EBPR) sludge communities. <i>Nature Biotechnology</i> , 2006, 24, 1263-1269.	17.5	634
4	Metabolic network analysis reveals microbial community interactions in anammox granules. <i>Nature Communications</i> , 2017, 8, 15416.	12.8	489
5	Tetracycline resistance genes in activated sludge wastewater treatment plants. <i>Water Research</i> , 2007, 41, 1143-1151.	11.3	478
6	A genomic catalog of Earth's microbiomes. <i>Nature Biotechnology</i> , 2021, 39, 499-509.	17.5	457
7	Common principles and best practices for engineering microbiomes. <i>Nature Reviews Microbiology</i> , 2019, 17, 725-741.	28.6	324
8	Methanogenic population dynamics during start-up of anaerobic digesters treating municipal solid waste and biosolids. <i>Biotechnology and Bioengineering</i> , 1998, 57, 342-355.	3.3	302
9	Anaerobic codigestion of municipal solid waste and biosolids under various mixing conditions I: digester performance. <i>Water Research</i> , 2001, 35, 1804-1816.	11.3	299
10	New Abundant Microbial Groups in Aquatic Hypersaline Environments. <i>Scientific Reports</i> , 2011, 1, 135.	3.3	288
11	Anaerobic codigestion of municipal solid waste and biosolids under various mixing conditions II: microbial population dynamics. <i>Water Research</i> , 2001, 35, 1817-1827.	11.3	268
12	<i>Candidatus</i> <i>Accumulibacter</i> Population Structure in Enhanced Biological Phosphorus Removal Sludges as Revealed by Polyphosphate Kinase Genes. <i>Applied and Environmental Microbiology</i> , 2007, 73, 5865-5874.	3.1	256
13	Genome-wide selective sweeps and gene-specific sweeps in natural bacterial populations. <i>ISME Journal</i> , 2016, 10, 1589-1601.	9.8	226
14	Synchrony in aquatic microbial community dynamics. <i>ISME Journal</i> , 2007, 1, 38-47.	9.8	225
15	Giant virus diversity and host interactions through global metagenomics. <i>Nature</i> , 2020, 578, 432-436.	27.8	207
16	Keystone taxa predict compositional change in microbial communities. <i>Environmental Microbiology</i> , 2018, 20, 2207-2217.	3.8	201
17	Lake microbial communities are resilient after a whole-ecosystem disturbance. <i>ISME Journal</i> , 2012, 6, 2153-2167.	9.8	198
18	Phylogenetic Ecology of the Freshwater <i>Actinobacteria</i> Lineage. <i>Applied and Environmental Microbiology</i> , 2007, 73, 7169-7176.	3.1	195

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19	Cohesion: a method for quantifying the connectivity of microbial communities. <i>ISME Journal</i> , 2017, 11, 2426-2438.	9.8	190
20	Denitrification capabilities of two biological phosphorus removal sludges dominated by different <i>Candidatus</i> <i>Accumulibacter</i> ™ clades. <i>Environmental Microbiology Reports</i> , 2009, 1, 583-588.	2.4	189
21	Metagenomics of the Water Column in the Pristine Upper Course of the Amazon River. <i>PLoS ONE</i> , 2011, 6, e23785.	2.5	183
22	IMG/VR: a database of cultured and uncultured DNA Viruses and retroviruses. <i>Nucleic Acids Research</i> , 2016, 45, D457-D465.	14.5	177
23	Interannual dynamics and phenology of bacterial communities in a eutrophic lake. <i>Limnology and Oceanography</i> , 2007, 52, 487-494.	3.1	167
24	Microbial population dynamics during start-up and overload conditions of anaerobic digesters treating municipal solid waste and sewage sludge. <i>Biotechnology and Bioengineering</i> , 2004, 87, 823-834.	3.3	160
25	A decade of seasonal dynamics and co-occurrences within freshwater bacterioplankton communities from eutrophic Lake Mendota, WI, USA. <i>ISME Journal</i> , 2013, 7, 680-684.	9.8	156
26	Microbial community dynamics in a humic lake: differential persistence of common freshwater phylotypes. <i>Environmental Microbiology</i> , 2006, 8, 956-970.	3.8	141
27	Comparative single-cell genomics reveals potential ecological niches for the freshwater actinobacteria lineage. <i>ISME Journal</i> , 2014, 8, 2503-2516.	9.8	137
28	A bacterial metapopulation adapts locally to phage predation despite global dispersal. <i>Genome Research</i> , 2008, 18, 293-297.	5.5	135
29	Understanding Regional Change: A Comparison of Two Lake Districts. <i>BioScience</i> , 2007, 57, 323-335.	4.9	129
30	Resistance, resilience and recovery: aquatic bacterial dynamics after water column disturbance. <i>Environmental Microbiology</i> , 2011, 13, 2752-2767.	3.8	127
31	The Role of Nitrogen Fixation in Cyanobacterial Bloom Toxicity in a Temperate, Eutrophic Lake. <i>PLoS ONE</i> , 2013, 8, e56103.	2.5	127
32	Evidence for structuring of bacterial community composition by organic carbon source in temperate lakes. <i>Environmental Microbiology</i> , 2009, 11, 2463-2472.	3.8	123
33	Polyphosphate Kinase from Activated Sludge Performing Enhanced Biological Phosphorus Removal. <i>Applied and Environmental Microbiology</i> , 2002, 68, 4971-4978.	3.1	121
34	The influence of habitat heterogeneity on freshwater bacterial community composition and dynamics. <i>Environmental Microbiology</i> , 2008, 10, 1057-1067.	3.8	120
35	Genome-Enabled Insights into the Ecophysiology of the Comammox Bacterium <i>Candidatus</i> <i>Nitrospira nitrosa</i> . <i>MSystems</i> , 2017, 2, .	3.8	119
36	Occurrence of Tetracycline Resistance Genes in Aquaculture Facilities with Varying Use of Oxytetracycline. <i>Microbial Ecology</i> , 2010, 59, 799-807.	2.8	114

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37	Microbial diversity and dynamics during methane production from municipal solid waste. <i>Waste Management</i> , 2013, 33, 1982-1992.	7.4	110
38	Ecogenomics of virophages and their giant virus hosts assessed through time series metagenomics. <i>Nature Communications</i> , 2017, 8, 858.	12.8	107
39	Microbiology of <i>Candidatus</i> <i>Accumulibacter</i> ™ in activated sludge. <i>Microbial Biotechnology</i> , 2011, 4, 603-619.	4.2	104
40	Environmental distribution and population biology of <i>Candidatus</i> <i>Accumulibacter</i> , a primary agent of biological phosphorus removal. <i>Environmental Microbiology</i> , 2008, 10, 2692-2703.	3.8	102
41	Comparative genomics of two <i>Candidatus</i> <i>Accumulibacter</i> ™ clades performing biological phosphorus removal. <i>ISME Journal</i> , 2013, 7, 2301-2314.	9.8	101
42	Development of a solar-powered microbial fuel cell. <i>Journal of Applied Microbiology</i> , 2008, 104, 640-650.	3.1	100
43	Metatranscriptomic insights on gene expression and regulatory controls in <i>Candidatus</i> <i>Accumulibacter phosphatis</i> . <i>ISME Journal</i> , 2016, 10, 810-822.	9.8	98
44	Whole-Community Metagenomics in Two Different Anammox Configurations: Process Performance and Community Structure. <i>Environmental Science &amp; Technology</i> , 2017, 51, 4317-4327.	10.0	98
45	Auxotrophy and intrapopulation complementarity in the <i>interactome</i> ™ of a cultivated freshwater model community. <i>Molecular Ecology</i> , 2015, 24, 4449-4459.	3.9	97
46	Metabolic potential of a single cell belonging to one of the most abundant lineages in freshwater bacterioplankton. <i>ISME Journal</i> , 2013, 7, 137-147.	9.8	94
47	<i>Candidatus</i> <i>Accumulibacter phosphatis</i> clades enriched under cyclic anaerobic and microaerobic conditions simultaneously use different electron acceptors. <i>Water Research</i> , 2016, 102, 125-137.	11.3	94
48	Seasonal differences in bacterial community composition following nutrient additions in a eutrophic lake. <i>Environmental Microbiology</i> , 2011, 13, 887-899.	3.8	87
49	Ecophysiology of Freshwater Verrucomicrobia Inferred from Metagenome-Assembled Genomes. <i>MSphere</i> , 2017, 2, .	2.9	87
50	Bridging the gap between micro - and macro-scale perspectives on the role of microbial communities in global change ecology. <i>Plant and Soil</i> , 2006, 289, 59-70.	3.7	86
51	Microbial Contributions to Phosphorus Cycling in Eutrophic Lakes and Wastewater. <i>Annual Review of Microbiology</i> , 2013, 67, 199-219.	7.3	86
52	Progress Toward Understanding the Distribution of <i>Accumulibacter</i> Among Full-Scale Enhanced Biological Phosphorus Removal Systems. <i>Microbial Ecology</i> , 2008, 55, 229-236.	2.8	85
53	Metagenomes of Mediterranean Coastal Lagoons. <i>Scientific Reports</i> , 2012, 2, 490.	3.3	85
54	Bacterial Community Composition and Dynamics Spanning Five Years in Freshwater Bog Lakes. <i>MSphere</i> , 2017, 2, .	2.9	84

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55	Speciesâ€orting may explain an apparent minimal effect of immigration on freshwater bacterial community dynamics. <i>Environmental Microbiology</i> , 2009, 11, 905-913.	3.8	82
56	Linking metagenomics to aquatic microbial ecology and biogeochemical cycles. <i>Limnology and Oceanography</i> , 2020, 65, S2.	3.1	82
57	Productivity and salinity structuring of the microplankton revealed by comparative freshwater metagenomics. <i>Environmental Microbiology</i> , 2014, 16, 2682-2698.	3.8	80
58	Polyphosphate kinase genes from full-scale activated sludge plants. <i>Applied Microbiology and Biotechnology</i> , 2007, 77, 167-173.	3.6	78
59	Contrasting patterns of genome-level diversity across distinct co-occurring bacterial populations. <i>ISME Journal</i> , 2018, 12, 742-755.	9.8	76
60	Spatial and temporal scales of aquatic bacterial beta diversity. <i>Frontiers in Microbiology</i> , 2012, 3, 318.	3.5	74
61	Typhoons initiate predictable change in aquatic bacterial communities. <i>Limnology and Oceanography</i> , 2008, 53, 1319-1326.	3.1	73
62	Metatranscriptomic array analysis of <i>Candidatus</i> <i>Accumulibacter phosphatis</i> â€enriched enhanced biological phosphorus removal sludge. <i>Environmental Microbiology</i> , 2010, 12, 1205-1217.	3.8	73
63	Phosphorus speciation in a eutrophic lake by 31P NMR spectroscopy. <i>Water Research</i> , 2014, 62, 229-240.	11.3	73
64	Depth-discrete metagenomics reveals the roles of microbes in biogeochemical cycling in the tropical freshwater Lake Tanganyika. <i>ISME Journal</i> , 2021, 15, 1971-1986.	9.8	69
65	Meteorological drivers of hypolimnetic anoxia in a eutrophic, north temperate lake. <i>Ecological Modelling</i> , 2017, 343, 39-53.	2.5	68
66	<i>Candidatus</i> <i>Accumulibacter</i> â€ gene expression in response to dynamic EBPR conditions. <i>ISME Journal</i> , 2011, 5, 329-340.	9.8	67
67	Breaking a paradigm: cosmopolitan and abundant freshwater actinobacteria are low GC. <i>Environmental Microbiology Reports</i> , 2012, 4, 29-35.	2.4	66
68	Tuning fresh: radiation through rewiring of central metabolism in streamlined bacteria. <i>ISME Journal</i> , 2016, 10, 1902-1914.	9.8	66
69	Large freshwater phages with the potential to augment aerobic methane oxidation. <i>Nature Microbiology</i> , 2020, 5, 1504-1515.	13.3	66
70	Seasonal bacterial community dynamics in a full-scale enhanced biological phosphorus removal plant. <i>Water Research</i> , 2013, 47, 7019-7031.	11.3	65
71	Freshwater carbon and nutrient cycles revealed through reconstructed population genomes. <i>PeerJ</i> , 2018, 6, e6075.	2.0	64
72	Autotrophic and mixotrophic metabolism of an anammox bacterium revealed by in vivo 13C and 2H metabolic network mapping. <i>ISME Journal</i> , 2021, 15, 673-687.	9.8	64

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73	Persistence of Pathogenic Prion Protein during Simulated Wastewater Treatment Processes. <i>Environmental Science &amp; Technology</i> , 2008, 42, 5254-5259.	10.0	61
74	TaxAss: Leveraging a Custom Freshwater Database Achieves Fine-Scale Taxonomic Resolution. <i>MSphere</i> , 2018, 3, .	2.9	60
75	Phage Encoded H-NS: A Potential Achilles Heel in the Bacterial Defence System. <i>PLoS ONE</i> , 2011, 6, e20095.	2.5	59
76	Integrating ecology into biotechnology. <i>Current Opinion in Biotechnology</i> , 2007, 18, 287-292.	6.6	57
77	Comparison of Primer Sets for Use in Automated Ribosomal Intergenic Spacer Analysis of Aquatic Bacterial Communities: an Ecological Perspective. <i>Applied and Environmental Microbiology</i> , 2007, 73, 659-662.	3.1	56
78	Expanded Phylogenetic Diversity and Metabolic Flexibility of Mercury-Methylating Microorganisms. <i>MSystems</i> , 2020, 5, .	3.8	56
79	Time-scale dependence in numerical simulations: Assessment of physical, chemical, and biological predictions in a stratified lake at temporal scales of hours to months. <i>Environmental Modelling and Software</i> , 2012, 35, 104-121.	4.5	55
80	Diversity, evolution, and classification of virophages uncovered through global metagenomics. <i>Microbiome</i> , 2019, 7, 157.	11.1	53
81	Mercury Methylation Genes Identified across Diverse Anaerobic Microbial Guilds in a Eutrophic Sulfate-Enriched Lake. <i>Environmental Science &amp; Technology</i> , 2020, 54, 15840-15851.	10.0	50
82	Microcystin mcyA and mcyE Gene Abundances Are Not Appropriate Indicators of Microcystin Concentrations in Lakes. <i>PLoS ONE</i> , 2015, 10, e0125353.	2.5	47
83	Experimental manipulations of microbial food web interactions in a humic lake: shifting biological drivers of bacterial community structure. <i>Environmental Microbiology</i> , 2006, 8, 1448-1459.	3.8	44
84	Differential bacterial dynamics promote emergent community robustness to lake mixing: an epilimnion to hypolimnion transplant experiment. <i>Environmental Microbiology</i> , 2010, 12, 455-466.	3.8	44
85	Integrated Omic Analyses Provide Evidence that a <i>Candidatus</i> <i>Accumulibacter phosphatis</i> Strain Performs Denitrification under Microaerobic Conditions. <i>MSystems</i> , 2019, 4, .	3.8	44
86	Ancestral genome reconstruction identifies the evolutionary basis for trait acquisition in polyphosphate accumulating bacteria. <i>ISME Journal</i> , 2016, 10, 2931-2945.	9.8	43
87	Potential for atmospheric deposition of bacteria to influence bacterioplankton communities. <i>FEMS Microbiology Ecology</i> , 2008, 64, 388-394.	2.7	40
88	Gut microbiomes of mobile predators vary with landscape context and species identity. <i>Ecology and Evolution</i> , 2017, 7, 8545-8557.	1.9	39
89	Engineering photosynthetic production of L-lysine. <i>Metabolic Engineering</i> , 2017, 44, 273-283.	7.0	36
90	Successful enrichment of the ubiquitous freshwater <i>Actinobacteria</i> . <i>Environmental Microbiology Reports</i> , 2014, 6, 21-27.	2.4	35

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91	Bacterial Community and <i>Candidatus</i> Accumulibacter Population Dynamics in Laboratory-Scale Enhanced Biological Phosphorus Removal Reactors. <i>Applied and Environmental Microbiology</i> , 2010, 76, 5479-5487.	3.1	34
92	Spatiotemporal Molecular Analysis of Cyanobacteria Blooms Reveals Microcystis-Aphanizomenon Interactions. <i>PLoS ONE</i> , 2013, 8, e74933.	2.5	33
93	Can the black box be cracked? The augmentation of microbial ecology by high-resolution, automated sensing technologies. <i>ISME Journal</i> , 2009, 3, 881-888.	9.8	32
94	Uranyl precipitation by biomass from an enhanced biological phosphorus removal reactor. <i>Biodegradation</i> , 2001, 12, 401-410.	3.0	31
95	Seasonal and Episodic Lake Mixing Stimulate Differential Planktonic Bacterial Dynamics. <i>Microbial Ecology</i> , 2010, 59, 546-554.	2.8	31
96	Bacterial production of free fatty acids from freshwater macroalgal cellulose. <i>Applied Microbiology and Biotechnology</i> , 2011, 91, 435-446.	3.6	31
97	Long-term monitoring reveals carbon and nitrogen metabolism key to microcystin production in eutrophic lakes. <i>Frontiers in Microbiology</i> , 2015, 6, 456.	3.5	28
98	Community Assembly and Ecology of Activated Sludge under Photosynthetic Feast-Famine Conditions. <i>Environmental Science &amp; Technology</i> , 2017, 51, 3165-3175.	10.0	28
99	Genetic diversity of cyanobacteria in four eutrophic lakes. <i>FEMS Microbiology Ecology</i> , 2011, 78, 336-348.	2.7	27
100	Prospects for multi-omics in the microbial ecology of water engineering. <i>Water Research</i> , 2021, 205, 117608.	11.3	26
101	Extracellular Electron Transfer May Be an Overlooked Contribution to Pelagic Respiration in Humic-Rich Freshwater Lakes. <i>MSphere</i> , 2019, 4, .	2.9	25
102	Ananke: temporal clustering reveals ecological dynamics of microbial communities. <i>PeerJ</i> , 2017, 5, e3812.	2.0	25
103	Influence of typhoons on annual CO <sub>2</sub> flux from a subtropical, humic lake. <i>Global Change Biology</i> , 2009, 15, 243-254.	9.5	23
104	Reevaluation of the Phylogenetic Diversity and Global Distribution of the Genus <i>Candidatus</i> Accumulibacter. <i>MSystems</i> , 2022, 7, e0001622.	3.8	22
105	Metabolic Network Analysis and Metatranscriptomics Reveal Auxotrophies and Nutrient Sources of the Cosmopolitan Freshwater Microbial Lineage <i>acI</i> . <i>MSystems</i> , 2017, 2, .	3.8	21
106	Lineage-Specific Responses of Microbial Communities to Environmental Change. <i>Applied and Environmental Microbiology</i> , 2013, 79, 39-47.	3.1	20
107	Model Communities Hint at Promiscuous Metabolic Linkages between Ubiquitous Free-Living Freshwater Bacteria. <i>MSphere</i> , 2018, 3, .	2.9	20
108	Time-series metatranscriptomes reveal conserved patterns between phototrophic and heterotrophic microbes in diverse freshwater systems. <i>Limnology and Oceanography</i> , 2020, 65, S101.	3.1	18

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109	A Comparison of the Use of In Vitro-Transcribed and Native rRNA for the Quantification of Microorganisms in the Environment. <i>Microbial Ecology</i> , 1998, 36, 362-371.	2.8	17
110	Contrasting factors drive within-lake bacterial community composition and functional traits in a large shallow subtropical lake. <i>Hydrobiologia</i> , 2016, 778, 105-120.	2.0	17
111	Host population diversity as a driver of viral infection cycle in wild populations of green sulfur bacteria with long standing virus-host interactions. <i>ISME Journal</i> , 2021, 15, 1569-1584.	9.8	16
112	act Actinobacteria Assemble a Functional Actinorhodopsin with Natively Synthesized Retinal. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	15
113	Metabolic Differentiation of Co-occurring <i>Accumulibacter</i> Clades Revealed through Genome-Resolved Metatranscriptomics. <i>MSystems</i> , 2021, 6, e0047421.	3.8	15
114	Prions: Novel Pathogens of Environmental Concern?. <i>Journal of Environmental Engineering, ASCE</i> , 2006, 132, 967-969.	1.4	14
115	Metagenomics 2.0™. <i>Environmental Microbiology Reports</i> , 2015, 7, 38-39.	2.4	14
116	Recognizing cross-ecosystem responses to changing temperatures: soil warming impacts pelagic food webs. <i>Oikos</i> , 2015, 124, 1473-1481.	2.7	13
117	Environmental Disturbances Decrease the Variability of Microbial Populations within Periphyton. <i>MSystems</i> , 2016, 1, .	3.8	13
118	Inhibition of Cyanobacterial Growth on a Municipal Wastewater Sidestream Is Impacted by Temperature. <i>MSphere</i> , 2018, 3, .	2.9	13
119	Wide Distribution of Phage That Infect Freshwater SAR11 Bacteria. <i>MSystems</i> , 2019, 4, .	3.8	11
120	Diazotroph Genomes and Their Seasonal Dynamics in a Stratified Humic Bog Lake. <i>Frontiers in Microbiology</i> , 2020, 11, 1500.	3.5	10
121	Genome-Resolved Metagenomics of a Photosynthetic Bioreactor Performing Biological Nutrient Removal. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	9
122	Freshwater <i>Chlorobia</i> Exhibit Metabolic Specialization among Cosmopolitan and Endemic Populations. <i>MSystems</i> , 2021, 6, .	3.8	8
123	Investigating the Chemolithoautotrophic and Formate Metabolism of <i>Nitrospira moscoviensis</i> by Constraint-Based Metabolic Modeling and <sup>13</sup> C-Tracer Analysis. <i>MSystems</i> , 2021, 6, e0017321.	3.8	8
124	Spatial and Temporal Variability of Dissolved Organic Matter Molecular Composition in a Stratified Eutrophic Lake. <i>Journal of Geophysical Research G: Biogeosciences</i> , 2022, 127, .	3.0	8
125	Defining Linkages between the GSC and NSF's LTER Program: How the Ecological Metadata Language (EML) Relates to GCDML and Other Outcomes. <i>OMICS A Journal of Integrative Biology</i> , 2008, 12, 151-156.	2.0	6
126	Ecological Differentiation of <i>Accumulibacter</i> in EBPR Reactors. <i>Proceedings of the Water Environment Federation</i> , 2008, 2008, 31-42.	0.0	5



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127	Molecular Methods in Biological Systems. <i>Water Environment Research</i> , 2009, 81, 986-1002.	2.7	5
128	The environment drives microbial trait variability in aquatic habitats. <i>Molecular Ecology</i> , 2020, 29, 4605-4617.	3.9	5
129	Pilot-scale comparison of biological nutrient removal (BNR) using intermittent and continuous ammonia-based low dissolved oxygen aeration control systems. <i>Water Science and Technology</i> , 2022, 85, 578-590.	2.5	5
130	Phosphorus Removal and PAOs Populations at a Full-Scale Integrated Fixed-Film Activated Sludge (IFAS) Plant. <i>Proceedings of the Water Environment Federation</i> , 2008, 2008, 1-17.	0.0	3
131	Effect of Sludge Residence Time on Phosphorus Removal Activities and Populations in Enhanced Biological Phosphorus Removal (EBPR) Systems. <i>Proceedings of the Water Environment Federation</i> , 2013, 2013, 121-132.	0.0	3
132	Turnover is replaced by nestedness with increasing geographical distance in bacterial communities of coastal shallow lakes. <i>Marine and Freshwater Research</i> , 2020, 71, 1086.	1.3	3
133	Tetracycline Resistance Genes in Activated Sludge Wastewater Treatment Plants. <i>Proceedings of the Water Environment Federation</i> , 2006, 2006, 1478-1493.	0.0	2
134	Molecular Methods in Biological Systems. <i>Water Environment Research</i> , 2007, 79, 1109-1151.	2.7	2
135	De novo synthesis and functional analysis of the phosphatase-encoding gene <i>acI-B</i> of uncultured Actinobacteria from Lake Stechlin (NE Germany). <i>International Microbiology</i> , 2015, 18, 39-47.	2.4	2
136	Genetic Blueprints for Enhanced Biological Phosphorus Removal (EBPR) Based on Environmental Shotgun Sequencing. <i>Proceedings of the Water Environment Federation</i> , 2006, 2006, 82-85.	0.0	1
137	Molecular Methods in Biological Systems. <i>Water Environment Research</i> , 2008, 80, 929-961.	2.7	1
138	Ecogenomics Reveals Distributed Metabolic Networks In Suspended And Attached Growth Anammox Bioreactors. <i>Proceedings of the Water Environment Federation</i> , 2015, 2015, 3194-3198.	0.0	1
139	POLYPHOSPHATE KINASE GENES FROM ACTIVATED SLUDGE CARRYING OUT ENHANCED BIOLOGICAL PHOSPHORUS REMOVAL. <i>Proceedings of the Water Environment Federation</i> , 2001, 2001, 20-33.	0.0	0
140	GENETIC AND BIOCHEMICAL MARKERS FOR ENHANCED BIOLOGICAL PHOSPHORUS REMOVAL. <i>Proceedings of the Water Environment Federation</i> , 2003, 2003, 529-549.	0.0	0
141	Molecular Methods in Biological Systems. <i>Water Environment Research</i> , 2005, 77, 718-779.	2.7	0
142	Molecular Methods in Biological Systems. <i>Water Environment Research</i> , 2006, 78, 1084-1118.	2.7	0
143	AQUACULTURE FACILITIES AS A POTENTIAL SOURCE OF ANTIBIOTIC RESISTANCE TO THE AQUATIC ENVIRONMENT. <i>Proceedings of the Water Environment Federation</i> , 2007, 2007, 3132-3143.	0.0	0
144	METAGENOMIC ARRAY ANALYSIS OF AN ENHANCED BIOLOGICAL PHOSPHORUS REMOVAL SLUDGE ENRICHED WITH ACCUMULIBACTER. <i>Proceedings of the Water Environment Federation</i> , 2007, 2007, 4979-4982.	0.0	0

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145	PHOSPHORUS ACCUMULATING ORGANISMS REVEAL THEIR SECRETS: A GENOME LEVEL UNDERSTANDING OF ENHANCED BIOLOGICAL PHOSPHORUS REMOVAL. Proceedings of the Water Environment Federation, 2007, 2007, 4920-4932.	0.0	0
146	BIOCHEMICAL PATHWAYS IN BIOLOGICAL PHOSPHORUS REMOVAL ASSESSED USING PROTEOMICS. Proceedings of the Water Environment Federation, 2007, 2007, 4933-4943.	0.0	0
147	Stream Monitoring using Antibiotic Resistance Detection and Microbial Fingerprinting Methods as Indicators of Anthropogenic Contamination. Proceedings of the Water Environment Federation, 2009, 2009, 5056-5067.	0.0	0
148	Bacterial Community Composition Dynamics in a Full-Scale Activated Sludge. Proceedings of the Water Environment Federation, 2009, 2009, 4065-4071.	0.0	0
149	mSphere of Influence: the View from the Microbiologists of the Future. MSphere, 2019, 4, .	2.9	0