

Katherine D McMahon

List of Publications by Year in descending order

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149
papers

15,219
citations

18436

62
h-index

21474

114
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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.	9.4	1,512
2	A Guide to the Natural History of Freshwater Lake Bacteria. <i>Microbiology and Molecular Biology Reviews</i> , 2011, 75, 14-49.	2.9	1,356
3	Metagenomic analysis of two enhanced biological phosphorus removal (EBPR) sludge communities. <i>Nature Biotechnology</i> , 2006, 24, 1263-1269.	9.4	634
4	Metabolic network analysis reveals microbial community interactions in anammox granules. <i>Nature Communications</i> , 2017, 8, 15416.	5.8	489
5	Tetracycline resistance genes in activated sludge wastewater treatment plants. <i>Water Research</i> , 2007, 41, 1143-1151.	5.3	478
6	A genomic catalog of Earth's microbiomes. <i>Nature Biotechnology</i> , 2021, 39, 499-509.	9.4	457
7	Common principles and best practices for engineering microbiomes. <i>Nature Reviews Microbiology</i> , 2019, 17, 725-741.	13.6	324
8	Methanogenic population dynamics during start-up of anaerobic digesters treating municipal solid waste and biosolids. , 1998, 57, 342-355.		302
9	Anaerobic codigestion of municipal solid waste and biosolids under various mixing conditionsâ€”I. digester performance. <i>Water Research</i> , 2001, 35, 1804-1816.	5.3	299
10	New Abundant Microbial Groups in Aquatic Hypersaline Environments. <i>Scientific Reports</i> , 2011, 1, 135.	1.6	288
11	Anaerobic codigestion of municipal solid waste and biosolids under various mixing conditionsâ€”II: microbial population dynamics. <i>Water Research</i> , 2001, 35, 1817-1827.	5.3	268
12	â€œ <i>Candidatus</i> Accumulibacterâ€•Population Structure in Enhanced Biological Phosphorus Removal Sludges as Revealed by Polyphosphate Kinase Genes. <i>Applied and Environmental Microbiology</i> , 2007, 73, 5865-5874.	1.4	256
13	Genome-wide selective sweeps and gene-specific sweeps in natural bacterial populations. <i>ISME Journal</i> , 2016, 10, 1589-1601.	4.4	226
14	Synchrony in aquatic microbial community dynamics. <i>ISME Journal</i> , 2007, 1, 38-47.	4.4	225
15	Giant virus diversity and host interactions through global metagenomics. <i>Nature</i> , 2020, 578, 432-436.	13.7	207
16	Keystone taxa predict compositional change in microbial communities. <i>Environmental Microbiology</i> , 2018, 20, 2207-2217.	1.8	201
17	Lake microbial communities are resilient after a whole-ecosystem disturbance. <i>ISME Journal</i> , 2012, 6, 2153-2167.	4.4	198
18	Phylogenetic Ecology of the Freshwater <i>Actinobacteria</i> Lineage. <i>Applied and Environmental Microbiology</i> , 2007, 73, 7169-7176.	1.4	195

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19	Cohesion: a method for quantifying the connectivity of microbial communities. <i>ISME Journal</i> , 2017, 11, 2426-2438.	4.4	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.	1.0	189
21	Metagenomics of the Water Column in the Pristine Upper Course of the Amazon River. <i>PLoS ONE</i> , 2011, 6, e23785.	1.1	183
22	IMG/VR: a database of cultured and uncultured DNA Viruses and retroviruses. <i>Nucleic Acids Research</i> , 2016, 45, D457-D465.	6.5	177
23	Interannual dynamics and phenology of bacterial communities in a eutrophic lake. <i>Limnology and Oceanography</i> , 2007, 52, 487-494.	1.6	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.	1.7	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.	4.4	156
26	Microbial community dynamics in a humic lake: differential persistence of common freshwater phylotypes. <i>Environmental Microbiology</i> , 2006, 8, 956-970.	1.8	141
27	Comparative single-cell genomics reveals potential ecological niches for the freshwater actinobacteria lineage. <i>ISME Journal</i> , 2014, 8, 2503-2516.	4.4	137
28	A bacterial metapopulation adapts locally to phage predation despite global dispersal. <i>Genome Research</i> , 2008, 18, 293-297.	2.4	135
29	Understanding Regional Change: A Comparison of Two Lake Districts. <i>BioScience</i> , 2007, 57, 323-335.	2.2	129
30	Resistance, resilience and recovery: aquatic bacterial dynamics after water column disturbance. <i>Environmental Microbiology</i> , 2011, 13, 2752-2767.	1.8	127
31	The Role of Nitrogen Fixation in Cyanobacterial Bloom Toxicity in a Temperate, Eutrophic Lake. <i>PLoS ONE</i> , 2013, 8, e56103.	1.1	127
32	Evidence for structuring of bacterial community composition by organic carbon source in temperate lakes. <i>Environmental Microbiology</i> , 2009, 11, 2463-2472.	1.8	123
33	Polyphosphate Kinase from Activated Sludge Performing Enhanced Biological Phosphorus Removal. <i>Applied and Environmental Microbiology</i> , 2002, 68, 4971-4978.	1.4	121
34	The influence of habitat heterogeneity on freshwater bacterial community composition and dynamics. <i>Environmental Microbiology</i> , 2008, 10, 1057-1067.	1.8	120
35	Genome-Enabled Insights into the Ecophysiology of the Comammox Bacterium <i>Candidatus</i> <i>Nitrospira nitrosa</i> . <i>MSystems</i> , 2017, 2, .	1.7	119
36	Occurrence of Tetracycline Resistance Genes in Aquaculture Facilities with Varying Use of Oxytetracycline. <i>Microbial Ecology</i> , 2010, 59, 799-807.	1.4	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.	3.7	110
38	Ecogenomics of virophages and their giant virus hosts assessed through time series metagenomics. <i>Nature Communications</i> , 2017, 8, 858.	5.8	107
39	Microbiology of <i>Candidatus</i> Accumulibacter TM in activated sludge. <i>Microbial Biotechnology</i> , 2011, 4, 603-619.	2.0	104
40	Environmental distribution and population biology of <i>Candidatus</i> Accumulibacter, a primary agent of biological phosphorus removal. <i>Environmental Microbiology</i> , 2008, 10, 2692-2703.	1.8	102
41	Comparative genomics of two <i>Candidatus</i> Accumulibacter TM clades performing biological phosphorus removal. <i>ISME Journal</i> , 2013, 7, 2301-2314.	4.4	101
42	Development of a solar-powered microbial fuel cell. <i>Journal of Applied Microbiology</i> , 2008, 104, 640-650.	1.4	100
43	Metatranscriptomic insights on gene expression and regulatory controls in <i>Candidatus</i> Accumulibacter phosphatis. <i>ISME Journal</i> , 2016, 10, 810-822.	4.4	98
44	Whole-Community Metagenomics in Two Different Anammox Configurations: Process Performance and Community Structure. <i>Environmental Science & Technology</i> , 2017, 51, 4317-4327.	4.6	98
45	Auxotrophy and intrapopulation complementarity in the interactome TM of a cultivated freshwater model community. <i>Molecular Ecology</i> , 2015, 24, 4449-4459.	2.0	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.	4.4	94
47	<i>Candidatus</i> Accumulibacter phosphatis clades enriched under cyclic anaerobic and microaerobic conditions simultaneously use different electron acceptors. <i>Water Research</i> , 2016, 102, 125-137.	5.3	94
48	Seasonal differences in bacterial community composition following nutrient additions in a eutrophic lake. <i>Environmental Microbiology</i> , 2011, 13, 887-899.	1.8	87
49	Ecophysiology of Freshwater Verrucomicrobia Inferred from Metagenome-Assembled Genomes. <i>MSphere</i> , 2017, 2, .	1.3	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.	1.8	86
51	Microbial Contributions to Phosphorus Cycling in Eutrophic Lakes and Wastewater. <i>Annual Review of Microbiology</i> , 2013, 67, 199-219.	2.9	86
52	Progress Toward Understanding the Distribution of Accumulibacter Among Full-Scale Enhanced Biological Phosphorus Removal Systems. <i>Microbial Ecology</i> , 2008, 55, 229-236.	1.4	85
53	Metagenomes of Mediterranean Coastal Lagoons. <i>Scientific Reports</i> , 2012, 2, 490.	1.6	85
54	Bacterial Community Composition and Dynamics Spanning Five Years in Freshwater Bog Lakes. <i>MSphere</i> , 2017, 2, .	1.3	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.	1.8	82
56	Linking metagenomics to aquatic microbial ecology and biogeochemical cycles. <i>Limnology and Oceanography</i> , 2020, 65, S2.	1.6	82
57	Productivity and salinity structuring of the microplankton revealed by comparative freshwater metagenomics. <i>Environmental Microbiology</i> , 2014, 16, 2682-2698.	1.8	80
58	Polyphosphate kinase genes from full-scale activated sludge plants. <i>Applied Microbiology and Biotechnology</i> , 2007, 77, 167-173.	1.7	78
59	Contrasting patterns of genome-level diversity across distinct co-occurring bacterial populations. <i>ISME Journal</i> , 2018, 12, 742-755.	4.4	76
60	Spatial and temporal scales of aquatic bacterial beta diversity. <i>Frontiers in Microbiology</i> , 2012, 3, 318.	1.5	74
61	Typhoons initiate predictable change in aquatic bacterial communities. <i>Limnology and Oceanography</i> , 2008, 53, 1319-1326.	1.6	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.	1.8	73
63	Phosphorus speciation in a eutrophic lake by 31P NMR spectroscopy. <i>Water Research</i> , 2014, 62, 229-240.	5.3	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.	4.4	69
65	Meteorological drivers of hypolimnetic anoxia in a eutrophic, north temperate lake. <i>Ecological Modelling</i> , 2017, 343, 39-53.	1.2	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.	4.4	67
67	Breaking a paradigm: cosmopolitan and abundant freshwater actinobacteria are low GC. <i>Environmental Microbiology Reports</i> , 2012, 4, 29-35.	1.0	66
68	Tuning fresh: radiation through rewiring of central metabolism in streamlined bacteria. <i>ISME Journal</i> , 2016, 10, 1902-1914.	4.4	66
69	Large freshwater phages with the potential to augment aerobic methane oxidation. <i>Nature Microbiology</i> , 2020, 5, 1504-1515.	5.9	66
70	Seasonal bacterial community dynamics in a full-scale enhanced biological phosphorus removal plant. <i>Water Research</i> , 2013, 47, 7019-7031.	5.3	65
71	Freshwater carbon and nutrient cycles revealed through reconstructed population genomes. <i>PeerJ</i> , 2018, 6, e6075.	0.9	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.	4.4	64

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73	Persistence of Pathogenic Prion Protein during Simulated Wastewater Treatment Processes. <i>Environmental Science & Technology</i> , 2008, 42, 5254-5259.	4.6	61
74	TaxAss: Leveraging a Custom Freshwater Database Achieves Fine-Scale Taxonomic Resolution. <i>MSphere</i> , 2018, 3, .	1.3	60
75	Phage Encoded H-NS: A Potential Achilles Heel in the Bacterial Defence System. <i>PLoS ONE</i> , 2011, 6, e20095.	1.1	59
76	Integrating ecology into biotechnology. <i>Current Opinion in Biotechnology</i> , 2007, 18, 287-292.	3.3	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.	1.4	56
78	Expanded Phylogenetic Diversity and Metabolic Flexibility of Mercury-Methylating Microorganisms. <i>MSystems</i> , 2020, 5, .	1.7	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.	1.9	55
80	Diversity, evolution, and classification of virophages uncovered through global metagenomics. <i>Microbiome</i> , 2019, 7, 157.	4.9	53
81	Mercury Methylation Genes Identified across Diverse Anaerobic Microbial Guilds in a Eutrophic Sulfate-Enriched Lake. <i>Environmental Science & Technology</i> , 2020, 54, 15840-15851.	4.6	50
82	Microcystin mcyA and mcyE Gene Abundances Are Not Appropriate Indicators of Microcystin Concentrations in Lakes. <i>PLoS ONE</i> , 2015, 10, e0125353.	1.1	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.	1.8	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.	1.8	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, .	1.7	44
86	Ancestral genome reconstruction identifies the evolutionary basis for trait acquisition in polyphosphate accumulating bacteria. <i>ISME Journal</i> , 2016, 10, 2931-2945.	4.4	43
87	Potential for atmospheric deposition of bacteria to influence bacterioplankton communities. <i>FEMS Microbiology Ecology</i> , 2008, 64, 388-394.	1.3	40
88	Gut microbiomes of mobile predators vary with landscape context and species identity. <i>Ecology and Evolution</i> , 2017, 7, 8545-8557.	0.8	39
89	Engineering photosynthetic production of L-lysine. <i>Metabolic Engineering</i> , 2017, 44, 273-283.	3.6	36
90	Successful enrichment of the ubiquitous freshwater cyanobacteria. <i>Environmental Microbiology Reports</i> , 2014, 6, 21-27.	1.0	35

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91	Bacterial Community and <i>Candidatus</i> Accumulibacter Population Dynamics in Laboratory-Scale Enhanced Biological Phosphorus Removal Reactors. Applied and Environmental Microbiology, 2010, 76, 5479-5487.	1.4	34
92	Spatiotemporal Molecular Analysis of Cyanobacteria Blooms Reveals Microcystis-Aphanizomenon Interactions. PLoS ONE, 2013, 8, e74933.	1.1	33
93	Can the black box be cracked? The augmentation of microbial ecology by high-resolution, automated sensing technologies. ISME Journal, 2009, 3, 881-888.	4.4	32
94	Uranyl precipitation by biomass from an enhanced biological phosphorus removal reactor. Biodegradation, 2001, 12, 401-410.	1.5	31
95	Seasonal and Episodic Lake Mixing Stimulate Differential Planktonic Bacterial Dynamics. Microbial Ecology, 2010, 59, 546-554.	1.4	31
96	Bacterial production of free fatty acids from freshwater macroalgal cellulose. Applied Microbiology and Biotechnology, 2011, 91, 435-446.	1.7	31
97	Long-term monitoring reveals carbon and nitrogen metabolism key to microcystin production in eutrophic lakes. Frontiers in Microbiology, 2015, 6, 456.	1.5	28
98	Community Assembly and Ecology of Activated Sludge under Photosynthetic Feast-Famine Conditions. Environmental Science & Technology, 2017, 51, 3165-3175.	4.6	28
99	Genetic diversity of cyanobacteria in four eutrophic lakes. FEMS Microbiology Ecology, 2011, 78, 336-348.	1.3	27
100	Prospects for multi-omics in the microbial ecology of water engineering. Water Research, 2021, 205, 117608.	5.3	26
101	Extracellular Electron Transfer May Be an Overlooked Contribution to Pelagic Respiration in Humic-Rich Freshwater Lakes. MSphere, 2019, 4, .	1.3	25
102	Ananke: temporal clustering reveals ecological dynamics of microbial communities. PeerJ, 2017, 5, e3812.	0.9	25
103	Influence of typhoons on annual CO ₂ flux from a subtropical, humic lake. Global Change Biology, 2009, 15, 243-254.	4.2	23
104	Reevaluation of the Phylogenetic Diversity and Global Distribution of the Genus <i>Candidatus</i> Accumulibacter. MSystems, 2022, 7, e0001622.	1.7	22
105	Metabolic Network Analysis and Metatranscriptomics Reveal Auxotrophies and Nutrient Sources of the Cosmopolitan Freshwater Microbial Lineage aql. MSystems, 2017, 2, .	1.7	21
106	Lineage-Specific Responses of Microbial Communities to Environmental Change. Applied and Environmental Microbiology, 2013, 79, 39-47.	1.4	20
107	Model Communities Hint at Promiscuous Metabolic Linkages between Ubiquitous Free-Living Freshwater Bacteria. MSphere, 2018, 3, .	1.3	20
108	Time-series metatranscriptomes reveal conserved patterns between phototrophic and heterotrophic microbes in diverse freshwater systems. Limnology and Oceanography, 2020, 65, S101.	1.6	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.	1.4	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.	1.0	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.	4.4	16
112	act Actinobacteria Assemble a Functional Actinorhodopsin with Natively Synthesized Retinal. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	15
113	Metabolic Differentiation of Co-occurring <i>Accumulibacter</i> Clades Revealed through Genome-Resolved Metatranscriptomics. <i>MSystems</i> , 2021, 6, e0047421.	1.7	15
114	Prions: Novel Pathogens of Environmental Concern?. <i>Journal of Environmental Engineering, ASCE</i> , 2006, 132, 967-969.	0.7	14
115	Metagenomics 2.0™. <i>Environmental Microbiology Reports</i> , 2015, 7, 38-39.	1.0	14
116	Recognizing cross-ecosystem responses to changing temperatures: soil warming impacts pelagic food webs. <i>Oikos</i> , 2015, 124, 1473-1481.	1.2	13
117	Environmental Disturbances Decrease the Variability of Microbial Populations within Periphyton. <i>MSystems</i> , 2016, 1, .	1.7	13
118	Inhibition of Cyanobacterial Growth on a Municipal Wastewater Sidestream Is Impacted by Temperature. <i>MSphere</i> , 2018, 3, .	1.3	13
119	Wide Distribution of Phage That Infect Freshwater SAR11 Bacteria. <i>MSystems</i> , 2019, 4, .	1.7	11
120	Diazotroph Genomes and Their Seasonal Dynamics in a Stratified Humic Bog Lake. <i>Frontiers in Microbiology</i> , 2020, 11, 1500.	1.5	10
121	Genome-Resolved Metagenomics of a Photosynthetic Bioreactor Performing Biological Nutrient Removal. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	9
122	Freshwater <i>Chlorobia</i> Exhibit Metabolic Specialization among Cosmopolitan and Endemic Populations. <i>MSystems</i> , 2021, 6, .	1.7	8
123	Investigating the Chemolithoautotrophic and Formate Metabolism of <i>Nitrospira moscoviensis</i> by Constraint-Based Metabolic Modeling and ¹³ C-Tracer Analysis. <i>MSystems</i> , 2021, 6, e0017321.	1.7	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, .	1.3	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.	1.0	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.	1.3	5
128	The environment drives microbial trait variability in aquatic habitats. <i>Molecular Ecology</i> , 2020, 29, 4605-4617.	2.0	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.	1.2	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.	0.7	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.	1.3	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.	1.1	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.	1.3	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.	1.3	0
142	Molecular Methods in Biological Systems. <i>Water Environment Research</i> , 2006, 78, 1084-1118.	1.3	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, .	1.3	0