

Ye Deng

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

222
papers

13,249
citations

58
h-index

110
g-index

238
ext. papers

18,006
ext. citations

7.4
avg, IF

6.37
L-index

#	Paper	IF	Citations
222	Molecular ecological network analyses. <i>BMC Bioinformatics</i> , 2012 , 13, 113	3.6	975
221	Deep-sea oil plume enriches indigenous oil-degrading bacteria. <i>Science</i> , 2010 , 330, 204-8	33.3	906
220	Phylogenetic molecular ecological network of soil microbial communities in response to elevated CO ₂ . <i>MBio</i> , 2011 , 2,	7.8	497
219	Functional molecular ecological networks. <i>MBio</i> , 2010 , 1,	7.8	431
218	Correlation detection strategies in microbial data sets vary widely in sensitivity and precision. <i>ISME Journal</i> , 2016 , 10, 1669-81	11.9	365
217	Stochasticity, succession, and environmental perturbations in a fluidic ecosystem. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, E836-45	11.5	363
216	Microbial mediation of carbon-cycle feedbacks to climate warming. <i>Nature Climate Change</i> , 2012 , 2, 106-110	11.0	348
215	Reproducibility and quantitation of amplicon sequencing-based detection. <i>ISME Journal</i> , 2011 , 5, 1303-1311	11.9	294
214	Temperature mediates continental-scale diversity of microbes in forest soils. <i>Nature Communications</i> , 2016 , 7, 12083	17.4	271
213	High-throughput metagenomic technologies for complex microbial community analysis: open and closed formats. <i>MBio</i> , 2015 , 6,	7.8	265
212	Metagenomic insights into evolution of a heavy metal-contaminated groundwater microbial community. <i>ISME Journal</i> , 2010 , 4, 660-72	11.9	249
211	GeoChip 3.0 as a high-throughput tool for analyzing microbial community composition, structure and functional activity. <i>ISME Journal</i> , 2010 , 4, 1167-79	11.9	249
210	Global diversity and biogeography of bacterial communities in wastewater treatment plants. <i>Nature Microbiology</i> , 2019 , 4, 1183-1195	26.6	248
209	Microbial gene functions enriched in the Deepwater Horizon deep-sea oil plume. <i>ISME Journal</i> , 2012 , 6, 451-60	11.9	212
208	Metagenomic analysis reveals a marked divergence in the structure of belowground microbial communities at elevated CO ₂ . <i>Ecology Letters</i> , 2010 , 13, 564-75	10	211
207	Network succession reveals the importance of competition in response to emulsified vegetable oil amendment for uranium bioremediation. <i>Environmental Microbiology</i> , 2016 , 18, 205-18	5.2	194
206	Stochastic assembly leads to alternative communities with distinct functions in a bioreactor microbial community. <i>MBio</i> , 2013 , 4,	7.8	192

205	The microbial gene diversity along an elevation gradient of the Tibetan grassland. <i>ISME Journal</i> , 2014 , 8, 430-40	11.9	166
204	Tundra soil carbon is vulnerable to rapid microbial decomposition under climate warming. <i>Nature Climate Change</i> , 2016 , 6, 595-600	21.4	164
203	Functional gene diversity of soil microbial communities from five oil-contaminated fields in China. <i>ISME Journal</i> , 2011 , 5, 403-13	11.9	161
202	Biodiversity and species competition regulate the resilience of microbial biofilm community. <i>Molecular Ecology</i> , 2017 , 26, 6170-6182	5.7	156
201	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	11.5	142
200	GeoChip 4: a functional gene-array-based high-throughput environmental technology for microbial community analysis. <i>Molecular Ecology Resources</i> , 2014 , 14, 914-28	8.4	134
199	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	7.5	127
198	Phasing amplicon sequencing on Illumina Miseq for robust environmental microbial community analysis. <i>BMC Microbiology</i> , 2015 , 15, 125	4.5	125
197	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	7.5	124
196	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, 4840-5	11.5	124
195	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	7.5	119
194	Phylogenetic and functional gene structure shifts of the oral microbiomes in periodontitis patients. <i>ISME Journal</i> , 2014 , 8, 1879-91	11.9	114
193	Habitat-specific patterns and drivers of bacterial diversity in China's drylands. <i>ISME Journal</i> , 2017 , 11, 1345-1358	11.9	111
192	Impacts of the Three Gorges Dam on microbial structure and potential function. <i>Scientific Reports</i> , 2015 , 5, 8605	4.9	106
191	The phylogenetic composition and structure of soil microbial communities shifts in response to elevated carbon dioxide. <i>ISME Journal</i> , 2012 , 6, 259-72	11.9	95
190	Soil microbial community responses to a decade of warming as revealed by comparative metagenomics. <i>Applied and Environmental Microbiology</i> , 2014 , 80, 1777-86	4.8	94
189	Meteorological factors had more impact on airborne bacterial communities than air pollutants. <i>Science of the Total Environment</i> , 2017 , 601-602, 703-712	10.2	92
188	Land use change alters functional gene diversity, composition and abundance in Amazon forest soil microbial communities. <i>Molecular Ecology</i> , 2014 , 23, 2988-99	5.7	91

187	Responses of microbial community functional structures to pilot-scale uranium in situ bioremediation. <i>ISME Journal</i> , 2010 , 4, 1060-70	11.9	89
186	GeoChip-based analysis of functional microbial communities during the reoxidation of a bio-reduced uranium-contaminated aquifer. <i>Environmental Microbiology</i> , 2009 , 11, 2611-26	5.2	87
185	Long-term soil transplant simulating climate change with latitude significantly alters microbial temporal turnover. <i>ISME Journal</i> , 2015 , 9, 2561-72	11.9	84
184	Higher precipitation strengthens the microbial interactions in semi-arid grassland soils. <i>Global Ecology and Biogeography</i> , 2018 , 27, 570-580	6.1	83
183	Warming enhances old organic carbon decomposition through altering functional microbial communities. <i>ISME Journal</i> , 2017 , 11, 1825-1835	11.9	80
182	Functional gene differences in soil microbial communities from conventional, low-input, and organic farmlands. <i>Applied and Environmental Microbiology</i> , 2013 , 79, 1284-92	4.8	73
181	Impact of metal pollution and <i>Thlaspi caerulescens</i> growth on soil microbial communities. <i>Applied and Environmental Microbiology</i> , 2010 , 76, 7843-53	4.8	73
180	Soil organic matter quantity and quality shape microbial community compositions of subtropical broadleaved forests. <i>Molecular Ecology</i> , 2015 , 24, 5175-85	5.7	72
179	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, 991-9	4.8	71
178	Geochip-based functional gene analysis of anodophilic communities in microbial electrolysis cells under different operational modes. <i>Environmental Science & Technology</i> , 2010 , 44, 7729-35	10.3	70
177	Soil bacterial quantification approaches coupling with relative abundances reflecting the changes of taxa. <i>Scientific Reports</i> , 2017 , 7, 4837	4.9	69
176	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, 1088-94	4.8	69
175	Response of chloramphenicol-reducing biocathode resistome to continuous electrical stimulation. <i>Water Research</i> , 2019 , 148, 398-406	12.5	69
174	Evaluation of the reproducibility of amplicon sequencing with Illumina MiSeq platform. <i>PLoS ONE</i> , 2017 , 12, e0176716	3.7	66
173	Elevated carbon dioxide alters the structure of soil microbial communities. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 2991-5	4.8	66
172	Microarray-based analysis of microbial functional diversity along an oil contamination gradient in oil field. <i>FEMS Microbiology Ecology</i> , 2009 , 70, 324-33	4.3	65
171	Development of functional gene microarrays for microbial community analysis. <i>Current Opinion in Biotechnology</i> , 2012 , 23, 49-55	11.4	64
170	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	5.2	64

169	Deterministic Assembly and Diversity Gradient Altered the Biofilm Community Performances of Bioreactors. <i>Environmental Science & Technology</i> , 2019 , 53, 1315-1324	10.3	64
168	Distinct microbial communities in the active and permafrost layers on the Tibetan Plateau. <i>Molecular Ecology</i> , 2017 , 26, 6608-6620	5.7	61
167	Integrated metagenomics and network analysis of soil microbial community of the forest timberline. <i>Scientific Reports</i> , 2015 , 5, 7994	4.9	61
166	mcrA sequencing reveals the role of basophilic methanogens in a cathodic methanogenic community. <i>Water Research</i> , 2018 , 136, 192-199	12.5	60
165	Random sampling process leads to overestimation of diversity of microbial communities. <i>MBio</i> , 2013 , 4, e00324-13	7.8	58
164	Responses of bacterial community to dibutyl phthalate pollution in a soil-vegetable ecosystem. <i>Journal of Hazardous Materials</i> , 2018 , 353, 142-150	12.8	57
163	Biogeographic patterns of soil diazotrophic communities across six forests in North America. <i>Molecular Ecology</i> , 2016 , 25, 2937-48	5.7	57
162	Long-Term Oil Contamination Alters the Molecular Ecological Networks of Soil Microbial Functional Genes. <i>Frontiers in Microbiology</i> , 2016 , 7, 60	5.7	57
161	Scale-dependent effects of climate and geographic distance on bacterial diversity patterns across northern China's grasslands. <i>FEMS Microbiology Ecology</i> , 2015 , 91,	4.3	56
160	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	10.7	52
159	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	5.7	51
158	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	11.9	51
157	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	7.5	50
156	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	10.2	50
155	Comparative metagenomics reveals impact of contaminants on groundwater microbiomes. <i>Frontiers in Microbiology</i> , 2015 , 6, 1205	5.7	50
154	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	6.5	49
153	Bacterioplankton community resilience to ocean acidification: evidence from microbial network analysis. <i>ICES Journal of Marine Science</i> , 2016 , 73, 865-875	2.7	48
152	GeoChip-based analysis of microbial functional gene diversity in a landfill leachate-contaminated aquifer. <i>Environmental Science & Technology</i> , 2012 , 46, 5824-33	10.3	46

151	Widespread distribution of soluble di-iron monooxygenase (SDIMO) genes in Arctic groundwater impacted by 1,4-dioxane. <i>Environmental Science & Technology</i> , 2013 , 47, 9950-8	10.3	46
150	Bacterioplankton assembly and interspecies interaction indicating increasing coastal eutrophication. <i>Chemosphere</i> , 2017 , 177, 317-325	8.4	45
149	Deforestation decreases spatial turnover and alters the network interactions in soil bacterial communities. <i>Soil Biology and Biochemistry</i> , 2018 , 123, 80-86	7.5	44
148	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	7.5	43
147	Soil bacterial diversity patterns and drivers along an elevational gradient on Shennongjia Mountain, China. <i>Microbial Biotechnology</i> , 2015 , 8, 739-46	6.3	43
146	Dynamics of microbial community composition and function during in situ bioremediation of a uranium-contaminated aquifer. <i>Applied and Environmental Microbiology</i> , 2011 , 77, 3860-9	4.8	42
145	NCycDB: a curated integrative database for fast and accurate metagenomic profiling of nitrogen cycling genes. <i>Bioinformatics</i> , 2019 , 35, 1040-1048	7.2	42
144	Shifts of functional gene representation in wheat rhizosphere microbial communities under elevated ozone. <i>ISME Journal</i> , 2013 , 7, 660-71	11.9	41
143	Recurrent horizontal transfer of arsenite methyltransferase genes facilitated adaptation of life to arsenic. <i>Scientific Reports</i> , 2017 , 7, 7741	4.9	40
142	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	5.7	40
141	Fungal communities respond to long-term CO ₂ elevation by community reassembly. <i>Applied and Environmental Microbiology</i> , 2015 , 81, 2445-54	4.8	39
140	Hydrogen peroxide-induced oxidative stress responses in <i>Desulfovibrio vulgaris</i> Hildenborough. <i>Environmental Microbiology</i> , 2010 , 12, 2645-57	5.2	39
139	Elevated carbon dioxide accelerates the spatial turnover of soil microbial communities. <i>Global Change Biology</i> , 2016 , 22, 957-64	11.4	39
138	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	3.7	38
137	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	11.5	37
136	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	5	37
135	Latitudinal distribution of ammonia-oxidizing bacteria and archaea in the agricultural soils of eastern China. <i>Applied and Environmental Microbiology</i> , 2014 , 80, 5593-602	4.8	36
134	Elevated CO ₂ influences microbial carbon and nitrogen cycling. <i>BMC Microbiology</i> , 2013 , 13, 124	4.5	36

133	Correlation of genomic and physiological traits of thermoanaerobacter species with biofuel yields. <i>Applied and Environmental Microbiology</i> , 2011 , 77, 7998-8008	4.8	36
132	Microbial functional gene diversity with a shift of subsurface redox conditions during In Situ uranium reduction. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 2966-72	4.8	36
131	Analysis of the functional gene structure and metabolic potential of microbial community in high arsenic groundwater. <i>Water Research</i> , 2017 , 123, 268-276	12.5	35
130	Elevated CO ₂ shifts the functional structure and metabolic potentials of soil microbial communities in a C ₄ agroecosystem. <i>Scientific Reports</i> , 2015 , 5, 9316	4.9	34
129	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	12.8	33
128	Over 150 years of long-term fertilization alters spatial scaling of microbial biodiversity. <i>MBio</i> , 2015 , 6,	7.8	32
127	Exploring abundance, diversity and variation of a widespread antibiotic resistance gene in wastewater treatment plants. <i>Environment International</i> , 2018 , 117, 186-195	12.9	31
126	Bacterial communities and potential waterborne pathogens within the typical urban surface waters. <i>Scientific Reports</i> , 2018 , 8, 13368	4.9	30
125	Functional Gene Array-Based Ultrasensitive and Quantitative Detection of Microbial Populations in Complex Communities. <i>MSystems</i> , 2019 , 4,	7.6	29
124	Characterising the interspecific variations and convergence of gut microbiota in Anseriformes herbivores at wintering areas. <i>Scientific Reports</i> , 2016 , 6, 32655	4.9	29
123	Constructed Wetland Effectively Removes Nitrogen in Swine Wastewater. <i>Frontiers in Microbiology</i> , 2017 , 8, 1932	5.7	29
122	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		29
121	Adaptive shifts of bacterioplankton communities in response to nitrogen enrichment in a highly polluted river. <i>Environmental Pollution</i> , 2019 , 245, 290-299	9.3	29
120	Network analysis infers the wilt pathogen invasion associated with non-detrimental bacteria. <i>Npj Biofilms and Microbiomes</i> , 2020 , 6, 8	8.2	28
119	Habitat environments impacted the gut microbiome of long-distance migratory swan geese but central species conserved. <i>Scientific Reports</i> , 2018 , 8, 13314	4.9	28
118	Biogeographic patterns of microbial co-occurrence ecological networks in six American forests. <i>Soil Biology and Biochemistry</i> , 2020 , 148, 107897	7.5	27
117	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, 13510-22	4.6	27
116	Toward a theory for diversity gradients: the abundance-adaptation hypothesis. <i>Ecography</i> , 2018 , 41, 2556-2564	26	26

115	Warming Alters Expressions of Microbial Functional Genes Important to Ecosystem Functioning. <i>Frontiers in Microbiology</i> , 2016 , 7, 668	5.7	26
114	-Harboring Bacterial Community Composition across an Alaskan Permafrost Thaw Gradient. <i>Frontiers in Microbiology</i> , 2016 , 7, 1894	5.7	26
113	Elevated CO and Warming Altered Grassland Microbial Communities in Soil Top-Layers. <i>Frontiers in Microbiology</i> , 2018 , 9, 1790	5.7	26
112	Available nitrogen is the key factor influencing soil microbial functional gene diversity in tropical rainforest. <i>BMC Microbiology</i> , 2015 , 15, 167	4.5	25
111	Forest conversion induces seasonal variation in microbial diversity. <i>Environmental Microbiology</i> , 2018 , 20, 111-123	5.2	25
110	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	10.2	24
109	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	3.4	24
108	The PathoChip, a functional gene array for assessing pathogenic properties of diverse microbial communities. <i>ISME Journal</i> , 2013 , 7, 1974-84	11.9	24
107	Functional gene arrays-based analysis of fecal microbiomes in patients with liver cirrhosis. <i>BMC Genomics</i> , 2014 , 15, 753	4.5	24
106	Exploring the accuracy of amplicon-based internal transcribed spacer markers for a fungal community. <i>Molecular Ecology Resources</i> , 2020 , 20, 170-184	8.4	23
105	Dramatic Increases of Soil Microbial Functional Gene Diversity at the Treeline Ecotone of Changbai Mountain. <i>Frontiers in Microbiology</i> , 2016 , 7, 1184	5.7	23
104	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	7.9	22
103	Electron acceptors for anaerobic oxidation of methane drive microbial community structure and diversity in mud volcanoes. <i>Environmental Microbiology</i> , 2018 , 20, 2370-2385	5.2	22
102	Interdomain ecological networks between plants and microbes. <i>Molecular Ecology Resources</i> , 2019 , 19, 1565-1577	8.4	22
101	An exploration of 3Send processing signals and their tissue distribution in <i>Oryza sativa</i> . <i>Gene</i> , 2007 , 389, 107-13	3.8	22
100	Salinity reduces bacterial diversity, but increases network complexity in Tibetan Plateau lakes. <i>FEMS Microbiology Ecology</i> , 2019 , 95,	4.3	22
99	Linking NO Emissions from Biofertilizer-Amended Soil of Tea Plantations to the Abundance and Structure of NO-Reducing Microbial Communities. <i>Environmental Science & Technology</i> , 2018 , 52, 11338-11345	10.3	21
98	Applying GeoChip Analysis to Disparate Microbial Communities. <i>Microbe Magazine</i> , 2010 , 5, 60-65		20

97	Distance-Decay Relationship for Biological Wastewater Treatment Plants. <i>Applied and Environmental Microbiology</i> , 2016 , 82, 4860-6	4.8	19
96	Electro-driven methanogenic microbial community diversity and variability in the electron abundant niche. <i>Science of the Total Environment</i> , 2019 , 661, 178-186	10.2	18
95	Dynamic Succession of Groundwater Functional Microbial Communities in Response to Emulsified Vegetable Oil Amendment during Sustained In Situ U(VI) Reduction. <i>Applied and Environmental Microbiology</i> , 2015 , 81, 4164-72	4.8	18
94	Identifying qualitative effects of different grazing types on below-ground communities and function in a long-term field experiment. <i>Environmental Microbiology</i> , 2015 , 17, 841-54	5.2	17
93	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	4.2	17
92	Continental scale structuring of forest and soil diversity via functional traits. <i>Nature Ecology and Evolution</i> , 2019 , 3, 1298-1308	12.3	17
91	Analyses of the influencing factors of soil microbial functional gene diversity in tropical rainforest based on GeoChip 5.0. <i>Genomics Data</i> , 2015 , 5, 397-8		17
90	Temperature and microbial interactions drive the deterministic assembly processes in sediments of hot springs. <i>Science of the Total Environment</i> , 2021 , 772, 145465	10.2	17
89	A Slow-Release Substrate Stimulates Groundwater Microbial Communities for Long-Term in Situ Cr(VI) Reduction. <i>Environmental Science & Technology</i> , 2015 , 49, 12922-31	10.3	16
88	Oriental DNA binding and directed transport on nanomaterial heterojunctions. <i>Nanoscale</i> , 2020 , 12, 5217-5226	7.7	16
87	Spatial scaling of forest soil microbial communities across a temperature gradient. <i>Environmental Microbiology</i> , 2018 , 20, 3504-3513	5.2	16
86	Design and analysis of mismatch probes for long oligonucleotide microarrays. <i>BMC Genomics</i> , 2008 , 9, 491	4.5	16
85	Dibutyl phthalate contamination remolded the fungal community in agro-environmental system. <i>Chemosphere</i> , 2019 , 215, 189-198	8.4	16
84	StressChip as a high-throughput tool for assessing microbial community responses to environmental stresses. <i>Environmental Science & Technology</i> , 2013 , 47, 9841-9	10.3	15
83	Large-scale expressed sequence tag analysis for the chestnut blight fungus <i>Cryphonectria parasitica</i> . <i>Fungal Genetics and Biology</i> , 2008 , 45, 319-27	3.9	15
82	Temperature sensitivity of SOM decomposition is linked with a K-selected microbial community. <i>Global Change Biology</i> , 2021 , 27, 2763-2779	11.4	15
81	Annual Removal of Aboveground Plant Biomass Alters Soil Microbial Responses to Warming. <i>MBio</i> , 2016 , 7,	7.8	15
80	Dynamic Succession of Groundwater Sulfate-Reducing Communities during Prolonged Reduction of Uranium in a Contaminated Aquifer. <i>Environmental Science & Technology</i> , 2017 , 51, 3609-3620	10.3	14

79	The shift of microbial communities and their roles in sulfur and iron cycling in a copper ore bioleaching system. <i>Scientific Reports</i> , 2016 , 6, 34744	4.9	14
78	Interaction of graphene-family nanomaterials with microbial communities in sequential batch reactors revealed by high-throughput sequencing. <i>Environmental Research</i> , 2020 , 184, 109392	7.9	14
77	Taxonomic and Functional Analyses of the Supragingival Microbiome from Caries-Affected and Caries-Free Hosts. <i>Microbial Ecology</i> , 2018 , 75, 543-554	4.4	13
76	Soil microbiome mediated nutrients decline during forest degradation process. <i>Soil Ecology Letters</i> , 2019 , 1, 59-71	2.7	13
75	Development of HuMiChip for functional profiling of human microbiomes. <i>PLoS ONE</i> , 2014 , 9, e90546	3.7	13
74	The microbially mediated soil organic carbon loss under degenerative succession in an alpine meadow. <i>Molecular Ecology</i> , 2017 , 26, 3676-3686	5.7	12
73	Responses of Microbial Communities and Interaction Networks to Different Management Practices in Tea Plantation Soils. <i>Sustainability</i> , 2019 , 11, 4428	3.6	12
72	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	4.2	12
71	Microbial functional diversity covaries with permafrost thaw-induced environmental heterogeneity in tundra soil. <i>Global Change Biology</i> , 2018 , 24, 297-307	11.4	12
70	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,	4.8	12
69	Soil bacterial endemism and potential functional redundancy in natural broadleaf forest along a latitudinal gradient. <i>Scientific Reports</i> , 2016 , 6, 28819	4.9	12
68	Geographical Distribution of Methanogenic Archaea in Nine Representative Paddy Soils in China. <i>Frontiers in Microbiology</i> , 2016 , 7, 1447	5.7	12
67	Assembly Patterns of the Rhizosphere Microbiome Along the Longitudinal Root Axis of Maize (L.). <i>Frontiers in Microbiology</i> , 2021 , 12, 614501	5.7	12
66	Florfenicol restructured the microbial interaction network for wastewater treatment by microbial electrolysis cells. <i>Environmental Research</i> , 2020 , 183, 109145	7.9	11
65	Impact of Rural Domestic Wastewater Irrigation on the Physicochemical and Microbiological Properties of Pakchoi and Soil. <i>Water (Switzerland)</i> , 2015 , 7, 1825-1839	3	11
64	Saliva microbiota carry caries-specific functional gene signatures. <i>PLoS ONE</i> , 2014 , 9, e76458	3.7	11
63	Chitinophaga caeni sp. nov., isolated from activated sludge. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018 , 68, 2209-2213	2.2	11
62	Characterization and Genomic Analysis of a Highly Efficient Dibutyl Phthalate-Degrading Bacterium Gordonia sp. Strain QH-12. <i>International Journal of Molecular Sciences</i> , 2016 , 17,	6.3	11

61	Contrasting Biogeographic Patterns of Bacterial and Archaeal Diversity in the Top- and Subsoils of Temperate Grasslands. <i>MSystems</i> , 2019 , 4,	7.6	10
60	Strain/species-specific probe design for microbial identification microarrays. <i>Applied and Environmental Microbiology</i> , 2013 , 79, 5085-8	4.8	10
59	Succession of microbial functional communities in response to a pilot-scale ethanol-blended fuel release throughout the plume life cycle. <i>Environmental Pollution</i> , 2015 , 198, 154-60	9.3	9
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