

Christopher Schadt

List of Publications by Year in descending order

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133
papers

13,127
citations

25034

57
h-index

24982

109
g-index

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, . | 3.8 | 2 |
| 2 | A genomic catalog of Earth's microbiomes. <i>Nature Biotechnology</i> , 2021, 39, 499-509. | 17.5 | 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. | 2.5 | 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. | 7.3 | 29 |
| 5 | Climate-driven divergence in plant-microbiome interactions generates range-wide variation in bud break phenology. <i>Communications Biology</i> , 2021, 4, 748. | 4.4 | 23 |
| 6 | Cultivating the Bacterial Microbiota of <i>Populus</i> Roots. <i>MSystems</i> , 2021, 6, e0130620. | 3.8 | 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, . | 3.3 | 7 |
| 8 | Precipitation and nitrogen application stimulate soil nitrous oxide emission. <i>Nutrient Cycling in Agroecosystems</i> , 2021, 120, 363-378. | 2.2 | 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. | 2.9 | 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, . | 7.1 | 54 |
| 11 | Nitrogen and phosphorus cycling in an ombrotrophic peatland: a benchmark for assessing change. <i>Plant and Soil</i> , 2021, 466, 649-674. | 3.7 | 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. | 7.3 | 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. | 3.0 | 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. | 3.0 | 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. | 2.7 | 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. | 4.1 | 10 |
| 17 | Heterospecific Neighbor Plants Impact Root Microbiome Diversity and Molecular Function of Root Fungi. <i>Frontiers in Microbiology</i> , 2021, 12, 680267. | 3.5 | 3 |
| 18 | Minnesota peat viromes reveal terrestrial and aquatic niche partitioning for local and global viral populations. <i>Microbiome</i> , 2021, 9, 233. | 11.1 | 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, , . | 1.8 | 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. | 3.9 | 21 |
| 21 | Microbial functional genes commonly respond to elevated carbon dioxide. <i>Environment International</i> , 2020, 144, 106068. | 10.0 | 20 |
| 22 | Multi-year incubation experiments boost confidence in model projections of long-term soil carbon dynamics. <i>Nature Communications</i> , 2020, 11, 5864. | 12.8 | 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, . | 0.6 | 2 |
| 24 | Peatland Microbial Community Composition Is Driven by a Natural Climate Gradient. <i>Microbial Ecology</i> , 2020, 80, 593-602. | 2.8 | 15 |
| 25 | Plant Hosts Modify Belowground Microbial Community Response to Extreme Drought. <i>MSystems</i> , 2020, 5, . | 3.8 | 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. | 3.7 | 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, . | 0.6 | 1 |
| 28 | Constraints on microbial communities, decomposition and methane production in deep peat deposits. <i>PLoS ONE</i> , 2020, 15, e0223744. | 2.5 | 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. | 5.3 | 63 |
| 30 | Methanogenic Archaea dominate mature heartwood habitats of Eastern Cottonwood (<i>Populus</i>) Tj ETQqO 0 0 rgBT /Overlock 10 Tf 50 | 7.3 | 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. | 9.5 | 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. | 2.6 | 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. | 2.5 | 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. | 11.1 | 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. | 3.5 | 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. | 16.4 | 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. | 7.3 | 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. | 9.5 | 436 |
| 39 | Abiotic Stresses Shift Belowground <i>Populus</i> -Associated Bacteria Toward a Core Stress Microbiome. <i>MSystems</i> , 2018, 3, . | 3.8 | 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, . | 3.1 | 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. | 2.5 | 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. | 8.8 | 25 |
| 43 | Linking Associations of Rare Low-Abundance Species to Their Environments by Association Networks. <i>Frontiers in Microbiology</i> , 2018, 9, 297. | 3.5 | 19 |
| 44 | The <i>Populus</i> holobiont: dissecting the effects of plant niches and genotype on the microbiome. <i>Microbiome</i> , 2018, 6, 31. | 11.1 | 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. | 3.7 | 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. | 1.9 | 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. | 3.8 | 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. | 1.6 | 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. | 10.0 | 22 |
| 50 | Molybdenum-Based Diazotrophy in a Sphagnum Peatland in Northern Minnesota. <i>Applied and Environmental Microbiology</i> , 2017, 83, . | 3.1 | 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. | 3.5 | 48 |
| 52 | Elevated carbon dioxide accelerates the spatial turnover of soil microbial communities. <i>Global Change Biology</i> , 2016, 22, 957-964. | 9.5 | 57 |
| 53 | Stability of peatland carbon to rising temperatures. <i>Nature Communications</i> , 2016, 7, 13723. | 12.8 | 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. | 3.8 | 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. | 1.6 | 88 |
| 56 | Enrichment of Root Endophytic Bacteria from Populus deltoides and Single-Cell-Genomics Analysis. Applied and Environmental Microbiology, 2016, 82, 5698-5708. | 3.1 | 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. | 3.1 | 55 |
| 58 | Diversity of Pseudomonas Genomes, Including Populus-Associated Isolates, as Revealed by Comparative Genome Analysis. Applied and Environmental Microbiology, 2016, 82, 375-383. | 3.1 | 70 |
| 59 | PanFP: pangenome-based functional profiles for microbial communities. BMC Research Notes, 2015, 8, 479. | 1.4 | 38 |
| 60 | Metabolic functions of Pseudomonas fluorescens strains from Populus deltoides depend on rhizosphere or endosphere isolation compartment. Frontiers in Microbiology, 2015, 6, 1118. | 3.5 | 60 |
| 61 | Towards a holistic understanding of the beneficial interactions across the <i>Populus</i> microbiome. New Phytologist, 2015, 205, 1424-1430. | 7.3 | 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. | 10.0 | 82 |
| 63 | Comment on "Global diversity and geography of soil fungi". Science, 2015, 348, 1438-1438. | 12.6 | 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. | 3.1 | 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. | 9.8 | 113 |
| 67 | Representation of Dormant and Active Microbial Dynamics for Ecosystem Modeling. PLoS ONE, 2014, 9, e89252. | 2.5 | 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. | 3.1 | 102 |
| 69 | Evaluation and validation of de novo and hybrid assembly techniques to derive high-quality genome sequences. Bioinformatics, 2014, 30, 2709-2716. | 4.1 | 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. | 3.1 | 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. | 3.0 | 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. | 3.1 | 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. | 3.9 | 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. | 10.0 | 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. | 3.8 | 202 |
| 76 | Variation in root architecture among switchgrass cultivars impacts root decomposition rates. <i>Soil Biology and Biochemistry</i> , 2013, 58, 198-206. | 8.8 | 77 |
| 77 | In Situ Bioremediation of Uranium with Emulsified Vegetable Oil as the Electron Donor. <i>Environmental Science & Technology</i> , 2013, 47, 6440-6448. | 10.0 | 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. | 10.0 | 26 |
| 79 | New North American truffles (<i>Tuber</i> spp.) and their ectomycorrhizal associations. <i>Mycologia</i> , 2013, 105, 194-209. | 1.9 | 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. | 2.5 | 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. | 3.1 | 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. | 3.1 | 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. | 2.2 | 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. | 3.1 | 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. | 3.1 | 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. | 2.2 | 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. | 2.6 | 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. | 4.3 | 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. | 3.8 | 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. | 3.8 | 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. | 3.8 | 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. | 3.1 | 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. | 3.8 | 56 |
| 96 | Elevated CO ₂ and plant species diversity interact to slow root decomposition. <i>Soil Biology and Biochemistry</i> , 2011, 43, 2347-2354. | 8.8 | 22 |
| 97 | 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. | 5.3 | 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. | 3.1 | 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. | 3.1 | 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. | 5.3 | 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. | 8.8 | 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. | 3.3 | 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. | 12.4 | 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. | 7.3 | 352 |
| 105 | Soil Microbial Community Responses to Multiple Experimental Climate Change Drivers. <i>Applied and Environmental Microbiology</i> , 2010, 76, 999-1007. | 3.1 | 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. | 9.8 | 134 |
| 107 | Sequencing of Multiple Clostridial Genomes Related to Biomass Conversion and Biofuel Production. <i>Journal of Bacteriology</i> , 2010, 192, 6494-6496. | 2.2 | 81 |
| 108 | Fruit and Soil Quality of Organic and Conventional Strawberry Agroecosystems. <i>PLoS ONE</i> , 2010, 5, e12346. | 2.5 | 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. | 2.0 | 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. | 8.8 | 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. | 10.0 | 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. | 3.1 | 60 |
| 113 | Fungal genome sequencing and bioenergy. <i>Fungal Biology Reviews</i> , 2008, 22, 1-5. | 4.7 | 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. | 2.7 | 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. | 3.8 | 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. | 7.1 | 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. | 1.1 | 93 |
| 118 | Microarray-Based Analysis of Microbial Community RNAs by Whole-Community RNA Amplification. <i>Applied and Environmental Microbiology</i> , 2007, 73, 563-571. | 3.1 | 98 |
| 119 | GeoChip: a comprehensive microarray for investigating biogeochemical, ecological and environmental processes. <i>ISME Journal</i> , 2007, 1, 67-77. | 9.8 | 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. | 8.8 | 78 |
| 121 | Microbial Diversity and Bioremediation of a Hydrocarbon-Contaminated Aquifer (Vega Baja, Puerto Rico). <i>Environmental Microbiology</i> , 2007, 9, 107-114. | 2.6 | 42 |
| 122 | Microarray Applications in Microbial Ecology Research. <i>Microbial Ecology</i> , 2006, 52, 159-175. | 2.8 | 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. | 3.6 | 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. | 3.1 | 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. | 3.1 | 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. | 0.8 | 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. | 3.1 | 87 |
| 129 | Seasonal Dynamics of Previously Unknown Fungal Lineages in Tundra Soils. <i>Science</i> , 2003, 301, 1359-1361. | 12.6 | 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. | 2.8 | 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. | 7.3 | 37 |
| 132 | Ectomycorrhizal transfer of amino acid-nitrogen to the alpine sedge <i>Kobresia myosuroides</i> . <i>New Phytologist</i> , 1999, 142, 163-167. | 7.3 | 36 |
| 133 | Single-Cell Genomics. , 0, , 267-278. | | 0 |