

Christopher Schadt

List of Publications by Year in descending order

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133
papers

13,127
citations

24978

57
h-index

24915

109
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148
all docs

148
docs citations

148
times ranked

14342
citing authors

#	ARTICLE	IF	CITATIONS
1	Relationships between <i>Sphaerulina musiva</i> Infection and the <i>Populus</i> Microbiome and Metabolome. <i>MSystems</i> , 2022, 7, .	1.7	2
2	A genomic catalog of Earth's microbiomes. <i>Nature Biotechnology</i> , 2021, 39, 499-509.	9.4	457
3	Phylogenetic diversity of 200+ isolates of the ectomycorrhizal fungus <i>Cenococcum geophilum</i> associated with <i>Populus trichocarpa</i> soils in the Pacific Northwest, USA and comparison to globally distributed representatives. <i>PLoS ONE</i> , 2021, 16, e0231367.	1.1	7
4	Fire alters plant microbiome assembly patterns: integrating the plant and soil microbial response to disturbance. <i>New Phytologist</i> , 2021, 230, 2433-2446.	3.5	29
5	Climate-driven divergence in plant-microbiome interactions generates range-wide variation in bud break phenology. <i>Communications Biology</i> , 2021, 4, 748.	2.0	23
6	Cultivating the Bacterial Microbiota of <i>Populus</i> Roots. <i>MSystems</i> , 2021, 6, e0130620.	1.7	17
7	Differential Organic Carbon Mineralization Responses to Soil Moisture in Three Different Soil Orders Under Mixed Forested System. <i>Frontiers in Environmental Science</i> , 2021, 9, .	1.5	7
8	Precipitation and nitrogen application stimulate soil nitrous oxide emission. <i>Nutrient Cycling in Agroecosystems</i> , 2021, 120, 363-378.	1.1	10
9	Assembly of the <i>Populus</i> Microbiome Is Temporally Dynamic and Determined by Selective and Stochastic Factors. <i>MSphere</i> , 2021, 6, e0131620.	1.3	25
10	Soil metabolome response to whole-ecosystem warming at the Spruce and Peatland Responses under Changing Environments experiment. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	54
11	Nitrogen and phosphorus cycling in an ombrotrophic peatland: a benchmark for assessing change. <i>Plant and Soil</i> , 2021, 466, 649-674.	1.8	15
12	Natural soil microbiome variation affects spring foliar phenology with consequences for plant productivity and climate-driven range shifts. <i>New Phytologist</i> , 2021, 232, 762-775.	3.5	12
13	Intensified Soil Moisture Extremes Decrease Soil Organic Carbon Decomposition: A Mechanistic Modeling Analysis. <i>Journal of Geophysical Research G: Biogeosciences</i> , 2021, 126, e2021JG006392.	1.3	3
14	An Integrative Model for Soil Biogeochemistry and Methane Processes: I. Model Structure and Sensitivity Analysis. <i>Journal of Geophysical Research G: Biogeosciences</i> , 2021, 126, e2019JG005468.	1.3	11
15	Plant-Microbe Interactions: From Genes to Ecosystems Using <i>Populus</i> as a Model System. <i>Phytobiomes Journal</i> , 2021, 5, 29-38.	1.4	31
16	A k-mer based approach for classifying viruses without taxonomy identifies viral associations in human autism and plant microbiomes. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 5911-5919.	1.9	10
17	Heterospecific Neighbor Plants Impact Root Microbiome Diversity and Molecular Function of Root Fungi. <i>Frontiers in Microbiology</i> , 2021, 12, 680267.	1.5	3
18	Minnesota peat viromes reveal terrestrial and aquatic niche partitioning for local and global viral populations. <i>Microbiome</i> , 2021, 9, 233.	4.9	53

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19	Beyond the usual suspects: methanogenic communities in eastern North American peatlands are also influenced by nickel and copper concentrations. <i>FEMS Microbiology Letters</i> , 2021, , .	0.7	4
20	Phosphorus rather than nitrogen enhances CO ₂ emissions in tropical forest soils: Evidence from a laboratory incubation study. <i>European Journal of Soil Science</i> , 2020, 71, 495-510.	1.8	21
21	Microbial functional genes commonly respond to elevated carbon dioxide. <i>Environment International</i> , 2020, 144, 106068.	4.8	20
22	Multi-year incubation experiments boost confidence in model projections of long-term soil carbon dynamics. <i>Nature Communications</i> , 2020, 11, 5864.	5.8	18
23	Draft Genome Sequence of <i>Larkinella</i> sp. Strain BK230, Isolated from <i>Populus deltoides</i> Roots. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	2
24	Peatland Microbial Community Composition Is Driven by a Natural Climate Gradient. <i>Microbial Ecology</i> , 2020, 80, 593-602.	1.4	15
25	Plant Hosts Modify Belowground Microbial Community Response to Extreme Drought. <i>MSystems</i> , 2020, 5, .	1.7	36
26	Ectomycorrhizal fungal diversity interacts with soil nutrients to predict plant growth despite weak plant-soil feedbacks. <i>Plant and Soil</i> , 2020, 453, 445-458.	1.8	9
27	Draft Genome Sequence of <i>Tumebacillus</i> sp. Strain BK434, Isolated from the Roots of Eastern Cottonwood. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
28	Constraints on microbial communities, decomposition and methane production in deep peat deposits. <i>PLoS ONE</i> , 2020, 15, e0223744.	1.1	13
29	Global meta-analyses show that conservation tillage practices promote soil fungal and bacterial biomass. <i>Agriculture, Ecosystems and Environment</i> , 2020, 293, 106841.	2.5	63
30	Methanogenic Archaea dominate mature heartwood habitats of Eastern Cottonwood (<i>Populus</i>) Tj ETQqO 0 0 rgBT/Overlock 10 Tf 50	3.5	53
31	Climate-driven reduction of genetic variation in plant phenology alters soil communities and nutrient pools. <i>Global Change Biology</i> , 2019, 25, 1514-1528.	4.2	23
32	Fungal Endophytes of <i>Populus trichocarpa</i> Alter Host Phenotype, Gene Expression, and Rhizobiome Composition. <i>Molecular Plant-Microbe Interactions</i> , 2019, 32, 853-864.	1.4	52
33	One-time nitrogen fertilization shifts switchgrass soil microbiomes within a context of larger spatial and temporal variation. <i>PLoS ONE</i> , 2019, 14, e0211310.	1.1	9
34	Rhizosphere microbiomes diverge among <i>Populus trichocarpa</i> plant-host genotypes and chemotypes, but it depends on soil origin. <i>Microbiome</i> , 2019, 7, 76.	4.9	109
35	Fungal-Bacterial Networks in the <i>Populus</i> Rhizobiome Are Impacted by Soil Properties and Host Genotype. <i>Frontiers in Microbiology</i> , 2019, 10, 481.	1.5	71
36	Influences of nitrogen fertilization and climate regime on the above-ground biomass yields of miscanthus and switchgrass: A meta-analysis. <i>Renewable and Sustainable Energy Reviews</i> , 2019, 108, 303-311.	8.2	31

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37	Methane emissions from tree stems: a new frontier in the global carbon cycle. <i>New Phytologist</i> , 2019, 222, 18-28.	3.5	104
38	Long-term nitrogen fertilization decreases bacterial diversity and favors the growth of <i>Actinobacteria</i> and <i>Proteobacteria</i> in agroecosystems across the globe. <i>Global Change Biology</i> , 2018, 24, 3452-3461.	4.2	436
39	Abiotic Stresses Shift Belowground <i>Populus</i> -Associated Bacteria Toward a Core Stress Microbiome. <i>MSystems</i> , 2018, 3, .	1.7	89
40	Divergent Responses of Forest Soil Microbial Communities under Elevated CO ₂ in Different Depths of Upper Soil Layers. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	31
41	Phylogenomics Reveal the Dynamic Evolution of Fungal Nitric Oxide Reductases and Their Relationship to Secondary Metabolism. <i>Genome Biology and Evolution</i> , 2018, 10, 2474-2489.	1.1	44
42	Temperature sensitivity of extracellular enzymes differs with peat depth but not with season in an ombrotrophic bog. <i>Soil Biology and Biochemistry</i> , 2018, 125, 244-250.	4.2	25
43	Linking Associations of Rare Low-Abundance Species to Their Environments by Association Networks. <i>Frontiers in Microbiology</i> , 2018, 9, 297.	1.5	19
44	The <i>Populus</i> holobiont: dissecting the effects of plant niches and genotype on the microbiome. <i>Microbiome</i> , 2018, 6, 31.	4.9	340
45	Modification of plant cell wall chemistry impacts metabolome and microbiome composition in <i>Populus</i> PdkOR1 RNAi plants. <i>Plant and Soil</i> , 2018, 429, 349-361.	1.8	16
46	<i>Atractiella rhizophila</i> , sp. nov., an endorhizal fungus isolated from the <i>Populus</i> root microbiome. <i>Mycologia</i> , 2017, 109, 18-26.	0.8	43
47	Comparative genomics of <i>Mortierella elongata</i> and its bacterial endosymbiont <i>Mycoavidus cysteinexigens</i> . <i>Environmental Microbiology</i> , 2017, 19, 2964-2983.	1.8	154
48	Characterization of a novel, ubiquitous fungal endophyte from the rhizosphere and root endosphere of <i>Populus</i> trees. <i>Fungal Ecology</i> , 2017, 27, 78-86.	0.7	27
49	Dynamic Succession of Groundwater Sulfate-Reducing Communities during Prolonged Reduction of Uranium in a Contaminated Aquifer. <i>Environmental Science & Technology</i> , 2017, 51, 3609-3620.	4.6	22
50	Molybdenum-Based Diazotrophy in a Sphagnum Peatland in Northern Minnesota. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	46
51	A Carotenoid-Deficient Mutant in <i>Pantoea</i> sp. YR343, a Bacteria Isolated from the Rhizosphere of <i>Populus deltoides</i> , Is Defective in Root Colonization. <i>Frontiers in Microbiology</i> , 2016, 7, 491.	1.5	48
52	Elevated carbon dioxide accelerates the spatial turnover of soil microbial communities. <i>Global Change Biology</i> , 2016, 22, 957-964.	4.2	57
53	Stability of peatland carbon to rising temperatures. <i>Nature Communications</i> , 2016, 7, 13723.	5.8	162
54	Network succession reveals the importance of competition in response to emulsified vegetable oil amendment for uranium bioremediation. <i>Environmental Microbiology</i> , 2016, 18, 205-218.	1.8	339

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55	Isolating a functionally relevant guild of fungi from the root microbiome of Populus. Fungal Ecology, 2016, 22, 35-42.	0.7	88
56	Enrichment of Root Endophytic Bacteria from Populus deltoides and Single-Cell-Genomics Analysis. Applied and Environmental Microbiology, 2016, 82, 5698-5708.	1.4	53
57	Detection and Diversity of Fungal Nitric Oxide Reductase Genes (<i>np450nor</i>) in Agricultural Soils. Applied and Environmental Microbiology, 2016, 82, 2919-2928.	1.4	55
58	Diversity of Pseudomonas Genomes, Including Populus-Associated Isolates, as Revealed by Comparative Genome Analysis. Applied and Environmental Microbiology, 2016, 82, 375-383.	1.4	70
59	PanFP: pangenome-based functional profiles for microbial communities. BMC Research Notes, 2015, 8, 479.	0.6	38
60	Metabolic functions of Pseudomonas fluorescens strains from Populus deltoides depend on rhizosphere or endosphere isolation compartment. Frontiers in Microbiology, 2015, 6, 1118.	1.5	60
61	Towards a holistic understanding of the beneficial interactions across the <i>Populus</i> microbiome. New Phytologist, 2015, 205, 1424-1430.	3.5	131
62	Bioavailability-Based In Situ Remediation To Meet Future Lead (Pb) Standards in Urban Soils and Gardens. Environmental Science & Technology, 2015, 49, 8948-8958.	4.6	82
63	Comment on "Global diversity and geography of soil fungi". Science, 2015, 348, 1438-1438.	6.0	23
64	Dynamic Succession of Groundwater Functional Microbial Communities in Response to Emulsified Vegetable Oil Amendment during Sustained <i>In Situ</i> U(VI) Reduction. Applied and Environmental Microbiology, 2015, 81, 4164-4172.	1.4	24
65	Draft Genome Sequences of Four Streptomyces Isolates from the Populus trichocarpa Root Endosphere and Rhizosphere. Genome Announcements, 2015, 3, .	0.8	7
66	Microbial dormancy improves development and experimental validation of ecosystem model. ISME Journal, 2015, 9, 226-237.	4.4	113
67	Representation of Dormant and Active Microbial Dynamics for Ecosystem Modeling. PLoS ONE, 2014, 9, e89252.	1.1	59
68	Microbial Metabolic Potential for Carbon Degradation and Nutrient (Nitrogen and Phosphorus) Acquisition in an Ombrotrophic Peatland. Applied and Environmental Microbiology, 2014, 80, 3531-3540.	1.4	102
69	Evaluation and validation of de novo and hybrid assembly techniques to derive high-quality genome sequences. Bioinformatics, 2014, 30, 2709-2716.	1.8	99
70	Microbial Community Stratification Linked to Utilization of Carbohydrates and Phosphorus Limitation in a Boreal Peatland at Marcell Experimental Forest, Minnesota, USA. Applied and Environmental Microbiology, 2014, 80, 3518-3530.	1.4	114
71	Organic matter transformation in the peat column at Marcell Experimental Forest: Humification and vertical stratification. Journal of Geophysical Research G: Biogeosciences, 2014, 119, 661-675.	1.3	170
72	Watershed-Scale Fungal Community Characterization along a pH Gradient in a Subsurface Environment Cocontaminated with Uranium and Nitrate. Applied and Environmental Microbiology, 2014, 80, 1810-1820.	1.4	15

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73	Plant host and soil origin influence fungal and bacterial assemblages in the roots of woody plants. <i>Molecular Ecology</i> , 2014, 23, 3356-3370.	2.0	285
74	U(VI) Bioreduction with Emulsified Vegetable Oil as the Electron Donor – Model Application to a Field Test. <i>Environmental Science & Technology</i> , 2013, 47, 3218-3225.	4.6	31
75	Comparative metagenomic and <i>16S</i> rRNA microbial diversity characterization using archaeal and bacterial synthetic communities. <i>Environmental Microbiology</i> , 2013, 15, 1882-1899.	1.8	202
76	Variation in root architecture among switchgrass cultivars impacts root decomposition rates. <i>Soil Biology and Biochemistry</i> , 2013, 58, 198-206.	4.2	77
77	In Situ Bioremediation of Uranium with Emulsified Vegetable Oil as the Electron Donor. <i>Environmental Science & Technology</i> , 2013, 47, 6440-6448.	4.6	81
78	U(VI) Bioreduction with Emulsified Vegetable Oil as the Electron Donor – Microcosm Tests and Model Development. <i>Environmental Science & Technology</i> , 2013, 47, 3209-3217.	4.6	26
79	New North American truffles (<i>Tuber</i> spp.) and their ectomycorrhizal associations. <i>Mycologia</i> , 2013, 105, 194-209.	0.8	34
80	A Multifactor Analysis of Fungal and Bacterial Community Structure in the Root Microbiome of Mature <i>Populus deltoides</i> Trees. <i>PLoS ONE</i> , 2013, 8, e76382.	1.1	315
81	Organic Versus Conventional Strawberry Agroecosystem. , 2013, , .		0
82	Microbial Community Succession during Lactate Amendment and Electron Acceptor Limitation Reveals a Predominance of Metal-Reducing <i>Pelosinus</i> spp. <i>Applied and Environmental Microbiology</i> , 2012, 78, 2082-2091.	1.4	42
83	Denitrifying Bacteria from the Genus <i>Rhodanobacter</i> Dominate Bacterial Communities in the Highly Contaminated Subsurface of a Nuclear Legacy Waste Site. <i>Applied and Environmental Microbiology</i> , 2012, 78, 1039-1047.	1.4	184
84	Draft Genome Sequence of <i>Rhizobium</i> sp. Strain PDO1-076, a Bacterium Isolated from <i>Populus deltoides</i> . <i>Journal of Bacteriology</i> , 2012, 194, 2383-2384.	1.0	16
85	Response of the Soil Microbial Community to Changes in Precipitation in a Semiarid Ecosystem. <i>Applied and Environmental Microbiology</i> , 2012, 78, 8587-8594.	1.4	179
86	Firing Range Soils Yield a Diverse Array of Fungal Isolates Capable of Organic Acid Production and Pb Mineral Solubilization. <i>Applied and Environmental Microbiology</i> , 2012, 78, 6078-6086.	1.4	36
87	Twenty-One Genome Sequences from <i>Pseudomonas</i> Species and 19 Genome Sequences from Diverse Bacteria Isolated from the Rhizosphere and Endosphere of <i>Populus deltoides</i> . <i>Journal of Bacteriology</i> , 2012, 194, 5991-5993.	1.0	164
88	<i>Pseudomonas fluorescens</i> Induces Strain-Dependent and Strain-Independent Host Plant Responses in Defense Networks, Primary Metabolism, Photosynthesis, and Fitness. <i>Molecular Plant-Microbe Interactions</i> , 2012, 25, 765-778.	1.4	100
89	Development and validation of a citrate synthase directed quantitative PCR marker for soil bacterial communities. <i>Applied Soil Ecology</i> , 2012, 61, 69-75.	2.1	13
90	Combined inactivation of the <i>Clostridium cellulolyticum</i> lactate and malate dehydrogenase genes substantially increases ethanol yield from cellulose and switchgrass fermentations. <i>Biotechnology for Biofuels</i> , 2012, 5, 2.	6.2	125

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91	Photoautotrophic symbiont and geography are major factors affecting highly structured and diverse bacterial communities in the lichen microbiome. <i>Environmental Microbiology</i> , 2012, 14, 147-161.	1.8	176
92	Massively parallel rRNA gene sequencing exacerbates the potential for biased community diversity comparisons due to variable library sizes. <i>Environmental Microbiology</i> , 2012, 14, 285-290.	1.8	386
93	Common bacterial responses in six ecosystems exposed to 10 years of elevated atmospheric carbon dioxide. <i>Environmental Microbiology</i> , 2012, 14, 1145-1158.	1.8	79
94	Sulfate-Reducing Bacterium <i>Desulfovibrio desulfuricans</i> ND132 as a Model for Understanding Bacterial Mercury Methylation. <i>Applied and Environmental Microbiology</i> , 2011, 77, 3938-3951.	1.4	252
95	Responses of soil cellulolytic fungal communities to elevated atmospheric CO ₂ are complex and variable across five ecosystems. <i>Environmental Microbiology</i> , 2011, 13, 2778-2793.	1.8	56
96	Elevated CO ₂ and plant species diversity interact to slow root decomposition. <i>Soil Biology and Biochemistry</i> , 2011, 43, 2347-2354.	4.2	22
97	Response of "Alamo" switchgrass tissue chemistry and biomass to nitrogen fertilization in West Tennessee, USA. <i>Agriculture, Ecosystems and Environment</i> , 2011, 140, 289-297.	2.5	42
98	A Limited Microbial Consortium Is Responsible for Extended Bioreduction of Uranium in a Contaminated Aquifer. <i>Applied and Environmental Microbiology</i> , 2011, 77, 5955-5965.	1.4	108
99	Distinct Microbial Communities within the Endosphere and Rhizosphere of <i>Populus deltoides</i> Roots across Contrasting Soil Types. <i>Applied and Environmental Microbiology</i> , 2011, 77, 5934-5944.	1.4	524
100	Intra-annual changes in biomass, carbon, and nitrogen dynamics at 4-year old switchgrass field trials in west Tennessee, USA. <i>Agriculture, Ecosystems and Environment</i> , 2010, 136, 177-184.	2.5	72
101	Structural and functional diversity of soil bacterial and fungal communities following woody plant encroachment in the southern Great Plains. <i>Soil Biology and Biochemistry</i> , 2010, 42, 1816-1824.	4.2	72
102	Establishment and metabolic analysis of a model microbial community for understanding trophic and electron accepting interactions of subsurface anaerobic environments. <i>BMC Microbiology</i> , 2010, 10, 149.	1.3	36
103	Kinetic analysis and modeling of oleate and ethanol stimulated uranium (VI) bio-reduction in contaminated sediments under sulfate reduction conditions. <i>Journal of Hazardous Materials</i> , 2010, 183, 482-489.	6.5	19
104	Labile soil carbon inputs mediate the soil microbial community composition and plant residue decomposition rates. <i>New Phytologist</i> , 2010, 188, 1055-1064.	3.5	352
105	Soil Microbial Community Responses to Multiple Experimental Climate Change Drivers. <i>Applied and Environmental Microbiology</i> , 2010, 76, 999-1007.	1.4	690
106	Effects of soil type and farm management on soil ecological functional genes and microbial activities. <i>ISME Journal</i> , 2010, 4, 1099-1107.	4.4	134
107	Sequencing of Multiple Clostridial Genomes Related to Biomass Conversion and Biofuel Production. <i>Journal of Bacteriology</i> , 2010, 192, 6494-6496.	1.0	81
108	Fruit and Soil Quality of Organic and Conventional Strawberry Agroecosystems. <i>PLoS ONE</i> , 2010, 5, e12346.	1.1	127

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109	Donor-dependent Extent of Uranium Reduction for Bioremediation of Contaminated Sediment Microcosms. <i>Journal of Environmental Quality</i> , 2009, 38, 53-60.	1.0	26
110	Assessment of 10 years of CO ₂ fumigation on soil microbial communities and function in a sweetgum plantation. <i>Soil Biology and Biochemistry</i> , 2009, 41, 514-520.	4.2	84
111	Functional Gene Array-Based Analysis of Microbial Community Structure in Groundwaters with a Gradient of Contaminant Levels. <i>Environmental Science & Technology</i> , 2009, 43, 3529-3534.	4.6	80
112	Afforestation Alters the Composition of Functional Genes in Soil and Biogeochemical Processes in South American Grasslands. <i>Applied and Environmental Microbiology</i> , 2009, 75, 6240-6248.	1.4	60
113	Fungal genome sequencing and bioenergy. <i>Fungal Biology Reviews</i> , 2008, 22, 1-5.	1.9	27
114	Widespread occurrence and phylogenetic placement of a soil clone group adds a prominent new branch to the fungal tree of life. <i>Molecular Phylogenetics and Evolution</i> , 2008, 46, 635-644.	1.2	95
115	The effects of chronic nitrogen fertilization on alpine tundra soil microbial communities: implications for carbon and nitrogen cycling. <i>Environmental Microbiology</i> , 2008, 10, 3093-3105.	1.8	252
116	Spatial scaling of functional gene diversity across various microbial taxa. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 7768-7773.	3.3	285
117	Mycorrhizal and Dark-Septate Fungi in Plant Roots Above 4270 Meters Elevation in the Andes and Rocky Mountains. <i>Arctic, Antarctic, and Alpine Research</i> , 2008, 40, 576-583.	0.4	93
118	Microarray-Based Analysis of Microbial Community RNAs by Whole-Community RNA Amplification. <i>Applied and Environmental Microbiology</i> , 2007, 73, 563-571.	1.4	98
119	GeoChip: a comprehensive microarray for investigating biogeochemical, ecological and environmental processes. <i>ISME Journal</i> , 2007, 1, 67-77.	4.4	554
120	Variability in soil properties at different spatial scales (1m ² –1km) in a deciduous forest ecosystem. <i>Soil Biology and Biochemistry</i> , 2007, 39, 2621-2627.	4.2	78
121	Microbial Diversity and Bioremediation of a Hydrocarbon-Contaminated Aquifer (Vega Baja, Puerto Rico). <i>Journal of Environmental Quality</i> , 2007, 36, 114-122.	1.2	42
122	Microarray Applications in Microbial Ecology Research. <i>Microbial Ecology</i> , 2006, 52, 159-175.	1.4	164
123	Changes in bacterial community structure correlate with initial operating conditions of a field-scale denitrifying fluidized bed reactor. <i>Applied Microbiology and Biotechnology</i> , 2006, 71, 748-760.	1.7	44
124	Improvement of Oligonucleotide Probe Design Criteria for Functional Gene Microarrays in Environmental Applications. <i>Applied and Environmental Microbiology</i> , 2006, 72, 1688-1691.	1.4	68
125	Microarray-Based Analysis of Subnanogram Quantities of Microbial Community DNAs by Using Whole-Community Genome Amplification. <i>Applied and Environmental Microbiology</i> , 2006, 72, 4931-4941.	1.4	263
126	Advances in Microarray-Based Technologies for Soil Microbial Community Analyses. <i>Soil Biology and Biochemistry</i> , 2006, 38, 189-203.		4

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127	Design and Use of Functional Gene Microarrays (FGAs) for the Characterization of Microbial Communities. <i>Methods in Microbiology</i> , 2004, 34, 331-368.	0.4	10
128	Molecular and Metabolic Characterization of Cold-Tolerant Alpine Soil <i>Pseudomonas Sensu Stricto</i> . <i>Applied and Environmental Microbiology</i> , 2004, 70, 483-489.	1.4	87
129	Seasonal Dynamics of Previously Unknown Fungal Lineages in Tundra Soils. <i>Science</i> , 2003, 301, 1359-1361.	6.0	586
130	Changes in Soil Microbial Community Structure and Function in an Alpine Dry Meadow Following Spring Snow Melt. <i>Microbial Ecology</i> , 2002, 43, 307-314.	1.4	269
131	Isolation and phylogenetic identification of a dark-septate fungus associated with the alpine plant <i>Ranunculus adoneus</i> . <i>New Phytologist</i> , 2001, 150, 747-755.	3.5	37
132	Ectomycorrhizal transfer of amino acid-nitrogen to the alpine sedge <i>Kobresia myosuroides</i> . <i>New Phytologist</i> , 1999, 142, 163-167.	3.5	36
133	Single-Cell Genomics. , 0, , 267-278.		0