

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	Soil Microbial Community Responses to Multiple Experimental Climate Change Drivers. <i>Applied and Environmental Microbiology</i> , 2010, 76, 999-1007.	1.4	690
2	Seasonal Dynamics of Previously Unknown Fungal Lineages in Tundra Soils. <i>Science</i> , 2003, 301, 1359-1361.	6.0	586
3	GeoChip: a comprehensive microarray for investigating biogeochemical, ecological and environmental processes. <i>ISME Journal</i> , 2007, 1, 67-77.	4.4	554
4	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
5	A genomic catalog of Earth's microbiomes. <i>Nature Biotechnology</i> , 2021, 39, 499-509.	9.4	457
6	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
7	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
8	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
9	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
10	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
11	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
12	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
13	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
14	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
15	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
16	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
17	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
18	Comparative metagenomic and rRNA microbial diversity characterization using archaeal and bacterial synthetic communities. <i>Environmental Microbiology</i> , 2013, 15, 1882-1899.	1.8	202

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19	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
20	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
21	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
22	Organic matter transformation in the peat column at Marcell Experimental Forest: Humification and vertical stratification. <i>Journal of Geophysical Research G: Biogeosciences</i> , 2014, 119, 661-675.	1.3	170
23	Microarray Applications in Microbial Ecology Research. <i>Microbial Ecology</i> , 2006, 52, 159-175.	1.4	164
24	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
25	Stability of peatland carbon to rising temperatures. <i>Nature Communications</i> , 2016, 7, 13723.	5.8	162
26	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
27	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
28	Towards a holistic understanding of the beneficial interactions across the <i>Populus</i> microbiome. <i>New Phytologist</i> , 2015, 205, 1424-1430.	3.5	131
29	Fruit and Soil Quality of Organic and Conventional Strawberry Agroecosystems. <i>PLoS ONE</i> , 2010, 5, e12346.	1.1	127
30	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
31	Microbial Community Stratification Linked to Utilization of Carbohydrates and Phosphorus Limitation in a Boreal Peatland at Marcell Experimental Forest, Minnesota, USA. <i>Applied and Environmental Microbiology</i> , 2014, 80, 3518-3530.	1.4	114
32	Microbial dormancy improves development and experimental validation of ecosystem model. <i>ISME Journal</i> , 2015, 9, 226-237.	4.4	113
33	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
34	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
35	Methane emissions from tree stems: a new frontier in the global carbon cycle. <i>New Phytologist</i> , 2019, 222, 18-28.	3.5	104
36	Microbial Metabolic Potential for Carbon Degradation and Nutrient (Nitrogen and Phosphorus) Acquisition in an Ombrotrophic Peatland. <i>Applied and Environmental Microbiology</i> , 2014, 80, 3531-3540.	1.4	102

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37	<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
38	Evaluation and validation of de novo and hybrid assembly techniques to derive high-quality genome sequences. <i>Bioinformatics</i> , 2014, 30, 2709-2716.	1.8	99
39	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
40	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
41	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
42	Abiotic Stresses Shift Belowground <i>Populus</i> -Associated Bacteria Toward a Core Stress Microbiome. <i>MSystems</i> , 2018, 3, .	1.7	89
43	Isolating a functionally relevant guild of fungi from the root microbiome of <i>Populus</i> . <i>Fungal Ecology</i> , 2016, 22, 35-42.	0.7	88
44	Molecular and Metabolic Characterization of Cold-Tolerant Alpine Soil <i>Pseudomonas</i> Sensu Stricto. <i>Applied and Environmental Microbiology</i> , 2004, 70, 483-489.	1.4	87
45	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
46	Bioavailability-Based In Situ Remediation To Meet Future Lead (Pb) Standards in Urban Soils and Gardens. <i>Environmental Science & Technology</i> , 2015, 49, 8948-8958.	4.6	82
47	Sequencing of Multiple Clostridial Genomes Related to Biomass Conversion and Biofuel Production. <i>Journal of Bacteriology</i> , 2010, 192, 6494-6496.	1.0	81
48	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
49	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
50	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
51	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
52	Variation in root architecture among switchgrass cultivars impacts root decomposition rates. <i>Soil Biology and Biochemistry</i> , 2013, 58, 198-206.	4.2	77
53	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
54	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

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55	Fungal-Bacterial Networks in the Populus Rhizobiome Are Impacted by Soil Properties and Host Genotype. <i>Frontiers in Microbiology</i> , 2019, 10, 481.	1.5	71
56	Diversity of Pseudomonas Genomes, Including Populus-Associated Isolates, as Revealed by Comparative Genome Analysis. <i>Applied and Environmental Microbiology</i> , 2016, 82, 375-383.	1.4	70
57	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
58	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
59	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
60	Metabolic functions of Pseudomonas fluorescens strains from Populus deltoides depend on rhizosphere or endosphere isolation compartment. <i>Frontiers in Microbiology</i> , 2015, 6, 1118.	1.5	60
61	Representation of Dormant and Active Microbial Dynamics for Ecosystem Modeling. <i>PLoS ONE</i> , 2014, 9, e89252.	1.1	59
62	Elevated carbon dioxide accelerates the spatial turnover of soil microbial communities. <i>Global Change Biology</i> , 2016, 22, 957-964.	4.2	57
63	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
64	Detection and Diversity of Fungal Nitric Oxide Reductase Genes (<i>nor</i>) in Agricultural Soils. <i>Applied and Environmental Microbiology</i> , 2016, 82, 2919-2928.	1.4	55
65	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
66	Enrichment of Root Endophytic Bacteria from Populus deltoides and Single-Cell-Genomics Analysis. <i>Applied and Environmental Microbiology</i> , 2016, 82, 5698-5708.	1.4	53
67	Methanogenic Archaea dominate mature heartwood habitats of Eastern Cottonwood (<i>Populus</i>) Tj ETQq1 1 0.784314 rgBT/Overlo	3.5	53
68	Minnesota peat viromes reveal terrestrial and aquatic niche partitioning for local and global viral populations. <i>Microbiome</i> , 2021, 9, 233.	4.9	53
69	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
70	A Carotenoid-Deficient Mutant in Pantoea sp. YR343, a Bacteria Isolated from the Rhizosphere of Populus deltoides, Is Defective in Root Colonization. <i>Frontiers in Microbiology</i> , 2016, 7, 491.	1.5	48
71	Molybdenum-Based Diazotrophy in a Sphagnum Peatland in Northern Minnesota. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	46
72	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

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73	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
74	<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
75	Microbial Diversity and Bioremediation of a Hydrocarbon-Contaminated Aquifer (Vega Baja, Puerto Rico). <i>Environmental Microbiology</i> , 2012, 14, 1243-1254.	1.2	42
76	Response of <i>Alamo</i> 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
77	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
78	PanFP: pangenome-based functional profiles for microbial communities. <i>BMC Research Notes</i> , 2015, 8, 479.	0.6	38
79	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
80	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
81	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
82	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
83	Plant Hosts Modify Belowground Microbial Community Response to Extreme Drought. <i>MSystems</i> , 2020, 5, .	1.7	36
84	New North American truffles (<i>Tuber</i> spp.) and their ectomycorrhizal associations. <i>Mycologia</i> , 2013, 105, 194-209.	0.8	34
85	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
86	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
87	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
88	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
89	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
90	Fungal genome sequencing and bioenergy. <i>Fungal Biology Reviews</i> , 2008, 22, 1-5.	1.9	27

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91	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
92	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
93	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
94	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
95	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
96	Dynamic Succession of Groundwater Functional Microbial Communities in Response to Emulsified Vegetable Oil Amendment during Sustained <i>In Situ</i> U(VI) Reduction. <i>Applied and Environmental Microbiology</i> , 2015, 81, 4164-4172.	1.4	24
97	Comment on “Global diversity and geography of soil fungi”. <i>Science</i> , 2015, 348, 1438-1438.	6.0	23
98	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
99	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
100	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
101	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
102	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
103	Microbial functional genes commonly respond to elevated carbon dioxide. <i>Environment International</i> , 2020, 144, 106068.	4.8	20
104	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
105	Linking Associations of Rare Low-Abundance Species to Their Environments by Association Networks. <i>Frontiers in Microbiology</i> , 2018, 9, 297.	1.5	19
106	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
107	Cultivating the Bacterial Microbiota of <i>Populus</i> Roots. <i>MSystems</i> , 2021, 6, e0130620.	1.7	17
108	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

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109	Modification of plant cell wall chemistry impacts metabolome and microbiome composition in <i>Populus PdkOR1</i> RNAi plants. <i>Plant and Soil</i> , 2018, 429, 349-361.	1.8	16
110	Watershed-Scale Fungal Community Characterization along a pH Gradient in a Subsurface Environment Cocontaminated with Uranium and Nitrate. <i>Applied and Environmental Microbiology</i> , 2014, 80, 1810-1820.	1.4	15
111	Peatland Microbial Community Composition Is Driven by a Natural Climate Gradient. <i>Microbial Ecology</i> , 2020, 80, 593-602.	1.4	15
112	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
113	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
114	Constraints on microbial communities, decomposition and methane production in deep peat deposits. <i>PLoS ONE</i> , 2020, 15, e0223744.	1.1	13
115	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
116	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
117	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
118	Precipitation and nitrogen application stimulate soil nitrous oxide emission. <i>Nutrient Cycling in Agroecosystems</i> , 2021, 120, 363-378.	1.1	10
119	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
120	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
121	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
122	Draft Genome Sequences of Four <i>Streptomyces</i> Isolates from the <i>Populus trichocarpa</i> Root Endosphere and Rhizosphere. <i>Genome Announcements</i> , 2015, 3, .	0.8	7
123	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
124	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
125	Advances in Microarray-Based Technologies for Soil Microbial Community Analyses. , 2006, , 189-203.		4
126	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

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127	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
128	Heterospecific Neighbor Plants Impact Root Microbiome Diversity and Molecular Function of Root Fungi. <i>Frontiers in Microbiology</i> , 2021, 12, 680267.	1.5	3
129	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
130	Relationships between <i>Sphaerulina musiva</i> Infection and the <i>Populus</i> Microbiome and Metabolome. <i>MSystems</i> , 2022, 7, .	1.7	2
131	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
132	Organic Versus Conventional Strawberry Agroecosystem. , 2013, , .		0
133	Single-Cell Genomics. , 0, , 267-278.		0