

# Zhili He

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1545331/publications.pdf>

Version: 2024-02-01

315  
papers

26,545  
citations

7551

77  
h-index

8835

145  
g-index

325  
all docs

325  
docs citations

325  
times ranked

19977  
citing authors

#	ARTICLE	IF	CITATIONS
1	Functional microbial community structures and chemical properties indicated mechanisms and potential risks of urban river eco-remediation. <i>Science of the Total Environment</i> , 2022, 803, 149868.	3.9	8
2	Environmental effects of nanoparticles on the ecological succession of gut microbiota across zebrafish development. <i>Science of the Total Environment</i> , 2022, 806, 150963.	3.9	22
3	Biogeography of soil protistan consumer and parasite is contrasting and linked to microbial nutrient mineralization in forest soils at a wide-scale. <i>Soil Biology and Biochemistry</i> , 2022, 165, 108513.	4.2	10
4	Extracellular proteins of <i>Desulfovibrio vulgaris</i> as adsorbents and redox shuttles promote biomineralization of antimony. <i>Journal of Hazardous Materials</i> , 2022, 426, 127795.	6.5	13
5	MCycDB: A curated database for comprehensively profiling methane cycling processes of environmental microbiomes. <i>Molecular Ecology Resources</i> , 2022, 22, 1803-1823.	2.2	16
6	Environmental Filtering by pH and Salinity Jointly Drives Prokaryotic Community Assembly in Coastal Wetland Sediments. <i>Frontiers in Marine Science</i> , 2022, 8, .	1.2	17
7	Environmental risk characteristics of bacterial antibiotic resistome in Antarctic krill. <i>Ecotoxicology and Environmental Safety</i> , 2022, 232, 113289.	2.9	9
8	Complex Bilateral Interactions Determine the Fate of Polystyrene Micro- and Nanoplastics and Soil Protists: Implications from a Soil Amoeba. <i>Environmental Science &amp; Technology</i> , 2022, 56, 4936-4949.	4.6	25
9	Ecological stability of microbial communities in Lake Donghu regulated by keystone taxa. <i>Ecological Indicators</i> , 2022, 136, 108695.	2.6	95
10	Interactions and Stability of Gut Microbiota in Zebrafish Increase with Host Development. <i>Microbiology Spectrum</i> , 2022, 10, e0169621.	1.2	11
11	Organic carbon and eukaryotic predation synergistically change resistance and resilience of aquatic microbial communities. <i>Science of the Total Environment</i> , 2022, 830, 154386.	3.9	7
12	Symbiont-Induced Phagosome Changes Rather than Extracellular Discrimination Contribute to the Formation of Social Amoeba Farming Symbiosis. <i>Microbiology Spectrum</i> , 2022, , e0172721.	1.2	6
13	Soil Amoebae Affect Iron and Chromium Reduction through Preferential Predation between Two Metal-Reducing Bacteria. <i>Environmental Science &amp; Technology</i> , 2022, 56, 9052-9062.	4.6	11
14	Organic fertilizer potentiates the transfer of typical antibiotic resistance gene among special bacterial species. <i>Journal of Hazardous Materials</i> , 2022, 435, 128985.	6.5	15
15	Nitrite and nitrate reduction drive sediment microbial nitrogen cycling in a eutrophic lake. <i>Water Research</i> , 2022, 220, 118637.	5.3	28
16	Evaluation of different primers of the 18S rRNA gene to profile amoeba communities in environmental samples. , 2022, 1, 100057.		5
17	PCycDB: a comprehensive and accurate database for fast analysis of phosphorus cycling genes. <i>Microbiome</i> , 2022, 10, .	4.9	30
18	Enhanced microbial nitrification-denitrification processes in a subtropical metropolitan river network. <i>Water Research</i> , 2022, 222, 118857.	5.3	19

#	ARTICLE	IF	CITATIONS
19	The Ecology and Evolution of Amoeba-Bacterium Interactions. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	42
20	Elevated nitrate simplifies microbial community compositions and interactions in sulfide-rich river sediments. <i>Science of the Total Environment</i> , 2021, 750, 141513.	3.9	21
21	Coexistence between antibiotic resistance genes and metal resistance genes in manure-fertilized soils. <i>Geoderma</i> , 2021, 382, 114760.	2.3	38
22	Host-microbiota interactions and responses to grass carp reovirus infection in <i>Ctenopharyngodon idellus</i> . <i>Environmental Microbiology</i> , 2021, 23, 431-447.	1.8	30
23	Microbially-driven sulfur cycling microbial communities in different mangrove sediments. <i>Chemosphere</i> , 2021, 273, 128597.	4.2	39
24	Synergistic interactions of <i>Desulfovibrio</i> and <i>Petrimonas</i> for sulfate-reduction coupling polycyclic aromatic hydrocarbon degradation. <i>Journal of Hazardous Materials</i> , 2021, 407, 124385.	6.5	46
25	Mechanistic insights into organic carbon-driven water blackening and odorization of urban rivers. <i>Journal of Hazardous Materials</i> , 2021, 405, 124663.	6.5	56
26	Water content as a primary parameter determines microbial reductive dechlorination activities in soil. <i>Chemosphere</i> , 2021, 267, 129152.	4.2	8
27	SCycDB: A curated functional gene database for metagenomic profiling of sulphur cycling pathways. <i>Molecular Ecology Resources</i> , 2021, 21, 924-940.	2.2	52
28	Sediment resuspension drives protist metacommunity structure and assembly in grass carp ( <i>Ctenopharyngodon idella</i> ) aquaculture ponds. <i>Science of the Total Environment</i> , 2021, 764, 142840.	3.9	19
29	Prevalence of antibiotic resistance genes and bacterial pathogens along the soil-mangrove root continuum. <i>Journal of Hazardous Materials</i> , 2021, 408, 124985.	6.5	27
30	Toxic and protective mechanisms of cyanobacterium <i>Synechocystis</i> sp. in response to titanium dioxide nanoparticles. <i>Environmental Pollution</i> , 2021, 274, 116508.	3.7	19
31	Spatial Distribution, Bioconversion and Ecological Risk of PCBs and PBDEs in the Surface Sediment of Contaminated Urban Rivers: A Nationwide Study in China. <i>Environmental Science &amp; Technology</i> , 2021, 55, 9579-9590.	4.6	50
32	Light modulates the effect of antibiotic norfloxacin on photosynthetic processes of <i>Microcystis aeruginosa</i> . <i>Aquatic Toxicology</i> , 2021, 235, 105826.	1.9	8
33	Substrate-dependent competition and cooperation relationships between <i>Geobacter</i> and <i>Dehalococcoides</i> for their organohalide respiration. <i>ISME Communications</i> , 2021, 1, .	1.7	27
34	A dormant amoeba species can selectively sense and predate on different soil bacteria. <i>Functional Ecology</i> , 2021, 35, 1708-1721.	1.7	18
35	VB <sub>12</sub> Path for Accurate Metagenomic Profiling of Microbially Driven Cobalamin Synthesis Pathways. <i>MSystems</i> , 2021, 6, e0049721.	1.7	5
36	Synergistic effects of antimony and arsenic contaminations on bacterial, archaeal and fungal communities in the rhizosphere of <i>Miscanthus sinensis</i> : Insights for nitrification and carbon mineralization. <i>Journal of Hazardous Materials</i> , 2021, 411, 125094.	6.5	42

#	ARTICLE	IF	CITATIONS
37	Microbial sulfur metabolism and environmental implications. <i>Science of the Total Environment</i> , 2021, 778, 146085.	3.9	80
38	Metagenomic insights into the effects of submerged plants on functional potential of microbial communities in wetland sediments. <i>Marine Life Science and Technology</i> , 2021, 3, 405-415.	1.8	19
39	Bacteria-driven phthalic acid ester biodegradation: Current status and emerging opportunities. <i>Environment International</i> , 2021, 154, 106560.	4.8	66
40	Resistance and Resilience of Fish Gut Microbiota to Silver Nanoparticles. <i>MSystems</i> , 2021, 6, e0063021.	1.7	17
41	Co-symbiosis of arbuscular mycorrhizal fungi (AMF) and diazotrophs promote biological nitrogen fixation in mangrove ecosystems. <i>Soil Biology and Biochemistry</i> , 2021, 161, 108382.	4.2	34
42	Stimulation of soil microbial functioning by elevated CO <sub>2</sub> may surpass effects mediated by irrigation in a semiarid grassland. <i>Geoderma</i> , 2021, 401, 115162.	2.3	10
43	Alkaline phosphatase activity mediates soil organic phosphorus mineralization in a subalpine forest ecosystem. <i>Geoderma</i> , 2021, 404, 115376.	2.3	60
44	Pollution alters methanogenic and methanotrophic communities and increases dissolved methane in small ponds. <i>Science of the Total Environment</i> , 2021, 801, 149723.	3.9	8
45	Host development overwhelms environmental dispersal in governing the ecological succession of zebrafish gut microbiota. <i>Npj Biofilms and Microbiomes</i> , 2021, 7, 5.	2.9	64
46	Genetic Elucidation of Quorum Sensing and Cobamide Biosynthesis in Divergent Bacterial-Fungal Associations Across the Soil-Mangrove Root Interface. <i>Frontiers in Microbiology</i> , 2021, 12, 698385.	1.5	0
47	Depth-dependent variability of biological nitrogen fixation and diazotrophic communities in mangrove sediments. <i>Microbiome</i> , 2021, 9, 212.	4.9	24
48	Environmental Water and Sediment Microbial Communities Shape Intestine Microbiota for Host Health: The Central Dogma in an Anthropogenic Aquaculture Ecosystem. <i>Frontiers in Microbiology</i> , 2021, 12, 772149.	1.5	8
49	Genome-Centric Metagenomic Insights into the Impact of Alkaline/Acid and Thermal Sludge Pretreatment on the Microbiome in Digestion Sludge. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	12
50	Microbial functional genes commonly respond to elevated carbon dioxide. <i>Environment International</i> , 2020, 144, 106068.	4.8	20
51	Protection of <i>Siganus oramin</i> , rabbitfish, from heavy metal toxicity by the selenium-enriched seaweed <i>Gracilaria lemaneiformis</i> . <i>Ecotoxicology and Environmental Safety</i> , 2020, 206, 111183.	2.9	10
52	Gene-informed decomposition model predicts lower soil carbon loss due to persistent microbial adaptation to warming. <i>Nature Communications</i> , 2020, 11, 4897.	5.8	67
53	Differential distribution of and similar biochemical responses to different species of arsenic and antimony in <i>Vetiveria zizanioides</i> . <i>Environmental Geochemistry and Health</i> , 2020, 42, 3995-4010.	1.8	11
54	Diversity, function and assembly of mangrove root-associated microbial communities at a continuous fine-scale. <i>Npj Biofilms and Microbiomes</i> , 2020, 6, 52.	2.9	68

#	ARTICLE	IF	CITATIONS
55	Experimental evolution reveals nitrate tolerance mechanisms in <i>Desulfovibrio vulgaris</i> . ISME Journal, 2020, 14, 2862-2876.	4.4	10
56	Effects of Titanium Dioxide Nanoparticles on Photosynthetic and Antioxidative Processes of <i>Scenedesmus obliquus</i> . Plants, 2020, 9, 1748.	1.6	19
57	Microbial functional gene diversity in natural secondary forest Ultisols. Acta Oecologica, 2020, 105, 103575.	0.5	1
58	Biogeographic patterns of microbial co-occurrence ecological networks in six American forests. Soil Biology and Biochemistry, 2020, 148, 107897.	4.2	68
59	Organohalide-Respiring Bacteria in Polluted Urban Rivers Employ Novel Bifunctional Reductive Dehalogenases to Dechlorinate Polychlorinated Biphenyls and Tetrachloroethene. Environmental Science & Technology, 2020, 54, 8791-8800.	4.6	61
60	Structure and distribution of nitrite-dependent anaerobic methane oxidation bacteria vary with water tables in Zoige peatlands. FEMS Microbiology Ecology, 2020, 96, .	1.3	14
61	Size-fractionated aggregates within phycosphere define functional bacterial communities related to <i>Microcystis aeruginosa</i> and <i>Euglena sanguinea</i> blooms. Aquatic Ecology, 2020, 54, 609-623.	0.7	3
62	Post-agricultural tropical forest regeneration shifts soil microbial functional potential for carbon and nutrient cycling. Soil Biology and Biochemistry, 2020, 145, 107784.	4.2	12
63	<i>Sonneratia apetala</i> introduction alters methane cycling microbial communities and increases methane emissions in mangrove ecosystems. Soil Biology and Biochemistry, 2020, 144, 107775.	4.2	42
64	The Beta-Diversity of <i>Siganus fuscescens</i> -Associated Microbial Communities From Different Habitats Increases With Body Weight. Frontiers in Microbiology, 2020, 11, 1562.	1.5	9
65	Fish growth enhances microbial sulfur cycling in aquaculture pond sediments. Microbial Biotechnology, 2020, 13, 1597-1610.	2.0	17
66	Functional Associations and Resilience in Microbial Communities. Microorganisms, 2020, 8, 951.	1.6	11
67	Distinct mechanisms shape soil bacterial and fungal co-occurrence networks in a mountain ecosystem. FEMS Microbiology Ecology, 2020, 96, .	1.3	62
68	Bacterial community responses to tourism development in the Xixi National Wetland Park, China. Science of the Total Environment, 2020, 720, 137570.	3.9	40
69	Warming-induced permafrost thaw exacerbates tundra soil carbon decomposition mediated by microbial community. Microbiome, 2020, 8, 3.	4.9	75
70	Revealing structure and assembly for rhizophyte-endophyte diazotrophic community in mangrove ecosystem after introduced <i>Sonneratia apetala</i> and <i>Laguncularia racemosa</i> . Science of the Total Environment, 2020, 721, 137807.	3.9	35
71	Small and mighty: adaptation of superphylum Patescibacteria to groundwater environment drives their genome simplicity. Microbiome, 2020, 8, 51.	4.9	205
72	Functional structures of soil microbial community relate to contrasting N <sub>2</sub> O emission patterns from a highly acidified forest. Science of the Total Environment, 2020, 725, 138504.	3.9	10

#	ARTICLE	IF	CITATIONS
73	Keystone taxa of water microbiome respond to environmental quality and predict water contamination. <i>Environmental Research</i> , 2020, 187, 109666.	3.7	33
74	Stimulation of soil respiration by elevated CO <sub>2</sub> is enhanced under nitrogen limitation in a decade-long grassland study. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 33317-33324.	3.3	34
75	The Impact of Anthropogenic Disturbance on Bacterioplankton Communities During the Construction of Donghu Tunnel (Wuhan, China). <i>Microbial Ecology</i> , 2019, 77, 277-287.	1.4	17
76	Continental scale structuring of forest and soil diversity via functional traits. <i>Nature Ecology and Evolution</i> , 2019, 3, 1298-1308.	3.4	34
77	Responses of tundra soil microbial communities to half a decade of experimental warming at two critical depths. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 15096-15105.	3.3	83
78	Interdomain ecological networks between plants and microbes. <i>Molecular Ecology Resources</i> , 2019, 19, 1565-1577.	2.2	64
79	Functional Gene Array-Based Ultrasensitive and Quantitative Detection of Microbial Populations in Complex Communities. <i>MSystems</i> , 2019, 4, .	1.7	54
80	Global diversity and biogeography of bacterial communities in wastewater treatment plants. <i>Nature Microbiology</i> , 2019, 4, 1183-1195.	5.9	491
81	Thermal disruption of soil bacterial assemblages decreases diversity and assemblage similarity. <i>Ecosphere</i> , 2019, 10, e02598.	1.0	2
82	Unraveling the diversity of sedimentary sulfate-reducing prokaryotes (SRP) across Tibetan saline lakes using epicPCR. <i>Microbiome</i> , 2019, 7, 71.	4.9	16
83	Floc-size effects of the pathogenic bacteria in a membrane bioreactor plant. <i>Environment International</i> , 2019, 127, 645-652.	4.8	10
84	Long-Term Warming in Alaska Enlarges the Diazotrophic Community in Deep Soils. <i>MBio</i> , 2019, 10, .	1.8	22
85	Climate warming accelerates temporal scaling of grassland soil microbial biodiversity. <i>Nature Ecology and Evolution</i> , 2019, 3, 612-619.	3.4	82
86	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
87	Protection of dietary selenium-enriched seaweed <i>Gracilaria lemaneiformis</i> against cadmium toxicity to abalone <i>Haliotis discus hannai</i> . <i>Ecotoxicology and Environmental Safety</i> , 2019, 171, 398-405.	2.9	21
88	Mangrove Sediment Microbiome: Adaptive Microbial Assemblages and Their Routed Biogeochemical Processes in Yunxiao Mangrove National Nature Reserve, China. <i>Microbial Ecology</i> , 2019, 78, 57-69.	1.4	66
89	Impacts of hydroxyphenylpyruvate dioxygenase (HPPD) inhibitor (mesotrione) on photosynthetic processes in <i>Chlamydomonas reinhardtii</i> . <i>Environmental Pollution</i> , 2019, 244, 295-303.	3.7	26
90	Microbial Functional Gene Diversity Predicts Groundwater Contamination and Ecosystem Functioning. <i>MBio</i> , 2018, 9, .	1.8	57

#	ARTICLE	IF	CITATIONS
91	Temperature determines the diversity and structure of N <sub>2</sub> -fixing microbial assemblages. <i>Functional Ecology</i> , 2018, 32, 1867-1878.	1.7	19
92	Electron transport chains in organohalide-respiring bacteria and bioremediation implications. <i>Biotechnology Advances</i> , 2018, 36, 1194-1206.	6.0	108
93	Oral microbiota of periodontal health and disease and their changes after nonsurgical periodontal therapy. <i>ISME Journal</i> , 2018, 12, 1210-1224.	4.4	188
94	Cultivation of seaweed <i>Gracilaria lemaneiformis</i> enhanced biodiversity in a eukaryotic plankton community as revealed via metagenomic analyses. <i>Molecular Ecology</i> , 2018, 27, 1081-1093.	2.0	35
95	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
96	Development of an Efficient Genome Editing Tool in <i>Bacillus licheniformis</i> Using CRISPR-Cas9 Nickase. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	74
97	Toward a theory for diversity gradients: the abundance–adaptation hypothesis. <i>Ecography</i> , 2018, 41, 255-264.	2.1	36
98	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
99	Divergent Responses of Forest Soil Microbial Communities under Elevated CO <sub>2</sub> in Different Depths of Upper Soil Layers. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	31
100	Enhanced synthesis of poly gamma glutamic acid by increasing the intracellular reactive oxygen species in the <i>Bacillus licheniformis</i> 1-pyrroline-5-carboxylate dehydrogenase gene <i>ycgN</i> -deficient strain. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 10127-10137.	1.7	9
101	Plant roots alter microbial functional genes supporting root litter decomposition. <i>Soil Biology and Biochemistry</i> , 2018, 127, 90-99.	4.2	35
102	Elevated CO <sub>2</sub> and Warming Altered Grassland Microbial Communities in Soil Top-Layers. <i>Frontiers in Microbiology</i> , 2018, 9, 1790.	1.5	51
103	Spatial scaling of forest soil microbial communities across a temperature gradient. <i>Environmental Microbiology</i> , 2018, 20, 3504-3513.	1.8	24
104	Taxonomic and Functional Responses of Soil Microbial Communities to Annual Removal of Aboveground Plant Biomass. <i>Frontiers in Microbiology</i> , 2018, 9, 954.	1.5	11
105	Climate warming leads to divergent succession of grassland microbial communities. <i>Nature Climate Change</i> , 2018, 8, 813-818.	8.1	208
106	Proteogenomic Analyses Revealed Favorable Metabolism Pattern Alterations in Rotifer <i>Brachionus plicatilis</i> Fed with Selenium-rich <i>Chlorella</i> . <i>Journal of Agricultural and Food Chemistry</i> , 2018, 66, 6699-6707.	2.4	17
107	The differentiation of soil bacterial communities along a precipitation and temperature gradient in the eastern Inner Mongolia steppe. <i>Catena</i> , 2017, 152, 47-56.	2.2	87
108	Metabolic and phylogenetic profiles of microbial communities from a mariculture base on the Chinese Guangdong coast. <i>Fisheries Science</i> , 2017, 83, 465-477.	0.7	11



#	ARTICLE	IF	CITATIONS
109	Microbial taxa and functional genes shift in degraded soil with bacterial wilt. <i>Scientific Reports</i> , 2017, 7, 39911.	1.6	63
110	Warming enhances old organic carbon decomposition through altering functional microbial communities. <i>ISME Journal</i> , 2017, 11, 1825-1835.	4.4	136
111	Large-scale seaweed cultivation diverges water and sediment microbial communities in the coast of Nan'ao Island, South China Sea. <i>Science of the Total Environment</i> , 2017, 598, 97-108.	3.9	49
112	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
113	Correspondence: Reply to "Analytical flaws in a continental-scale forest soil microbial diversity study". <i>Nature Communications</i> , 2017, 8, 15583.	5.8	4
114	Alpine soil carbon is vulnerable to rapid microbial decomposition under climate cooling. <i>ISME Journal</i> , 2017, 11, 2102-2111.	4.4	33
115	Lichenysin production is improved in <i>codY</i> null <i>Bacillus licheniformis</i> by addition of precursor amino acids. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 6375-6383.	1.7	16
116	A novel method to determine the minimum number of sequences required for reliable microbial community analysis. <i>Journal of Microbiological Methods</i> , 2017, 139, 196-201.	0.7	44
117	Dynamic Succession of Groundwater Sulfate-Reducing Communities during Prolonged Reduction of Uranium in a Contaminated Aquifer. <i>Environmental Science &amp; Technology</i> , 2017, 51, 3609-3620.	4.6	22
118	Metagenomic reconstruction of nitrogen cycling pathways in a CO <sub>2</sub> -enriched grassland ecosystem. <i>Soil Biology and Biochemistry</i> , 2017, 106, 99-108.	4.2	63
119	Microbial functional trait of rRNA operon copy numbers increases with organic levels in anaerobic digesters. <i>ISME Journal</i> , 2017, 11, 2874-2878.	4.4	70
120	Biodiversity and species competition regulate the resilience of microbial biofilm community. <i>Molecular Ecology</i> , 2017, 26, 6170-6182.	2.0	299
121	Key Metabolites and Mechanistic Changes for Salt Tolerance in an Experimentally Evolved Sulfate-Reducing Bacterium, <i>Desulfovibrio vulgaris</i> . <i>MBio</i> , 2017, 8, .	1.8	13
122	Interconnection of Key Microbial Functional Genes for Enhanced Benzo[ <i>a</i> ]pyrene Biodegradation in Sediments by Microbial Electrochemistry. <i>Environmental Science &amp; Technology</i> , 2017, 51, 8519-8529.	4.6	64
123	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
124	HuMiChip2 for strain level identification and functional profiling of human microbiomes. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 423-435.	1.7	16
125	Functional Gene Diversity and Metabolic Potential of the Microbial Community in an Estuary-Shelf Environment. <i>Frontiers in Microbiology</i> , 2017, 8, 1153.	1.5	25
126	Dehalococcoides as a Potential Biomarker Evidence for Uncharacterized Organohalides in Environmental Samples. <i>Frontiers in Microbiology</i> , 2017, 8, 1677.	1.5	18



#	ARTICLE	IF	CITATIONS
127	Cas9 Nickase-Assisted RNA Repression Enables Stable and Efficient Manipulation of Essential Metabolic Genes in <i>Clostridium cellulolyticum</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 1744.	1.5	19
128	Environmental Factors Shape Water Microbial Community Structure and Function in Shrimp Cultural Enclosure Ecosystems. <i>Frontiers in Microbiology</i> , 2017, 8, 2359.	1.5	137
129	Bacterial community and arsenic functional genes diversity in arsenic contaminated soils from different geographic locations. <i>PLoS ONE</i> , 2017, 12, e0176696.	1.1	40
130	Metagenomics Reveals Pervasive Bacterial Populations and Reduced Community Diversity across the Alaska Tundra Ecosystem. <i>Frontiers in Microbiology</i> , 2016, 7, 579.	1.5	66
131	Warming Alters Expressions of Microbial Functional Genes Important to Ecosystem Functioning. <i>Frontiers in Microbiology</i> , 2016, 7, 668.	1.5	46
132	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
133	Elevated carbon dioxide accelerates the spatial turnover of soil microbial communities. <i>Global Change Biology</i> , 2016, 22, 957-964.	4.2	57
134	The interconnected rhizosphere: High network complexity dominates rhizosphere assemblages. <i>Ecology Letters</i> , 2016, 19, 926-936.	3.0	803
135	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.	1.8	339
136	Lateral Gene Transfer in a Heavy Metal-Contaminated-Groundwater Microbial Community. <i>MBio</i> , 2016, 7, e02234-15.	1.8	105
137	Annual Removal of Aboveground Plant Biomass Alters Soil Microbial Responses to Warming. <i>MBio</i> , 2016, 7, .	1.8	43
138	Long-term successional dynamics of microbial association networks in anaerobic digestion processes. <i>Water Research</i> , 2016, 104, 1-10.	5.3	177
139	Temperature mediates continental-scale diversity of microbes in forest soils. <i>Nature Communications</i> , 2016, 7, 12083.	5.8	419
140	The shifts of sediment microbial community phylogenetic and functional structures during chromium (VI) reduction. <i>Ecotoxicology</i> , 2016, 25, 1759-1770.	1.1	48
141	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.	1.6	18
142	A comprehensive insight into functional profiles of free-living microbial community responses to a toxic <i>Akashiwo sanguinea</i> bloom. <i>Scientific Reports</i> , 2016, 6, 34645.	1.6	25
143	Differential Regulation of the Two Ferrochelatase Paralogues in <i>Shewanella loihica</i> PV-4 in Response to Environmental Stresses. <i>Applied and Environmental Microbiology</i> , 2016, 82, 5077-5088.	1.4	5
144	Biogeographic patterns of soil diazotrophic communities across six forests in the North America. <i>Molecular Ecology</i> , 2016, 25, 2937-2948.	2.0	76

#	ARTICLE	IF	CITATIONS
145	Environmental filtering decreases with fish development for the assembly of gut microbiota. <i>Environmental Microbiology</i> , 2016, 18, 4739-4754.	1.8	267
146	Effects of <i>Bacillus amyloliquefaciens</i> ZM9 on bacterial wilt and rhizosphere microbial communities of tobacco. <i>Applied Soil Ecology</i> , 2016, 103, 1-12.	2.1	71
147	Microbial genetic and enzymatic responses to an anthropogenic phosphorus gradient within a subtropical peatland. <i>Geoderma</i> , 2016, 268, 119-127.	2.3	30
148	Tundra soil carbon is vulnerable to rapid microbial decomposition under climate warming. <i>Nature Climate Change</i> , 2016, 6, 595-600.	8.1	260
149	Predicting taxonomic and functional structure of microbial communities in acid mine drainage. <i>ISME Journal</i> , 2016, 10, 1527-1539.	4.4	130
150	The Diversity and Co-occurrence Patterns of N <sub>2</sub> -Fixing Communities in a CO <sub>2</sub> -Enriched Grassland Ecosystem. <i>Microbial Ecology</i> , 2016, 71, 604-615.	1.4	52
151	NOVEL INSIGHT INTO EVOLUTIONARY PROCESS FROM AVERAGE GENOME SIZE IN MARINE BACTERIOPLANKTONIC BIOTA. <i>Applied Ecology and Environmental Research</i> , 2016, 14, 65-75.	0.2	8
152	An integrated insight into the response of sedimentary microbial communities to heavy metal contamination. <i>Scientific Reports</i> , 2015, 5, 14266.	1.6	235
153	Comparative metagenomics reveals impact of contaminants on groundwater microbiomes. <i>Frontiers in Microbiology</i> , 2015, 6, 1205.	1.5	77
154	Natural Bacterial Communities Serve as Quantitative Geochemical Biosensors. <i>MBio</i> , 2015, 6, e00326-15.	1.8	173
155	Illumina sequencing-based analysis of free-living bacterial community dynamics during an <i>Akashiwo sanguine</i> bloom in Xiamen sea, China. <i>Scientific Reports</i> , 2015, 5, 8476.	1.6	101
156	The microbe-mediated mechanisms affecting topsoil carbon stock in Tibetan grasslands. <i>ISME Journal</i> , 2015, 9, 2012-2020.	4.4	98
157	High-Throughput Metagenomic Technologies for Complex Microbial Community Analysis: Open and Closed Formats. <i>MBio</i> , 2015, 6, .	1.8	357
158	Redox potential and microbial functional gene diversity in wetland sediments under simulated warming conditions: implications for phosphorus mobilization. <i>Hydrobiologia</i> , 2015, 743, 221-235.	1.0	16
159	Microbial community composition and functions are resilient to metal pollution along two forest soil gradients. <i>FEMS Microbiology Ecology</i> , 2015, 91, 1-11.	1.3	120
160	Ecogenomics Reveals Metals and Land-Use Pressures on Microbial Communities in the Waterways of a Megacity. <i>Environmental Science &amp; Technology</i> , 2015, 49, 1462-1471.	4.6	53
161	Impacts of the Three Gorges Dam on microbial structure and potential function. <i>Scientific Reports</i> , 2015, 5, 8605.	1.6	129
162	Responses of Microbial Communities to Single-Walled Carbon Nanotubes in Phenol Wastewater Treatment Systems. <i>Environmental Science &amp; Technology</i> , 2015, 49, 4627-4635.	4.6	81

#	ARTICLE	IF	CITATIONS
163	Fungal Communities Respond to Long-Term CO <sub>2</sub> Elevation by Community Reassembly. <i>Applied and Environmental Microbiology</i> , 2015, 81, 2445-2454.	1.4	48
164	Responses of Bacterial Communities to Simulated Climate Changes in Alpine Meadow Soil of the Qinghai-Tibet Plateau. <i>Applied and Environmental Microbiology</i> , 2015, 81, 6070-6077.	1.4	107
165	Efficient Genome Editing in <i>Clostridium cellulolyticum</i> via CRISPR-Cas9 Nickase. <i>Applied and Environmental Microbiology</i> , 2015, 81, 4423-4431.	1.4	195
166	Elevated CO <sub>2</sub> 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
167	Cultivation of seaweed <i>Gracilaria</i> in Chinese coastal waters and its contribution to environmental improvements. <i>Algal Research</i> , 2015, 9, 236-244.	2.4	190
168	Over 150 Years of Long-Term Fertilization Alters Spatial Scaling of Microbial Biodiversity. <i>MBio</i> , 2015, 6, .	1.8	57
169	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
170	A Slow-Release Substrate Stimulates Groundwater Microbial Communities for Long-Term <i>In Situ</i> Cr(VI) Reduction. <i>Environmental Science &amp; Technology</i> , 2015, 49, 12922-12931.	4.6	19
171	Rapid selective sweep of pre-existing polymorphisms and slow fixation of new mutations in experimental evolution of <i>Desulfovibrio vulgaris</i> . <i>ISME Journal</i> , 2015, 9, 2360-2372.	4.4	24
172	Responses of Aromatic-Degrading Microbial Communities to Elevated Nitrate in Sediments. <i>Environmental Science &amp; Technology</i> , 2015, 49, 12422-12431.	4.6	72
173	Functional Gene Composition, Diversity and Redundancy in Microbial Stream Biofilm Communities. <i>PLoS ONE</i> , 2015, 10, e0123179.	1.1	41
174	Successional Trajectories of Rhizosphere Bacterial Communities over Consecutive Seasons. <i>MBio</i> , 2015, 6, e00746.	1.8	232
175	Declined soil suppressiveness to <i>Fusarium oxysporum</i> by rhizosphere microflora of cotton in soil sickness. <i>Biology and Fertility of Soils</i> , 2015, 51, 935-946.	2.3	58
176	The complicated substrates enhance the microbial diversity and zinc leaching efficiency in sphalerite bioleaching system. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 10311-10322.	1.7	26
177	Shifts of tundra bacterial and archaeal communities along a permafrost thaw gradient in Alaska. <i>Molecular Ecology</i> , 2015, 24, 222-234.	2.0	127
178	The interactive effects of soil transplant into colder regions and cropping on soil microbiology and biogeochemistry. <i>Environmental Microbiology</i> , 2015, 17, 566-576.	1.8	47
179	Microbial Community Dynamics and Activity Link to Indigo Production from Indole in Bioaugmented Activated Sludge Systems. <i>PLoS ONE</i> , 2015, 10, e0138455.	1.1	7
180	Saliva Microbiota Carry Caries-Specific Functional Gene Signatures. <i>PLoS ONE</i> , 2014, 9, e76458.	1.1	16

#	ARTICLE	IF	CITATIONS
181	Phylogenetic and Functional Diversity of Microbial Communities Associated with Subsurface Sediments of the Sonora Margin, Guaymas Basin. <i>PLoS ONE</i> , 2014, 9, e104427.	1.1	29
182	Whole-genome sequencing reveals novel insights into sulfur oxidation in the extremophile <i>Acidithiobacillus thiooxidans</i> . <i>BMC Microbiology</i> , 2014, 14, 179.	1.3	102
183	Functional gene arrays-based analysis of fecal microbiomes in patients with liver cirrhosis. <i>BMC Genomics</i> , 2014, 15, 753.	1.2	36
184	Metagenomic-based analysis of biofilm communities for electrohydrogenesis: From wastewater to hydrogen. <i>International Journal of Hydrogen Energy</i> , 2014, 39, 4222-4233.	3.8	19
185	Phylogenetic and functional gene structure shifts of the oral microbiomes in periodontitis patients. <i>ISME Journal</i> , 2014, 8, 1879-1891.	4.4	157
186	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
187	Cas9-Based Tools for Targeted Genome Editing and Transcriptional Control. <i>Applied and Environmental Microbiology</i> , 2014, 80, 1544-1552.	1.4	59
188	Dockerinâ€containing protease inhibitor protects key cellulosomal cellulases from proteolysis in <i>Clostridium cellulolyticum</i> . <i>Molecular Microbiology</i> , 2014, 91, 694-705.	1.2	5
189	Distinct responses of soil microbial communities to elevated CO <sub>2</sub> and O <sub>3</sub> in a soybean agro-ecosystem. <i>ISME Journal</i> , 2014, 8, 714-726.	4.4	80
190	GeoChip 4: a functional geneâ€arrayâ€based highâ€throughput environmental technology for microbial community analysis. <i>Molecular Ecology Resources</i> , 2014, 14, 914-928.	2.2	183
191	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.	3.3	595
192	Loss of microbial diversity in soils is coincident with reductions in some specialized functions. <i>Environmental Microbiology</i> , 2014, 16, 2408-2420.	1.8	232
193	GeoChip profiling of microbial community in response to global changes simulated by soil transplant and cropping. <i>Genomics Data</i> , 2014, 2, 166-169.	1.3	3
194	GeoChip as a metagenomics tool to analyze the microbial gene diversity along an elevation gradient. <i>Genomics Data</i> , 2014, 2, 132-134.	1.3	5
195	The microbial gene diversity along an elevation gradient of the Tibetan grassland. <i>ISME Journal</i> , 2014, 8, 430-440.	4.4	249
196	Metabolic and phylogenetic profile of bacterial community in Guishan coastal water (Pearl River) Tj ETQq0 0 0 rgBT /Overlock_10 Tf 50 1	0.6	3
197	Rate-specific responses of prokaryotic diversity and structure to nitrogen deposition in the <i>Leymus chinensis</i> steppe. <i>Soil Biology and Biochemistry</i> , 2014, 79, 81-90.	4.2	175
198	Improvement of cellulose catabolism in <i>Clostridium cellulolyticum</i> by sporulation abolishment and carbon alleviation. <i>Biotechnology for Biofuels</i> , 2014, 7, 25.	6.2	25

#	ARTICLE	IF	CITATIONS
199	Strain/species identification in metagenomes using genome-specific markers. <i>Nucleic Acids Research</i> , 2014, 42, e67-e67.	6.5	72
200	Elevated nitrate enriches microbial functional genes for potential bioremediation of complexly contaminated sediments. <i>ISME Journal</i> , 2014, 8, 1932-1944.	4.4	164
201	Development of HuMiChip for Functional Profiling of Human Microbiomes. <i>PLoS ONE</i> , 2014, 9, e90546.	1.1	18
202	Functional Potential of Soil Microbial Communities in the Maize Rhizosphere. <i>PLoS ONE</i> , 2014, 9, e112609.	1.1	127
203	Elevated CO <sub>2</sub> influences microbial carbon and nitrogen cycling. <i>BMC Microbiology</i> , 2013, 13, 124.	1.3	47
204	GeoChip-based analysis of microbial communities in alpine meadow soils in the Qinghai-Tibetan plateau. <i>BMC Microbiology</i> , 2013, 13, 72.	1.3	28
205	Microevolution from shock to adaptation revealed strategies improving ethanol tolerance and production in <i>Thermoanaerobacter</i> . <i>Biotechnology for Biofuels</i> , 2013, 6, 103.	6.2	12
206	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
207	Strain/Species-Specific Probe Design for Microbial Identification Microarrays. <i>Applied and Environmental Microbiology</i> , 2013, 79, 5085-5088.	1.4	15
208	Stochastic Assembly Leads to Alternative Communities with Distinct Functions in a Bioreactor Microbial Community. <i>MBio</i> , 2013, 4, .	1.8	293
209	Shifts of functional gene representation in wheat rhizosphere microbial communities under elevated ozone. <i>ISME Journal</i> , 2013, 7, 660-671.	4.4	59
210	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
211	GeoChip-based analysis of the functional gene diversity and metabolic potential of soil microbial communities of mangroves. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 7035-7048.	1.7	66
212	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.	4.2	216
213	Shifts in the phylogenetic structure and functional capacity of soil microbial communities follow alteration of native tussock grassland ecosystems. <i>Soil Biology and Biochemistry</i> , 2013, 57, 675-682.	4.2	28
214	Microbial biogeochemistry of boiling springs lake: a physically dynamic, oligotrophic, low-enthalpy geothermal ecosystem. <i>Geobiology</i> , 2013, 11, 356-376.	1.1	17
215	Characterization of NaCl tolerance in <i>Desulfovibrio vulgaris</i> Hildenborough through experimental evolution. <i>ISME Journal</i> , 2013, 7, 1790-1802.	4.4	46
216	Functional gene array-based analysis of microbial communities in heavy metals-contaminated lake sediments. <i>FEMS Microbiology Ecology</i> , 2013, 86, 200-214.	1.3	39

#	ARTICLE	IF	CITATIONS
217	StressChip as a High-Throughput Tool for Assessing Microbial Community Responses to Environmental Stresses. <i>Environmental Science &amp; Technology</i> , 2013, 47, 9841-9849.	4.6	17
218	Microbial community functional structure in response to antibiotics in pharmaceutical wastewater treatment systems. <i>Water Research</i> , 2013, 47, 6298-6308.	5.3	103
219	Towards a molecular understanding of N cycling in northern hardwood forests under future rates of N deposition. <i>Soil Biology and Biochemistry</i> , 2013, 66, 130-138.	4.2	38
220	Correction to GeoChip-Based Analysis of Microbial Functional Gene Diversity in a Landfill Leachate-Contaminated Aquifer. <i>Environmental Science &amp; Technology</i> , 2013, 47, 2142-2142.	4.6	1
221	Widespread Distribution of Soluble Di-Iron Monooxygenase (SDIMO) Genes in Arctic Groundwater Impacted by 1,4-Dioxane. <i>Environmental Science &amp; Technology</i> , 2013, 47, 9950-9958.	4.6	51
222	Random Sampling Process Leads to Overestimation of $\beta$ -Diversity of Microbial Communities. <i>MBio</i> , 2013, 4, e00324-13.	1.8	96
223	Microbial Mechanisms Mediating Increased Soil C Storage under Elevated Atmospheric N Deposition. <i>Applied and Environmental Microbiology</i> , 2013, 79, 1191-1199.	1.4	75
224	Combined Genomics and Experimental Analyses of Respiratory Characteristics of <i>Shewanella putrefaciens</i> W3-18-1. <i>Applied and Environmental Microbiology</i> , 2013, 79, 5250-5257.	1.4	22
225	Continuous Cellulosic Bioethanol Fermentation by Cyclic Fed-Batch Cocultivation. <i>Applied and Environmental Microbiology</i> , 2013, 79, 1580-1589.	1.4	23
226	Microbial Electricity Generation Enhances Decabromodiphenyl Ether (BDE-209) Degradation. <i>PLoS ONE</i> , 2013, 8, e70686.	1.1	19
227	GeoChip-Based Metagenomic Technologies for Analyzing Microbial Community Functional Structure and Activities. , 2013, , 1-13.		2
228	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
229	Functional responses of methanogenic archaea to syntrophic growth. <i>ISME Journal</i> , 2012, 6, 2045-2055.	4.4	66
230	Genetic Linkage of Soil Carbon Pools and Microbial Functions in Subtropical Freshwater Wetlands in Response to Experimental Warming. <i>Applied and Environmental Microbiology</i> , 2012, 78, 7652-7661.	1.4	52
231	Elevated Carbon Dioxide Alters the Structure of Soil Microbial Communities. <i>Applied and Environmental Microbiology</i> , 2012, 78, 2991-2995.	1.4	93
232	Assessing the Microbial Community and Functional Genes in a Vertical Soil Profile with Long-Term Arsenic Contamination. <i>PLoS ONE</i> , 2012, 7, e50507.	1.1	37
233	Functional Characterization of Crp/Fnr-Type Global Transcriptional Regulators in <i>Desulfovibrio vulgaris</i> Hildenborough. <i>Applied and Environmental Microbiology</i> , 2012, 78, 1168-1177.	1.4	32
234	Influence of geogenic factors on microbial communities in metallogenic Australian soils. <i>ISME Journal</i> , 2012, 6, 2107-2118.	4.4	79

#	ARTICLE	IF	CITATIONS
235	GeoChip-Based Analysis of Microbial Functional Gene Diversity in a Landfill Leachate-Contaminated Aquifer. <i>Environmental Science &amp; Technology</i> , 2012, 46, 5824-5833.	4.6	64
236	Deletion of the <i>Desulfovibrio vulgaris</i> Carbon Monoxide Sensor Invokes Global Changes in Transcription. <i>Journal of Bacteriology</i> , 2012, 194, 5783-5793.	1.0	20
237	Molecular ecological network analyses. <i>BMC Bioinformatics</i> , 2012, 13, 113.	1.2	1,917
238	Transcriptomic and proteomic analyses of <i>Desulfovibrio vulgaris</i> biofilms: Carbon and energy flow contribute to the distinct biofilm growth state. <i>BMC Genomics</i> , 2012, 13, 138.	1.2	67
239	Huanglongbing alters the structure and functional diversity of microbial communities associated with citrus rhizosphere. <i>ISME Journal</i> , 2012, 6, 363-383.	4.4	162
240	Applications of functional gene microarrays for profiling microbial communities. <i>Current Opinion in Biotechnology</i> , 2012, 23, 460-466.	3.3	55
241	Microbial mediation of carbon-cycle feedbacks to climate warming. <i>Nature Climate Change</i> , 2012, 2, 106-110.	8.1	502
242	Microbial gene functions enriched in the Deepwater Horizon deep-sea oil plume. <i>ISME Journal</i> , 2012, 6, 451-460.	4.4	240
243	Use of functional gene arrays for elucidating in situ biodegradation. <i>Frontiers in Microbiology</i> , 2012, 3, 339.	1.5	21
244	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
245	Transcriptome analysis of pellicle formation of <i>Shewanella oneidensis</i> . <i>Archives of Microbiology</i> , 2012, 194, 473-482.	1.0	9
246	Development of functional gene microarrays for microbial community analysis. <i>Current Opinion in Biotechnology</i> , 2012, 23, 49-55.	3.3	73
247	More functional genes and convergent overall functional patterns detected by geochip in phenanthrene-spiked soils. <i>FEMS Microbiology Ecology</i> , 2012, 82, 148-156.	1.3	8
248	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
249	How sulphate-reducing microorganisms cope with stress: lessons from systems biology. <i>Nature Reviews Microbiology</i> , 2011, 9, 452-466.	13.6	169
250	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
251	Reproducibility and quantitation of amplicon sequencing-based detection. <i>ISME Journal</i> , 2011, 5, 1303-1313.	4.4	412
252	Mechanisms of enhanced cellulosic bioethanol fermentation by co-cultivation of <i>Clostridium</i> and <i>Thermoanaerobacter</i> spp.. <i>Bioresource Technology</i> , 2011, 102, 9586-9592.	4.8	66



#	ARTICLE	IF	CITATIONS
253	Development of highly fluorescent silica nanoparticles chemically doped with organic dye for sensitive DNA microarray detection. <i>Analytical and Bioanalytical Chemistry</i> , 2011, 401, 2003-2011.	1.9	17
254	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
255	Phylogenetic Molecular Ecological Network of Soil Microbial Communities in Response to Elevated CO <sub>2</sub> . <i>MBio</i> , 2011, 2, .	1.8	771
256	Dynamics of Microbial Community Composition and Function during In Situ Bioremediation of a Uranium-Contaminated Aquifer. <i>Applied and Environmental Microbiology</i> , 2011, 77, 5063-5063.	1.4	4
257	Isolation and Characterization of <i>Shigella flexneri</i> G3, Capable of Effective Cellulosic Saccharification under Mesophilic Conditions. <i>Applied and Environmental Microbiology</i> , 2011, 77, 517-523.	1.4	22
258	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
259	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
260	Microarray-Based Evaluation of Whole-Community Genome DNA Amplification Methods. <i>Applied and Environmental Microbiology</i> , 2011, 77, 4241-4245.	1.4	20
261	The <i>Thermoanaerobacter</i> Glycobiome Reveals Mechanisms of Pentose and Hexose Co-Utilization in Bacteria. <i>PLoS Genetics</i> , 2011, 7, e1002318.	1.5	37
262	Pellicle formation in <i>Shewanella oneidensis</i> . <i>BMC Microbiology</i> , 2010, 10, 291.	1.3	55
263	Impacts of <i>Shewanella oneidensis</i> cytochromes on aerobic and anaerobic respiration. <i>Microbial Biotechnology</i> , 2010, 3, 455-466.	2.0	91
264	Metagenomic insights into evolution of a heavy metal-contaminated groundwater microbial community. <i>ISME Journal</i> , 2010, 4, 660-672.	4.4	332
265	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
266	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.	4.4	300
267	Impact of elevated nitrate on sulfate-reducing bacteria: a comparative Study of <i>Desulfovibrio vulgaris</i> . <i>ISME Journal</i> , 2010, 4, 1386-1397.	4.4	67
268	Metagenomic analysis reveals a marked divergence in the structure of belowground microbial communities at elevated CO <sub>2</sub> . <i>Ecology Letters</i> , 2010, 13, 564-575.	3.0	252
269	Hydrogen peroxide-induced oxidative stress responses in <i>Desulfovibrio vulgaris</i> Hildenborough. <i>Environmental Microbiology</i> , 2010, 12, 2645-2657.	1.8	46
270	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

#	ARTICLE	IF	CITATIONS
271	Functional Molecular Ecological Networks. <i>MBio</i> , 2010, 1, .	1.8	717
272	Microbial Communities and Functional Genes Associated with Soil Arsenic Contamination and the Rhizosphere of the Arsenic-Hyperaccumulating Plant <i>Pteris vittata</i> L. <i>Applied and Environmental Microbiology</i> , 2010, 76, 7277-7284.	1.4	102
273	Functional Biogeography as Evidence of Gene Transfer in Hypersaline Microbial Communities. <i>PLoS ONE</i> , 2010, 5, e12919.	1.1	57
274	Global Transcriptional, Physiological, and Metabolite Analyses of the Responses of <i>Desulfovibrio vulgaris</i> Hildenborough to Salt Adaptation. <i>Applied and Environmental Microbiology</i> , 2010, 76, 1574-1586.	1.4	64
275	GeoChip-Based Functional Gene Analysis of Anodophilic Communities in Microbial Electrolysis Cells under Different Operational Modes. <i>Environmental Science &amp; Technology</i> , 2010, 44, 7729-7735.	4.6	76
276	Sequencing of Multiple Clostridial Genomes Related to Biomass Conversion and Biofuel Production. <i>Journal of Bacteriology</i> , 2010, 192, 6494-6496.	1.0	81
277	Applying GeoChip Analysis to Disparate Microbial Communities. <i>Microbe Magazine</i> , 2010, 5, 60-65.	0.4	25
278	Ultrasound-Mediated DNA Transformation in Thermophilic Gram-Positive Anaerobes. <i>PLoS ONE</i> , 2010, 5, e12582.	1.1	36
279	Analysis of Microbial Communities by Functional Gene Arrays. , 2010, , 109-126.		0
280	Characterization of the Central Metabolic Pathways in <i>Thermoanaerobacter</i> sp. Strain X514 via Isotopomer-Assisted Metabolite Analysis. <i>Applied and Environmental Microbiology</i> , 2009, 75, 5001-5008.	1.4	57
281	The Electron Transfer System of Syntrophically Grown <i>Desulfovibrio vulgaris</i> . <i>Journal of Bacteriology</i> , 2009, 191, 5793-5801.	1.0	133
282	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
283	Contribution of mobile genetic elements to <i>Desulfovibrio vulgaris</i> genome plasticity. <i>Environmental Microbiology</i> , 2009, 11, 2244-2252.	1.8	20
284	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
285	Functional Gene Array-Based Analysis of Microbial Community Structure in Groundwaters with a Gradient of Contaminant Levels. <i>Environmental Science &amp; Technology</i> , 2009, 43, 3529-3534.	4.6	80
286	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
287	Characterization of cytochrome mutants for pellicle formation in <i>Shewanella onedensis</i> MR-1. <i>Transactions of Nonferrous Metals Society of China</i> , 2009, 19, 700-706.	1.7	4
288	Detection and Characterization of Uncultivated Microorganisms Using Microarrays. <i>Microbiology Monographs</i> , 2009, , 179-202.	0.3	0

#	ARTICLE	IF	CITATIONS
289	Detection and Characterization of Uncultivated Microorganisms Using Microarrays. <i>Microbiology Monographs</i> , 2009, , 35-58.	0.3	1
290	Design and analysis of mismatch probes for long oligonucleotide microarrays. <i>BMC Genomics</i> , 2008, 9, 491.	1.2	21
291	Architecture of thermal adaptation in an <i>Exiguobacterium sibiricum</i> strain isolated from 3 million year old permafrost: A genome and transcriptome approach. <i>BMC Genomics</i> , 2008, 9, 547.	1.2	134
292	Development and application of functional gene arrays for microbial community analysis. <i>Transactions of Nonferrous Metals Society of China</i> , 2008, 18, 1319-1327.	1.7	16
293	Empirical Evaluation of a New Method for Calculating Signal-to-Noise Ratio for Microarray Data Analysis. <i>Applied and Environmental Microbiology</i> , 2008, 74, 2957-2966.	1.4	81
294	Section 7 Update - Selection of oligonucleotide probes for microarrays. , 2008, , 1880-1891.		0
295	Function of Periplasmic Hydrogenases in the Sulfate-Reducing Bacterium <i>Desulfovibrio vulgaris</i> Hildenborough. <i>Journal of Bacteriology</i> , 2007, 189, 6159-6167.	1.0	78
296	Analysis of a Ferric Uptake Regulator (Fur) Mutant of <i>Desulfovibrio vulgaris</i> Hildenborough. <i>Applied and Environmental Microbiology</i> , 2007, 73, 5389-5400.	1.4	70
297	Response of <i>Desulfovibrio vulgaris</i> to Alkaline Stress. <i>Journal of Bacteriology</i> , 2007, 189, 8944-8952.	1.0	62
298	GeoChip: a comprehensive microarray for investigating biogeochemical, ecological and environmental processes. <i>ISME Journal</i> , 2007, 1, 67-77.	4.4	554
299	Functional microarray analysis of nitrogen and carbon cycling genes across an Antarctic latitudinal transect. <i>ISME Journal</i> , 2007, 1, 163-179.	4.4	232
300	Genomic and microarray analysis of aromatics degradation in <i>Geobacter metallireducens</i> and comparison to a <i>Geobacter</i> isolate from a contaminated field site. <i>BMC Genomics</i> , 2007, 8, 180.	1.2	87
301	Construction and evaluation of a <i>Clostridium thermocellum</i> ATCC 27405 whole-genome oligonucleotide microarray. <i>Applied Biochemistry and Biotechnology</i> , 2007, 137-140, 663-674.	1.4	17
302	Construction and Evaluation of a <i>Clostridium thermocellum</i> ATCC 27405 Whole-Genome Oligonucleotide Microarray. , 2007, , 663-674.		1
303	Salt Stress in <i>Desulfovibrio vulgaris</i> Hildenborough: an Integrated Genomics Approach. <i>Journal of Bacteriology</i> , 2006, 188, 4068-4078.	1.0	155
304	Recovery of temperate <i>Desulfovibrio vulgaris</i> bacteriophage using a novel host strain. <i>Environmental Microbiology</i> , 2006, 8, 1950-1959.	1.8	14
305	Microarray Applications in Microbial Ecology Research. <i>Microbial Ecology</i> , 2006, 52, 159-175.	1.4	164
306	Improvement of Oligonucleotide Probe Design Criteria for Functional Gene Microarrays in Environmental Applications. <i>Applied and Environmental Microbiology</i> , 2006, 72, 1688-1691.	1.4	68

#	ARTICLE	IF	CITATIONS
307	Temporal Transcriptomic Analysis as <i>Desulfovibrio vulgaris</i> Hildenborough Transitions into Stationary Phase during Electron Donor Depletion. <i>Applied and Environmental Microbiology</i> , 2006, 72, 5578-5588.	1.4	57
308	Global Analysis of Heat Shock Response in <i>Desulfovibrio vulgaris</i> Hildenborough. <i>Journal of Bacteriology</i> , 2006, 188, 1817-1828.	1.0	106
309	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.	1.4	92
310	Empirical Establishment of Oligonucleotide Probe Design Criteria. <i>Applied and Environmental Microbiology</i> , 2005, 71, 3753-3760.	1.4	155
311	Selection of optimal oligonucleotide probes for microarrays using multiple criteria, global alignment and parameter estimation. <i>Nucleic Acids Research</i> , 2005, 33, 6114-6123.	6.5	113
312	Use of Microarrays with Different Probe Sizes for Monitoring Gene Expression. <i>Applied and Environmental Microbiology</i> , 2005, 71, 5154-5162.	1.4	59
313	Design and Use of Functional Gene Microarrays (FGAs) for the Characterization of Microbial Communities. <i>Methods in Microbiology</i> , 2004, 34, 331-368.	0.4	10
314	Ribulose-1,5-Bisphosphate Carboxylase/Oxygenase Deficiency Delays Senescence of Ribulose-1,5-Bisphosphate Carboxylase/Oxygenase but Progressively Impairs Its Catalysis during Tobacco Leaf Development. <i>Plant Physiology</i> , 1997, 115, 1569-1580.	2.3	78
315	Monitoring Microbial Activity with GeoChip. , 0, , 261-P1.		0