

Jizhong Zhou

List of Publications by Year in descending order

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Version: 2024-02-01

333
papers

32,093
citations

4388

86
h-index

5679

162
g-index

353
all docs

353
docs citations

353
times ranked

23298
citing authors

#	ARTICLE	IF	CITATIONS
1	Antibiotic resistome mostly relates to bacterial taxonomy along a suburban transmission chain. <i>Frontiers of Environmental Science and Engineering</i> , 2022, 16, 1.	6.0	5
2	Conversion of marginal land into switchgrass conditionally accrues soil carbon but reduces methane consumption. <i>ISME Journal</i> , 2022, 16, 10-25.	9.8	4
3	Macroecological distributions of gene variants highlight the functional organization of soil microbial systems. <i>ISME Journal</i> , 2022, 16, 726-737.	9.8	8
4	Sustained Ability of a Natural Microbial Community to Remove Nitrate from Groundwater. <i>Ground Water</i> , 2022, 60, 99-111.	1.3	6
5	Functional microbial community structures and chemical properties indicated mechanisms and potential risks of urban river eco-remediation. <i>Science of the Total Environment</i> , 2022, 803, 149868.	8.0	8
6	Antibiotic resistance genes in manure-amended paddy soils across eastern China: Occurrence and influencing factors. <i>Frontiers of Environmental Science and Engineering</i> , 2022, 16, 1.	6.0	15
7	Nutrient supply controls the linkage between species abundance and ecological interactions in marine bacterial communities. <i>Nature Communications</i> , 2022, 13, 175.	12.8	95
8	Disentangling direct from indirect relationships in association networks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	61
9	Long-Term Effects of Soil Remediation with Willow Short Rotation Coppice on Biogeographic Pattern of Microbial Functional Genes. <i>Microorganisms</i> , 2022, 10, 140.	3.6	1
10	Origin of eukaryotes: What can be learned from the first successfully isolated Asgard archaeon. <i>Faculty Reviews</i> , 2022, 11, 3.	3.9	2
11	Functional Traits Resolve Mechanisms Governing the Assembly and Distribution of Nitrogen-Cycling Microbial Communities in the Global Ocean. <i>MBio</i> , 2022, 13, e0383221.	4.1	31
12	<i>mLife</i> : Your journal for cutting-edge research in all microbiological disciplines. , 2022, 1, 1-2.		0
13	Microbial Community Structure and Ecological Networks during Simulation of Diatom Sinking. <i>Microorganisms</i> , 2022, 10, 639.	3.6	4
14	Embracing mountain microbiome and ecosystem functions under global change. <i>New Phytologist</i> , 2022, 234, 1987-2002.	7.3	57
15	In vivo Functional Characterization of Hydrophilic X2 Modules in the Cellulosomal Scaffolding Protein. <i>Frontiers in Microbiology</i> , 2022, 13, 861549.	3.5	1
16	Precipitation balances deterministic and stochastic processes of bacterial community assembly in grassland soils. <i>Soil Biology and Biochemistry</i> , 2022, 168, 108635.	8.8	38
17	Permafrost thaw with warming reduces microbial metabolic capacities in subsurface soils. <i>Molecular Ecology</i> , 2022, 31, 1403-1415.	3.9	12
18	Soil enzymes as indicators of soil function: A step toward greater realism in microbial ecological modeling. <i>Global Change Biology</i> , 2022, 28, 1935-1950.	9.5	31

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19	Microbes and Climate Change: a Research Prospectus for the Future. <i>MBio</i> , 2022, 13, e0080022.	4.1	53
20	Temporal Dynamics of Bacterial Communities along a Gradient of Disturbance in a U.S. Southern Plains Agroecosystem. <i>MBio</i> , 2022, 13, e0382921.	4.1	4
21	Functional profiles of soil microbial communities in the alpine and temperate grasslands of China. , 2022, 1, 3-13.		1
22	Cas9 Nickase-Based Genome Editing in <i>Clostridium cellulolyticum</i> . <i>Methods in Molecular Biology</i> , 2022, 2479, 227-243.	0.9	0
23	Development of a Markerless Deletion Mutagenesis System in Nitrate-Reducing Bacterium <i>Rhodanobacter denitrificans</i> . <i>Applied and Environmental Microbiology</i> , 2022, 88, .	3.1	3
24	Reduction of microbial diversity in grassland soil is driven by long-term climate warming. <i>Nature Microbiology</i> , 2022, 7, 1054-1062.	13.3	86
25	The microbial network property as a bio-indicator of antibiotic transmission in the environment. <i>Science of the Total Environment</i> , 2021, 758, 143712.	8.0	24
26	Dissimilatory Nitrate Reduction to Ammonium (DNRA) and Denitrification Pathways Are Leveraged by Cyclic AMP Receptor Protein (CRP) Paralogues Based on Electron Donor/Acceptor Limitation in <i>Shewanella loihica</i> PV-4. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	3.1	20
27	Microscale heterogeneity of the soil nitrogen cycling microbial functional structure and potential metabolism. <i>Environmental Microbiology</i> , 2021, 23, 1199-1209.	3.8	16
28	Winter warming rapidly increases carbon degradation capacities of fungal communities in tundra soil: Potential consequences on carbon stability. <i>Molecular Ecology</i> , 2021, 30, 926-937.	3.9	16
29	Links among extracellular enzymes, lignin degradation and cell growth establish the models to identify marine lignin-utilizing bacteria. <i>Environmental Microbiology</i> , 2021, 23, 160-173.	3.8	14
30	Excessive nitrogen addition accelerates N assimilation and P utilization by enhancing organic carbon decomposition in a Tibetan alpine steppe. <i>Science of the Total Environment</i> , 2021, 764, 142848.	8.0	25
31	Root exudates drive soil-microbe-nutrient feedbacks in response to plant growth. <i>Plant, Cell and Environment</i> , 2021, 44, 613-628.	5.7	150
32	Coexistence patterns of soil methanogens are closely tied to methane generation and community assembly in rice paddies. <i>Microbiome</i> , 2021, 9, 20.	11.1	66
33	Temporal changes in global soil respiration since 1987. <i>Nature Communications</i> , 2021, 12, 403.	12.8	57
34	Synergistic epistasis enhances the co-operativity of mutualistic interspecies interactions. <i>ISME Journal</i> , 2021, 15, 2233-2247.	9.8	6
35	Microbial Functional Responses Explain Alpine Soil Carbon Fluxes under Future Climate Scenarios. <i>MBio</i> , 2021, 12, .	4.1	10
36	A latitudinal gradient of microbial β -diversity in continental paddy soils. <i>Global Ecology and Biogeography</i> , 2021, 30, 909-919.	5.8	17

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37	Microbial metabolic response to winter warming stabilizes soil carbon. <i>Global Change Biology</i> , 2021, 27, 2011-2028.	9.5	50
38	Climate warming enhances microbial network complexity and stability. <i>Nature Climate Change</i> , 2021, 11, 343-348.	18.8	672
39	Long-term warming in a Mediterranean-type grassland affects soil bacterial functional potential but not bacterial taxonomic composition. <i>Npj Biofilms and Microbiomes</i> , 2021, 7, 17.	6.4	12
40	Mechanism Across Scales: A Holistic Modeling Framework Integrating Laboratory and Field Studies for Microbial Ecology. <i>Frontiers in Microbiology</i> , 2021, 12, 642422.	3.5	12
41	Soil Biogeochemical Cycle Couplings Inferred from a Function-Taxon Network. <i>Research</i> , 2021, 2021, 7102769.	5.7	30
42	The call for regional design code from the regional discrepancy of microbial communities in activated sludge. <i>Environmental Pollution</i> , 2021, 273, 116487.	7.5	10
43	Warming exacerbates the impact of nutrient enrichment on microbial functional potentials important to the nutrient cycling in shallow lake mesocosms. <i>Limnology and Oceanography</i> , 2021, 66, 2481-2495.	3.1	6
44	Direct cell extraction from fresh and stored soil samples: Impact on microbial viability and community compositions. <i>Soil Biology and Biochemistry</i> , 2021, 155, 108178.	8.8	12
45	Dissolved organic matter (DOM) quality drives biogeographic patterns of soil bacterial communities and their association networks in semi-arid regions. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	2.7	6
46	Temporal Changes of Virus-Like Particle Abundance and Metagenomic Comparison of Viral Communities in Cropland and Prairie Soils. <i>MSphere</i> , 2021, 6, e0116020.	2.9	12
47	Aboveground and Belowground Plant Traits Explain Latitudinal Patterns in Topsoil Fungal Communities From Tropical to Cold Temperate Forests. <i>Frontiers in Microbiology</i> , 2021, 12, 633751.	3.5	5
48	Edaphic variables are better indicators of soil microbial functional structure than plant-related ones in subtropical broad-leaved forests. <i>Science of the Total Environment</i> , 2021, 773, 145630.	8.0	9
49	Rare prokaryotic sub-communities dominate the complexity of ecological networks and soil multinutrient cycling during long-term secondary succession in China's Loess Plateau. <i>Science of the Total Environment</i> , 2021, 774, 145737.	8.0	47
50	VB ₁₂ Path for Accurate Metagenomic Profiling of Microbially Driven Cobalamin Synthesis Pathways. <i>MSystems</i> , 2021, 6, e0049721.	3.8	5
51	Genetic Basis of Chromate Adaptation and the Role of the Pre-existing Genetic Divergence during an Experimental Evolution Study with <i>Desulfovibrio vulgaris</i> Populations. <i>MSystems</i> , 2021, 6, e0049321.	3.8	0
52	Seasonal dynamics of the microbial community in two full-scale wastewater treatment plants: Diversity, composition, phylogenetic group based assembly and co-occurrence pattern. <i>Water Research</i> , 2021, 200, 117295.	11.3	83
53	Pathogenic and Indigenous Denitrifying Bacteria are Transcriptionally Active and Key Multi-Antibiotic-Resistant Players in Wastewater Treatment Plants. <i>Environmental Science & Technology</i> , 2021, 55, 10862-10874.	10.0	60
54	High historical variability weakens the effects of current climate differentiation on microbial community dissimilarity and assembly. <i>Global Change Biology</i> , 2021, 27, 5963-5975.	9.5	2

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55	Theory of microbial coexistence in promoting soil–plant ecosystem health. <i>Biology and Fertility of Soils</i> , 2021, 57, 897-911.	4.3	21
56	Patterns of microbial arsenic detoxification genes in low-arsenic continental paddy soils. <i>Environmental Research</i> , 2021, 201, 111584.	7.5	13
57	Warming-driven migration of core microbiota indicates soil property changes at continental scale. <i>Science Bulletin</i> , 2021, 66, 2025-2035.	9.0	12
58	Efficient extracellular laccase secretion via bio-designed secretory apparatuses to enhance bacterial utilization of recalcitrant lignin. <i>Green Chemistry</i> , 2021, 23, 2079-2094.	9.0	17
59	Rhizosphere Carbon Turnover from Cradle to Grave: The Role of Microbe–Plant Interactions. <i>Rhizosphere Biology</i> , 2021, , 51-73.	0.6	33
60	Electrical selection for planktonic sludge microbial community function and assembly. <i>Water Research</i> , 2021, 206, 117744.	11.3	81
61	Environmental Water and Sediment Microbial Communities Shape Intestine Microbiota for Host Health: The Central Dogma in an Anthropogenic Aquaculture Ecosystem. <i>Frontiers in Microbiology</i> , 2021, 12, 772149.	3.5	8
62	Improving a Biogeochemical Model to Simulate Microbial-mediated Carbon Dynamics in Agricultural ecosystems. <i>Journal of Advances in Modeling Earth Systems</i> , 2021, 13, e2021MS002752.	3.8	1
63	Behaviors of Homologous Antibiotic Resistance Genes in a Cephalosporin WWTP, Subsequent WWTP and the Receiving River. <i>Frontiers in Environmental Science</i> , 2021, 9, .	3.3	2
64	Fire affects the taxonomic and functional composition of soil microbial communities, with cascading effects on grassland ecosystem functioning. <i>Global Change Biology</i> , 2020, 26, 431-442.	9.5	45
65	Biodegradability of wastewater determines microbial assembly mechanisms in full-scale wastewater treatment plants. <i>Water Research</i> , 2020, 169, 115276.	11.3	109
66	Environmental antibiotics drives the genetic functions of resistome dynamics. <i>Environment International</i> , 2020, 135, 105398.	10.0	29
67	Mechanisms of soil bacterial and fungal community assembly differ among and within islands. <i>Environmental Microbiology</i> , 2020, 22, 1559-1571.	3.8	47
68	Temperature drives local contributions to beta diversity in mountain streams: Stochastic and deterministic processes. <i>Global Ecology and Biogeography</i> , 2020, 29, 420-432.	5.8	30
69	Mountain biodiversity and ecosystem functions: interplay between geology and contemporary environments. <i>ISME Journal</i> , 2020, 14, 931-944.	9.8	64
70	Microbial functional genes commonly respond to elevated carbon dioxide. <i>Environment International</i> , 2020, 144, 106068.	10.0	20
71	Gene-informed decomposition model predicts lower soil carbon loss due to persistent microbial adaptation to warming. <i>Nature Communications</i> , 2020, 11, 4897.	12.8	67
72	Phytomanagement Reduces Metal Availability and Microbial Metal Resistance in a Metal Contaminated Soil. <i>Frontiers in Microbiology</i> , 2020, 11, 1899.	3.5	7

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73	Century long fertilization reduces stochasticity controlling grassland microbial community succession. <i>Soil Biology and Biochemistry</i> , 2020, 151, 108023.	8.8	60
74	Experimental evolution reveals nitrate tolerance mechanisms in <i>Desulfovibrio vulgaris</i> . <i>ISME Journal</i> , 2020, 14, 2862-2876.	9.8	10
75	A quantitative framework reveals ecological drivers of grassland microbial community assembly in response to warming. <i>Nature Communications</i> , 2020, 11, 4717.	12.8	417
76	Stabilities of soil organic carbon and carbon cycling genes are higher in natural secondary forests than in artificial plantations in southern China. <i>Land Degradation and Development</i> , 2020, 31, 2986-2995.	3.9	6
77	Climate mediates continental scale patterns of stream microbial functional diversity. <i>Microbiome</i> , 2020, 8, 92.	11.1	28
78	Winter warming in Alaska accelerates lignin decomposition contributed by Proteobacteria. <i>Microbiome</i> , 2020, 8, 84.	11.1	47
79	Targeted assemblies of <i>cas1</i> suggest CRISPR-Cas™s response to soil warming. <i>ISME Journal</i> , 2020, 14, 1651-1662.	9.8	6
80	Microecological Koch's postulates reveal that intestinal microbiota dysbiosis contributes to shrimp white feces syndrome. <i>Microbiome</i> , 2020, 8, 32.	11.1	126
81	Modeling the processes of soil moisture in regulating microbial and carbon-nitrogen cycling. <i>Journal of Hydrology</i> , 2020, 585, 124777.	5.4	27
82	Soil Microbial Community Assembly and Interactions Are Constrained by Nitrogen and Phosphorus in Broadleaf Forests of Southern China. <i>Forests</i> , 2020, 11, 285.	2.1	10
83	Development of a CRISPR/Cas9n-based tool for metabolic engineering of <i>Pseudomonas putida</i> for ferulic acid-to-polyhydroxyalkanoate bioconversion. <i>Communications Biology</i> , 2020, 3, 98.	4.4	44
84	Alternative strategies of nutrient acquisition and energy conservation map to the biogeography of marine ammonia-oxidizing archaea. <i>ISME Journal</i> , 2020, 14, 2595-2609.	9.8	62
85	Functional Associations and Resilience in Microbial Communities. <i>Microorganisms</i> , 2020, 8, 951.	3.6	11
86	Microbial extracellular polysaccharide production and aggregate stability controlled by switchgrass (<i>Panicum virgatum</i>) root biomass and soil water potential. <i>Soil Biology and Biochemistry</i> , 2020, 143, 107742.	8.8	69
87	Differentiation strategies of soil rare and abundant microbial taxa in response to changing climatic regimes. <i>Environmental Microbiology</i> , 2020, 22, 1327-1340.	3.8	164
88	Warming-induced permafrost thaw exacerbates tundra soil carbon decomposition mediated by microbial community. <i>Microbiome</i> , 2020, 8, 3.	11.1	75
89	Niche differentiation is spatially and temporally regulated in the rhizosphere. <i>ISME Journal</i> , 2020, 14, 999-1014.	9.8	135
90	Changes of microbial functional capacities in the rhizosphere contribute to aluminum tolerance by genotype-specific soybeans in acid soils. <i>Biology and Fertility of Soils</i> , 2020, 56, 771-783.	4.3	13

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91	Soil pH exerts stronger impacts than vegetation type and plant diversity on soil bacterial community composition in subtropical broad-leaved forests. <i>Plant and Soil</i> , 2020, 450, 273-286.	3.7	27
92	Precise promoter integration improves cellulose bioconversion and thermotolerance in <i>Clostridium cellulolyticum</i> . <i>Metabolic Engineering</i> , 2020, 60, 110-118.	7.0	18
93	Biogeography and Assembly of Microbial Communities in Wastewater Treatment Plants in China. <i>Environmental Science & Technology</i> , 2020, 54, 5884-5892.	10.0	34
94	Multilevel Nitrogen Additions Alter Chemical Composition and Turnover of the Labile Fraction Soil Organic Matter via Effects on Vegetation and Microorganisms. <i>Journal of Geophysical Research C: Biogeosciences</i> , 2020, 125, e2019JG005316.	3.0	7
95	Stochasticity in microbiology: managing unpredictability to reach the Sustainable Development Goals. <i>Microbial Biotechnology</i> , 2020, 13, 829-843.	4.2	26
96	Small and mighty: adaptation of superphylum Patescibacteria to groundwater environment drives their genome simplicity. <i>Microbiome</i> , 2020, 8, 51.	11.1	205
97	Functional structures of soil microbial community relate to contrasting N ₂ O emission patterns from a highly acidified forest. <i>Science of the Total Environment</i> , 2020, 725, 138504.	8.0	10
98	Stimulation of soil respiration by elevated CO ₂ is enhanced under nitrogen limitation in a decade-long grassland study. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 33317-33324.	7.1	34
99	Continental scale structuring of forest and soil diversity via functional traits. <i>Nature Ecology and Evolution</i> , 2019, 3, 1298-1308.	7.8	34
100	A general framework for quantitatively assessing ecological stochasticity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 16892-16898.	7.1	482
101	Complete Genome Sequence of <i>Desulfovibrio desulfuricans</i> IC1, a Sulfonate-Respiring Anaerobe. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	3
102	Differential gene content and gene expression for bacterial evolution and speciation of <i>Shewanella</i> in terms of biosynthesis of heme and heme-requiring proteins. <i>BMC Microbiology</i> , 2019, 19, 173.	3.3	8
103	Long-term nitrogen addition modifies microbial composition and functions for slow carbon cycling and increased sequestration in tropical forest soil. <i>Global Change Biology</i> , 2019, 25, 3267-3281.	9.5	121
104	Salivary mycobiome dysbiosis and its potential impact on bacteriome shifts and host immunity in oral lichen planus. <i>International Journal of Oral Science</i> , 2019, 11, 13.	8.6	54
105	Adaptive Evolution of <i>Sphingobium hydrophobicum</i> C1T in Electronic Waste Contaminated River Sediment. <i>Frontiers in Microbiology</i> , 2019, 10, 2263.	3.5	7
106	Microbial functional diversity: From concepts to applications. <i>Ecology and Evolution</i> , 2019, 9, 12000-12016.	1.9	133
107	Plant-microbe networks in soil are weakened by century-long use of inorganic fertilizers. <i>Microbial Biotechnology</i> , 2019, 12, 1464-1475.	4.2	77
108	Microbial functional traits are sensitive indicators of mild disturbance by lamb grazing. <i>ISME Journal</i> , 2019, 13, 1370-1373.	9.8	44

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109	Functional Gene Array-Based Ultrasensitive and Quantitative Detection of Microbial Populations in Complex Communities. <i>MSystems</i> , 2019, 4, .	3.8	54
110	<i>Ageratina adenophora</i> invasions are associated with microbially mediated differences in biogeochemical cycles. <i>Science of the Total Environment</i> , 2019, 677, 47-56.	8.0	38
111	Global diversity and biogeography of bacterial communities in wastewater treatment plants. <i>Nature Microbiology</i> , 2019, 4, 1183-1195.	13.3	491
112	The spatial scale dependence of diazotrophic and bacterial community assembly in paddy soil. <i>Global Ecology and Biogeography</i> , 2019, 28, 1093-1105.	5.8	42
113	Thermal disruption of soil bacterial assemblages decreases diversity and assemblage similarity. <i>Ecosphere</i> , 2019, 10, e02598.	2.2	2
114	Ocean Acidification Regulates the Activity, Community Structure, and Functional Potential of Heterotrophic Bacterioplankton in an Oligotrophic Gyre. <i>Journal of Geophysical Research G: Biogeosciences</i> , 2019, 124, 1001-1017.	3.0	10
115	Climate warming accelerates temporal scaling of grassland soil microbial biodiversity. <i>Nature Ecology and Evolution</i> , 2019, 3, 612-619.	7.8	82
116	Genomic dynamics of full-scale temperature-phased anaerobic digestion treating waste activated sludge: Focusing on temperature differentiation. <i>Waste Management</i> , 2019, 87, 621-628.	7.4	17
117	High variations of methanogenic microorganisms drive full-scale anaerobic digestion process. <i>Environment International</i> , 2019, 126, 543-551.	10.0	52
118	A comparative proteomic analysis of <i>Desulfovibrio vulgaris</i> Hildenborough in response to the antimicrobial agent free nitrous acid. <i>Science of the Total Environment</i> , 2019, 672, 625-633.	8.0	13
119	Dissimilar responses of fungal and bacterial communities to soil transplantation simulating abrupt climate changes. <i>Molecular Ecology</i> , 2019, 28, 1842-1856.	3.9	13
120	Artificial reforestation produces less diverse soil nitrogen cycling genes than natural restoration. <i>Ecosphere</i> , 2019, 10, e02562.	2.2	13
121	Long-term elevated CO ₂ shifts composition of soil microbial communities in a Californian annual grassland, reducing growth and N utilization potentials. <i>Science of the Total Environment</i> , 2019, 652, 1474-1481.	8.0	34
122	Response of chloramphenicol-reducing biocathode resistome to continuous electrical stimulation. <i>Water Research</i> , 2019, 148, 398-406.	11.3	90
123	Temperature determines the diversity and structure of N ₂ O-reducing microbial assemblages. <i>Functional Ecology</i> , 2018, 32, 1867-1878.	3.6	19
124	Comment on "The whole-soil carbon flux in response to warming". <i>Science</i> , 2018, 359, .	12.6	12
125	Oral microbiota of periodontal health and disease and their changes after nonsurgical periodontal therapy. <i>ISME Journal</i> , 2018, 12, 1210-1224.	9.8	188
126	Soil microbial beta-diversity is linked with compositional variation in aboveground plant biomass in a semi-arid grassland. <i>Plant and Soil</i> , 2018, 423, 465-480.	3.7	33

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127	Toward a theory for diversity gradients: the abundance–adaptation hypothesis. <i>Ecography</i> , 2018, 41, 255-264.	4.5	36
128	Effects of residual organics in municipal wastewater on hydrogenotrophic denitrifying microbial communities. <i>Journal of Environmental Sciences</i> , 2018, 65, 262-270.	6.1	94
129	Biodegradation of polystyrene wastes in yellow mealworms (larvae of <i>Tenebrio molitor</i> Linnaeus): Factors affecting biodegradation rates and the ability of polystyrene-fed larvae to complete their life cycle. <i>Chemosphere</i> , 2018, 191, 979-989.	8.2	168
130	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
131	Taxonomic and Functional Analyses of the Supragingival Microbiome from Caries-Affected and Caries-Free Hosts. <i>Microbial Ecology</i> , 2018, 75, 543-554.	2.8	23
132	Taxonomic decomposition of the latitudinal gradient in species diversity of North American floras. <i>Journal of Biogeography</i> , 2018, 45, 418-428.	3.0	22
133	Soil organic matter availability and climate drive latitudinal patterns in bacterial diversity from tropical to cold temperate forests. <i>Functional Ecology</i> , 2018, 32, 61-70.	3.6	106
134	Contradictory effects of silver nanoparticles on activated sludge wastewater treatment. <i>Journal of Hazardous Materials</i> , 2018, 341, 448-456.	12.4	38
135	Biotic responses buffer warming-induced soil organic carbon loss in Arctic tundra. <i>Global Change Biology</i> , 2018, 24, 4946-4959.	9.5	21
136	Successional change in species composition alters climate sensitivity of grassland productivity. <i>Global Change Biology</i> , 2018, 24, 4993-5003.	9.5	21
137	Biodegradation of Polyethylene and Plastic Mixtures in Mealworms (Larvae of <i>Tenebrio</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 6526-6533.	10.0	316
138	Functional activity and functional gene diversity of a Cu-contaminated soil remediated by aided phytostabilization using compost, dolomitic limestone and a mixed tree stand. <i>Environmental Pollution</i> , 2018, 242, 229-238.	7.5	24
139	Microbial responses to inorganic nutrient amendment overridden by warming: Consequences on soil carbon stability. <i>Environmental Microbiology</i> , 2018, 20, 2509-2522.	3.8	12
140	Microbial community assembly differs across minerals in a rhizosphere microcosm. <i>Environmental Microbiology</i> , 2018, 20, 4444-4460.	3.8	77
141	Spatial scaling of forest soil microbial communities across a temperature gradient. <i>Environmental Microbiology</i> , 2018, 20, 3504-3513.	3.8	24
142	Climate warming leads to divergent succession of grassland microbial communities. <i>Nature Climate Change</i> , 2018, 8, 813-818.	18.8	208
143	Differential Sensitivity of Wetland-Derived Nitrogen Cycling Microorganisms to Copper Nanoparticles. <i>ACS Sustainable Chemistry and Engineering</i> , 2018, 6, 11642-11652.	6.7	10
144	More replenishment than priming loss of soil organic carbon with additional carbon input. <i>Nature Communications</i> , 2018, 9, 3175.	12.8	69

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145	Ubiquity of polystyrene digestion and biodegradation within yellow mealworms, larvae of <i>Tenebrio molitor</i> Linnaeus (Coleoptera: Tenebrionidae). <i>Chemosphere</i> , 2018, 212, 262-271.	8.2	130
146	Differential Sensitivity of Wetland-Derived Nitrogen Cycling Microorganisms to Copper Nanoparticles. <i>ACS Sustainable Chemistry and Engineering</i> , 2018, 6, 11642-11652.	6.7	1
147	Regional and global elevational patterns of microbial species richness and evenness. <i>Ecography</i> , 2017, 40, 393-402.	4.5	79
148	Temporal Dynamics of In-Field Bioreactor Populations Reflect the Groundwater System and Respond Predictably to Perturbation. <i>Environmental Science & Technology</i> , 2017, 51, 2879-2889.	10.0	15
149	Warming enhances old organic carbon decomposition through altering functional microbial communities. <i>ISME Journal</i> , 2017, 11, 1825-1835.	9.8	136
150	The microbially mediated soil organic carbon loss under degenerative succession in an alpine meadow. <i>Molecular Ecology</i> , 2017, 26, 3676-3686.	3.9	22
151	Biogeochemistry drives diversity in the prokaryotes, fungi, and invertebrates of a Panama forest. <i>Ecology</i> , 2017, 98, 2019-2028.	3.2	46
152	RpoN (⁵⁴) Is Required for Floc Formation but Not for Extracellular Polysaccharide Biosynthesis in a Floc-Forming <i>Aquicola tertiaricarbonis</i> Strain. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	14
153	Nearly a decade-long repeatable seasonal diversity patterns of bacterioplankton communities in the eutrophic Lake Donghu (Wuhan, China). <i>Molecular Ecology</i> , 2017, 26, 3839-3850.	3.9	76
154	Functional diversity and redundancy across fish gut, sediment and water bacterial communities. <i>Environmental Microbiology</i> , 2017, 19, 3268-3282.	3.8	30
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