

Ye Deng

List of Publications by Year in descending order

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Version: 2024-02-01

227
papers

21,551
citations

11608

70
h-index

11581

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.	1.2	1,917
2	Deep-Sea Oil Plume Enriches Indigenous Oil-Degrading Bacteria. Science, 2010, 330, 204-208.	6.0	1,109
3	Phylogenetic Molecular Ecological Network of Soil Microbial Communities in Response to Elevated CO ₂ . MBio, 2011, 2, .	1.8	771
4	Functional Molecular Ecological Networks. MBio, 2010, 1, .	1.8	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.	3.3	595
6	Correlation detection strategies in microbial data sets vary widely in sensitivity and precision. ISME Journal, 2016, 10, 1669-1681.	4.4	593
7	Microbial mediation of carbon-cycle feedbacks to climate warming. Nature Climate Change, 2012, 2, 106-110.	8.1	502
8	Global diversity and biogeography of bacterial communities in wastewater treatment plants. Nature Microbiology, 2019, 4, 1183-1195.	5.9	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.	3.3	482
10	Temperature mediates continental-scale diversity of microbes in forest soils. Nature Communications, 2016, 7, 12083.	5.8	419
11	Reproducibility and quantitation of amplicon sequencing-based detection. ISME Journal, 2011, 5, 1303-1313.	4.4	412
12	High-Throughput Metagenomic Technologies for Complex Microbial Community Analysis: Open and Closed Formats. MBio, 2015, 6, .	1.8	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.	1.8	339
14	Metagenomic insights into evolution of a heavy metal-contaminated groundwater microbial community. ISME Journal, 2010, 4, 660-672.	4.4	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.	4.4	300
16	Biodiversity and species competition regulate the resilience of microbial biofilm community. Molecular Ecology, 2017, 26, 6170-6182.	2.0	299
17	Stochastic Assembly Leads to Alternative Communities with Distinct Functions in a Bioreactor Microbial Community. MBio, 2013, 4, .	1.8	293
18	Tundra soil carbon is vulnerable to rapid microbial decomposition under climate warming. Nature Climate Change, 2016, 6, 595-600.	8.1	260

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19	Metagenomic analysis reveals a marked divergence in the structure of belowground microbial communities at elevated CO ₂ . <i>Ecology Letters</i> , 2010, 13, 564-575.	3.0	252
20	The microbial gene diversity along an elevation gradient of the Tibetan grassland. <i>ISME Journal</i> , 2014, 8, 430-440.	4.4	249
21	Microbial gene functions enriched in the Deepwater Horizon deep-sea oil plume. <i>ISME Journal</i> , 2012, 6, 451-460.	4.4	240
22	Phasing amplicon sequencing on Illumina Miseq for robust environmental microbial community analysis. <i>BMC Microbiology</i> , 2015, 15, 125.	1.3	222
23	Habitat-specific patterns and drivers of bacterial β -diversity in China's drylands. <i>ISME Journal</i> , 2017, 11, 1345-1358.	4.4	218
24	Thirty-one years of rice-rice-green manure rotations shape the rhizosphere microbial community and enrich beneficial bacteria. <i>Soil Biology and Biochemistry</i> , 2017, 104, 208-217.	4.2	205
25	Plant diversity represents the prevalent determinant of soil fungal community structure across temperate grasslands in northern China. <i>Soil Biology and Biochemistry</i> , 2017, 110, 12-21.	4.2	202
26	Tropical agricultural land management influences on soil microbial communities through its effect on soil organic carbon. <i>Soil Biology and Biochemistry</i> , 2013, 65, 33-38.	4.2	189
27	GeoChip 4: a functional gene-based high-throughput environmental technology for microbial community analysis. <i>Molecular Ecology Resources</i> , 2014, 14, 914-928.	2.2	183
28	Functional gene diversity of soil microbial communities from five oil-contaminated fields in China. <i>ISME Journal</i> , 2011, 5, 403-413.	4.4	178
29	Phylogenetic and functional gene structure shifts of the oral microbiomes in periodontitis patients. <i>ISME Journal</i> , 2014, 8, 1879-1891.	4.4	157
30	Temperature sensitivity of SOM decomposition is linked with a selected microbial community. <i>Global Change Biology</i> , 2021, 27, 2763-2779.	4.2	155
31	Land use change alters functional gene diversity, composition and abundance in Amazon forest soil microbial communities. <i>Molecular Ecology</i> , 2014, 23, 2988-2999.	2.0	152
32	Higher precipitation strengthens the microbial interactions in semi-arid grassland soils. <i>Global Ecology and Biogeography</i> , 2018, 27, 570-580.	2.7	151
33	GeoChip-based analysis of metabolic diversity of microbial communities at the Juan de Fuca Ridge hydrothermal vent. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 4840-4845.	3.3	139
34	Meteorological factors had more impact on airborne bacterial communities than air pollutants. <i>Science of the Total Environment</i> , 2017, 601-602, 703-712.	3.9	138
35	Warming enhances old organic carbon decomposition through altering functional microbial communities. <i>ISME Journal</i> , 2017, 11, 1825-1835.	4.4	136
36	Long-term soil transplant simulating climate change with latitude significantly alters microbial temporal turnover. <i>ISME Journal</i> , 2015, 9, 2561-2572.	4.4	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.	1.8	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.	1.4	131
39	Soil bacterial quantification approaches coupling with relative abundances reflecting the changes of taxa. <i>Scientific Reports</i> , 2017, 7, 4837.	1.6	131
40	Impacts of the Three Gorges Dam on microbial structure and potential function. <i>Scientific Reports</i> , 2015, 5, 8605.	1.6	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.	2.6	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.	4.4	110
44	Deterministic Assembly and Diversity Gradient Altered the Biofilm Community Performances of Bioreactors. <i>Environmental Science & Technology</i> , 2019, 53, 1315-1324.	4.6	109
45	Evaluation of the reproducibility of amplicon sequencing with Illumina MiSeq platform. <i>PLoS ONE</i> , 2017, 12, e0176716.	1.1	107
46	Soil organic matter quantity and quality shape microbial community compositions of subtropical broadleaved forests. <i>Molecular Ecology</i> , 2015, 24, 5175-5185.	2.0	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.	6.5	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.	4.4	98
49	Integrated metagenomics and network analysis of soil microbial community of the forest timberline. <i>Scientific Reports</i> , 2015, 5, 7994.	1.6	97
50	Random Sampling Process Leads to Overestimation of β -Diversity of Microbial Communities. <i>MBio</i> , 2013, 4, e00324-13.	1.8	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.	3.3	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.	1.8	95
53	Soil bacterial diversity patterns and drivers along an elevational gradient on <i>S</i> hennongjia Mountain, <i>C</i> hina. <i>Microbial Biotechnology</i> , 2015, 8, 739-746.	2.0	94
54	Elevated Carbon Dioxide Alters the Structure of Soil Microbial Communities. <i>Applied and Environmental Microbiology</i> , 2012, 78, 2991-2995.	1.4	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.	2.0	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.	1.8	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.	1.4	90
58	Response of chloramphenicol-reducing biocathode resistome to continuous electrical stimulation. <i>Water Research</i> , 2019, 148, 398-406.	5.3	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.	1.3	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.	3.9	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.	1.4	83
62	Warming reshaped the microbial hierarchical interactions. <i>Global Change Biology</i> , 2021, 27, 6331-6347.	4.2	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.	1.4	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.	4.4	80
65	Long-Term Oil Contamination Alters the Molecular Ecological Networks of Soil Microbial Functional Genes. <i>Frontiers in Microbiology</i> , 2016, 7, 60.	1.5	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.	3.9	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.	1.4	78
68	Comparative metagenomics reveals impact of contaminants on groundwater microbiomes. <i>Frontiers in Microbiology</i> , 2015, 6, 1205.	1.5	77
69	mcrA sequencing reveals the role of basophilic methanogens in a cathodic methanogenic community. <i>Water Research</i> , 2018, 136, 192-199.	5.3	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.	4.6	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.	5.1	76
72	Biogeographic patterns of soil diazotrophic communities across six forests in the North America. <i>Molecular Ecology</i> , 2016, 25, 2937-2948.	2.0	76

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73	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.	2.0	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.	2.1	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.	1.5	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.	4.2	75
77	Development of functional gene microarrays for microbial community analysis. <i>Current Opinion in Biotechnology</i> , 2012, 23, 49-55.	3.3	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.	4.2	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.	4.2	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.	1.3	70
81	Bacterioplankton assembly and interspecies interaction indicating increasing coastal eutrophication. <i>Chemosphere</i> , 2017, 177, 317-325.	4.2	70
82	Biogeographic patterns of microbial co-occurrence ecological networks in six American forests. <i>Soil Biology and Biochemistry</i> , 2020, 148, 107897.	4.2	68
83	Network analysis infers the wilt pathogen invasion associated with non-detrimental bacteria. <i>Npj Biofilms and Microbiomes</i> , 2020, 6, 8.	2.9	68
84	Bacterioplankton community resilience to ocean acidification: evidence from microbial network analysis. <i>ICES Journal of Marine Science</i> , 2016, 73, 865-875.	1.2	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.	1.0	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.	4.6	64
87	Interdomain ecological networks between plants and microbes. <i>Molecular Ecology Resources</i> , 2019, 19, 1565-1577.	2.2	64
88	Salinity reduces bacterial diversity, but increases network complexity in Tibetan Plateau lakes. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	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.	5.3	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.	1.4	60

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91	Recurrent horizontal transfer of arsenite methyltransferase genes facilitated adaptation of life to arsenic. <i>Scientific Reports</i> , 2017, 7, 7741.	1.6	60
92	Shifts of functional gene representation in wheat rhizosphere microbial communities under elevated ozone. <i>ISME Journal</i> , 2013, 7, 660-671.	4.4	59
93	Over 150 Years of Long-Term Fertilization Alters Spatial Scaling of Microbial Biodiversity. <i>MBio</i> , 2015, 6, .	1.8	57
94	Elevated carbon dioxide accelerates the spatial turnover of soil microbial communities. <i>Global Change Biology</i> , 2016, 22, 957-964.	4.2	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	1.5	57
96	Adaptive shifts of bacterioplankton communities in response to nitrogen enrichment in a highly polluted river. <i>Environmental Pollution</i> , 2019, 245, 290-299.	3.7	55
97	Habitat environments impacted the gut microbiome of long-distance migratory swan geese but central species conserved. <i>Scientific Reports</i> , 2018, 8, 13314.	1.6	54
98	Bacterial communities and potential waterborne pathogens within the typical urban surface waters. <i>Scientific Reports</i> , 2018, 8, 13368.	1.6	54
99	Functional Gene Array-Based Ultrasensitive and Quantitative Detection of Microbial Populations in Complex Communities. <i>MSystems</i> , 2019, 4, .	1.7	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. <i>Science of the Total Environment</i> , 2019, 667, 691-700.	3.9	54
101	Dynamics of Microbial Community Composition and Function during In Situ Bioremediation of a Uranium-Contaminated Aquifer. <i>Applied and Environmental Microbiology</i> , 2011, 77, 3860-3869.	1.4	51
102	Widespread Distribution of Soluble Di-Iron Monooxygenase (SDIMO) Genes in Arctic Groundwater Impacted by 1,4-Dioxane. <i>Environmental Science & Technology</i> , 2013, 47, 9950-9958.	4.6	51
103	Elevated CO ₂ and Warming Altered Grassland Microbial Communities in Soil Top-Layers. <i>Frontiers in Microbiology</i> , 2018, 9, 1790.	1.5	51
104	Exploring the accuracy of amplicon-based internal transcribed spacer markers for a fungal community. <i>Molecular Ecology Resources</i> , 2020, 20, 170-184.	2.2	49
105	Fungal Communities Respond to Long-Term CO ₂ Elevation by Community Reassembly. <i>Applied and Environmental Microbiology</i> , 2015, 81, 2445-2454.	1.4	48
106	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.	1.6	48
107	Elevated CO ₂ influences microbial carbon and nitrogen cycling. <i>BMC Microbiology</i> , 2013, 13, 124.	1.3	47
108	Hydrogen peroxide-induced oxidative stress responses in <i>Desulfovibrio vulgaris</i> Hildenborough. <i>Environmental Microbiology</i> , 2010, 12, 2645-2657.	1.8	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.	1.5	46
110	Characterising the interspecific variations and convergence of gut microbiota in Anseriformes herbivores at wintering areas. <i>Scientific Reports</i> , 2016, 6, 32655.	1.6	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.	4.6	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.	6.5	44
113	<i>Myriophyllum aquaticum</i> Constructed Wetland Effectively Removes Nitrogen in Swine Wastewater. <i>Frontiers in Microbiology</i> , 2017, 8, 1932.	1.5	44
114	Annual Removal of Aboveground Plant Biomass Alters Soil Microbial Responses to Warming. <i>MBio</i> , 2016, 7, .	1.8	43
115	Steeper spatial scaling patterns of subsoil microbiota are shaped by deterministic assembly process. <i>Molecular Ecology</i> , 2021, 30, 1072-1085.	2.0	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.	1.4	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.	1.4	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.	3.8	42
119	Available nitrogen is the key factor influencing soil microbial functional gene diversity in tropical rainforest. <i>BMC Microbiology</i> , 2015, 15, 167.	1.3	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.	4.8	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.	1.2	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.	1.5	38
124	Functional gene arrays-based analysis of fecal microbiomes in patients with liver cirrhosis. <i>BMC Genomics</i> , 2014, 15, 753.	1.2	36
125	Toward a theory for diversity gradients: the abundance–adaptation hypothesis. <i>Ecography</i> , 2018, 41, 255-264.	2.1	36
126	NifH-Harboring Bacterial Community Composition across an Alaskan Permafrost Thaw Gradient. <i>Frontiers in Microbiology</i> , 2016, 7, 1894.	1.5	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.	1.5	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.	1.8	34
129	Continental scale structuring of forest and soil diversity via functional traits. <i>Nature Ecology and Evolution</i> , 2019, 3, 1298-1308.	3.4	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.	1.8	33
131	Forest conversion induces seasonal variation in microbial α -diversity. <i>Environmental Microbiology</i> , 2018, 20, 111-123.	1.8	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.	4.6	33
133	The PathoChip, a functional gene array for assessing pathogenic properties of diverse microbial communities. <i>ISME Journal</i> , 2013, 7, 1974-1984.	4.4	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, .	1.4	31
135	Soil microbiome mediated nutrients decline during forest degradation process. <i>Soil Ecology Letters</i> , 2019, 1, 59-71.	2.4	29
136	Orientational DNA binding and directed transport on nanomaterial heterojunctions. <i>Nanoscale</i> , 2020, 12, 5217-5226.	2.8	29
137	Stochastic processes regulate belowground community assembly in alpine grasslands on the Tibetan Plateau. <i>Environmental Microbiology</i> , 2022, 24, 179-194.	1.8	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.	0.9	27
139	Dibutyl phthalate contamination remodeled the fungal community in agro-environmental system. <i>Chemosphere</i> , 2019, 215, 189-198.	4.2	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.	1.8	27
141	Distance-Decay Relationship for Biological Wastewater Treatment Plants. <i>Applied and Environmental Microbiology</i> , 2016, 82, 4860-4866.	1.4	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.	3.9	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.	1.5	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.	3.7	26

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145	Applying GeoChip Analysis to Disparate Microbial Communities. <i>Microbe Magazine</i> , 2010, 5, 60-65.	0.4	25
146	The Succession of Bacterial Community Attached on Biodegradable Plastic Mulches During the Degradation in Soil. <i>Frontiers in Microbiology</i> , 2021, 12, 785737.	1.5	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. <i>Applied and Environmental Microbiology</i> , 2015, 81, 4164-4172.	1.4	24
148	Spatial scaling of forest soil microbial communities across a temperature gradient. <i>Environmental Microbiology</i> , 2018, 20, 3504-3513.	1.8	24
149	Contrasting Biogeographic Patterns of Bacterial and Archaeal Diversity in the Top- and Subsoils of Temperate Grasslands. <i>MSystems</i> , 2019, 4, .	1.7	24
150	Responses of Microbial Communities and Interaction Networks to Different Management Practices in Tea Plantation Soils. <i>Sustainability</i> , 2019, 11, 4428.	1.6	24
151	Meadow degradation increases spatial turnover rates of the fungal community through both niche selection and dispersal limitation. <i>Science of the Total Environment</i> , 2021, 798, 149362.	3.9	24
152	Interaction of graphene-family nanomaterials with microbial communities in sequential batch reactors revealed by high-throughput sequencing. <i>Environmental Research</i> , 2020, 184, 109392.	3.7	24
153	Taxonomic and Functional Analyses of the Supragingival Microbiome from Caries-Affected and Caries-Free Hosts. <i>Microbial Ecology</i> , 2018, 75, 543-554.	1.4	23
154	<i>Chitinophaga caeni</i> sp. nov., isolated from activated sludge. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 2209-2213.	0.8	23
155	An exploration of 3'-end processing signals and their tissue distribution in <i>Oryza sativa</i> . <i>Gene</i> , 2007, 389, 107-113.	1.0	22
156	The microbially mediated soil organic carbon loss under degenerative succession in an alpine meadow. <i>Molecular Ecology</i> , 2017, 26, 3676-3686.	2.0	22
157	Dynamic Succession of Groundwater Sulfate-Reducing Communities during Prolonged Reduction of Uranium in a Contaminated Aquifer. <i>Environmental Science & Technology</i> , 2017, 51, 3609-3620.	4.6	22
158	Microbial functional diversity covaries with permafrost thaw-induced environmental heterogeneity in tundra soil. <i>Global Change Biology</i> , 2018, 24, 297-307.	4.2	22
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