

Ye Deng

List of Publications by Year in descending order

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Version: 2024-02-01

227
papers

21,551
citations

11651

70
h-index

11607

135
g-index

238
all docs

238
docs citations

238
times ranked

16331
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Molecular ecological network analyses. BMC Bioinformatics, 2012, 13, 113. | 2.6 | 1,917 |
| 2 | Deep-Sea Oil Plume Enriches Indigenous Oil-Degrading Bacteria. Science, 2010, 330, 204-208. | 12.6 | 1,109 |
| 3 | Phylogenetic Molecular Ecological Network of Soil Microbial Communities in Response to Elevated CO ₂ . MBio, 2011, 2, . | 4.1 | 771 |
| 4 | Functional Molecular Ecological Networks. MBio, 2010, 1, . | 4.1 | 717 |
| 5 | 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 |
| 6 | Correlation detection strategies in microbial data sets vary widely in sensitivity and precision. ISME Journal, 2016, 10, 1669-1681. | 9.8 | 593 |
| 7 | Microbial mediation of carbon-cycle feedbacks to climate warming. Nature Climate Change, 2012, 2, 106-110. | 18.8 | 502 |
| 8 | Global diversity and biogeography of bacterial communities in wastewater treatment plants. Nature Microbiology, 2019, 4, 1183-1195. | 13.3 | 491 |
| 9 | 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 |
| 10 | Temperature mediates continental-scale diversity of microbes in forest soils. Nature Communications, 2016, 7, 12083. | 12.8 | 419 |
| 11 | Reproducibility and quantitation of amplicon sequencing-based detection. ISME Journal, 2011, 5, 1303-1313. | 9.8 | 412 |
| 12 | High-Throughput Metagenomic Technologies for Complex Microbial Community Analysis: Open and Closed Formats. MBio, 2015, 6, . | 4.1 | 357 |
| 13 | Network succession reveals the importance of competition in response to emulsified vegetable oil amendment for uranium bioremediation. Environmental Microbiology, 2016, 18, 205-218. | 3.8 | 339 |
| 14 | Metagenomic insights into evolution of a heavy metal-contaminated groundwater microbial community. ISME Journal, 2010, 4, 660-672. | 9.8 | 332 |
| 15 | GeoChip 3.0 as a high-throughput tool for analyzing microbial community composition, structure and functional activity. ISME Journal, 2010, 4, 1167-1179. | 9.8 | 300 |
| 16 | Biodiversity and species competition regulate the resilience of microbial biofilm community. Molecular Ecology, 2017, 26, 6170-6182. | 3.9 | 299 |
| 17 | Stochastic Assembly Leads to Alternative Communities with Distinct Functions in a Bioreactor Microbial Community. MBio, 2013, 4, . | 4.1 | 293 |
| 18 | Tundra soil carbon is vulnerable to rapid microbial decomposition under climate warming. Nature Climate Change, 2016, 6, 595-600. | 18.8 | 260 |

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 19 | Metagenomic analysis reveals a marked divergence in the structure of belowground microbial communities at elevated CO ₂ . Ecology Letters, 2010, 13, 564-575. | 6.4 | 252 |
| 20 | The microbial gene diversity along an elevation gradient of the Tibetan grassland. ISME Journal, 2014, 8, 430-440. | 9.8 | 249 |
| 21 | Microbial gene functions enriched in the Deepwater Horizon deep-sea oil plume. ISME Journal, 2012, 6, 451-460. | 9.8 | 240 |
| 22 | Phasing amplicon sequencing on Illumina Miseq for robust environmental microbial community analysis. BMC Microbiology, 2015, 15, 125. | 3.3 | 222 |
| 23 | Habitat-specific patterns and drivers of bacterial α -diversity in China's drylands. ISME Journal, 2017, 11, 1345-1358. | 9.8 | 218 |
| 24 | Thirty-one years of rice-rice-green manure rotations shape the rhizosphere microbial community and enrich beneficial bacteria. Soil Biology and Biochemistry, 2017, 104, 208-217. | 8.8 | 205 |
| 25 | Plant diversity represents the prevalent determinant of soil fungal community structure across temperate grasslands in northern China. Soil Biology and Biochemistry, 2017, 110, 12-21. | 8.8 | 202 |
| 26 | Tropical agricultural land management influences on soil microbial communities through its effect on soil organic carbon. Soil Biology and Biochemistry, 2013, 65, 33-38. | 8.8 | 189 |
| 27 | GeoChip 4: a functional gene-array-based high-throughput environmental technology for microbial community analysis. Molecular Ecology Resources, 2014, 14, 914-928. | 4.8 | 183 |
| 28 | Functional gene diversity of soil microbial communities from five oil-contaminated fields in China. ISME Journal, 2011, 5, 403-413. | 9.8 | 178 |
| 29 | Phylogenetic and functional gene structure shifts of the oral microbiomes in periodontitis patients. ISME Journal, 2014, 8, 1879-1891. | 9.8 | 157 |
| 30 | Temperature sensitivity of SOM decomposition is linked with a selected microbial community. Global Change Biology, 2021, 27, 2763-2779. | 9.5 | 155 |
| 31 | Land use change alters functional gene diversity, composition and abundance in Amazon forest soil microbial communities. Molecular Ecology, 2014, 23, 2988-2999. | 3.9 | 152 |
| 32 | Higher precipitation strengthens the microbial interactions in semi-arid grassland soils. Global Ecology and Biogeography, 2018, 27, 570-580. | 5.8 | 151 |
| 33 | GeoChip-based analysis of metabolic diversity of microbial communities at the Juan de Fuca Ridge hydrothermal vent. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 4840-4845. | 7.1 | 139 |
| 34 | Meteorological factors had more impact on airborne bacterial communities than air pollutants. Science of the Total Environment, 2017, 601-602, 703-712. | 8.0 | 138 |
| 35 | Warming enhances old organic carbon decomposition through altering functional microbial communities. ISME Journal, 2017, 11, 1825-1835. | 9.8 | 136 |
| 36 | Long-term soil transplant simulating climate change with latitude significantly alters microbial temporal turnover. ISME Journal, 2015, 9, 2561-2572. | 9.8 | 134 |

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|----|---|------|-----------|
| 37 | NCycDB: a curated integrative database for fast and accurate metagenomic profiling of nitrogen cycling genes. <i>Bioinformatics</i> , 2019, 35, 1040-1048. | 4.1 | 134 |
| 38 | 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 |
| 39 | Soil bacterial quantification approaches coupling with relative abundances reflecting the changes of taxa. <i>Scientific Reports</i> , 2017, 7, 4837. | 3.3 | 131 |
| 40 | Impacts of the Three Gorges Dam on microbial structure and potential function. <i>Scientific Reports</i> , 2015, 5, 8605. | 3.3 | 129 |
| 41 | iNAP: An integrated network analysis pipeline for microbiome studies. , 2022, 1, . | | 126 |
| 42 | Application of organic fertilizer improves microbial community diversity and alters microbial network structure in tea (<i>Camellia sinensis</i>) plantation soils. <i>Soil and Tillage Research</i> , 2019, 195, 104356. | 5.6 | 117 |
| 43 | The phylogenetic composition and structure of soil microbial communities shifts in response to elevated carbon dioxide. <i>ISME Journal</i> , 2012, 6, 259-272. | 9.8 | 110 |
| 44 | Deterministic Assembly and Diversity Gradient Altered the Biofilm Community Performances of Bioreactors. <i>Environmental Science & Technology</i> , 2019, 53, 1315-1324. | 10.0 | 109 |
| 45 | Evaluation of the reproducibility of amplicon sequencing with Illumina MiSeq platform. <i>PLoS ONE</i> , 2017, 12, e0176716. | 2.5 | 107 |
| 46 | 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 |
| 47 | Responses of bacterial community to dibutyl phthalate pollution in a soil-vegetable ecosystem. <i>Journal of Hazardous Materials</i> , 2018, 353, 142-150. | 12.4 | 104 |
| 48 | Responses of microbial community functional structures to pilot-scale uranium <i>in situ</i> bioremediation. <i>ISME Journal</i> , 2010, 4, 1060-1070. | 9.8 | 98 |
| 49 | Integrated metagenomics and network analysis of soil microbial community of the forest timberline. <i>Scientific Reports</i> , 2015, 5, 7994. | 3.3 | 97 |
| 50 | Random Sampling Process Leads to Overestimation of β -Diversity of Microbial Communities. <i>MBio</i> , 2013, 4, e00324-13. | 4.1 | 96 |
| 51 | The Great Oxidation Event expanded the genetic repertoire of arsenic metabolism and cycling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 10414-10421. | 7.1 | 96 |
| 52 | GeoChip-based analysis of functional microbial communities during the reoxidation of a bioreduced uranium-contaminated aquifer. <i>Environmental Microbiology</i> , 2009, 11, 2611-2626. | 3.8 | 95 |
| 53 | Soil bacterial diversity patterns and drivers along an elevational gradient on <i>S<hennongjia china<="" i="" mountain,="">. <i>Microbial Biotechnology</i>, 2015, 8, 739-746.</hennongjia></i> | 4.2 | 94 |
| 54 | Elevated Carbon Dioxide Alters the Structure of Soil Microbial Communities. <i>Applied and Environmental Microbiology</i> , 2012, 78, 2991-2995. | 3.1 | 93 |

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|----|--|------|-----------|
| 55 | Distinct microbial communities in the active and permafrost layers on the Tibetan Plateau. <i>Molecular Ecology</i> , 2017, 26, 6608-6620. | 3.9 | 92 |
| 56 | A multiplayer game: species of <i>Clostridium</i> , <i>Acinetobacter</i> , and <i>Pseudomonas</i> are responsible for the persistence of antibiotic resistance genes in manure-treated soils. <i>Environmental Microbiology</i> , 2016, 18, 3494-3508. | 3.8 | 91 |
| 57 | Functional Gene Differences in Soil Microbial Communities from Conventional, Low-Input, and Organic Farmlands. <i>Applied and Environmental Microbiology</i> , 2013, 79, 1284-1292. | 3.1 | 90 |
| 58 | Response of chloramphenicol-reducing biocathode resistome to continuous electrical stimulation. <i>Water Research</i> , 2019, 148, 398-406. | 11.3 | 90 |
| 59 | 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 |
| 60 | Temperature and microbial interactions drive the deterministic assembly processes in sediments of hot springs. <i>Science of the Total Environment</i> , 2021, 772, 145465. | 8.0 | 85 |
| 61 | Development of a Common Oligonucleotide Reference Standard for Microarray Data Normalization and Comparison across Different Microbial Communities. <i>Applied and Environmental Microbiology</i> , 2010, 76, 1088-1094. | 3.1 | 83 |
| 62 | Warming reshaped the microbial hierarchical interactions. <i>Global Change Biology</i> , 2021, 27, 6331-6347. | 9.5 | 81 |
| 63 | Impact of Metal Pollution and <i>Thlaspi caerulescens</i> Growth on Soil Microbial Communities. <i>Applied and Environmental Microbiology</i> , 2010, 76, 7843-7853. | 3.1 | 80 |
| 64 | 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 |
| 65 | 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 |
| 66 | The divergence between fungal and bacterial communities in seasonal and spatial variations of wastewater treatment plants. <i>Science of the Total Environment</i> , 2018, 628-629, 969-978. | 8.0 | 79 |
| 67 | GeoChip-Based Analysis of the Functional Gene Diversity and Metabolic Potential of Microbial Communities in Acid Mine Drainage. <i>Applied and Environmental Microbiology</i> , 2011, 77, 991-999. | 3.1 | 78 |
| 68 | Comparative metagenomics reveals impact of contaminants on groundwater microbiomes. <i>Frontiers in Microbiology</i> , 2015, 6, 1205. | 3.5 | 77 |
| 69 | mcrA sequencing reveals the role of basophilic methanogens in a cathodic methanogenic community. <i>Water Research</i> , 2018, 136, 192-199. | 11.3 | 77 |
| 70 | GeoChip-Based Functional Gene Analysis of Anodophilic Communities in Microbial Electrolysis Cells under Different Operational Modes. <i>Environmental Science & Technology</i> , 2010, 44, 7729-7735. | 10.0 | 76 |
| 71 | Quorum sensing alters the microbial community of electrode-respiring bacteria and hydrogen scavengers toward improving hydrogen yield in microbial electrolysis cells. <i>Applied Energy</i> , 2016, 183, 1133-1141. | 10.1 | 76 |
| 72 | Biogeographic patterns of soil diazotrophic communities across six forests in the North America. <i>Molecular Ecology</i> , 2016, 25, 2937-2948. | 3.9 | 76 |

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|----|--|------|-----------|
| 73 | Nearly a decadeâ€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 |
| 74 | The responses and adaptations of microbial communities to salinity in farmland soils: A molecular ecological network analysis. <i>Applied Soil Ecology</i> , 2017, 120, 239-246. | 4.3 | 76 |
| 75 | Microbial Community and Functional Structure Significantly Varied among Distinct Types of Paddy Soils But Responded Differently along Gradients of Soil Depth Layers. <i>Frontiers in Microbiology</i> , 2017, 8, 945. | 3.5 | 76 |
| 76 | Responses of soil microbial functional genes to global changes are indirectly influenced by aboveground plant biomass variation. <i>Soil Biology and Biochemistry</i> , 2017, 104, 18-29. | 8.8 | 75 |
| 77 | Development of functional gene microarrays for microbial community analysis. <i>Current Opinion in Biotechnology</i> , 2012, 23, 49-55. | 6.6 | 73 |
| 78 | Deforestation decreases spatial turnover and alters the network interactions in soil bacterial communities. <i>Soil Biology and Biochemistry</i> , 2018, 123, 80-86. | 8.8 | 73 |
| 79 | Combined use of network inference tools identifies ecologically meaningful bacterial associations in a paddy soil. <i>Soil Biology and Biochemistry</i> , 2017, 105, 227-235. | 8.8 | 72 |
| 80 | Microarray-based analysis of microbial functional diversity along an oil contamination gradient in oil field. <i>FEMS Microbiology Ecology</i> , 2009, 70, 324-333. | 2.7 | 70 |
| 81 | Bacterioplankton assembly and interspecies interaction indicating increasing coastal eutrophication. <i>Chemosphere</i> , 2017, 177, 317-325. | 8.2 | 70 |
| 82 | Biogeographic patterns of microbial co-occurrence ecological networks in six American forests. <i>Soil Biology and Biochemistry</i> , 2020, 148, 107897. | 8.8 | 68 |
| 83 | Network analysis infers the wilt pathogen invasion associated with non-detrimental bacteria. <i>Npj Biofilms and Microbiomes</i> , 2020, 6, 8. | 6.4 | 68 |
| 84 | Bacterioplankton community resilience to ocean acidification: evidence from microbial network analysis. <i>ICES Journal of Marine Science</i> , 2016, 73, 865-875. | 2.5 | 67 |
| 85 | Plant community, geographic distance and abiotic factors play different roles in predicting AMF biogeography at the regional scale in northern China. <i>Environmental Microbiology Reports</i> , 2016, 8, 1048-1057. | 2.4 | 66 |
| 86 | GeoChip-Based Analysis of Microbial Functional Gene Diversity in a Landfill Leachate-Contaminated Aquifer. <i>Environmental Science & Technology</i> , 2012, 46, 5824-5833. | 10.0 | 64 |
| 87 | Interdomain ecological networks between plants and microbes. <i>Molecular Ecology Resources</i> , 2019, 19, 1565-1577. | 4.8 | 64 |
| 88 | Salinity reduces bacterial diversity, but increases network complexity in Tibetan Plateau lakes. <i>FEMS Microbiology Ecology</i> , 2019, 95, . | 2.7 | 62 |
| 89 | Analysis of the functional gene structure and metabolic potential of microbial community in high arsenic groundwater. <i>Water Research</i> , 2017, 123, 268-276. | 11.3 | 61 |
| 90 | Latitudinal Distribution of Ammonia-Oxidizing Bacteria and Archaea in the Agricultural Soils of Eastern China. <i>Applied and Environmental Microbiology</i> , 2014, 80, 5593-5602. | 3.1 | 60 |

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|-----|---|------|-----------|
| 91 | Recurrent horizontal transfer of arsenite methyltransferase genes facilitated adaptation of life to arsenic. Scientific Reports, 2017, 7, 7741. | 3.3 | 60 |
| 92 | Shifts of functional gene representation in wheat rhizosphere microbial communities under elevated ozone. ISME Journal, 2013, 7, 660-671. | 9.8 | 59 |
| 93 | Over 150 Years of Long-Term Fertilization Alters Spatial Scaling of Microbial Biodiversity. MBio, 2015, 6, . | 4.1 | 57 |
| 94 | Elevated carbon dioxide accelerates the spatial turnover of soil microbial communities. Global Change Biology, 2016, 22, 957-964. | 9.5 | 57 |
| 95 | Assembly Patterns of the Rhizosphere Microbiome Along the Longitudinal Root Axis of Maize (<i>Zea mays</i>) Tj ETQq1 1 0.784314rgBT /Qv | 3.5 | 57 |
| 96 | Adaptive shifts of bacterioplankton communities in response to nitrogen enrichment in a highly polluted river. Environmental Pollution, 2019, 245, 290-299. | 7.5 | 55 |
| 97 | Habitat environments impacted the gut microbiome of long-distance migratory swan geese but central species conserved. Scientific Reports, 2018, 8, 13314. | 3.3 | 54 |
| 98 | Bacterial communities and potential waterborne pathogens within the typical urban surface waters. Scientific Reports, 2018, 8, 13368. | 3.3 | 54 |
| 99 | Functional Gene Array-Based Ultrasensitive and Quantitative Detection of Microbial Populations in Complex Communities. MSystems, 2019, 4, . | 3.8 | 54 |
| 100 | Bioremediation of dibutyl phthalate in a simulated agricultural ecosystem by <i>Gordonia</i> sp. strain QH-11 and the microbial ecological effects in soil. Science of the Total Environment, 2019, 667, 691-700. | 8.0 | 54 |
| 101 | Dynamics of Microbial Community Composition and Function during In Situ Bioremediation of a Uranium-Contaminated Aquifer. Applied and Environmental Microbiology, 2011, 77, 3860-3869. | 3.1 | 51 |
| 102 | Widespread Distribution of Soluble Di-Iron Monooxygenase (SDIMO) Genes in Arctic Groundwater Impacted by 1,4-Dioxane. Environmental Science & Technology, 2013, 47, 9950-9958. | 10.0 | 51 |
| 103 | Elevated CO ₂ and Warming Altered Grassland Microbial Communities in Soil Top-Layers. Frontiers in Microbiology, 2018, 9, 1790. | 3.5 | 51 |
| 104 | Exploring the accuracy of amplicon-based internal transcribed spacer markers for a fungal community. Molecular Ecology Resources, 2020, 20, 170-184. | 4.8 | 49 |
| 105 | Fungal Communities Respond to Long-Term CO ₂ Elevation by Community Reassembly. Applied and Environmental Microbiology, 2015, 81, 2445-2454. | 3.1 | 48 |
| 106 | Elevated CO ₂ shifts the functional structure and metabolic potentials of soil microbial communities in a C ₄ agroecosystem. Scientific Reports, 2015, 5, 9316. | 3.3 | 48 |
| 107 | Elevated CO ₂ influences microbial carbon and nitrogen cycling. BMC Microbiology, 2013, 13, 124. | 3.3 | 47 |
| 108 | Hydrogen peroxide-induced oxidative stress responses in <i>Desulfovibrio vulgaris</i> Hildenborough. Environmental Microbiology, 2010, 12, 2645-2657. | 3.8 | 46 |

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|-----|---|------|-----------|
| 109 | Warming Alters Expressions of Microbial Functional Genes Important to Ecosystem Functioning. <i>Frontiers in Microbiology</i> , 2016, 7, 668. | 3.5 | 46 |
| 110 | Characterising the interspecific variations and convergence of gut microbiota in Anseriformes herbivores at wintering areas. <i>Scientific Reports</i> , 2016, 6, 32655. | 3.3 | 46 |
| 111 | Linking N ₂ O Emissions from Biofertilizer-Amended Soil of Tea Plantations to the Abundance and Structure of N ₂ O-Reducing Microbial Communities. <i>Environmental Science & Technology</i> , 2018, 52, 11338-11345. | 10.0 | 46 |
| 112 | Reconstruction of metabolic networks in a fluoranthene-degrading enrichments from polycyclic aromatic hydrocarbon polluted soil. <i>Journal of Hazardous Materials</i> , 2016, 318, 90-98. | 12.4 | 44 |
| 113 | Myriophyllum aquaticum Constructed Wetland Effectively Removes Nitrogen in Swine Wastewater. <i>Frontiers in Microbiology</i> , 2017, 8, 1932. | 3.5 | 44 |
| 114 | Annual Removal of Aboveground Plant Biomass Alters Soil Microbial Responses to Warming. <i>MBio</i> , 2016, 7, . | 4.1 | 43 |
| 115 | Steeper spatial scaling patterns of subsoil microbiota are shaped by deterministic assembly process. <i>Molecular Ecology</i> , 2021, 30, 1072-1085. | 3.9 | 43 |
| 116 | Correlation of Genomic and Physiological Traits of <i>Thermoanaerobacter</i> Species with Biofuel Yields. <i>Applied and Environmental Microbiology</i> , 2011, 77, 7998-8008. | 3.1 | 42 |
| 117 | Microbial Functional Gene Diversity with a Shift of Subsurface Redox Conditions during <i>In Situ</i> Uranium Reduction. <i>Applied and Environmental Microbiology</i> , 2012, 78, 2966-2972. | 3.1 | 42 |
| 118 | Enhancement of facultative anaerobic denitrifying communities by oxygen release from roots of the macrophyte in constructed wetlands. <i>Journal of Environmental Management</i> , 2019, 246, 157-163. | 7.8 | 42 |
| 119 | Available nitrogen is the key factor influencing soil microbial functional gene diversity in tropical rainforest. <i>BMC Microbiology</i> , 2015, 15, 167. | 3.3 | 41 |
| 120 | Development and applications of functional gene microarrays in the analysis of the functional diversity, composition, and structure of microbial communities. <i>Frontiers of Environmental Science and Engineering in China</i> , 2011, 5, 1-20. | 0.8 | 40 |
| 121 | Exploring abundance, diversity and variation of a widespread antibiotic resistance gene in wastewater treatment plants. <i>Environment International</i> , 2018, 117, 186-195. | 10.0 | 40 |
| 122 | Biodegradation of di-n-Butyl Phthalate by <i>Achromobacter</i> sp. Isolated from Rural Domestic Wastewater. <i>International Journal of Environmental Research and Public Health</i> , 2015, 12, 13510-13522. | 2.6 | 38 |
| 123 | Dramatic Increases of Soil Microbial Functional Gene Diversity at the Treeline Ecotone of Changbai Mountain. <i>Frontiers in Microbiology</i> , 2016, 7, 1184. | 3.5 | 38 |
| 124 | Functional gene arrays-based analysis of fecal microbiomes in patients with liver cirrhosis. <i>BMC Genomics</i> , 2014, 15, 753. | 2.8 | 36 |
| 125 | Toward a theory for diversity gradients: the abundance–adaptation hypothesis. <i>Ecography</i> , 2018, 41, 255-264. | 4.5 | 36 |
| 126 | NifH-Harboring Bacterial Community Composition across an Alaskan Permafrost Thaw Gradient. <i>Frontiers in Microbiology</i> , 2016, 7, 1894. | 3.5 | 35 |

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|-----|--|------|-----------|
| 127 | Geographic distance and amorphous iron affect the abundance and distribution of Geobacteraceae in paddy soils in China. <i>Journal of Soils and Sediments</i> , 2016, 16, 2657-2665. | 3.0 | 35 |
| 128 | Electron acceptors for anaerobic oxidation of methane drive microbial community structure and diversity in mud volcanoes. <i>Environmental Microbiology</i> , 2018, 20, 2370-2385. | 3.8 | 34 |
| 129 | Continental scale structuring of forest and soil diversity via functional traits. <i>Nature Ecology and Evolution</i> , 2019, 3, 1298-1308. | 7.8 | 34 |
| 130 | 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 |
| 131 | Forest conversion induces seasonal variation in microbial α -diversity. <i>Environmental Microbiology</i> , 2018, 20, 111-123. | 3.8 | 33 |
| 132 | High-Throughput Single-Cell Technology Reveals the Contribution of Horizontal Gene Transfer to Typical Antibiotic Resistance Gene Dissemination in Wastewater Treatment Plants. <i>Environmental Science & Technology</i> , 2021, 55, 11824-11834. | 10.0 | 33 |
| 133 | The PathoChip, a functional gene array for assessing pathogenic properties of diverse microbial communities. <i>ISME Journal</i> , 2013, 7, 1974-1984. | 9.8 | 32 |
| 134 | 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 |
| 135 | Soil microbiome mediated nutrients decline during forest degradation process. <i>Soil Ecology Letters</i> , 2019, 1, 59-71. | 4.5 | 29 |
| 136 | Orientational DNA binding and directed transport on nanomaterial heterojunctions. <i>Nanoscale</i> , 2020, 12, 5217-5226. | 5.6 | 29 |
| 137 | Stochastic processes regulate belowground community assembly in alpine grasslands on the Tibetan Plateau. <i>Environmental Microbiology</i> , 2022, 24, 179-194. | 3.8 | 28 |
| 138 | Large-scale expressed sequence tag analysis for the chestnut blight fungus <i>Cryphonectria parasitica</i> . <i>Fungal Genetics and Biology</i> , 2008, 45, 319-327. | 2.1 | 27 |
| 139 | Dibutyl phthalate contamination remodeled the fungal community in agro-environmental system. <i>Chemosphere</i> , 2019, 215, 189-198. | 8.2 | 27 |
| 140 | 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 |
| 141 | Distance-Decay Relationship for Biological Wastewater Treatment Plants. <i>Applied and Environmental Microbiology</i> , 2016, 82, 4860-4866. | 3.1 | 26 |
| 142 | Electro-driven methanogenic microbial community diversity and variability in the electron abundant niche. <i>Science of the Total Environment</i> , 2019, 661, 178-186. | 8.0 | 26 |
| 143 | Distinct Functions and Assembly Mechanisms of Soil Abundant and Rare Bacterial Taxa Under Increasing Pyrene Stresses. <i>Frontiers in Microbiology</i> , 2021, 12, 689762. | 3.5 | 26 |
| 144 | Succession of diversity, functions, and interactions of the fungal community in activated sludge under aromatic hydrocarbon stress. <i>Environmental Research</i> , 2022, 204, 112143. | 7.5 | 26 |

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|-----|--|------|-----------|
| 145 | Applying GeoChip Analysis to Disparate Microbial Communities. Microbe Magazine, 2010, 5, 60-65. | 0.4 | 25 |
| 146 | The Succession of Bacterial Community Attached on Biodegradable Plastic Mulches During the Degradation in Soil. Frontiers in Microbiology, 2021, 12, 785737. | 3.5 | 25 |
| 147 | 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 |
| 148 | Spatial scaling of forest soil microbial communities across a temperature gradient. Environmental Microbiology, 2018, 20, 3504-3513. | 3.8 | 24 |
| 149 | Contrasting Biogeographic Patterns of Bacterial and Archaeal Diversity in the Top- and Subsoils of Temperate Grasslands. MSystems, 2019, 4, . | 3.8 | 24 |
| 150 | Responses of Microbial Communities and Interaction Networks to Different Management Practices in Tea Plantation Soils. Sustainability, 2019, 11, 4428. | 3.2 | 24 |
| 151 | Meadow degradation increases spatial turnover rates of the fungal community through both niche selection and dispersal limitation. Science of the Total Environment, 2021, 798, 149362. | 8.0 | 24 |
| 152 | Interaction of graphene-family nanomaterials with microbial communities in sequential batch reactors revealed by high-throughput sequencing. Environmental Research, 2020, 184, 109392. | 7.5 | 24 |
| 153 | Taxonomic and Functional Analyses of the Supragingival Microbiome from Caries-Affected and Caries-Free Hosts. Microbial Ecology, 2018, 75, 543-554. | 2.8 | 23 |
| 154 | Chitinophaga caeni sp. nov., isolated from activated sludge. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 2209-2213. | 1.7 | 23 |
| 155 | An exploration of 3'-end processing signals and their tissue distribution in Oryza sativa. Gene, 2007, 389, 107-113. | 2.2 | 22 |
| 156 | The microbially mediated soil organic carbon loss under degenerative succession in an alpine meadow. Molecular Ecology, 2017, 26, 3676-3686. | 3.9 | 22 |
| 157 | Dynamic Succession of Groundwater Sulfate-Reducing Communities during Prolonged Reduction of Uranium in a Contaminated Aquifer. Environmental Science & Technology, 2017, 51, 3609-3620. | 10.0 | 22 |
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