

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 | Molecular ecological network analyses. BMC Bioinformatics, 2012, 13, 113. | 2.6 | 1,917 |
| 2 | Stochastic Community Assembly: Does It Matter in Microbial Ecology?. Microbiology and Molecular Biology Reviews, 2017, 81, . | 6.6 | 1,291 |
| 3 | The interconnected rhizosphere: High network complexity dominates rhizosphere assemblages. Ecology Letters, 2016, 19, 926-936. | 6.4 | 803 |
| 4 | Phylogenetic Molecular Ecological Network of Soil Microbial Communities in Response to Elevated CO ₂ . MBio, 2011, 2, . | 4.1 | 771 |
| 5 | Functional Molecular Ecological Networks. MBio, 2010, 1, . | 4.1 | 717 |
| 6 | A Proposed Genus Boundary for the Prokaryotes Based on Genomic Insights. Journal of Bacteriology, 2014, 196, 2210-2215. | 2.2 | 708 |
| 7 | Climate warming enhances microbial network complexity and stability. Nature Climate Change, 2021, 11, 343-348. | 18.8 | 672 |
| 8 | Spatial and Resource Factors Influencing High Microbial Diversity in Soil. Applied and Environmental Microbiology, 2002, 68, 326-334. | 3.1 | 599 |
| 9 | Stochasticity, succession, and environmental perturbations in a fluidic ecosystem. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E836-45. | 7.1 | 595 |
| 10 | Correlation detection strategies in microbial data sets vary widely in sensitivity and precision. ISME Journal, 2016, 10, 1669-1681. | 9.8 | 593 |
| 11 | GeoChip: a comprehensive microarray for investigating biogeochemical, ecological and environmental processes. ISME Journal, 2007, 1, 67-77. | 9.8 | 554 |
| 12 | Microbial mediation of carbon-cycle feedbacks to climate warming. Nature Climate Change, 2012, 2, 106-110. | 18.8 | 502 |
| 13 | Global diversity and biogeography of bacterial communities in wastewater treatment plants. Nature Microbiology, 2019, 4, 1183-1195. | 13.3 | 491 |
| 14 | A general framework for quantitatively assessing ecological stochasticity. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 16892-16898. | 7.1 | 482 |
| 15 | Temperature mediates continental-scale diversity of microbes in forest soils. Nature Communications, 2016, 7, 12083. | 12.8 | 419 |
| 16 | A quantitative framework reveals ecological drivers of grassland microbial community assembly in response to warming. Nature Communications, 2020, 11, 4717. | 12.8 | 417 |
| 17 | Reproducibility and quantitation of amplicon sequencing-based detection. ISME Journal, 2011, 5, 1303-1313. | 9.8 | 412 |
| 18 | High-Throughput Metagenomic Technologies for Complex Microbial Community Analysis: Open and Closed Formats. MBio, 2015, 6, . | 4.1 | 357 |

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 19 | Simultaneous Recovery of RNA and DNA from Soils and Sediments. <i>Applied and Environmental Microbiology</i> , 2001, 67, 4495-4503. | 3.1 | 341 |
| 20 | 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 |
| 21 | Microbial regulation of the soil carbon cycle: evidence from gene-enzyme relationships. <i>ISME Journal</i> , 2016, 10, 2593-2604. | 9.8 | 324 |
| 22 | Biodegradation of Polyethylene and Plastic Mixtures in Mealworms (Larvae of <i>Tenebrio</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 627 Td 6526-6533. | 10.0 | 316 |
| 23 | GeoChip 3.0 as a high-throughput tool for analyzing microbial community composition, structure and functional activity. <i>ISME Journal</i> , 2010, 4, 1167-1179. | 9.8 | 300 |
| 24 | Stochastic Assembly Leads to Alternative Communities with Distinct Functions in a Bioreactor Microbial Community. <i>MBio</i> , 2013, 4, . | 4.1 | 293 |
| 25 | 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 |
| 26 | Environmental filtering decreases with fish development for the assembly of gut microbiota. <i>Environmental Microbiology</i> , 2016, 18, 4739-4754. | 3.8 | 267 |
| 27 | 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 |
| 28 | Tundra soil carbon is vulnerable to rapid microbial decomposition under climate warming. <i>Nature Climate Change</i> , 2016, 6, 595-600. | 18.8 | 260 |
| 29 | Shifts in soil microorganisms in response to warming are consistent across a range of Antarctic environments. <i>ISME Journal</i> , 2012, 6, 692-702. | 9.8 | 258 |
| 30 | Aridity threshold in controlling ecosystem nitrogen cycling in arid and semi-arid grasslands. <i>Nature Communications</i> , 2014, 5, 4799. | 12.8 | 254 |
| 31 | The microbial gene diversity along an elevation gradient of the Tibetan grassland. <i>ISME Journal</i> , 2014, 8, 430-440. | 9.8 | 249 |
| 32 | An integrated insight into the response of sedimentary microbial communities to heavy metal contamination. <i>Scientific Reports</i> , 2015, 5, 14266. | 3.3 | 235 |
| 33 | Successional Trajectories of Rhizosphere Bacterial Communities over Consecutive Seasons. <i>MBio</i> , 2015, 6, e00746. | 4.1 | 232 |
| 34 | Phasing amplicon sequencing on Illumina Miseq for robust environmental microbial community analysis. <i>BMC Microbiology</i> , 2015, 15, 125. | 3.3 | 222 |
| 35 | Constructing gene co-expression networks and predicting functions of unknown genes by random matrix theory. <i>BMC Bioinformatics</i> , 2007, 8, 299. | 2.6 | 221 |
| 36 | Responses of the functional structure of soil microbial community to livestock grazing in the Tibetan alpine grassland. <i>Global Change Biology</i> , 2013, 19, 637-648. | 9.5 | 216 |

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|----|--|------|-----------|
| 37 | Climate warming leads to divergent succession of grassland microbial communities. <i>Nature Climate Change</i> , 2018, 8, 813-818. | 18.8 | 208 |
| 38 | Small and mighty: adaptation of superphylum Patescibacteria to groundwater environment drives their genome simplicity. <i>Microbiome</i> , 2020, 8, 51. | 11.1 | 205 |
| 39 | Efficient Genome Editing in <i>Clostridium cellulolyticum</i> via CRISPR-Cas9 Nickase. <i>Applied and Environmental Microbiology</i> , 2015, 81, 4423-4431. | 3.1 | 195 |
| 40 | 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 |
| 41 | GeoChip 4: a functional gene array-based high-throughput environmental technology for microbial community analysis. <i>Molecular Ecology Resources</i> , 2014, 14, 914-928. | 4.8 | 183 |
| 42 | The energetic and carbon economic origins of leaf thermoregulation. <i>Nature Plants</i> , 2016, 2, 16129. | 9.3 | 178 |
| 43 | Long-term successional dynamics of microbial association networks in anaerobic digestion processes. <i>Water Research</i> , 2016, 104, 1-10. | 11.3 | 177 |
| 44 | Natural Bacterial Communities Serve as Quantitative Geochemical Biosensors. <i>MBio</i> , 2015, 6, e00326-15. | 4.1 | 173 |
| 45 | Application of random matrix theory to biological networks. <i>Physics Letters, Section A: General, Atomic and Solid State Physics</i> , 2006, 357, 420-423. | 2.1 | 172 |
| 46 | How sulphate-reducing microorganisms cope with stress: lessons from systems biology. <i>Nature Reviews Microbiology</i> , 2011, 9, 452-466. | 28.6 | 169 |
| 47 | 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 |
| 48 | Elevated nitrate enriches microbial functional genes for potential bioremediation of complexly contaminated sediments. <i>ISME Journal</i> , 2014, 8, 1932-1944. | 9.8 | 164 |
| 49 | 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 |
| 50 | Analyses of soil microbial community compositions and functional genes reveal potential consequences of natural forest succession. <i>Scientific Reports</i> , 2015, 5, 10007. | 3.3 | 162 |
| 51 | Phylogenetic and functional gene structure shifts of the oral microbiomes in periodontitis patients. <i>ISME Journal</i> , 2014, 8, 1879-1891. | 9.8 | 157 |
| 52 | Salt Stress in <i>Desulfovibrio vulgaris</i> Hildenborough: an Integrated Genomics Approach. <i>Journal of Bacteriology</i> , 2006, 188, 4068-4078. | 2.2 | 155 |
| 53 | Plant Thermoregulation: Energetics, Trait-Environment Interactions, and Carbon Economics. <i>Trends in Ecology and Evolution</i> , 2015, 30, 714-724. | 8.7 | 154 |
| 54 | Land use change alters functional gene diversity, composition and abundance in Amazon forest soil microbial communities. <i>Molecular Ecology</i> , 2014, 23, 2988-2999. | 3.9 | 152 |

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|----|---|------|-----------|
| 55 | 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 |
| 56 | Warming enhances old organic carbon decomposition through altering functional microbial communities. <i>ISME Journal</i> , 2017, 11, 1825-1835. | 9.8 | 136 |
| 57 | Niche differentiation is spatially and temporally regulated in the rhizosphere. <i>ISME Journal</i> , 2020, 14, 999-1014. | 9.8 | 135 |
| 58 | Microbial Diversity and Heterogeneity in Sandy Subsurface Soils. <i>Applied and Environmental Microbiology</i> , 2004, 70, 1723-1734. | 3.1 | 134 |
| 59 | Microbial community structure and function of Nitrobenzene reduction biocathode in response to carbon source switchover. <i>Water Research</i> , 2014, 54, 137-148. | 11.3 | 134 |
| 60 | Long-term soil transplant simulating climate change with latitude significantly alters microbial temporal turnover. <i>ISME Journal</i> , 2015, 9, 2561-2572. | 9.8 | 134 |
| 61 | The Electron Transfer System of Syntrophically Grown <i>Desulfovibrio vulgaris</i> . <i>Journal of Bacteriology</i> , 2009, 191, 5793-5801. | 2.2 | 133 |
| 62 | Microbial functional diversity: From concepts to applications. <i>Ecology and Evolution</i> , 2019, 9, 12000-12016. | 1.9 | 133 |
| 63 | Soil Microbial Community Responses to a Decade of Warming as Revealed by Comparative Metagenomics. <i>Applied and Environmental Microbiology</i> , 2014, 80, 1777-1786. | 3.1 | 131 |
| 64 | Predicting taxonomic and functional structure of microbial communities in acid mine drainage. <i>ISME Journal</i> , 2016, 10, 1527-1539. | 9.8 | 130 |
| 65 | 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 |
| 66 | Impacts of the Three Gorges Dam on microbial structure and potential function. <i>Scientific Reports</i> , 2015, 5, 8605. | 3.3 | 129 |
| 67 | Functional Potential of Soil Microbial Communities in the Maize Rhizosphere. <i>PLoS ONE</i> , 2014, 9, e112609. | 2.5 | 127 |
| 68 | Microecological Koch's postulates reveal that intestinal microbiota dysbiosis contributes to shrimp white feces syndrome. <i>Microbiome</i> , 2020, 8, 32. | 11.1 | 126 |
| 69 | 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 |
| 70 | Microbial community composition and functions are resilient to metal pollution along two forest soil gradients. <i>FEMS Microbiology Ecology</i> , 2015, 91, 1-11. | 2.7 | 120 |
| 71 | Selection of optimal oligonucleotide probes for microarrays using multiple criteria, global alignment and parameter estimation. <i>Nucleic Acids Research</i> , 2005, 33, 6114-6123. | 14.5 | 113 |
| 72 | Biodegradability of wastewater determines microbial assembly mechanisms in full-scale wastewater treatment plants. <i>Water Research</i> , 2020, 169, 115276. | 11.3 | 109 |

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|----|--|------|-----------|
| 73 | Community structure and elevational diversity patterns of soil Acidobacteria. <i>Journal of Environmental Sciences</i> , 2014, 26, 1717-1724. | 6.1 | 107 |
| 74 | Evaluation of the reproducibility of amplicon sequencing with Illumina MiSeq platform. <i>PLoS ONE</i> , 2017, 12, e0176716. | 2.5 | 107 |
| 75 | Soil organic matter quantity and quality shape microbial community compositions of subtropical broadleaved forests. <i>Molecular Ecology</i> , 2015, 24, 5175-5185. | 3.9 | 106 |
| 76 | 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 |
| 77 | Lateral Gene Transfer in a Heavy Metal-Contaminated-Groundwater Microbial Community. <i>MBio</i> , 2016, 7, e02234-15. | 4.1 | 105 |
| 78 | Illumina sequencing-based analysis of free-living bacterial community dynamics during an Akashiwo sanguine bloom in Xiamen sea, China. <i>Scientific Reports</i> , 2015, 5, 8476. | 3.3 | 101 |
| 79 | Belowground Response to Drought in a Tropical Forest Soil. I. Changes in Microbial Functional Potential and Metabolism. <i>Frontiers in Microbiology</i> , 2016, 7, 525. | 3.5 | 100 |
| 80 | Preliminary analysis of salivary microbiome and their potential roles in oral lichen planus. <i>Scientific Reports</i> , 2016, 6, 22943. | 3.3 | 99 |
| 81 | The polycyclic aromatic hydrocarbon degradation potential of Gulf of Mexico native coastal microbial communities after the Deepwater Horizon oil spill. <i>Frontiers in Microbiology</i> , 2014, 5, 205. | 3.5 | 98 |
| 82 | The microbe-mediated mechanisms affecting topsoil carbon stock in Tibetan grasslands. <i>ISME Journal</i> , 2015, 9, 2012-2020. | 9.8 | 98 |
| 83 | Microbial mediation of biogeochemical cycles revealed by simulation of global changes with soil transplant and cropping. <i>ISME Journal</i> , 2014, 8, 2045-2055. | 9.8 | 97 |
| 84 | Integrated metagenomics and network analysis of soil microbial community of the forest timberline. <i>Scientific Reports</i> , 2015, 5, 7994. | 3.3 | 97 |
| 85 | Random Sampling Process Leads to Overestimation of $\hat{\pi}^2$ -Diversity of Microbial Communities. <i>MBio</i> , 2013, 4, e00324-13. | 4.1 | 96 |
| 86 | 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 |
| 87 | Soil bacterial diversity patterns and drivers along an elevational gradient on Hennongjia Mountain, China. <i>Microbial Biotechnology</i> , 2015, 8, 739-746. | 4.2 | 94 |
| 88 | 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 |
| 89 | Taxonomic and Functional Diversity of Soil and Hypolithic Microbial Communities in Miers Valley, McMurdo Dry Valleys, Antarctica. <i>Frontiers in Microbiology</i> , 2016, 7, 1642. | 3.5 | 93 |
| 90 | Energetic Consequences of Nitrite Stress in <i>Desulfovibrio vulgaris</i> Hildenborough, Inferred from Global Transcriptional Analysis. <i>Applied and Environmental Microbiology</i> , 2006, 72, 4370-4381. | 3.1 | 92 |

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|-----|---|------|-----------|
| 91 | Response of chloramphenicol-reducing biocathode resistome to continuous electrical stimulation. <i>Water Research</i> , 2019, 148, 398-406. | 11.3 | 90 |
| 92 | Scale-dependent effects of climate and geographic distance on bacterial diversity patterns across northern China's grasslands. <i>FEMS Microbiology Ecology</i> , 2015, 91, fiv133. | 2.7 | 87 |
| 93 | 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 |
| 94 | 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 |
| 95 | Climate warming accelerates temporal scaling of grassland soil microbial biodiversity. <i>Nature Ecology and Evolution</i> , 2019, 3, 612-619. | 7.8 | 82 |
| 96 | Responses of Microbial Communities to Single-Walled Carbon Nanotubes in Phenol Wastewater Treatment Systems. <i>Environmental Science & Technology</i> , 2015, 49, 4627-4635. | 10.0 | 81 |
| 97 | Electrical selection for planktonic sludge microbial community function and assembly. <i>Water Research</i> , 2021, 206, 117744. | 11.3 | 81 |
| 98 | Distinct responses of soil microbial communities to elevated CO ₂ and O ₃ in a soybean agro-ecosystem. <i>ISME Journal</i> , 2014, 8, 714-726. | 9.8 | 80 |
| 99 | Long-Term Oil Contamination Alters the Molecular Ecological Networks of Soil Microbial Functional Genes. <i>Frontiers in Microbiology</i> , 2016, 7, 60. | 3.5 | 80 |
| 100 | Interannual variability in responses of belowground net primary productivity ($\langle \text{NPP} \rangle$) and $\langle \text{NPP} \rangle$ partitioning to long-term warming and clipping in a tallgrass prairie. <i>Global Change Biology</i> , 2012, 18, 1648-1656. | 9.5 | 79 |
| 101 | Long-term cultivation of a stable <i>Methylocystis</i> -dominated methanotrophic enrichment enabling tailored production of poly(3-hydroxybutyrate-co-3-hydroxyvalerate). <i>Bioresource Technology</i> , 2015, 198, 811-818. | 9.6 | 79 |
| 102 | Regional and global elevational patterns of microbial species richness and evenness. <i>Ecography</i> , 2017, 40, 393-402. | 4.5 | 79 |
| 103 | Comparative metagenomics reveals impact of contaminants on groundwater microbiomes. <i>Frontiers in Microbiology</i> , 2015, 6, 1205. | 3.5 | 77 |
| 104 | Microbial community assembly differs across minerals in a rhizosphere microcosm. <i>Environmental Microbiology</i> , 2018, 20, 4444-4460. | 3.8 | 77 |
| 105 | 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 |
| 106 | Biogeographic patterns of soil diazotrophic communities across six forests in the North America. <i>Molecular Ecology</i> , 2016, 25, 2937-2948. | 3.9 | 76 |
| 107 | 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 |
| 108 | Molecular mechanisms of water table lowering and nitrogen deposition in affecting greenhouse gas emissions from a Tibetan alpine wetland. <i>Global Change Biology</i> , 2017, 23, 815-829. | 9.5 | 75 |

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|-----|--|------|-----------|
| 109 | Warming-induced permafrost thaw exacerbates tundra soil carbon decomposition mediated by microbial community. <i>Microbiome</i> , 2020, 8, 3. | 11.1 | 75 |
| 110 | Enhanced decomposition of stable soil organic carbon and microbial catabolic potentials by long-term field warming. <i>Global Change Biology</i> , 2017, 23, 4765-4776. | 9.5 | 74 |
| 111 | Responses of Aromatic-Degrading Microbial Communities to Elevated Nitrate in Sediments. <i>Environmental Science & Technology</i> , 2015, 49, 12422-12431. | 10.0 | 72 |
| 112 | The functional gene composition and metabolic potential of coral-associated microbial communities. <i>Scientific Reports</i> , 2015, 5, 16191. | 3.3 | 71 |
| 113 | Analysis of a Ferric Uptake Regulator (Fur) Mutant of <i>Desulfovibrio vulgaris</i> Hildenborough. <i>Applied and Environmental Microbiology</i> , 2007, 73, 5389-5400. | 3.1 | 70 |
| 114 | Microbial functional trait of rRNA operon copy numbers increases with organic levels in anaerobic digesters. <i>ISME Journal</i> , 2017, 11, 2874-2878. | 9.8 | 70 |
| 115 | More replenishment than priming loss of soil organic carbon with additional carbon input. <i>Nature Communications</i> , 2018, 9, 3175. | 12.8 | 69 |
| 116 | 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 |
| 117 | Bacteriophage-prokaryote dynamics and interaction within anaerobic digestion processes across time and space. <i>Microbiome</i> , 2017, 5, 57. | 11.1 | 68 |
| 118 | Impact of elevated nitrate on sulfate-reducing bacteria: a comparative Study of <i>Desulfovibrio vulgaris</i> . <i>ISME Journal</i> , 2010, 4, 1386-1397. | 9.8 | 67 |
| 119 | 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 |
| 120 | Functional responses of methanogenic archaea to syntrophic growth. <i>ISME Journal</i> , 2012, 6, 2045-2055. | 9.8 | 66 |
| 121 | Crude oil as a microbial seed bank with unexpected functional potentials. <i>Scientific Reports</i> , 2015, 5, 16057. | 3.3 | 66 |
| 122 | Metagenomics Reveals Pervasive Bacterial Populations and Reduced Community Diversity across the Alaska Tundra Ecosystem. <i>Frontiers in Microbiology</i> , 2016, 7, 579. | 3.5 | 66 |
| 123 | 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 |
| 124 | From lithotroph- to organotroph-dominant: directional shift of microbial community in sulphidic tailings during phytostabilization. <i>Scientific Reports</i> , 2015, 5, 12978. | 3.3 | 64 |
| 125 | Interconnection of Key Microbial Functional Genes for Enhanced Benzo[<i>a</i>]pyrene Biodegradation in Sediments by Microbial Electrochemistry. <i>Environmental Science & Technology</i> , 2017, 51, 8519-8529. | 10.0 | 64 |
| 126 | Mountain biodiversity and ecosystem functions: interplay between geology and contemporary environments. <i>ISME Journal</i> , 2020, 14, 931-944. | 9.8 | 64 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 127 | Erosion of functional independence early in the evolution of a microbial mutualism. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 14822-14827. | 7.1 | 63 |
| 128 | Alternative strategies of nutrient acquisition and energy conservation map to the biogeography of marine ammonia-oxidizing archaea. ISME Journal, 2020, 14, 2595-2609. | 9.8 | 62 |
| 129 | Methods for estimating temperature sensitivity of soil organic matter based on incubation data: A comparative evaluation. Soil Biology and Biochemistry, 2015, 80, 127-135. | 8.8 | 61 |
| 130 | Analysis of the functional gene structure and metabolic potential of microbial community in high arsenic groundwater. Water Research, 2017, 123, 268-276. | 11.3 | 61 |
| 131 | Disentangling direct from indirect relationships in association networks. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, . | 7.1 | 61 |
| 132 | Contrasting responses of heterotrophic and autotrophic respiration to experimental warming in a winter annual-dominated prairie. Global Change Biology, 2013, 19, 3553-3564. | 9.5 | 60 |
| 133 | Century long fertilization reduces stochasticity controlling grassland microbial community succession. Soil Biology and Biochemistry, 2020, 151, 108023. | 8.8 | 60 |
| 134 | Pathogenic and Indigenous Denitrifying Bacteria are Transcriptionally Active and Key Multi-Antibiotic-Resistant Players in Wastewater Treatment Plants. Environmental Science & Technology, 2021, 55, 10862-10874. | 10.0 | 60 |
| 135 | High Concentrations of the Antibiotic Spiramycin in Wastewater Lead to High Abundance of Ammonia-Oxidizing Archaea in Nitrifying Populations. Environmental Science & Technology, 2015, 49, 9124-9132. | 10.0 | 57 |
| 136 | Elevated carbon dioxide accelerates the spatial turnover of soil microbial communities. Global Change Biology, 2016, 22, 957-964. | 9.5 | 57 |
| 137 | Temporal changes in global soil respiration since 1987. Nature Communications, 2021, 12, 403. | 12.8 | 57 |
| 138 | Embracing mountain microbiome and ecosystem functions under global change. New Phytologist, 2022, 234, 1987-2002. | 7.3 | 57 |
| 139 | Salivary mycobiome dysbiosis and its potential impact on bacteriome shifts and host immunity in oral lichen planus. International Journal of Oral Science, 2019, 11, 13. | 8.6 | 54 |
| 140 | Functional Gene Array-Based Ultrasensitive and Quantitative Detection of Microbial Populations in Complex Communities. MSystems, 2019, 4, . | 3.8 | 54 |
| 141 | Microbes and Climate Change: a Research Prospectus for the Future. MBio, 2022, 13, e0080022. | 4.1 | 53 |
| 142 | An Integrated Study to Analyze Soil Microbial Community Structure and Metabolic Potential in Two Forest Types. PLoS ONE, 2014, 9, e93773. | 2.5 | 52 |
| 143 | The Diversity and Co-occurrence Patterns of N ₂ -Fixing Communities in a CO ₂ -Enriched Grassland Ecosystem. Microbial Ecology, 2016, 71, 604-615. | 2.8 | 52 |
| 144 | High variations of methanogenic microorganisms drive full-scale anaerobic digestion process. Environment International, 2019, 126, 543-551. | 10.0 | 52 |

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|-----|---|------|-----------|
| 145 | Microbial metabolic response to winter warming stabilizes soil carbon. <i>Global Change Biology</i> , 2021, 27, 2011-2028. | 9.5 | 50 |
| 146 | Structure and regulation of the cellulose degradome in <i>Clostridium cellulolyticum</i> . <i>Biotechnology for Biofuels</i> , 2013, 6, 73. | 6.2 | 49 |
| 147 | Diversity and Structure of Diazotrophic Communities in Mangrove Rhizosphere, Revealed by High-Throughput Sequencing. <i>Frontiers in Microbiology</i> , 2017, 8, 2032. | 3.5 | 49 |
| 148 | Fungal Communities Respond to Long-Term CO ₂ Elevation by Community Reassembly. <i>Applied and Environmental Microbiology</i> , 2015, 81, 2445-2454. | 3.1 | 48 |
| 149 | Elevated CO ₂ shifts the functional structure and metabolic potentials of soil microbial communities in a C4 agroecosystem. <i>Scientific Reports</i> , 2015, 5, 9316. | 3.3 | 48 |
| 150 | The shifts of sediment microbial community phylogenetic and functional structures during chromium (VI) reduction. <i>Ecotoxicology</i> , 2016, 25, 1759-1770. | 2.4 | 48 |
| 151 | Low temperature acclimation with electrical stimulation enhance the biocathode functioning stability for antibiotics detoxification. <i>Water Research</i> , 2016, 100, 157-168. | 11.3 | 47 |
| 152 | Mechanisms of soil bacterial and fungal community assembly differ among and within islands. <i>Environmental Microbiology</i> , 2020, 22, 1559-1571. | 3.8 | 47 |
| 153 | Winter warming in Alaska accelerates lignin decomposition contributed by Proteobacteria. <i>Microbiome</i> , 2020, 8, 84. | 11.1 | 47 |
| 154 | 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 |
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