

Katherine D McMahon

List of Publications by Year in descending order

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149
papers

15,219
citations

18436

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183
docs citations

183
times ranked

13888
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	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
3	Reevaluation of the Phylogenetic Diversity and Global Distribution of the Genus <i>Candidatus Accumulibacter</i> . <i>MSystems</i> , 2022, 7, e0001622.	1.7	22
4	A genomic catalog of Earth's microbiomes. <i>Nature Biotechnology</i> , 2021, 39, 499-509.	9.4	457
5	Autotrophic and mixotrophic metabolism of an anammox bacterium revealed by in vivo ¹³ C and ² H metabolic network mapping. <i>ISME Journal</i> , 2021, 15, 673-687.	4.4	64
6	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
7	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
8	Genome-Resolved Metagenomics of a Photosynthetic Bioreactor Performing Biological Nutrient Removal. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	9
9	Freshwater <i>Chlorobia</i> Exhibit Metabolic Specialization among Cosmopolitan and Endemic Populations. <i>MSystems</i> , 2021, 6, .	1.7	8
10	Metabolic Differentiation of Co-occurring <i>Accumulibacter</i> Clades Revealed through Genome-Resolved Metatranscriptomics. <i>MSystems</i> , 2021, 6, e0047421.	1.7	15
11	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
12	Prospects for multi-omics in the microbial ecology of water engineering. <i>Water Research</i> , 2021, 205, 117608.	5.3	26
13	Time-series metatranscriptomes reveal conserved patterns between phototrophic and heterotrophic microbes in diverse freshwater systems. <i>Limnology and Oceanography</i> , 2020, 65, S101.	1.6	18
14	Linking metagenomics to aquatic microbial ecology and biogeochemical cycles. <i>Limnology and Oceanography</i> , 2020, 65, S2.	1.6	82
15	The environment drives microbial trait variability in aquatic habitats. <i>Molecular Ecology</i> , 2020, 29, 4605-4617.	2.0	5
16	Diazotroph Genomes and Their Seasonal Dynamics in a Stratified Humic Bog Lake. <i>Frontiers in Microbiology</i> , 2020, 11, 1500.	1.5	10
17	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
18	Expanded Phylogenetic Diversity and Metabolic Flexibility of Mercury-Methylating Microorganisms. <i>MSystems</i> , 2020, 5, .	1.7	56

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19	Large freshwater phages with the potential to augment aerobic methane oxidation. <i>Nature Microbiology</i> , 2020, 5, 1504-1515.	5.9	66
20	Giant virus diversity and host interactions through global metagenomics. <i>Nature</i> , 2020, 578, 432-436.	13.7	207
21	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
22	Common principles and best practices for engineering microbiomes. <i>Nature Reviews Microbiology</i> , 2019, 17, 725-741.	13.6	324
23	Extracellular Electron Transfer May Be an Overlooked Contribution to Pelagic Respiration in Humic-Rich Freshwater Lakes. <i>MSphere</i> , 2019, 4, .	1.3	25
24	mSphere of Influence: the View from the Microbiologists of the Future. <i>MSphere</i> , 2019, 4, .	1.3	0
25	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
26	Wide Distribution of Phage That Infect Freshwater SAR11 Bacteria. <i>MSystems</i> , 2019, 4, .	1.7	11
27	Diversity, evolution, and classification of virophages uncovered through global metagenomics. <i>Microbiome</i> , 2019, 7, 157.	4.9	53
28	Keystone taxa predict compositional change in microbial communities. <i>Environmental Microbiology</i> , 2018, 20, 2207-2217.	1.8	201
29	Contrasting patterns of genome-level diversity across distinct co-occurring bacterial populations. <i>ISME Journal</i> , 2018, 12, 742-755.	4.4	76
30	Freshwater carbon and nutrient cycles revealed through reconstructed population genomes. <i>PeerJ</i> , 2018, 6, e6075.	0.9	64
31	Inhibition of Cyanobacterial Growth on a Municipal Wastewater Sidestream Is Impacted by Temperature. <i>MSphere</i> , 2018, 3, .	1.3	13
32	act Actinobacteria Assemble a Functional Actinorhodopsin with Natively Synthesized Retinal. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	15
33	TaxAss: Leveraging a Custom Freshwater Database Achieves Fine-Scale Taxonomic Resolution. <i>MSphere</i> , 2018, 3, .	1.3	60
34	Model Communities Hint at Promiscuous Metabolic Linkages between Ubiquitous Free-Living Freshwater Bacteria. <i>MSphere</i> , 2018, 3, .	1.3	20
35	Community Assembly and Ecology of Activated Sludge under Photosynthetic Feast-Famine Conditions. <i>Environmental Science & Technology</i> , 2017, 51, 3165-3175.	4.6	28
36	Metabolic network analysis reveals microbial community interactions in anammox granules. <i>Nature Communications</i> , 2017, 8, 15416.	5.8	489

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37	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
38	Engineering photosynthetic production of L-lysine. <i>Metabolic Engineering</i> , 2017, 44, 273-283.	3.6	36
39	Ecophysiology of Freshwater Verrucomicrobia Inferred from Metagenome-Assembled Genomes. <i>MSphere</i> , 2017, 2, .	1.3	87
40	Ecogenomics of virophages and their giant virus hosts assessed through time series metagenomics. <i>Nature Communications</i> , 2017, 8, 858.	5.8	107
41	Metabolic Network Analysis and Metatranscriptomics Reveal Auxotrophies and Nutrient Sources of the Cosmopolitan Freshwater Microbial Lineage acl. <i>MSystems</i> , 2017, 2, .	1.7	21
42	Genome-Enabled Insights into the Ecophysiology of the Comammox Bacterium <i>Candidatus</i> Nitrospira nitrosa. <i>MSystems</i> , 2017, 2, .	1.7	119
43	Cohesion: a method for quantifying the connectivity of microbial communities. <i>ISME Journal</i> , 2017, 11, 2426-2438.	4.4	190
44	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
45	Bacterial Community Composition and Dynamics Spanning Five Years in Freshwater Bog Lakes. <i>MSphere</i> , 2017, 2, .	1.3	84
46	Meteorological drivers of hypolimnetic anoxia in a eutrophic, north temperate lake. <i>Ecological Modelling</i> , 2017, 343, 39-53.	1.2	68
47	Gut microbiomes of mobile predators vary with landscape context and species identity. <i>Ecology and Evolution</i> , 2017, 7, 8545-8557.	0.8	39
48	Ananke: temporal clustering reveals ecological dynamics of microbial communities. <i>PeerJ</i> , 2017, 5, e3812.	0.9	25
49	Environmental Disturbances Decrease the Variability of Microbial Populations within Periphyton. <i>MSystems</i> , 2016, 1, .	1.7	13
50	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
51	<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
52	IMG/VR: a database of cultured and uncultured DNA Viruses and retroviruses. <i>Nucleic Acids Research</i> , 2016, 45, D457-D465.	6.5	177
53	Genome-wide selective sweeps and gene-specific sweeps in natural bacterial populations. <i>ISME Journal</i> , 2016, 10, 1589-1601.	4.4	226
54	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

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55	Tuning fresh: radiation through rewiring of central metabolism in streamlined bacteria. <i>ISME Journal</i> , 2016, 10, 1902-1914.	4.4	66
56	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
57	Auxotrophy and intrapopulation complementary in the interactome™ of a cultivated freshwater model community. <i>Molecular Ecology</i> , 2015, 24, 4449-4459.	2.0	97
58	Recognizing cross-ecosystem responses to changing temperatures: soil warming impacts pelagic food webs. <i>Oikos</i> , 2015, 124, 1473-1481.	1.2	13
59	Long-term monitoring reveals carbon- and nitrogen metabolism key to microcystin production in eutrophic lakes. <i>Frontiers in Microbiology</i> , 2015, 6, 456.	1.5	28
60	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
61	Metagenomics 2.0™. <i>Environmental Microbiology Reports</i> , 2015, 7, 38-39.	1.0	14
62	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
63	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
64	Comparative single-cell genomics reveals potential ecological niches for the freshwater <i>acI</i> Actinobacteria lineage. <i>ISME Journal</i> , 2014, 8, 2503-2516.	4.4	137
65	Successful enrichment of the ubiquitous freshwater Actinobacteria. <i>Environmental Microbiology Reports</i> , 2014, 6, 21-27.	1.0	35
66	Productivity and salinity structuring of the microplankton revealed by comparative freshwater metagenomics. <i>Environmental Microbiology</i> , 2014, 16, 2682-2698.	1.8	80
67	Phosphorus speciation in a eutrophic lake by 31P NMR spectroscopy. <i>Water Research</i> , 2014, 62, 229-240.	5.3	73
68	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
69	Seasonal bacterial community dynamics in a full-scale enhanced biological phosphorus removal plant. <i>Water Research</i> , 2013, 47, 7019-7031.	5.3	65
70	Comparative genomics of two <i>Candidatus</i> <i>Accumulibacter</i> ™ clades performing biological phosphorus removal. <i>ISME Journal</i> , 2013, 7, 2301-2314.	4.4	101
71	Microbial Contributions to Phosphorus Cycling in Eutrophic Lakes and Wastewater. <i>Annual Review of Microbiology</i> , 2013, 67, 199-219.	2.9	86
72	Lineage-Specific Responses of Microbial Communities to Environmental Change. <i>Applied and Environmental Microbiology</i> , 2013, 79, 39-47.	1.4	20

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73	Microbial diversity and dynamics during methane production from municipal solid waste. Waste Management, 2013, 33, 1982-1992.	3.7	110
74	A decade of seasonal dynamics and co-occurrences within freshwater bacterioplankton communities from eutrophic Lake Mendota, WI, USA. ISME Journal, 2013, 7, 680-684.	4.4	156
75	Effect of Sludge Residence Time on Phosphorus Removal Activities and Populations in Enhanced Biological Phosphorus Removal (EBPR) Systems. Proceedings of the Water Environment Federation, 2013, 2013, 121-132.	0.0	3
76	The Role of Nitrogen Fixation in Cyanobacterial Bloom Toxicity in a Temperate, Eutrophic Lake. PLoS ONE, 2013, 8, e56103.	1.1	127
77	Spatiotemporal Molecular Analysis of Cyanobacteria Blooms Reveals Microcystis-Aphanizomenon Interactions. PLoS ONE, 2013, 8, e74933.	1.1	33
78	Lake microbial communities are resilient after a whole-ecosystem disturbance. ISME Journal, 2012, 6, 2153-2167.	4.4	198
79	Spatial and temporal scales of aquatic bacterial beta diversity. Frontiers in Microbiology, 2012, 3, 318.	1.5	74
80	Metagenomes of Mediterranean Coastal Lagoons. Scientific Reports, 2012, 2, 490.	1.6	85
81	Time-scale dependence in numerical simulations: Assessment of physical, chemical, and biological predictions in a stratified lake at temporal scales of hours to months. Environmental Modelling and Software, 2012, 35, 104-121.	1.9	55
82	Breaking a paradigm: cosmopolitan and abundant freshwater actinobacteria are low GC. Environmental Microbiology Reports, 2012, 4, 29-35.	1.0	66
83	New Abundant Microbial Groups in Aquatic Hypersaline Environments. Scientific Reports, 2011, 1, 135.	1.6	288
84	Microbiology of <i>Candidatus</i> Accumulibacter™ in activated sludge. Microbial Biotechnology, 2011, 4, 603-619.	2.0	104
85	Metagenomics of the Water Column in the Pristine Upper Course of the Amazon River. PLoS ONE, 2011, 6, e23785.	1.1	183
86	Seasonal differences in bacterial community composition following nutrient additions in a eutrophic lake. Environmental Microbiology, 2011, 13, 887-899.	1.8	87
87	Resistance, resilience and recovery: aquatic bacterial dynamics after water column disturbance. Environmental Microbiology, 2011, 13, 2752-2767.	1.8	127
88	Genetic diversity of cyanobacteria in four eutrophic lakes. FEMS Microbiology Ecology, 2011, 78, 336-348.	1.3	27
89	<i>Candidatus</i> Accumulibacter™ gene expression in response to dynamic EBPR conditions. ISME Journal, 2011, 5, 329-340.	4.4	67
90	A Guide to the Natural History of Freshwater Lake Bacteria. Microbiology and Molecular Biology Reviews, 2011, 75, 14-49.	2.9	1,356

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91	Bacterial production of free fatty acids from freshwater macroalgal cellulose. <i>Applied Microbiology and Biotechnology</i> , 2011, 91, 435-446.	1.7	31
92	Phage Encoded H-NS: A Potential Achilles Heel in the Bacterial Defence System. <i>PLoS ONE</i> , 2011, 6, e20095.	1.1	59
93	Seasonal and Episodic Lake Mixing Stimulate Differential Planktonic Bacterial Dynamics. <i>Microbial Ecology</i> , 2010, 59, 546-554.	1.4	31
94	Occurrence of Tetracycline Resistance Genes in Aquaculture Facilities with Varying Use of Oxytetracycline. <i>Microbial Ecology</i> , 2010, 59, 799-807.	1.4	114
95	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
96	Metatranscriptomic array analysis of <i>Candidatus</i> <i>Accumulibacter phosphatis</i> ™-enriched enhanced biological phosphorus removal sludge. <i>Environmental Microbiology</i> , 2010, 12, 1205-1217.	1.8	73
97	Bacterial Community and <i>Candidatus</i> <i>Accumulibacter</i> ™-Population Dynamics in Laboratory-Scale Enhanced Biological Phosphorus Removal Reactors. <i>Applied and Environmental Microbiology</i> , 2010, 76, 5479-5487.	1.4	34
98	Stream Monitoring using Antibiotic Resistance Detection and Microbial Fingerprinting Methods as Indicators of Anthropogenic Contamination. <i>Proceedings of the Water Environment Federation</i> , 2009, 2009, 5056-5067.	0.0	0
99	Influence of typhoons on annual CO ₂ flux from a subtropical, humic lake. <i>Global Change Biology</i> , 2009, 15, 243-254.	4.2	23
100	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.	4.4	32
101	Species sorting may explain an apparent minimal effect of immigration on freshwater bacterial community dynamics. <i>Environmental Microbiology</i> , 2009, 11, 905-913.	1.8	82
102	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
103	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
104	Bacterial Community Composition Dynamics in a Full-Scale Activated Sludge. <i>Proceedings of the Water Environment Federation</i> , 2009, 2009, 4065-4071.	0.0	0
105	Molecular Methods in Biological Systems. <i>Water Environment Research</i> , 2009, 81, 986-1002.	1.3	5
106	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.	1.4	85
107	Potential for atmospheric deposition of bacteria to influence bacterioplankton communities. <i>FEMS Microbiology Ecology</i> , 2008, 64, 388-394.	1.3	40
108	The influence of habitat heterogeneity on freshwater bacterial community composition and dynamics. <i>Environmental Microbiology</i> , 2008, 10, 1057-1067.	1.8	120

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109	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
110	Development of a solar-powered microbial fuel cell. <i>Journal of Applied Microbiology</i> , 2008, 104, 640-650.	1.4	100
111	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
112	Persistence of Pathogenic Prion Protein during Simulated Wastewater Treatment Processes. <i>Environmental Science & Technology</i> , 2008, 42, 5254-5259.	4.6	61
113	A bacterial metapopulation adapts locally to phage predation despite global dispersal. <i>Genome Research</i> , 2008, 18, 293-297.	2.4	135
114	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
115	Ecological Differentiation of Accumulibacter in EBPR Reactors. <i>Proceedings of the Water Environment Federation</i> , 2008, 2008, 31-42.	0.0	5
116	Typhoons initiate predictable change in aquatic bacterial communities. <i>Limnology and Oceanography</i> , 2008, 53, 1319-1326.	1.6	73
117	Molecular Methods in Biological Systems. <i>Water Environment Research</i> , 2008, 80, 929-961.	1.3	1
118	<i>Candidatus</i> Accumulibacter 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
119	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
120	Molecular Methods in Biological Systems. <i>Water Environment Research</i> , 2007, 79, 1109-1151.	1.3	2
121	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
122	PHOSPHORUS ACCUMULATING ORGANISMS REVEAL THEIR SECRETS: A GENOME LEVEL UNDERSTANDING OF ENHANCED BIOLOGICAL PHOSPHORUS REMOVAL. <i>Proceedings of the Water Environment Federation</i> , 2007, 2007, 4920-4932.	0.0	0
123	BIOCHEMICAL PATHWAYS IN BIOLOGICAL PHOSPHORUS REMOVAL ASSESSED USING PROTEOMICS. <i>Proceedings of the Water Environment Federation</i> , 2007, 2007, 4933-4943.	0.0	0
124	Interannual dynamics and phenology of bacterial communities in a eutrophic lake. <i>Limnology and Oceanography</i> , 2007, 52, 487-494.	1.6	167
125	Tetracycline resistance genes in activated sludge wastewater treatment plants. <i>Water Research</i> , 2007, 41, 1143-1151.	5.3	478
126	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

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127	Phylogenetic Ecology of the Freshwater <i>Actinobacteria</i> Lineage. Applied and Environmental Microbiology, 2007, 73, 7169-7176.	1.4	195
128	Understanding Regional Change: A Comparison of Two Lake Districts. BioScience, 2007, 57, 323-335.	2.2	129
129	Integrating ecology into biotechnology. Current Opinion in Biotechnology, 2007, 18, 287-292.	3.3	57
130	Synchrony in aquatic microbial community dynamics. ISME Journal, 2007, 1, 38-47.	4.4	225
131	Polyphosphate kinase genes from full-scale activated sludge plants. Applied Microbiology and Biotechnology, 2007, 77, 167-173.	1.7	78
132	Molecular Methods in Biological Systems. Water Environment Research, 2006, 78, 1084-1118.	1.3	0
133	Genetic Blueprints for Enhanced Biological Phosphorus Removal (EBPR) Based on Environmental Shotgun Sequencing. Proceedings of the Water Environment Federation, 2006, 2006, 82-85.	0.0	1
134	Microbial community dynamics in a humic lake: differential persistence of common freshwater phylotypes. Environmental Microbiology, 2006, 8, 956-970.	1.8	141
135	Experimental manipulations of microbial food web interactions in a humic lake: shifting biological drivers of bacterial community structure. Environmental Microbiology, 2006, 8, 1448-1459.	1.8	44
136	Metagenomic analysis of two enhanced biological phosphorus removal (EBPR) sludge communities. Nature Biotechnology, 2006, 24, 1263-1269.	9.4	634
137	Bridging the gap between micro - and macro-scale perspectives on the role of microbial communities in global change ecology. Plant and Soil, 2006, 289, 59-70.	1.8	86
138	Tetracycline Resistance Genes in Activated Sludge Wastewater Treatment Plants. Proceedings of the Water Environment Federation, 2006, 2006, 1478-1493.	0.0	2
139	Prions: Novel Pathogens of Environmental Concern?. Journal of Environmental Engineering, ASCE, 2006, 132, 967-969.	0.7	14
140	Molecular Methods in Biological Systems. Water Environment Research, 2005, 77, 718-779.	1.3	0
141	Microbial population dynamics during start-up and overload conditions of anaerobic digesters treating municipal solid waste and sewage sludge. Biotechnology and Bioengineering, 2004, 87, 823-834.	1.7	160
142	GENETIC AND BIOCHEMICAL MARKERS FOR ENHANCED BIOLOGICAL PHOSPHORUS REMOVAL. Proceedings of the Water Environment Federation, 2003, 2003, 529-549.	0.0	0
143	Polyphosphate Kinase from Activated Sludge Performing Enhanced Biological Phosphorus Removal. Applied and Environmental Microbiology, 2002, 68, 4971-4978.	1.4	121
144	Anaerobic codigestion of municipal solid waste and biosolids under various mixing conditions: microbial population dynamics. Water Research, 2001, 35, 1817-1827.	5.3	268

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145	Anaerobic codigestion of municipal solid waste and biosolids under various mixing conditionsâ€™l. digester performance. <i>Water Research</i> , 2001, 35, 1804-1816.	5.3	299
146	Uranyl precipitation by biomass from an enhanced biological phosphorus removal reactor. <i>Biodegradation</i> , 2001, 12, 401-410.	1.5	31
147	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
148	Methanogenic population dynamics during start-up of anaerobic digesters treating municipal solid waste and biosolids. , 1998, 57, 342-355.		302
149	A Comparison of the Use of In VitroÂ–Transcribed and Native rRNA for the Quantification of Microorganisms in the Environment. <i>Microbial Ecology</i> , 1998, 36, 362-371.	1.4	17