

A communal catalogue reveals Earth's multiscale mic

Nature

551, 457-463

DOI: [10.1038/nature24621](https://doi.org/10.1038/nature24621)

Citation Report

#	ARTICLE	IF	CITATIONS
1	Crowdsourcing Earth's microbes. <i>Nature</i> , 2017, 551, 446-447.	13.7	2
2	Super-reactive catalyst for bond cleavage. <i>Nature</i> , 2017, 551, 447-448.	13.7	0
3	The soil microbiome "from metagenomics to metaproteomics". <i>Current Opinion in Microbiology</i> , 2018, 43, 162-168.	2.3	330
4	Bacterial-fungal interactions: ecology, mechanisms and challenges. <i>FEMS Microbiology Reviews</i> , 2018, 42, 335-352.	3.9	468
5	Towards a Natural History of Soil Bacterial Communities. <i>Trends in Microbiology</i> , 2018, 26, 250-252.	3.5	7
6	The Gills of Reef Fish Support a Distinct Microbiome Influenced by Host-Specific Factors. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	96
7	Marine microbes in 4D "using time series observation to assess the dynamics of the ocean microbiome and its links to ocean health". <i>Current Opinion in Microbiology</i> , 2018, 43, 169-185.	2.3	54
8	Phylogenetic Placement of Exact Amplicon Sequences Improves Associations with Clinical Information. <i>MSystems</i> , 2018, 3, .	1.7	376
9	In Search of Model Ecological Systems for Understanding Specialized Metabolism. <i>MSystems</i> , 2018, 3, .	1.7	10
10	The impact of vegan production on the kimchi microbiome. <i>Food Microbiology</i> , 2018, 74, 171-178.	2.1	37
11	What will it take to understand the ecology of symbiotic microorganisms?. <i>Environmental Microbiology</i> , 2018, 20, 1920-1924.	1.8	9
12	Ecological medicine. <i>Environmental Microbiology</i> , 2018, 20, 1917-1919.	1.8	3
13	Standard methods for the assessment of structural and functional diversity of soil organisms: A review. <i>Integrated Environmental Assessment and Management</i> , 2018, 14, 463-479.	1.6	17
14	The hunt for the most-wanted chemolithoautotrophic spookmicrobes. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	28
15	Exploiting ecosystem services in agriculture for increased food security. <i>Global Food Security</i> , 2018, 17, 57-63.	4.0	84
16	Select and resequence reveals relative fitness of bacteria in symbiotic and free-living environments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 2425-2430.	3.3	88
17	Hemolymph Microbiomes of Three Aquatic Invertebrates as Revealed by a New Cell Extraction Method. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	49
18	The Madness of Microbiome: Attempting To Find Consensus "Best Practice" for 16S Microbiome Studies. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	422

#	ARTICLE	IF	CITATIONS
19	Bacterial density rather than diversity correlates with hatching success across different avian species. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	21
20	Discerning autotrophy, mixotrophy, and heterotrophy in marine TACK archaea from the North Atlantic. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	6
21	A global atlas of the dominant bacteria found in soil. <i>Science</i> , 2018, 359, 320-325.	6.0	1,386
22	Microbial diversity knows no borders. <i>Nature Reviews Microbiology</i> , 2018, 16, 66-66.	13.6	13
23	Scaling up: A guide to high-throughput genomic approaches for biodiversity analysis. <i>Molecular Ecology</i> , 2018, 27, 313-338.	2.0	248
24	Testing association between soil bacterial diversity and soil carbon storage on the Loess Plateau. <i>Science of the Total Environment</i> , 2018, 626, 48-58.	3.9	53
26	Gut microbiota utilize immunoglobulin A for mucosal colonization. <i>Science</i> , 2018, 360, 795-800.	6.0	447
27	Metagenome Sequences of Sediment from a Recovering Industrialized Appalachian River in West Virginia. <i>Genome Announcements</i> , 2018, 6, .	0.8	10
28	Introduction: The host-associated microbiome: Pattern, process and function. <i>Molecular Ecology</i> , 2018, 27, 1749-1765.	2.0	46
29	The social network of microorganisms – how auxotrophies shape complex communities. <i>Nature Reviews Microbiology</i> , 2018, 16, 383-390.	13.6	311
30	Understanding the thermal properties of amorphous solids using machine-learning-based interatomic potentials. <i>Molecular Simulation</i> , 2018, 44, 866-880.	0.9	69
31	Soil pH is equally important as salinity in shaping bacterial communities in saline soils under halophytic vegetation. <i>Scientific Reports</i> , 2018, 8, 4550.	1.6	68
32	Chemical regulation of body feather microbiota in a wild bird. <i>Molecular Ecology</i> , 2018, 27, 1727-1738.	2.0	25
33	Microbiomes <i>In Natura</i> : Importance of Invertebrates in Understanding the Natural Variety of Animal-Microbe Interactions. <i>MSystems</i> , 2018, 3, .	1.7	54
34	The Who, Why, and How of Small-Molecule Production in Invertebrate Microbiomes: Basic Insights Fueling Drug Discovery. <i>MSystems</i> , 2018, 3, .	1.7	8
35	Around the globe in 2.2 billion sequences. <i>Nature Reviews Microbiology</i> , 2018, 16, 3-3.	13.6	4
36	Wildlife-microbiome interactions and disease: exploring opportunities for disease mitigation across ecological scales. <i>Drug Discovery Today: Disease Models</i> , 2018, 28, 105-115.	1.2	25
37	pH as a Primary Control in Environmental Microbiology: 2. Kinetic Perspective. <i>Frontiers in Environmental Science</i> , 0, 6, .	1.5	23

#	ARTICLE	IF	CITATIONS
38	An exploration of Prevotella-rich microbiomes in HIV and men who have sex with men. <i>Microbiome</i> , 2018, 6, 198.	4.9	111
39	Plant Selenium Hyperaccumulation Affects Rhizosphere: Enhanced Species Richness and Altered Species Composition. <i>Phytobiomes Journal</i> , 2018, 2, 82-91.	1.4	9
40	The murine vaginal microbiota and its perturbation by the human pathogen group B Streptococcus. <i>BMC Microbiology</i> , 2018, 18, 197.	1.3	52
41	Evaluating the Information Content of Shallow Shotgun Metagenomics. <i>MSystems</i> , 2018, 3, .	1.7	293
42	Reevaluating the Salty Divide: Phylogenetic Specificity of Transitions between Marine and Freshwater Systems. <i>MSystems</i> , 2018, 3, .	1.7	37
43	Identifying and Predicting Novelty in Microbiome Studies. <i>MBio</i> , 2018, 9, .	1.8	28
44	High-Throughput Miniaturized 16S rRNA Amplicon Library Preparation Reduces Costs while Preserving Microbiome Integrity. <i>MSystems</i> , 2018, 3, .	1.7	58
45	The Rootstock Regulates Microbiome Diversity in Root and Rhizosphere Compartments of <i>Vitis vinifera</i> Cultivar Lambrusco. <i>Frontiers in Microbiology</i> , 2018, 9, 2240.	1.5	54
46	Experimental bacterial adaptation to the zebrafish gut reveals a primary role for immigration. <i>PLoS Biology</i> , 2018, 16, e2006893.	2.6	83
47	Gut microbial features can predict host phenotype response to protein deficiency. <i>Physiological Reports</i> , 2018, 6, e13932.	0.7	17
48	Identification of Microbial Dark Matter in Antarctic Environments. <i>Frontiers in Microbiology</i> , 2018, 9, 3165.	1.5	26
49	SEDE-GPS: socio-economic data enrichment based on GPS information. <i>BMC Bioinformatics</i> , 2018, 19, 440.	1.2	4
50	A practical introduction to microbial molecular ecology through the use of isolation chips. <i>Ecology and Evolution</i> , 2018, 8, 12286-12298.	0.8	5
51	Practical considerations for sampling and data analysis in contemporary metagenomics-based environmental studies. <i>Journal of Microbiological Methods</i> , 2018, 154, 14-18.	0.7	12
52	Microbial Community Composition and Predicted Functional Attributes of Antarctic Lithobionts Using Targeted Next-Generation Sequencing and Bioinformatics Tools. <i>Methods in Microbiology</i> , 2018, , 243-290.	0.4	3
53	Microbial forensics: new breakthroughs and future prospects. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 10377-10391.	1.7	76
54	Clinician Guide to Microbiome Testing. <i>Digestive Diseases and Sciences</i> , 2018, 63, 3167-3177.	1.1	22
55	Alpha-diversity is strongly influenced by the composition of other samples when using multiplexed sequencing approaches. <i>Soil Biology and Biochemistry</i> , 2018, 127, 79-81.	4.2	4

#	ARTICLE	IF	CITATIONS
56	Progress of analytical tools and techniques for human gut microbiome research. <i>Journal of Microbiology</i> , 2018, 56, 693-705.	1.3	49
57	Qiita: rapid, web-enabled microbiome meta-analysis. <i>Nature Methods</i> , 2018, 15, 796-798.	9.0	459
58	On the Road to Breeding 4.0: Unraveling the Good, the Bad, and the Boring of Crop Quantitative Genomics. <i>Annual Review of Genetics</i> , 2018, 52, 421-444.	3.2	182
59	A metagenomics roadmap to the uncultured genome diversity in hypersaline soda lake sediments. <i>Microbiome</i> , 2018, 6, 168.	4.9	120
60	Diversity-Function Relationships in Natural, Applied, and Engineered Microbial Ecosystems. <i>Advances in Applied Microbiology</i> , 2018, 105, 131-189.	1.3	13
61	Comparative genomics of cocci-shaped <i>Sporosarcina</i> strains with diverse spatial isolation. <i>BMC Genomics</i> , 2018, 19, 310.	1.2	9
62	Differences in the fecal microbiota of neonates born at home or in the hospital. <i>Scientific Reports</i> , 2018, 8, 15660.	1.6	38
63	Community profiling of the urinary microbiota: considerations for low-biomass samples. <i>Nature Reviews Urology</i> , 2018, 15, 735-749.	1.9	87
64	Differential Activation of Hepatic Invariant NKT Cell Subsets Plays a Key Role in Progression of Nonalcoholic Steatohepatitis. <i>Journal of Immunology</i> , 2018, 201, 3017-3035.	0.4	69
65	Daylight exposure modulates bacterial communities associated with household dust. <i>Microbiome</i> , 2018, 6, 175.	4.9	62
66	Striped UniFrac: enabling microbiome analysis at unprecedented scale. <i>Nature Methods</i> , 2018, 15, 847-848.	9.0	71
67	A Comparative Analysis of Microbial DNA Preparation Methods for Use With Massive and Branching Coral Growth Forms. <i>Frontiers in Microbiology</i> , 2018, 9, 2146.	1.5	15
68	Microbial effects of livestock manure fertilization on freshwater aquaculture ponds rearing tilapia ( <i>Oreochromis shiranus</i> ) and North African catfish ( <i>Clarias gariepinus</i> ). <i>MicrobiologyOpen</i> , 2018, 7, e00716.	1.2	23
69	Dynamic Human Environmental Exposome Revealed by Longitudinal Personal Monitoring. <i>Cell</i> , 2018, 175, 277-291.e31.	13.5	137
70	Macroecology to Unite All Life, Large and Small. <i>Trends in Ecology and Evolution</i> , 2018, 33, 731-744.	4.2	118
71	Detecting eukaryotic microbiota with single-cell sensitivity in human tissue. <i>Microbiome</i> , 2018, 6, 151.	4.9	21
73	Manipulating the soil microbiome for improved nitrogen management. <i>Microbiology Australia</i> , 2018, 39, 24.	0.1	16
74	Environmental microbiology â€” the next 20 years: bioconnectivity and meta'omics 2.0. <i>Environmental Microbiology</i> , 2018, 20, 1949-1954.	1.8	3

#	ARTICLE	IF	CITATIONS
75	American Gut: an Open Platform for Citizen Science Microbiome Research. <i>MSystems</i> , 2018, 3, .	1.7	604
76	Earth Microbiome Project and Global Systems Biology. <i>MSystems</i> , 2018, 3, .	1.7	65
77	The future of biotic indices in the ecogenomic era: Integrating (e)DNA metabarcoding in biological assessment of aquatic ecosystems. <i>Science of the Total Environment</i> , 2018, 637-638, 1295-1310.	3.9	377
78	Best practices for analysing microbiomes. <i>Nature Reviews Microbiology</i> , 2018, 16, 410-422.	13.6	1,138
79	A Mechanistic Model for Gas Ebullition in the Presence of NAPLs in Sediments. , 2018, , .		0
80	Soil quality indicators: critical tools in ecosystem restoration. <i>Current Opinion in Environmental Science and Health</i> , 2018, 5, 47-52.	2.1	106
81	Benchmarking taxonomic assignments based on 16S rRNA gene profiling of the microbiota from commonly sampled environments. <i>GigaScience</i> , 2018, 7, .	3.3	95
82	A simple cleanup method for the removal of humic substances from soil protein extracts using aluminum coagulation. <i>Environmental Science and Pollution Research</i> , 2018, 25, 23845-23856.	2.7	10
83	Microbiome Yarns: microbiome of the built environment, paranormal microbiology, and the power of single cell genomics <sup>1,2,3,4</sup> . <i>Microbial Biotechnology</i> , 2018, 11, 575-587.	2.0	2
84	Biogeography of soil bacteria and archaea across France. <i>Science Advances</i> , 2018, 4, eaat1808.	4.7	185
85	Metagenomics Sheds Light on the Ecology of Marine Microbes and Their Viruses. <i>Trends in Microbiology</i> , 2018, 26, 955-965.	3.5	49
86	Bacterial diversification through geological time. <i>Nature Ecology and Evolution</i> , 2018, 2, 1458-1467.	3.4	81
87	Species-Associated Differences in the Below-Ground Microbiomes of Wild and Domesticated <i>Setaria</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 1183.	1.7	31
88	From hairballs to hypotheses—biological insights from microbial networks. <i>FEMS Microbiology Reviews</i> , 2018, 42, 761-780.	3.9	374
89	Gut microbiota, short chain fatty acids, and obesity across the epidemiologic transition: the METS-Microbiome study protocol. <i>BMC Public Health</i> , 2018, 18, 978.	1.2	32
90	Microbiome Data Accurately Predicts the Postmortem Interval Using Random Forest Regression Models. <i>Genes</i> , 2018, 9, 104.	1.0	80
91	Are microbiome studies ready for hypothesis-driven research?. <i>Current Opinion in Microbiology</i> , 2018, 44, 61-69.	2.3	27
92	Microbial biogeography of 925 geothermal springs in New Zealand. <i>Nature Communications</i> , 2018, 9, 2876.	5.8	163

#	ARTICLE	IF	CITATIONS
93	The Microbial Landscape of Sea Stars and the Anatomical and Interspecies Variability of Their Microbiome. <i>Frontiers in Microbiology</i> , 2018, 9, 1829.	1.5	35
94	pH as a Primary Control in Environmental Microbiology: 1. Thermodynamic Perspective. <i>Frontiers in Environmental Science</i> , 2018, 6, .	1.5	153
95	Microbiome Research Is Becoming the Key to Better Understanding Health and Nutrition. <i>Frontiers in Genetics</i> , 2018, 9, 212.	1.1	79
96	Microbial Community Analysis of Sauerkraut Fermentation Reveals a Stable and Rapidly Established Community. <i>Foods</i> , 2018, 7, 77.	1.9	73
97	Coupled Biological and Abiotic Mechanisms Driving Carbonyl Sulfide Production in Soils. <i>Soil Systems</i> , 2018, 2, 37.	1.0	24
98	Optimizing taxonomic classification of marker-gene amplicon sequences with QIIME 2's q2-feature-classifier plugin. <i>Microbiome</i> , 2018, 6, 90.	4.9	3,159
99	Need for Laboratory Ecosystems To Unravel the Structures and Functions of Soil Microbial Communities Mediated by Chemistry. <i>MBio</i> , 2018, 9, .	1.8	34
100	Opportunities and limitations for DNA metabarcoding in Australasian plant-pathogen biosecurity. <i>Australasian Plant Pathology</i> , 2018, 47, 467-474.	0.5	19
101	Microbial diversity and biogeography in Arctic soils. <i>Environmental Microbiology Reports</i> , 2018, 10, 611-625.	1.0	84
102	A Genomic Outlook on Bioremediation: The Case of Arsenic Removal. <i>Frontiers in Microbiology</i> , 2018, 9, 820.	1.5	49
103	Oxic Methane Cycling: New Evidence for Methane Formation in Oxic Lake Water. , 2018, , 1-22.		13
104	Assessment of the impact of three pesticides on microbial dynamics and functions in a lab-to-field experimental approach. <i>Science of the Total Environment</i> , 2018, 637-638, 636-646.	3.9	61
105	Exploring the Root Microbiome: Extracting Bacterial Community Data from the Soil, Rhizosphere, and Root Endosphere. <i>Journal of Visualized Experiments</i> , 2018, , .	0.2	28
106	Interaction between ferruginous clay sediment and an iron-reducing hyperthermophilic <i>Pyrobaculum</i> sp. in a terrestrial hot spring. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	2
107	The Nile River Microbiome Reveals a Remarkably Stable Community Between Wet and Dry Seasons, and Sampling Sites, in a Large Urban Metropolis (Cairo, Egypt). <i>OMICS A Journal of Integrative Biology</i> , 2018, 22, 553-564.	1.0	8
108	Metagenomic Approaches for Understanding New Concepts in Microbial Science. <i>International Journal of Genomics</i> , 2018, 2018, 1-15.	0.8	100
109	Latent environment allocation of microbial community data. <i>PLoS Computational Biology</i> , 2018, 14, e1006143.	1.5	10
110	Marchantia liverworts as a proxy to plants' basal microbiomes. <i>Scientific Reports</i> , 2018, 8, 12712.	1.6	46

#	ARTICLE	IF	CITATIONS
111	Broadscale Ecological Patterns Are Robust to Use of Exact Sequence Variants versus Operational Taxonomic Units. <i>MSphere</i> , 2018, 3, .	1.3	168
112	Nano-Sized and Filterable Bacteria and Archaea: Biodiversity and Function. <i>Frontiers in Microbiology</i> , 2018, 9, 1971.	1.5	51
113	The gut microbiome of nonhuman primates: Lessons in ecology and evolution. <i>American Journal of Primatology</i> , 2018, 80, e22867.	0.8	100
114	Environment and host as large-scale controls of ectomycorrhizal fungi. <i>Nature</i> , 2018, 558, 243-248.	13.7	282
115	Transient Osmotic Perturbation Causes Long-Term Alteration to the Gut Microbiota. <i>Cell</i> , 2018, 173, 1742-1754.e17.	13.5	171
116	Quantifying Crop Rhizosphere Microbiome Ecology: The Next Frontier in Enhancing the Commercial Utility of Agricultural Microbes. <i>Industrial Biotechnology</i> , 2018, 14, 116-119.	0.5	19
117	Comparative Genomics of Nitrogen Cycling Pathways in Bacteria and Archaea. <i>Microbial Ecology</i> , 2019, 77, 597-606.	1.4	21
118	Reply to Sun et al., "Identifying Composition Novelty in Microbiome Studies: Improvement of Prediction Accuracy". <i>MBio</i> , 2019, 10, .	1.8	0
119	Longitudinal Comparison of Bacterial Diversity and Antibiotic Resistance Genes in New York City Sewage. <i>MSystems</i> , 2019, 4, .	1.7	19
120	Global Observational Needs and Resources for Marine Biodiversity. <i>Frontiers in Marine Science</i> , 2019, 6, .	1.2	77
121	Phylogenetic, genomic, and biogeographic characterization of a novel and ubiquitous marine invertebrate-associated Rickettsiales parasite, <i>Candidatus Aquarickettsia rohweri</i> , gen. nov., sp. nov. <i>ISME Journal</i> , 2019, 13, 2938-2953.	4.4	82
122	Understanding soil biodiversity using two orthogonal 1000km transects across New South Wales, Australia. <i>Geoderma</i> , 2019, 354, 113860.	2.3	10
123	Thermophilic methanotrophs: in hot pursuit. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	18
124	Microbes: An Important Resource for Sustainable Agriculture. , 2019, , 53-77.		2
125	Microbial Transformations of Organically Fermented Foods. <i>Metabolites</i> , 2019, 9, 165.	1.3	20
126	Biogeographical patterns in soil bacterial communities across the Arctic region. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	53
127	The Human Gut Microbiome is Structured to Optimize Molecular Interaction Networks. <i>Computational and Structural Biotechnology Journal</i> , 2019, 17, 1040-1046.	1.9	6
128	The occurrence of <i>Listeria monocytogenes</i> is associated with built environment microbiota in three tree fruit processing facilities. <i>Microbiome</i> , 2019, 7, 115.	4.9	61



#	ARTICLE	IF	CITATIONS
129	A hierarchy of environmental covariates control the global biogeography of soil bacterial richness. <i>Scientific Reports</i> , 2019, 9, 12129.	1.6	16
130	A Response to Scientific and Societal Needs for Marine Biological Observations. <i>Frontiers in Marine Science</i> , 2019, 6, .	1.2	26
131	DAIRYdb: a manually curated reference database for improved taxonomy annotation of 16S rRNA gene sequences from dairy products. <i>BMC Genomics</i> , 2019, 20, 560.	1.2	48
132	A methodological framework to embrace soil biodiversity. <i>Soil Biology and Biochemistry</i> , 2019, 136, 107536.	4.2	88
133	Strong spatial and temporal turnover of soil bacterial communities in South Africa's hyperdiverse fynbos biome. <i>Soil Biology and Biochemistry</i> , 2019, 136, 107541.	4.2	25
134	Inferring macroecological patterns from local presence/absence data. <i>Oikos</i> , 2019, 128, 1641-1652.	1.2	5
135	Models in Microbial Ecology. , 2019, , 211-211.		6
136	Quantifying spatiotemporal variability and noise in absolute microbiota abundances using replicate sampling. <i>Nature Methods</i> , 2019, 16, 731-736.	9.0	54
137	Soil nematode abundance and functional group composition at a global scale. <i>Nature</i> , 2019, 572, 194-198.	13.7	635
138	Associations between fungal and bacterial microbiota of airways and asthma endotypes. <i>Journal of Allergy and Clinical Immunology</i> , 2019, 144, 1214-1227.e7.	1.5	96
139	The relative importance of ecological drivers of arbuscular mycorrhizal fungal distribution varies with taxon phylogenetic resolution. <i>New Phytologist</i> , 2019, 224, 936-948.	3.5	17
140	Identifying Composition Novelty in Microbiome Studies: Improvement for Prediction Accuracy. <i>MBio</i> , 2019, 10, .	1.8	2
141	The Role of Soil Fungi in K+ Plant Nutrition. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3169.	1.8	40
142	Microbial Diversity Exploration of Marine Hosts at Serrana Bank, a Coral Atoll of the Seaflower Biosphere Reserve. <i>Frontiers in Marine Science</i> , 2019, 6, .	1.2	18
143	Interactome-based abiotic and biotic impacts on biodiversity of plankton communities in disturbed wetlands. <i>Diversity and Distributions</i> , 2019, 25, 1416-1428.	1.9	8
144	Erythritol as a single carbon source improves cultural isolation of <i>Burkholderia pseudomallei</i> from rice paddy soils. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007821.	1.3	7
145	Unconventional Oil and Gas Energy Systems: An Unidentified Hotspot of Antimicrobial Resistance?. <i>Frontiers in Microbiology</i> , 2019, 10, 2392.	1.5	7
146	Antibiotic Resistance Genes in the Human-Impacted Environment: A One Health Perspective. <i>Pedosphere</i> , 2019, 29, 273-282.	2.1	100

#	ARTICLE	IF	CITATIONS
147	MetaMiner: A Scalable Peptidogenomics Approach for Discovery of Ribosomal Peptide Natural Products with Blind Modifications from Microbial Communities. <i>Cell Systems</i> , 2019, 9, 600-608.e4.	2.9	46
148	Effects of Warming and Nitrogen Addition on the Soil Bacterial Community in a Subtropical Chinese Fir Plantation. <i>Forests</i> , 2019, 10, 861.	0.9	12
149	Parasite microbiome project: Grand challenges. <i>PLoS Pathogens</i> , 2019, 15, e1008028.	2.1	50
150	Species abundance information improves sequence taxonomy classification accuracy. <i>Nature Communications</i> , 2019, 10, 4643.	5.8	86
151	The Extent of Fault-Associated Modern Authigenic Barite Deposits Offshore Northern Baja California Revealed by High-Resolution Mapping. <i>Frontiers in Marine Science</i> , 2019, 6, .	1.2	5
152	A conceptual framework for the phylogenetically constrained assembly of microbial communities. <i>Microbiome</i> , 2019, 7, 142.	4.9	28
153	MGnify: the microbiome analysis resource in 2020. <i>Nucleic Acids Research</i> , 2020, 48, D570-D578.	6.5	296
154	Microbiome of vineyard soils is shaped by geography and management. <i>Microbiome</i> , 2019, 7, 140.	4.9	94
156	Optimizing sequencing protocols for leaderboard metagenomics by combining long and short reads. <i>Genome Biology</i> , 2019, 20, 226.	3.8	47
157	Latitudinal gradient of cyanobacterial diversity in tidal flats. <i>PLoS ONE</i> , 2019, 14, e0224444.	1.1	4
158	A meta-analysis of global fungal distribution reveals climate-driven patterns. <i>Nature Communications</i> , 2019, 10, 5142.	5.8	232
159	Fueling ab initio folding with marine metagenomics enables structure and function predictions of new protein families. <i>Genome Biology</i> , 2019, 20, 229.	3.8	28
160	Impact of quality trimming on the efficiency of reads joining and diversity analysis of Illumina paired-end reads in the context of QIIME1 and QIIME2 microbiome analysis frameworks. <i>BMC Bioinformatics</i> , 2019, 20, 581.	1.2	52
161	The effect of captivity on the primate gut microbiome varies with host dietary niche. <i>American Journal of Primatology</i> , 2019, 81, e23061.	0.8	56
163	Cooperation in Microbial Populations: Theory and Experimental Model Systems. <i>Journal of Molecular Biology</i> , 2019, 431, 4599-4644.	2.0	30
164	Interdomain ecological networks between plants and microbes. <i>Molecular Ecology Resources</i> , 2019, 19, 1565-1577.	2.2	64
165	A case of spontaneous hepatic hemangioma rupture: Successful management with transarterial chemoembolization alone. <i>Journal of Interventional Medicine</i> , 2019, 2, 131-133.	0.2	2
166	A horizon scan of priorities for coastal marine microbiome research. <i>Nature Ecology and Evolution</i> , 2019, 3, 1509-1520.	3.4	77

#	ARTICLE	IF	CITATIONS
167	Defining the Distinct Skin and Gut Microbiomes of the Northern Pike ( <i>Esox lucius</i> ). <i>Frontiers in Microbiology</i> , 2019, 10, 2118.	1.5	25
168	High-throughput DNA sequencing technologies for water and wastewater analysis. <i>Science Progress</i> , 2019, 102, 351-376.	1.0	16
169	Accurate estimation of microbial sequence diversity with Distanced. <i>Bioinformatics</i> , 2020, 36, 728-734.	1.8	5
170	Does Soil Contribute to the Human Gut Microbiome?. <i>Microorganisms</i> , 2019, 7, 287.	1.6	95
171	Manipulation of Biodiversity to Steer and Optimize Microbial Community Function. , 2019, , 29-41.		0
172	Uncovering the biosynthetic potential of rare metagenomic DNA using co-occurrence network analysis of targeted sequences. <i>Nature Communications</i> , 2019, 10, 3848.	5.8	47
173	Inevitable future: space colonization beyond Earth with microbes first. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	22
174	Expanding the scope and scale of microbiome research. <i>Genome Biology</i> , 2019, 20, 191.	3.8	1
175	Challenges in the construction of knowledge bases for human microbiome-disease associations. <i>Microbiome</i> , 2019, 7, 129.	4.9	36
176	Potential Interactions between Clade SUP05 Sulfur-Oxidizing Bacteria and Phages in Hydrothermal Vent Sponges. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	22
177	Influence of 16S rRNA variable region on perceived diversity of marine microbial communities of the Northern North Atlantic. <i>FEMS Microbiology Letters</i> , 2019, 366, .	0.7	45
178	Asexual Reproduction Can Account for the High Diversity and Prevalence of Rare Taxa Observed in Microbial Communities. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	1
179	Evolutionary and Ecological Consequences of Gut Microbial Communities. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2019, 50, 451-475.	3.8	175
180	Untapped sponge microbiomes: structure specificity at host order and family levels. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	14
181	Gut microbiome in serious mental illnesses: A systematic review and critical evaluation. <i>Schizophrenia Research</i> , 2021, 234, 24-40.	1.1	47
182	The power of crowds: Grand challenges in the Asia-Pacific region. <i>Australian Journal of Management</i> , 2019, 44, 551-570.	1.2	11
183	Characterization of the microbiome and bioluminescent symbionts across life stages of Ceratioid Anglerfishes of the Gulf of Mexico. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	14
184	Microbial diversity and distribution differ between water column and biofilm assemblages in arid-land waterbodies. <i>Freshwater Science</i> , 2019, 38, 869-882.	0.9	4

#	ARTICLE	IF	CITATIONS
185	Beyond the gut: Skin microbiome compositional changes are associated with BMI. <i>Human Microbiome Journal</i> , 2019, 13, 100063.	3.8	38
186	Bacterial Candidates for Colonization and Degradation of Marine Plastic Debris. <i>Environmental Science &amp; Technology</i> , 2019, 53, 11636-11643.	4.6	178
187	MALDI-TOF MS protein fingerprinting of mixed samples. <i>Biology Methods and Protocols</i> , 2019, 4, bpz013.	1.0	8
188	Inclusive innovation: Enhancing global participation in and benefit sharing linked to the utilization of marine genetic resources from areas beyond national jurisdiction. <i>Marine Policy</i> , 2019, 109, 103696.	1.5	14
189	Microbiome Multi-Omics Network Analysis: Statistical Considerations, Limitations, and Opportunities. <i>Frontiers in Genetics</i> , 2019, 10, 995.	1.1	101
190	Soil parameters, land use, and geographical distance drive soil bacterial communities along a European transect. <i>Scientific Reports</i> , 2019, 9, 605.	1.6	56
191	Urogenital schistosomiasis is associated with signatures of microbiome dysbiosis in Nigerian adolescents. <i>Scientific Reports</i> , 2019, 9, 829.	1.6	41
192	Rapid alignment-free phylogenetic identification of metagenomic sequences. <i>Bioinformatics</i> , 2019, 35, 3303-3312.	1.8	35
193	High similarity in bacterial bioaerosol compositions between the free troposphere and atmospheric depositions collected at high-elevation mountains. <i>Atmospheric Environment</i> , 2019, 203, 79-86.	1.9	28
194	Use of a Fluorescent Analog of Glucose (2-NBDG) To Identify Uncultured Rumen Bacteria That Take Up Glucose. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	11
195	Siderophore profiling of co-habiting soil bacteria by ultra-high resolution mass spectrometry. <i>Metallomics</i> , 2019, 11, 166-175.	1.0	19
196	Optimal Microbiome Networks: Macroecology and Criticality. <i>Entropy</i> , 2019, 21, 506.	1.1	23
197	TYGS is an automated high-throughput platform for state-of-the-art genome-based taxonomy. <i>Nature Communications</i> , 2019, 10, 2182.	5.8	1,588
198	Advancing integration of data on food microbiome studies: FoodMicrobionet 3.1, a major upgrade of the FoodMicrobionet database. <i>International Journal of Food Microbiology</i> , 2019, 305, 108249.	2.1	32
199	EcoFABs: advancing microbiome science through standardized fabricated ecosystems. <i>Nature Methods</i> , 2019, 16, 567-571.	9.0	90
200	Uncovering prokaryotic biodiversity within aerosols of the pristine Amazon forest. <i>Science of the Total Environment</i> , 2019, 688, 83-86.	3.9	13
201	Kelp beds and their local effects on seawater chemistry, productivity, and microbial communities. <i>Ecology</i> , 2019, 100, e02798.	1.5	75
202	Visualization and prediction of CRISPR incidence in microbial trait-space to identify drivers of antiviral immune strategy. <i>ISME Journal</i> , 2019, 13, 2589-2602.	4.4	34

#	ARTICLE	IF	CITATIONS
203	redbiom: a Rapid Sample Discovery and Feature Characterization System. <i>MSystems</i> , 2019, 4, .	1.7	35
204	A Lot on Your Plate? Well-to-Well Contamination as an Additional Confounder in Microbiome Sequence Analyses. <i>MSystems</i> , 2019, 4, .	1.7	9
205	Exploring the Hospital Microbiome by High-Resolution 16S rRNA Profiling. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3099.	1.8	37
206	Quantifying and Understanding Well-to-Well Contamination in Microbiome Research. <i>MSystems</i> , 2019, 4, .	1.7	132
207	Microbial assemblages and bioindicators as proxies for ecosystem health status: potential and limitations. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 6407-6421.	1.7	45
208	How sample heterogeneity can obscure the signal of microbial interactions. <i>ISME Journal</i> , 2019, 13, 2639-2646.	4.4	39
209	FEAST: fast expectation-maximization for microbial source tracking. <i>Nature Methods</i> , 2019, 16, 627-632.	9.0	275
210	Multi-omics of the gut microbial ecosystem in inflammatory bowel diseases. <i>Nature</i> , 2019, 569, 655-662.	13.7	1,638
211	Host genetic determinants of the gut microbiota of wild mice. <i>Molecular Ecology</i> , 2019, 28, 3197-3207.	2.0	76
212	A global survey of arsenic-related genes in soil microbiomes. <i>BMC Biology</i> , 2019, 17, 45.	1.7	70
213	A comprehensive census of lake microbial diversity on a global scale. <i>Science China Life Sciences</i> , 2019, 62, 1320-1331.	2.3	56
214	Is there convergence of gut microbes in blood-feeding vertebrates?. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20180249.	1.8	21
215	A eukaryotic community succession based method for postmortem interval (PMI) estimation of decomposing porcine remains. <i>Forensic Science International</i> , 2019, 302, 109838.	1.3	17
216	Metaphenomic Responses of a Native Prairie Soil Microbiome to Moisture Perturbations. <i>MSystems</i> , 2019, 4, .	1.7	56
217	Next-Generation Metagenomics: Methodological Challenges and Opportunities. <i>OMICS A Journal of Integrative Biology</i> , 2019, 23, 327-333.	1.0	47
218	Longitudinal homogenization of the microbiome between both occupants and the built environment in a cohort of United States Air Force Cadets. <i>Microbiome</i> , 2019, 7, 70.	4.9	33
219	Modelling the influence of environmental parameters over marine planktonic microbial communities using artificial neural networks. <i>Science of the Total Environment</i> , 2019, 677, 205-214.	3.9	21
220	Global change microbiology – big questions about small life for our future. <i>Nature Reviews Microbiology</i> , 2019, 17, 331-332.	13.6	20

#	ARTICLE	IF	CITATIONS
221	Selection, Succession, and Stabilization of Soil Microbial Consortia. <i>MSystems</i> , 2019, 4, .	1.7	64
222	Global diversity and biogeography of bacterial communities in wastewater treatment plants. <i>Nature Microbiology</i> , 2019, 4, 1183-1195.	5.9	491
223	The cooling tower water microbiota: Seasonal dynamics and co-occurrence of bacterial and protist phylotypes. <i>Water Research</i> , 2019, 159, 464-479.	5.3	51
224	Establishment Limitation Constrains the Abundance of Lactic Acid Bacteria in the Napa Cabbage Phyllosphere. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	26
225	Microbial Biodeterioration of Cultural Heritage: Events, Colonization, and Analyses. <i>Microbial Ecology</i> , 2019, 78, 1014-1029.	1.4	75
226	Bacterial community structure and function distinguish gut sites in captive red-shanked doucs ( <i>Pygathrix nemaeus</i> ). <i>American Journal of Primatology</i> , 2019, 81, e22977.	0.8	9
227	Latitudinal variation in soil nematode communities under climate warming-related range-expanding and native plants. <i>Global Change Biology</i> , 2019, 25, 2714-2726.	4.2	45
228	Uncovering the hidden marine sponge microbiome by applying a multi-primer approach. <i>Scientific Reports</i> , 2019, 9, 6214.	1.6	12
229	The Characterization of Microbial Communities Response to Shallow Groundwater Contamination in Typical Piedmont Region of Taihang Mountains in the North China Plain. <i>Water (Switzerland)</i> , 2019, 11, 736.	1.2	4
230	DNA metabarcoding—Need for robust experimental designs to draw sound ecological conclusions. <i>Molecular Ecology</i> , 2019, 28, 1857-1862.	2.0	300
231	Spatial, Temporal, and Phylogenetic Scales of Microbial Ecology. <i>Trends in Microbiology</i> , 2019, 27, 662-669.	3.5	105
232	Drinking Water Microbiome Project: Is it Time?. <i>Trends in Microbiology</i> , 2019, 27, 670-677.	3.5	50
233	Genomic Characterization of Candidate Division LCP-89 Reveals an Atypical Cell Wall Structure, Microcompartment Production, and Dual Respiratory and Fermentative Capacities. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	14
234	Two Chloroflexi classes independently evolved the ability to persist on atmospheric hydrogen and carbon monoxide. <i>ISME Journal</i> , 2019, 13, 1801-1813.	4.4	129
235	A novel, nature-based alternative for photobioreactor decontaminations. <i>Scientific Reports</i> , 2019, 9, 2864.	1.6	14
236	Exploring the links between bacterial communities and magnetic susceptibility in bulk soil and rhizosphere of beech ( <i>Fagus sylvatica</i> L.). <i>Applied Soil Ecology</i> , 2019, 138, 69-79.	2.1	6
237	Sponges from Zanzibar host diverse prokaryotic communities with potential for natural product synthesis. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	29
238	Available energy fluxes drive a transition in the diversity, stability, and functional structure of microbial communities. <i>PLoS Computational Biology</i> , 2019, 15, e1006793.	1.5	101

#	ARTICLE	IF	CITATIONS
239	A Developing Symbiosis: Enabling Cross-Talk Between Ecologists and Microbiome Scientists. <i>Frontiers in Microbiology</i> , 2019, 10, 292.	1.5	50
240	Initial Evidence of the Relationships between the Human Postmortem Microbiome and Neighborhood Blight and Greening Efforts. <i>Annals of the American Association of Geographers</i> , 2019, 109, 958-978.	1.5	18
241	Subsurface Microbial Habitats in an Extreme Desert Mars-Analog Environment. <i>Frontiers in Microbiology</i> , 2019, 10, 69.	1.5	44
242	Modularity and predicted functions of the global sponge-microbiome network. <i>Nature Communications</i> , 2019, 10, 992.	5.8	94
243	Airborne microbial transport limitation to isolated Antarctic soil habitats. <i>Nature Microbiology</i> , 2019, 4, 925-932.	5.9	114
244	Urban metagenomics uncover antibiotic resistance reservoirs in coastal beach and sewage waters. <i>Microbiome</i> , 2019, 7, 35.	4.9	109
245	Transmission of human-associated microbiota along family and social networks. <i>Nature Microbiology</i> , 2019, 4, 964-971.	5.9	149
246	Fitness and microbial networks of the common wasp, <i>Vespula vulgaris</i> (Hymenoptera: Vespidae), in its native and introduced ranges. <i>Ecological Entomology</i> , 2019, 44, 512-523.	1.1	11
247	A census-based estimate of Earth's bacterial and archaeal diversity. <i>PLoS Biology</i> , 2019, 17, e3000106.	2.6	139
248	Nutrient-based diet modifications impact on the gut microbiome of the Javan slow loris ( <i>Nycticebus</i> ) Tj ETQq1 1 0.784314 rgBT /Overbo 1.6 24	1.6	24
249	Bacterial and viral respiratory tract microbiota and host characteristics in children with lower respiratory tract infections: a matched case-control study. <i>Lancet Respiratory Medicine</i> , 2019, 7, 417-426.	5.2	140
250	Streaming histogram sketching for rapid microbiome analytics. <i>Microbiome</i> , 2019, 7, 40.	4.9	18
251	Characterization of the total and viable bacterial and fungal communities associated with the International Space Station surfaces. <i>Microbiome</i> , 2019, 7, 50.	4.9	158
252	Restoring subtidal marine macrophytes in the Anthropocene: trajectories and future-proofing. <i>Marine and Freshwater Research</i> , 2019, 70, 936.	0.7	71
253	Future climate change is predicted to affect the microbiome and condition of habitat-forming kelp. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20181887.	1.2	101
254	Impacts of indoor surface finishes on bacterial viability. <i>Indoor Air</i> , 2019, 29, 551-562.	2.0	28
255	Dispersal homogenizes communities via immigration even at low rates in a simplified synthetic bacterial metacommunity. <i>Nature Communications</i> , 2019, 10, 1314.	5.8	47
256	Salt Marsh Greenhouse Gas Fluxes and Microbial Communities Are Not Sensitive to the First Year of Precipitation Change. <i>Journal of Geophysical Research G: Biogeosciences</i> , 2019, 124, 1071-1087.	1.3	17



#	ARTICLE	IF	CITATIONS
257	Pharmacobiomics: The Holy Grail to Variability in Drug Response?. <i>Clinical Pharmacology and Therapeutics</i> , 2019, 106, 317-328.	2.3	49
258	Role of the Plant Root Microbiome in Abiotic Stress Tolerance. , 2019, , 273-311.		20
259	Human and Extracellular DNA Depletion for Metagenomic Analysis of Complex Clinical Infection Samples Yields Optimized Viable Microbiome Profiles. <i>Cell Reports</i> , 2019, 26, 2227-2240.e5.	2.9	104
260	Tracing seafood at high spatial resolution using NGS-generated data and machine learning: Comparing microbiome versus SNPs. <i>Food Chemistry</i> , 2019, 286, 413-420.	4.2	22
261	CAMISIM: simulating metagenomes and microbial communities. <i>Microbiome</i> , 2019, 7, 17.	4.9	117
262	Changes of paradigms in agriculture soil microbiology and new challenges in microbial ecology. <i>Acta Oecologica</i> , 2019, 95, 68-73.	0.5	12
263	Redox traits characterize the organization of global microbial communities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 3630-3635.	3.3	44
264	Evaluating Metagenomic Prediction of the Metaproteome in a 4.5-Year Study of a Patient with Crohn's Disease. <i>MSystems</i> , 2019, 4, .	1.7	40
265	Community richness of amphibian skin bacteria correlates with bioclimate at the global scale. <i>Nature Ecology and Evolution</i> , 2019, 3, 381-389.	3.4	68
266	Amphibian microbiome linked to climate. <i>Nature Ecology and Evolution</i> , 2019, 3, 332-333.	3.4	1
267	Sequence and cultivation study of Muribaculaceae reveals novel species, host preference, and functional potential of this yet undescribed family. <i>Microbiome</i> , 2019, 7, 28.	4.9	481
268	Current State of and Future Opportunities for Prediction in Microbiome Research: Report from the Mid-Atlantic Microbiome Meet-up in Baltimore on 9 January 2019. <i>MSystems</i> , 2019, 4, .	1.7	6
269	Chemical and microbial diversity covary in fresh water to influence ecosystem functioning. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 24689-24695.	3.3	98
270	Unaltered Fungal Burden and Lethality in Human CEACAM1-Transgenic Mice During <i>Candida albicans</i> Dissemination and Systemic Infection. <i>Frontiers in Microbiology</i> , 2019, 10, 2703.	1.5	5
271	AMON: annotation of metabolite origins via networks to integrate microbiome and metabolome data. <i>BMC Bioinformatics</i> , 2019, 20, 614.	1.2	40
272	Temporal stability of the rumen microbiota in beef cattle, and response to diet and supplements. <i>Animal Microbiome</i> , 2019, 1, 16.	1.5	29
273	Microbes and Enzymes in Soil Health and Bioremediation. <i>Microorganisms for Sustainability</i> , 2019, , .	0.4	20
274	Prokaryotic Diversity in Mangrove Sediments across Southeastern China Fundamentally Differs from That in Other Biomes. <i>MSystems</i> , 2019, 4, .	1.7	57



#	ARTICLE	IF	CITATIONS
275	Charting the diversity of uncultured viruses of Archaea and Bacteria. <i>BMC Biology</i> , 2019, 17, 109.	1.7	26
276	Synergistic effects of APOE and sex on the gut microbiome of young EFAD transgenic mice. <i>Molecular Neurodegeneration</i> , 2019, 14, 47.	4.4	33
277	tmap: an integrative framework based on topological data analysis for population-scale microbiome stratification and association studies. <i>Genome Biology</i> , 2019, 20, 293.	3.8	20
278	Changes in bacterial community composition across natural grassland and pine forests in the Bunya Mountains in subtropical Australia. <i>Soil Research</i> , 2019, 57, 825.	0.6	5
279	Systematic processing of ribosomal RNA gene amplicon sequencing data. <i>GigaScience</i> , 2019, 8, .	3.3	49
280	High-order interactions distort the functional landscape of microbial consortia. <i>PLoS Biology</i> , 2019, 17, e3000550.	2.6	114
281	Host-mediated microbiome engineering (HMME) of drought tolerance in the wheat rhizosphere. <i>PLoS ONE</i> , 2019, 14, e0225933.	1.1	80
282	The Microbiome and Its Potential for Pharmacology. <i>Handbook of Experimental Pharmacology</i> , 2019, 260, 301-326.	0.9	14
283	Clustering and Classification of Human Microbiome Data: Evaluating the Impact of Different Settings in Bioinformatics Workflows. , 2019, , .		2
284	Methods for automatic reference trees and multilevel phylogenetic placement. <i>Bioinformatics</i> , 2019, 35, 1151-1158.	1.8	33
285	Contrasting patterns of plant and microbial diversity during long-term ecosystem development. <i>Journal of Ecology</i> , 2019, 107, 606-621.	1.9	48
286	The Microbiome Stress Project: Toward a Global Meta-Analysis of Environmental Stressors and Their Effects on Microbial Communities. <i>Frontiers in Microbiology</i> , 2018, 9, 3272.	1.5	126
287	gcMeta: a Global Catalogue of Metagenomics platform to support the archiving, standardization and analysis of microbiome data. <i>Nucleic Acids Research</i> , 2019, 47, D637-D648.	6.5	70
288	Cross-Biome Drivers of Soil Bacterial Alpha Diversity on a Worldwide Scale. <i>Ecosystems</i> , 2019, 22, 1220-1231.	1.6	71
289	Evolutionary constraints on species diversity in marine bacterioplankton communities. <i>ISME Journal</i> , 2019, 13, 1032-1041.	4.4	11
290	Towards a systematic understanding of differences between archaeal and bacterial diversity. <i>Environmental Microbiology Reports</i> , 2019, 11, 9-12.	1.0	3
291	Trace Evidence Potential in Postmortem Skin Microbiomes: From Death Scene to Morgue. <i>Journal of Forensic Sciences</i> , 2019, 64, 791-798.	0.9	40
292	Linking bacterial community composition to soil salinity along environmental gradients. <i>ISME Journal</i> , 2019, 13, 836-846.	4.4	283

#	ARTICLE	IF	CITATIONS
293	Estimating the postmortem interval using microbes: Knowledge gaps and a path to technology adoption. <i>Forensic Science International: Genetics</i> , 2019, 38, 211-218.	1.6	86
294	Microbiome 101: Studying, Analyzing, and Interpreting Gut Microbiome Data for Clinicians. <i>Clinical Gastroenterology and Hepatology</i> , 2019, 17, 218-230.	2.4	187
295	The Ecological Role of Micro-organisms in the Antarctic Environment. <i>Springer Polar Sciences</i> , 2019, , .	0.0	11
296	Antarctic Soil Microbial Communities in a Changing Environment: Their Contributions to the Sustainability of Antarctic Ecosystems and the Bioremediation of Anthropogenic Pollution. <i>Springer Polar Sciences</i> , 2019, , 133-161.	0.0	11
297	The known and the unknown in soil microbial ecology. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	64
298	Uncovering the hidden microbiota in hospital and built environments: New approaches and solutions. <i>Experimental Biology and Medicine</i> , 2019, 244, 534-542.	1.1	23
299	Soil Bacterial Community Associated With High Potato Production and Minimal Water Use. <i>Frontiers in Environmental Science</i> , 2019, 6, .	1.5	12
300	Ecological selection for small microbial genomes along a temperate-to-thermal soil gradient. <i>Nature Microbiology</i> , 2019, 4, 55-61.	5.9	42
301	Teamwork makes the dream work: Disentangling cross-taxon congruence across soil biota in black pine plantations. <i>Science of the Total Environment</i> , 2019, 656, 659-669.	3.9	16
302	Designing Spatially Distributed Gene Regulatory Networks To Elicit Contrasting Patterns. <i>ACS Synthetic Biology</i> , 2019, 8, 119-126.	1.9	6
303	Multiple Facets of Marine Invertebrate Conservation Genomics. <i>Annual Review of Animal Biosciences</i> , 2019, 7, 473-497.	3.6	16
304	Microbiomes and Holobionts. , 2019, , 157-164.		1
305	Geographical pattern of methanogenesis in paddy and wetland soils across eastern China. <i>Science of the Total Environment</i> , 2019, 651, 281-290.	3.9	6
306	Molecular Approaches for an Operational Marine Biodiversity Observation Network. , 2019, , 613-631.		5
307	Microbial Diversity of Thermophiles Through the Lens of Next Generation Sequencing. , 2019, , 217-226.		6
308	Pangenomic comparison of globally distributed Poribacteria associated with sponge hosts and marine particles. <i>ISME Journal</i> , 2019, 13, 468-481.	4.4	63
309	Elucidating the ecological networks in stoneâ€dwelling microbiomes. <i>Environmental Microbiology</i> , 2020, 22, 1467-1480.	1.8	38
310	Belowground microbial communities respond to water deficit and are shaped by decades of maize hybrid breeding. <i>Environmental Microbiology</i> , 2020, 22, 889-904.	1.8	15

#	ARTICLE	IF	CITATIONS
311	Soil microbiomes and climate change. <i>Nature Reviews Microbiology</i> , 2020, 18, 35-46.	13.6	725
312	Interactive Effects of Microbes and Nitrogen on <i>Panicum virgatum</i> Root Functional Traits and Patterns of Phenotypic Selection. <i>International Journal of Plant Sciences</i> , 2020, 181, 20-32.	0.6	10
313	Spatiotemporal patterns of microbial composition and diversity in precipitation. <i>Ecological Monographs</i> , 2020, 90, e01394.	2.4	14
314	<i>phylogenize</i> : correcting for phylogeny reveals genes associated with microbial distributions. <i>Bioinformatics</i> , 2020, 36, 1289-1290.	1.8	3
315	A General and Efficient Algorithm for the Likelihood of Diversification and Discrete-Trait Evolutionary Models. <i>Systematic Biology</i> , 2020, 69, 545-556.	2.7	16
316	ReClustOR: a clustering tool using an open-reference method that improves operational taxonomic unit definition. <i>Methods in Ecology and Evolution</i> , 2020, 11, 168-180.	2.2	8
317	Structural equation models to disentangle the biological relationship between microbiota and complex traits: Methane production in dairy cattle as a case of study. <i>Journal of Animal Breeding and Genetics</i> , 2020, 137, 36-48.	0.8	30
318	Analysis of bacterial microbiome associated with nylon and copper nets in an aquaculture context. <i>Aquaculture</i> , 2020, 516, 734540.	1.7	10
319	Response and driving factors of soil microbial diversity related to global nitrogen addition. <i>Land Degradation and Development</i> , 2020, 31, 190-204.	1.8	60
320	Latent Dirichlet Allocation reveals spatial and taxonomic structure in a DNA-based census of soil biodiversity from a tropical forest. <i>Molecular Ecology Resources</i> , 2020, 20, 371-386.	2.2	16
321	Expression of Free Fatty Acid Receptor 2 by Dendritic Cells Prevents Their Expression of Interleukin 27 and Is Required for Maintenance of Mucosal Barrier and Immune Response Against Colorectal Tumors in Mice. <i>Gastroenterology</i> , 2020, 158, 1359-1372.e9.	0.6	54
322	Mobile resistome of human gut and pathogen drives anthropogenic bloom of antibiotic resistance. <i>Microbiome</i> , 2020, 8, 2.	4.9	80
323	DNA metabarcoding reveals organisms contributing to particulate matter flux to abyssal depths in the North East Pacific ocean. <i>Deep-Sea Research Part II: Topical Studies in Oceanography</i> , 2020, 173, 104708.	0.6	51
324	Comparison of extraction methods for recovering ancient microbial DNA from paleofeces. <i>American Journal of Physical Anthropology</i> , 2020, 171, 275-284.	2.1	71
325	Evaluation of accuracy and precision in an amplicon sequencing workflow for marine protist communities. <i>Limnology and Oceanography: Methods</i> , 2020, 18, 20-40.	1.0	18
326	Structural changes of the microplankton community following a pulse of inorganic nitrogen in a eutrophic river. <i>Limnology and Oceanography</i> , 2020, 65, S264.	1.6	5
327	Mechanisms of soil bacterial and fungal community assembly differ among and within islands. <i>Environmental Microbiology</i> , 2020, 22, 1559-1571.	1.8	47
328	Linking metagenomics to aquatic microbial ecology and biogeochemical cycles. <i>Limnology and Oceanography</i> , 2020, 65, S2.	1.6	82

#	ARTICLE	IF	CITATIONS
329	Panel 4: Recent advances in understanding the natural history of the otitis media microbiome and its response to environmental pressures. <i>International Journal of Pediatric Otorhinolaryngology</i> , 2020, 130, 109836.	0.4	16
330	Biogeographical distribution of bacterial communities in saline agricultural soil. <i>Geoderma</i> , 2020, 361, 114095.	2.3	39
331	Key Questions for Next-Generation Biomonitoring. <i>Frontiers in Environmental Science</i> , 2020, 7, .	1.5	68
332	Conserving the holobiont. <i>Functional Ecology</i> , 2020, 34, 764-776.	1.7	61
333	Home chemical and microbial transitions across urbanization. <i>Nature Microbiology</i> , 2020, 5, 108-115.	5.9	83
334	Plant and soil traits driving soil fungal community due to tree plantation on the Loess Plateau. <i>Science of the Total Environment</i> , 2020, 708, 134560.	3.9	33
335	The Ecobiomics project: Advancing metagenomics assessment of soil health and freshwater quality in Canada. <i>Science of the Total Environment</i> , 2020, 710, 135906.	3.9	25
336	Characterizing the Composition of the Pediatric Gut Microbiome: A Systematic Review. <i>Nutrients</i> , 2020, 12, 16.	1.7	27
337	Sediment-associated bacterial community and predictive functionalities are influenced by choice of 16S ribosomal RNA hypervariable region(s): An amplicon-based diversity study. <i>Genomics</i> , 2020, 112, 4968-4979.	1.3	10
338	Microbial succession from a subsequent secondary death event following mass mortality. <i>BMC Microbiology</i> , 2020, 20, 309.	1.3	15
339	Alpha-, beta-, and gamma-diversity of bacteria varies across habitats. <i>PLoS ONE</i> , 2020, 15, e0233872.	1.1	105
340	Mapping the bacterial metabolic niche space. <i>Nature Communications</i> , 2020, 11, 4887.	5.8	27
341	Analysis of the intestinal microbiota in COVID-19 patients and its correlation with the inflammatory factor IL-18. <i>Medicine in Microecology</i> , 2020, 5, 100023.	0.7	112
342	Diversity of gut microbiomes in marine fishes is shaped by host-related factors. <i>Molecular Ecology</i> , 2020, 29, 5019-5034.	2.0	57
343	Introducing the Mangrove Microbiome Initiative: Identifying Microbial Research Priorities and Approaches To Better Understand, Protect, and Rehabilitate Mangrove Ecosystems. <i>MSystems</i> , 2020, 5, .	1.7	40
344	Effects of increasing dietary level of organic acids and nature-identical compounds on growth, intestinal cytokine gene expression and gut microbiota of rainbow trout ( <i>Oncorhynchus mykiss</i> ) reared at normal and high temperature. <i>Fish and Shellfish Immunology</i> , 2020, 107, 324-335.	1.6	33
345	Manipulation of the gut microbiota by the use of prebiotic fibre does not override a genetic predisposition to heart failure. <i>Scientific Reports</i> , 2020, 10, 17919.	1.6	8
346	The Central Role of Interbacterial Antagonism in Bacterial Life. <i>Current Biology</i> , 2020, 30, R1203-R1214.	1.8	59

#	ARTICLE	IF	CITATIONS
347	Environmental Atlas of Prokaryotes Enables Powerful and Intuitive Habitat-Based Analysis of Community Structures. <i>IScience</i> , 2020, 23, 101624.	1.9	14
348	Biodiversity intervention enhances immune regulation and health-associated commensal microbiota among daycare children. <i>Science Advances</i> , 2020, 6, .	4.7	174
349	Leveling up citizen science. <i>Nature Biotechnology</i> , 2020, 38, 1124-1126.	9.4	20
350	Changes in soil microbial communities in post mine ecological restoration: Implications for monitoring using high throughput DNA sequencing. <i>Science of the Total Environment</i> , 2020, 749, 142262.	3.9	33
351	Microbes and microbiomes in 2020 and beyond. <i>Nature Communications</i> , 2020, 11, 4988.	5.8	7
352	Salinity, Water Level, and Forest Structure Contribute to Baldcypress ( <i>Taxodium distichum</i> ) Rhizosphere and Endosphere Community Structure. <i>Wetlands</i> , 2020, 40, 2179-2188.	0.7	3
353	The microbiome: An emerging key player in aging and longevity. <i>Translational Medicine of Aging</i> , 2020, 4, 103-116.	0.6	76
354	Implications of Peat Soil Conceptualization for Groundwater Exfiltration in Numerical Modeling: A Study on a Hypothetical Peatland Hillslope. <i>Water Resources Research</i> , 2020, 56, e2019WR026203.	1.7	8
355	Conventional seed coating reduces prevalence of proteobacterial endophytes in <i>Nicotiana tabacum</i> . <i>Industrial Crops and Products</i> , 2020, 155, 112784.	2.5	16
356	The gut microbiota of brood parasite and host nestlings reared within the same environment: disentangling genetic and environmental effects. <i>ISME Journal</i> , 2020, 14, 2691-2702.	4.4	19
357	GlobalFungi, a global database of fungal occurrences from high-throughput-sequencing metabarcoding studies. <i>Scientific Data</i> , 2020, 7, 228.	2.4	92
358	The limits of lead (Pb) phytoextraction and possibilities of phytostabilization in contaminated soil: a critical review. <i>International Journal of Phytoremediation</i> , 2020, 22, 916-930.	1.7	42
359	When nature goes digital: routes for responsible innovation. <i>Journal of Responsible Innovation</i> , 2020, 7, 342-360.	2.3	10
360	Infant Skin Bacterial Communities Vary by Skin Site and Infant Age across Populations in Mexico and the United States. <i>MSystems</i> , 2020, 5, .	1.7	16
361	Effects of Bacterial Supplementation on Black Soldier Fly Growth and Development at Benchtop and Industrial Scale. <i>Frontiers in Microbiology</i> , 2020, 11, 587979.	1.5	23
362	Vitamin D metabolites and the gut microbiome in older men. <i>Nature Communications</i> , 2020, 11, 5997.	5.8	88
363	Many roads to bacterial generalism. <i>FEMS Microbiology Ecology</i> , 2020, 97, .	1.3	21
364	Carbon and nitrogen cycling in Yedoma permafrost controlled by microbial functional limitations. <i>Nature Geoscience</i> , 2020, 13, 794-798.	5.4	45

#	ARTICLE	IF	CITATIONS
365	Unravelling the importance of the eukaryotic and bacterial communities and their relationship with <i>Legionella</i> spp. ecology in cooling towers: a complex network. <i>Microbiome</i> , 2020, 8, 157.	4.9	19
366	Microbiomes for All. <i>Frontiers in Microbiology</i> , 2020, 11, 593472.	1.5	4
367	Aquatic virus culture collection: an absent (but necessary) safety net for environmental microbiologists. <i>Applied Phycology</i> , 2022, 3, 211-225.	0.6	7
368	DRAM for distilling microbial metabolism to automate the curation of microbiome function. <i>Nucleic Acids Research</i> , 2020, 48, 8883-8900.	6.5	410
369	Maternal administration of probiotics promotes gut development in mouse offsprings. <i>PLoS ONE</i> , 2020, 15, e0237182.	1.1	18
370	Microbial community shift under exposure of dredged sediments from a eutrophic bay. <i>Environmental Monitoring and Assessment</i> , 2020, 192, 539.	1.3	7
371	Temperature-Induced Annual Variation in Microbial Community Changes and Resulting Metabolome Shifts in a Controlled Fermentation System. <i>MSystems</i> , 2020, 5, .	1.7	47
372	Microbiome Shifts Associated With the Introduction of Wild Atlantic Horseshoe Crabs ( <i>Limulus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock	1.5	12
373	The Challenges of Reconstructing Tropical Biodiversity With Sedimentary Ancient DNA: A 2200-Year-Long Metagenomic Record From Bwindi Impenetrable Forest, Uganda. <i>Frontiers in Ecology and Evolution</i> , 2020, 8, .	1.1	23
374	Rapid biodegradation of renewable polyurethane foams with identification of associated microorganisms and decomposition products. <i>Bioresource Technology Reports</i> , 2020, 11, 100513.	1.5	37
375	Microbial diversity drives carbon use efficiency in a model soil. <i>Nature Communications</i> , 2020, 11, 3684.	5.8	217
376	Evaluating metagenomics tools for genome binning with real metagenomic datasets and CAMI datasets. <i>BMC Bioinformatics</i> , 2020, 21, 334.	1.2	53
377	Method development for cross-study microbiome data mining: Challenges and opportunities. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 2075-2080.	1.9	27
378	Microbial macroecology: In search of mechanisms governing microbial biogeographic patterns. <i>Global Ecology and Biogeography</i> , 2020, 29, 1870-1886.	2.7	55
379	Blind spots in global soil biodiversity and ecosystem function research. <i>Nature Communications</i> , 2020, 11, 3870.	5.8	192
380	Consumption of a Western-Style Diet Modulates the Response of the Murine Gut Microbiome to Ciprofloxacin. <i>MSystems</i> , 2020, 5, .	1.7	23
381	Methods and approaches to advance soil macroecology. <i>Global Ecology and Biogeography</i> , 2020, 29, 1674-1690.	2.7	28
382	Putting COI Metabarcoding in Context: The Utility of Exact Sequence Variants (ESVs) in Biodiversity Analysis. <i>Frontiers in Ecology and Evolution</i> , 2020, 8, .	1.1	37

#	ARTICLE	IF	CITATIONS
383	Soil microbial composition varies in response to coffee agroecosystem management. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	16
385	Testing the Two-Step Model of Plant Root Microbiome Acquisition Under Multiple Plant Species and Soil Sources. <i>Frontiers in Microbiology</i> , 2020, 11, 542742.	1.5	20
386	Microbiota of the Therapeutic Euganean Thermal Muds with a Focus on the Main Cyanobacteria Species. <i>Microorganisms</i> , 2020, 8, 1590.	1.6	23
387	The earthworm microbiome is resilient to exposure to biocidal metal nanoparticles. <i>Environmental Pollution</i> , 2020, 267, 115633.	3.7	17
388	Molecular detection of opportunistic pathogens and insights into microbial diversity in private well water and premise plumbing. <i>Journal of Water and Health</i> , 2020, 18, 820-834.	1.1	9
389	Phylotype-Level Characterization of Complex Communities of Lactobacilli Using a High-Throughput, High-Resolution Phenylalanyl-tRNA Synthetase ( <i>pheS</i> ) Gene Amplicon Sequencing Approach. <i>Applied and Environmental Microbiology</i> , 2020, 87, .	1.4	4
390	Antibiotics in hives and their effects on honey bee physiology and behavioral development. <i>Biology Open</i> , 2020, 9, .	0.6	22
391	Daring to be differential: metabarcoding analysis of soil and plant-related microbial communities using amplicon sequence variants and operational taxonomical units. <i>BMC Genomics</i> , 2020, 21, 733.	1.2	58
392	Analysis of molecular diversity within single cyanobacterial colonies from environmental samples. <i>Scientific Reports</i> , 2020, 10, 18453.	1.6	5
393	The archives are half-empty: an assessment of the availability of microbial community sequencing data. <i>Communications Biology</i> , 2020, 3, 474.	2.0	22
394	Activity-based cell sorting reveals responses of uncultured archaea and bacteria to substrate amendment. <i>ISME Journal</i> , 2020, 14, 2851-2861.	4.4	40
395	Macroecological laws describe variation and diversity in microbial communities. <i>Nature Communications</i> , 2020, 11, 4743.	5.8	84
396	On the way to specificity â€•Microbiome reflects sponge genetic cluster primarily in highly structured populations. <i>Molecular Ecology</i> , 2020, 29, 4412-4427.	2.0	22
397	Metagenomic Profiling and Microbial Metabolic Potential of Perdido Fold Belt (NW) and Campeche Knolls (SE) in the Gulf of Mexico. <i>Frontiers in Microbiology</i> , 2020, 11, 1825.	1.5	16
398	Generation of Comprehensive Ecosystem-Specific Reference Databases with Species-Level Resolution by High-Throughput Full-Length 16S rRNA Gene Sequencing and Automated Taxonomy Assignment (AutoTax). <i>MBio</i> , 2020, 11, .	1.8	66
399	CD8 T cells drive anorexia, dysbiosis, and blooms of a commensal with immunosuppressive potential after viral infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 24998-25007.	3.3	10
400	Applying the Anna Karenina principle for wild animal gut microbiota: Temporal stability of the bank vole gut microbiota in a disturbed environment. <i>Journal of Animal Ecology</i> , 2020, 89, 2617-2630.	1.3	28
401	Fructose stimulated de novo lipogenesis is promoted by inflammation. <i>Nature Metabolism</i> , 2020, 2, 1034-1045.	5.1	174



#	ARTICLE	IF	CITATIONS
402	Decoupled Spatial Distribution of PAHs Degraders Determined by Taxonomic 16S rRNA and Degrading Genes Across Chinese Forest Soils. <i>Journal of Geophysical Research G: Biogeosciences</i> , 2020, 125, e2020JG005659.	1.3	1
403	A lab in the field: applications of real-time, in situ metagenomic sequencing. <i>Biology Methods and Protocols</i> , 2020, 5, bpa016.	1.0	10
404	Sub-Lethal Effects of Pesticides on the DNA of Soil Organisms as Early Ecotoxicological Biomarkers. <i>Frontiers in Microbiology</i> , 2020, 11, 1892.	1.5	26
405	Gut mycobiome and its interaction with diet, gut bacteria and alzheimer's disease markers in subjects with mild cognitive impairment: A pilot study. <i>EBioMedicine</i> , 2020, 59, 102950.	2.7	98
406	Contrasting environmental preferences of photosynthetic and non-photosynthetic soil cyanobacteria across the globe. <i>Global Ecology and Biogeography</i> , 2020, 29, 2025-2038.	2.7	24
407	Biosulfidogenesis Mediates Natural Attenuation in Acidic Mine Pit Lakes. <i>Microorganisms</i> , 2020, 8, 1275.	1.6	19
408	Estimate of the sequenced proportion of the global prokaryotic genome. <i>Microbiome</i> , 2020, 8, 134.	4.9	58
409	Lactose-reduced infant formula with added corn syrup solids is associated with a distinct gut microbiota in Hispanic infants. <i>Gut Microbes</i> , 2020, 12, 1813534.	4.3	18
410	Diverse Bacterial Communities From Qaidam Basin of the Qinghai-Tibet Plateau: Insights Into Variations in Bacterial Diversity Across Different Regions. <i>Frontiers in Microbiology</i> , 2020, 11, 554105.	1.5	8
411	A total crapshoot? Evaluating bioinformatic decisions in animal diet metabarcoding analyses. <i>Ecology and Evolution</i> , 2020, 10, 9721-9739.	0.8	40
412	Roles of the gut microbiota in the adaptive evolution of mammalian species. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190597.	1.8	83
413	Skin Microbiome and its Interplay with the Environment. <i>American Journal of Clinical Dermatology</i> , 2020, 21, 4-11.	3.3	54
414	A specific combination of dual index adaptors decreases the sensitivity of amplicon sequencing with the Illumina platform. <i>DNA Research</i> , 2020, 27, .	1.5	0
415	Microbe-Metabolite Associations Linked to the Rebounding Murine Gut Microbiome Postcolonization with Vancomycin-Resistant <i>Enterococcus faecium</i> . <i>MSystems</i> , 2020, 5, .	1.7	3
416	Phenotypic Parallelism during Experimental Adaptation of a Free-Living Bacterium to the Zebrafish Gut. <i>MBio</i> , 2020, 11, .	1.8	12
417	Organism body size structures the soil microbial and nematode community assembly at a continental and global scale. <i>Nature Communications</i> , 2020, 11, 6406.	5.8	113
418	Using the Microbiome Amplification Preference Tool (MAPT) to Reveal <i>Medicago sativa</i> -Associated Eukaryotic Microbes. <i>Phytobiomes Journal</i> , 2020, 4, 340-350.	1.4	3
419	Comprehensive Survey of the Litter Bacterial Communities in Commercial Turkey Farms. <i>Frontiers in Veterinary Science</i> , 2020, 7, 596933.	0.9	8



#	ARTICLE	IF	CITATIONS
420	Dichloromethane Degradation Pathway from Unsequenced Hyphomicrobium sp. MC8b Rapidly Explored by Pan-Proteomics. <i>Microorganisms</i> , 2020, 8, 1876.	1.6	6
421	Synthetic Sequencing Standards: A Guide to Database Choice for Rumen Microbiota Amplicon Sequencing Analysis. <i>Frontiers in Microbiology</i> , 2020, 11, 606825.	1.5	14
422	Systematic evaluation of supervised machine learning for sample origin prediction using metagenomic sequencing data. <i>Biology Direct</i> , 2020, 15, 29.	1.9	11
423	The Southern Bluefin Tuna Mucosal Microbiome Is Influenced by Husbandry Method, Net Pen Location, and Anti-parasite Treatment. <i>Frontiers in Microbiology</i> , 2020, 11, 2015.	1.5	12
424	BIOCOM-PIPE: a new user-friendly metabarcoding pipeline for the characterization of microbial diversity from 16S, 18S and 23S rRNA gene amplicons. <i>BMC Bioinformatics</i> , 2020, 21, 492.	1.2	16
425	Abiotic factors influence patterns of bacterial diversity and community composition in the Dry Valleys of Antarctica. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	23
426	Sea Cucumber Intestinal Regeneration Reveals Deterministic Assembly of the Gut Microbiome. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	21
427	The ocean genome and future prospects for conservation and equity. <i>Nature Sustainability</i> , 2020, 3, 588-596.	11.5	38
428	Archaea in boreal Swedish lakes are diverse, dominated by Woesearchaeota and follow deterministic community assembly. <i>Environmental Microbiology</i> , 2020, 22, 3158-3171.	1.8	19
429	Continental-Scale Microbiome Study Reveals Different Environmental Characteristics Determining Microbial Richness, Composition, and Quantity in Hotel Rooms. <i>MSystems</i> , 2020, 5, .	1.7	20
430	Microbiome profile associated with malignant pleural effusion. <i>PLoS ONE</i> , 2020, 15, e0232181.	1.1	7
431	The next frontier of the anaerobic digestion microbiome: From ecology to process control. <i>Environmental Science and Ecotechnology</i> , 2020, 3, 100032.	6.7	26
432	Online searching platform for the antibiotic resistome in bacterial tree of life and global habitats. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	19
433	The NADP-dependent malic enzyme MaeB is a central metabolic hub controlled by the acetyl-CoA to CoASH ratio. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2020, 1868, 140462.	1.1	4
434	Detecting personal microbiota signatures at artificial crime scenes. <i>Forensic Science International</i> , 2020, 313, 110351.	1.3	19
435	Fiber Force: A Fiber Diet Intervention in an Advanced Course-Based Undergraduate Research Experience (CURE) Course. <i>Journal of Microbiology and Biology Education</i> , 2020, 21, .	0.5	15
436	Soil Microbiomes Under Climate Change and Implications for Carbon Cycling. <i>Annual Review of Environment and Resources</i> , 2020, 45, 29-59.	5.6	145
437	Space Is More Important than Season when Shaping Soil Microbial Communities at a Large Spatial Scale. <i>MSystems</i> , 2020, 5, .	1.7	71

#	ARTICLE	IF	CITATIONS
438	FORENSIC: an Online Platform for Fecal Source Identification. <i>MSystems</i> , 2020, 5, .	1.7	12
439	Unique Gut Microbiome Signatures Depict Diet-Versus Genetically Induced Obesity in Mice. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3434.	1.8	16
440	Controlled lacustrine microcosms show a brGDGT response to environmental perturbations. <i>Organic Geochemistry</i> , 2020, 145, 104041.	0.9	22
441	Community-level signatures of ecological succession in natural bacterial communities. <i>Nature Communications</i> , 2020, 11, 2386.	5.8	33
442	Maternal <i>H. pylori</i> is associated with differential fecal microbiota in infants born by vaginal delivery. <i>Scientific Reports</i> , 2020, 10, 7305.	1.6	2
443	Development and Application of Performance Assessment Criteria for Next-Generation Sequencing-Based HIV Drug Resistance Assays. <i>Viruses</i> , 2020, 12, 627.	1.5	10
444	Correlation and association analyses in microbiome study integrating multiomics in health and disease. <i>Progress in Molecular Biology and Translational Science</i> , 2020, 171, 309-491.	0.9	103
445	Characterising the soil fungal microbiome in metropolitan green spaces across a vegetation biodiversity gradient. <i>Fungal Ecology</i> , 2020, 47, 100939.	0.7	20
446	Earth microbial co-occurrence network reveals interconnection pattern across microbiomes. <i>Microbiome</i> , 2020, 8, 82.	4.9	239
447	Temperate Forests Dominated by Arbuscular or Ectomycorrhizal Fungi Are Characterized by Strong Shifts from Saprotrophic to Mycorrhizal Fungi with Increasing Soil Depth. <i>Microbial Ecology</i> , 2021, 82, 377-390.	1.4	28
448	Mainstreaming Microbes across Biomes. <i>BioScience</i> , 2020, 70, 589-596.	2.2	11
449	The food-gut axis: lactic acid bacteria and their link to food, the gut microbiome and human health. <i>FEMS Microbiology Reviews</i> , 2020, 44, 454-489.	3.9	139
450	Effects of historical legacies on soil nematode communities are mediated by contemporary environmental conditions. <i>Ecology and Evolution</i> , 2020, 10, 6732-6740.	0.8	5
451	Soil microbial succession following surface mining is governed primarily by deterministic factors. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	19
452	High <i>Oscillospira</i> abundance indicates constipation and low BMI in the Guangdong Gut Microbiome Project. <i>Scientific Reports</i> , 2020, 10, 9364.	1.6	74
453	Host identity and symbiotic association affects the taxonomic and functional diversity of the clownfish-hosting sea anemone microbiome. <i>Biology Letters</i> , 2020, 16, 20190738.	1.0	8
454	Carbon Use Efficiency and Its Temperature Sensitivity Covary in Soil Bacteria. <i>MBio</i> , 2020, 11, .	1.8	52
455	The Effects of Temperature on Animal Gut Microbiomes. <i>Frontiers in Microbiology</i> , 2020, 11, 384.	1.5	150

#	ARTICLE	IF	CITATIONS
456	Plant Microbiomes for Sustainable Agriculture. <i>Sustainable Development and Biodiversity</i> , 2020, , .	1.4	134
457	Factors that shape the host microbiome. , 2020, , 55-77.		5
458	HAMAP as SPARQL rulesâ€”A portable annotation pipeline for genomes and proteomes. <i>GigaScience</i> , 2020, 9, .	3.3	6
459	Low mutational load and high mutation rate variation in gut commensal bacteria. <i>PLoS Biology</i> , 2020, 18, e3000617.	2.6	59
460	Use of standardized bioinformatics for the analysis of fungal DNA signatures applied to sample provenance. <i>Forensic Science International</i> , 2020, 310, 110250.	1.3	9
461	A framework to bridge scales in distribution modeling of soil microbiota. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	8
462	The Community Simulator: A Python package for microbial ecology. <i>PLoS ONE</i> , 2020, 15, e0230430.	1.1	31
463	Surveying the Sweetpotato Rhizosphere, Endophyte, and Surrounding Soil Microbiomes at Two North Carolina Farms Reveals Underpinnings of Sweetpotato Microbiome Community Assembly. <i>Phytobiomes Journal</i> , 2020, 4, 75-89.	1.4	7
464	Simultaneous Metabarcoding of Eukaryotes and Prokaryotes to Elucidate the Community Structures within Tardigrade Microhabitats. <i>Diversity</i> , 2020, 12, 110.	0.7	8
465	Enhanced Characterization of Drug Metabolism and the Influence of the Intestinal Microbiome: A Pharmacokinetic, Microbiome, and Untargeted Metabolomics Study. <i>Clinical and Translational Science</i> , 2020, 13, 972-984.	1.5	16
466	Coexistence and cooperation in structured habitats. <i>BMC Ecology</i> , 2020, 20, 14.	3.0	19
467	Predicting Microbiome Function Across Space Is Confounded by Strain-Level Differences and Functional Redundancy Across Taxa. <i>Frontiers in Microbiology</i> , 2020, 11, 101.	1.5	27
468	Disturbance is more important than seeding or grazing in determining soil microbial communities in a semiarid grassland. <i>Restoration Ecology</i> , 2020, 28, S335.	1.4	14
469	Marine Sediments Illuminate Chlamydiae Diversity and Evolution. <i>Current Biology</i> , 2020, 30, 1032-1048.e7.	1.8	52
470	Effects of Housing Types on Cecal Microbiota of Two Different Strains of Laying Hens During the Late Production Phase. <i>Frontiers in Veterinary Science</i> , 2020, 7, 331.	0.9	12
471	Digital microbiology. <i>Clinical Microbiology and Infection</i> , 2020, 26, 1324-1331.	2.8	20
472	Life-long dynamics of the swine gut microbiome and their implications in probiotics development and food safety. <i>Gut Microbes</i> , 2020, 11, 1824-1832.	4.3	38
473	Evaluation of primer pairs for microbiome profiling from soils to humans within the One Health framework. <i>Molecular Ecology Resources</i> , 2020, 20, 1558-1571.	2.2	61

#	ARTICLE	IF	CITATIONS
474	Interindividual Variation in Dietary Carbohydrate Metabolism by Gut Bacteria Revealed with Droplet Microfluidic Culture. <i>MSystems</i> , 2020, 5, .	1.7	34
475	Taxonomic classification method for metagenomics based on core protein families with Core-Kaiju. <i>Nucleic Acids Research</i> , 2020, 48, e93-e93.	6.5	19
476	Microbial communities from arid environments on a global scale. A systematic review. <i>Biological Research</i> , 2020, 53, 29.	1.5	30
477	Shotgun metagenomics of dust microbiome from flight deck and cabin in civil aviation aircraft. <i>Indoor Air</i> , 2020, 30, 1199-1212.	2.0	19
478	High-Resolution Longitudinal Dynamics of the Cystic Fibrosis Sputum Microbiome and Metabolome through Antibiotic Therapy. <i>MSystems</i> , 2020, 5, .	1.7	47
479	Non-specific protection from respiratory tract infections in cattle generated by intranasal administration of an innate immune stimulant. <i>PLoS ONE</i> , 2020, 15, e0235422.	1.1	9
480	Nutrient enrichment increases size of <i>Zostera marina</i> shoots and enriches for sulfur and nitrogen cycling bacteria in root-associated microbiomes. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	22
481	Developing standards for the microbiome field. <i>Microbiome</i> , 2020, 8, 98.	4.9	63
482	Disentangling the seasonal co-occurrence patterns and ecological stochasticity of planktonic and benthic bacterial communities within multiple lakes. <i>Science of the Total Environment</i> , 2020, 740, 140010.	3.9	62
483	Metagenomic-based approach to a comprehensive understanding of cave microbial diversity. , 2020, , 561-586.		4
484	Host-associated microbiomes are predicted by immune system complexity and climate. <i>Genome Biology</i> , 2020, 21, 23.	3.8	54
485	Think global, act local: The small-scale environment mainly influences microbial community development and function in lake sediment. <i>Limnology and Oceanography</i> , 2020, 65, S88.	1.6	17
486	Bacterial adaptation is constrained in complex communities. <i>Nature Communications</i> , 2020, 11, 754.	5.8	111
487	Patterns of Oral Microbiota Diversity in Adults and Children: A Crowdsourced Population Study. <i>Scientific Reports</i> , 2020, 10, 2133.	1.6	82
488	Tropical Occurrence and Agricultural Importance of <i>Beauveria bassiana</i> and <i>Metarhizium anisopliae</i> . <i>Frontiers in Sustainable Food Systems</i> , 2020, 4, .	1.8	37
489	Microbial community analysis using high-throughput sequencing technology: a beginner's guide for microbiologists. <i>Journal of Microbiology</i> , 2020, 58, 176-192.	1.3	42
490	Advances and prospects of environmental DNA in neotropical rainforests. <i>Advances in Ecological Research</i> , 2020, , 331-373.	1.4	27
491	<i>Nicotiana tabacum</i> seed endophytic communities share a common core structure and genotype-specific signatures in diverging cultivars. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 287-295.	1.9	35

#	ARTICLE	IF	CITATIONS
492	Precision medicine in perinatal depression in light of the human microbiome. <i>Psychopharmacology</i> , 2020, 237, 915-941.	1.5	18
493	Metaphylogenetic analysis of global sewage reveals that bacterial strains associated with human disease show less degree of geographic clustering. <i>Scientific Reports</i> , 2020, 10, 3033.	1.6	7
494	Insights into the microbiome of farmed Asian sea bass ( <i>Lates calcarifer</i> ) with symptoms of tenacibaculosis and description of <i>Tenacibaculum singaporense</i> sp. nov.. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 737-752.	0.7	28
495	A minimal model for microbial biodiversity can reproduce experimentally observed ecological patterns. <i>Scientific Reports</i> , 2020, 10, 3308.	1.6	56
496	18S-V9 DNA metabarcoding detects the effect of water-quality impairment on stream biofilm eukaryotic assemblages. <i>Ecological Indicators</i> , 2020, 113, 106225.	2.6	19
497	Decoupled diversity patterns in bacteria and fungi across continental forest ecosystems. <i>Soil Biology and Biochemistry</i> , 2020, 144, 107763.	4.2	78
498	Strength of species interactions determines biodiversity and stability in microbial communities. <i>Nature Ecology and Evolution</i> , 2020, 4, 376-383.	3.4	287
499	Mediterranean seasonality and the halophyte <i>Arthrocnemum macrostachyum</i> determine the bacterial community in salt marsh soils in Southwest Spain. <i>Applied Soil Ecology</i> , 2020, 151, 103532.	2.1	7
500	Differing salivary microbiome diversity, community and diurnal rhythmicity in association with affective state and peripheral inflammation in adults. <i>Brain, Behavior, and Immunity</i> , 2020, 87, 591-602.	2.0	11
501	Metagenomic insights into the profile of antibiotic resistomes in a large drinking water reservoir. <i>Environment International</i> , 2020, 136, 105449.	4.8	65
502	<i>Candidatus Mcinerneyibacterium aminivorans</i> gen. nov., sp. nov., the first representative of the candidate phylum <i>Mcinerneyibacteriota</i> phyl. nov. recovered from a high temperature, high salinity tertiary oil reservoir in north central Oklahoma, USA. <i>Systematic and Applied Microbiology</i> , 2020, 43, 126057.	1.2	23
503	Microbiome applications for pathology: challenges of low microbial biomass samples during diagnostic testing. <i>Journal of Pathology: Clinical Research</i> , 2020, 6, 97-106.	1.3	24
504	Next-generation sequencing as a screening tool for foodborne pathogens in fresh produce. <i>Journal of Microbiological Methods</i> , 2020, 171, 105840.	0.7	19
505	Depression phenotype identified by using single nucleotide exact amplicon sequence variants of the human gut microbiome. <i>Molecular Psychiatry</i> , 2021, 26, 4277-4287.	4.1	46
506	Insect herbivory reshapes a native leaf microbiome. <i>Nature Ecology and Evolution</i> , 2020, 4, 221-229.	3.4	78
507	Comparative Analyses of Vertebrate Gut Microbiomes Reveal Convergence between Birds and Bats. <i>MBio</i> , 2020, 11, .	1.8	204
508	Doing More with Less: A Comparison of 16S Hypervariable Regions in Search of Defining the Shrimp Microbiota. <i>Microorganisms</i> , 2020, 8, 134.	1.6	37
509	Soil bacterial diversity mediated by microscale aqueous-phase processes across biomes. <i>Nature Communications</i> , 2020, 11, 116.	5.8	78

#	ARTICLE	IF	CITATIONS
510	Common structuring principles of the <i>Drosophila melanogaster</i> microbiome on a continental scale and between host and substrate. <i>Environmental Microbiology Reports</i> , 2020, 12, 220-228.	1.0	24
511	QIIME 2 Enables Comprehensive End-to-End Analysis of Diverse Microbiome Data and Comparative Studies with Publicly Available Data. <i>Current Protocols in Bioinformatics</i> , 2020, 70, e100.	25.8	212
512	Microbial Community Response to a Novel Salmon Resource Subsidy. <i>Frontiers in Ecology and Evolution</i> , 2020, 7, .	1.1	5
513	Introducing the North American project to evaluate soil health measurements. <i>Agronomy Journal</i> , 2020, 112, 3195-3215.	0.9	94
514	Reductions in anti-inflammatory gut bacteria are associated with depression in a sample of young adults. <i>Brain, Behavior, and Immunity</i> , 2020, 88, 308-324.	2.0	115
515	Bacterial dispersal and biogeography as underappreciated influences on phytobiomes. <i>Current Opinion in Plant Biology</i> , 2020, 56, 37-46.	3.5	5
516	Changes in soil fungal communities following anthropogenic disturbance are linked to decreased lodgepole pine seedling performance. <i>Journal of Applied Ecology</i> , 2020, 57, 1292-1302.	1.9	6
517	Microbiotyping the Sinonasal Microbiome. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 137.	1.8	21
518	Small molecule inhibition of gut microbial choline trimethylamine lyase activity alters host cholesterol and bile acid metabolism. <i>American Journal of Physiology - Heart and Circulatory Physiology</i> , 2020, 318, H1474-H1486.	1.5	48
519	Soil bacterial populations are shaped by recombination and gene-specific selection across a grassland meadow. <i>ISME Journal</i> , 2020, 14, 1834-1846.	4.4	43
520	Bacterial and archaeal taxa are reliable indicators of soil restoration across distributed calcareous grasslands. <i>European Journal of Soil Science</i> , 2021, 72, 2430-2444.	1.8	12
521	MICOM: Metagenome-Scale Modeling To Infer Metabolic Interactions in the Gut Microbiota. <i>MSystems</i> , 2020, 5, .	1.7	126
522	Pan-metagenomics: An overview of the human microbiome. , 2020, , 335-342.		0
523	Community-Driven Metadata Standards for Agricultural Microbiome Research. <i>Phytobiomes Journal</i> , 2020, 4, 115-121.	1.4	21
524	Dormancy dynamics and dispersal contribute to soil microbiome resilience. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190255.	1.8	38
525	Metabolome-Informed Microbiome Analysis Refines Metadata Classifications and Reveals Unexpected Medication Transfer in Captive Cheetahs. <i>MSystems</i> , 2020, 5, .	1.7	12
526	Soil Microbial Biogeography in a Changing World: Recent Advances and Future Perspectives. <i>MSystems</i> , 2020, 5, .	1.7	84
527	Strategies for culturing active/dormant marine microbes. <i>Marine Life Science and Technology</i> , 2021, 3, 121-131.	1.8	31

#	ARTICLE	IF	CITATIONS
528	Meta-Prism: Ultra-fast and highly accurate microbial community structure search utilizing dual indexing and parallel computation. <i>Briefings in Bioinformatics</i> , 2021, 22, 557-567.	3.2	10
529	Root exudates mediate plant defense against foliar pathogens by recruiting beneficial microbes. <i>Soil Ecology Letters</i> , 2021, 3, 42-51.	2.4	71
530	Deciphering cell-cell interactions and communication from gene expression. <i>Nature Reviews Genetics</i> , 2021, 22, 71-88.	7.7	575
531	Microbial co-occurrence network analysis of soils receiving short- and long-term applications of alkaline treated biosolids. <i>Science of the Total Environment</i> , 2021, 751, 141687.	3.9	37
532	Dietary sphinganine is selectively assimilated by members of the mammalian gut microbiome. <i>Journal of Lipid Research</i> , 2021, 62, 100034.	2.0	32
533	Does Intraspecific Variation in rDNA Copy Number Affect Analysis of Microbial Communities?. <i>Trends in Microbiology</i> , 2021, 29, 19-27.	3.5	71
534	Temporal succession of water microbiomes and resistomes during carcass decomposition in a fish model. <i>Journal of Hazardous Materials</i> , 2021, 403, 123795.	6.5	26
535	Bacterial communities in the plant phyllosphere harbour distinct responders to a broad-spectrum pesticide. <i>Science of the Total Environment</i> , 2021, 751, 141799.	3.9	46
536	Functional Genomics Platform, A Cloud-Based Platform for Studying Microbial Life at Scale. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 940-952.	1.9	18
537	Ecogenomics and metabolic potential of the South Atlantic Ocean microbiome. <i>Science of the Total Environment</i> , 2021, 765, 142758.	3.9	16
538	Spatial variation of the soil bacterial community in major apple producing regions of China. <i>Journal of Applied Microbiology</i> , 2021, 130, 1294-1306.	1.4	7
539	Seasonal changes and the unexpected impact of environmental disturbance on skin bacteria of individual amphibians in a natural habitat. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	10
540	Ecological features and global distribution of Asgard archaea. <i>Science of the Total Environment</i> , 2021, 758, 143581.	3.9	12
541	Metagenomic assessment of the global diversity and distribution of bacteria and fungi. <i>Environmental Microbiology</i> , 2021, 23, 316-326.	1.8	42
542	Predicting microbiomes through a deep latent space. <i>Bioinformatics</i> , 2021, 37, 1444-1451.	1.8	21
543	In-depth Spatiotemporal Characterization of Planktonic Archaeal and Bacterial Communities in North and South San Francisco Bay. <i>Microbial Ecology</i> , 2021, 81, 601-616.	1.4	11
544	Host-Association as major driver of microbiome structure and composition in Red Sea seagrass ecosystems. <i>Environmental Microbiology</i> , 2021, 23, 2021-2034.	1.8	9
545	Getting back to the nature of the microbial world: from the description and inductive reasoning to deductive study after "meta-omics". <i>Microbial Biotechnology</i> , 2021, 14, 22-25.	2.0	1



#	ARTICLE	IF	CITATIONS
546	Ecological drivers switch from bottomâ€“up to topâ€“down during model microbial community successions. <i>ISME Journal</i> , 2021, 15, 1085-1097.	4.4	21
547	Chemically informed analyses of metabolomics mass spectrometry data with Qemistree. <i>Nature Chemical Biology</i> , 2021, 17, 146-151.	3.9	73
548	Plant part and a steep environmental gradient predict plant microbial composition in a tropical watershed. <i>ISME Journal</i> , 2021, 15, 999-1009.	4.4	21
549	Coinfection and infection duration shape how pathogens affect the African buffalo gut microbiota. <i>ISME Journal</i> , 2021, 15, 1359-1371.	4.4	17
550	Epilithic biofilm as a reservoir for functional virulence factors in wastewater-dominant rivers after WWTP upgrade. <i>Journal of Environmental Sciences</i> , 2021, 101, 27-35.	3.2	13
551	Bacterial community variations with salinity in the saltwater-intruded estuarine aquifer. <i>Science of the Total Environment</i> , 2021, 755, 142423.	3.9	26
552	Steeper spatial scaling patterns of subsoil microbiota are shaped by deterministic assembly process. <i>Molecular Ecology</i> , 2021, 30, 1072-1085.	2.0	43
553	High-accuracy long-read amplicon sequences using unique molecular identifiers with Nanopore or PacBio sequencing. <i>Nature Methods</i> , 2021, 18, 165-169.	9.0	198
554	Effects of anthropogenic habitat disturbance and <i>Giardia duodenalis</i> infection on a sentinel species' gut bacteria. <i>Ecology and Evolution</i> , 2021, 11, 45-57.	0.8	3
555	Gut microbiome in Schizophrenia: Altered functional pathways related to immune modulation and atherosclerotic risk. <i>Brain, Behavior, and Immunity</i> , 2021, 91, 245-256.	2.0	44
556	Enrichment of potential pathogens in marine microbiomes with different degrees of anthropogenic activity. <i>Environmental Pollution</i> , 2021, 268, 115757.	3.7	12
557	Comparing DNA Extraction and 16S rRNA Gene Amplification Methods for Plant-Associated Bacterial Communities. <i>Phytobiomes Journal</i> , 2021, 5, 190-201.	1.4	5
558	The assembly of methanotrophic communities regulated by soil pH in a mountain ecosystem. <i>Catena</i> , 2021, 196, 104883.	2.2	14
559	Effects of vegetation type, season, and soil properties on soil microbial community in subtropical forests. <i>Applied Soil Ecology</i> , 2021, 158, 103813.	2.1	30
560	How the â€“kitomeâ€™ influences the characterization of bacterial communities in lepidopteran samples with low bacterial biomass. <i>Journal of Applied Microbiology</i> , 2021, 130, 1780-1793.	1.4	9
561	Major Depressive Disorder and gut microbiota â€“ Association not causation. A scoping review. <i>Progress in Neuro-Psychopharmacology and Biological Psychiatry</i> , 2021, 106, 110111.	2.5	32
562	Metagenome Across a Geochemical Gradient of Indian Stone Ruins Found at Historic Sites in Tamil Nadu, India. <i>Microbial Ecology</i> , 2021, 81, 385-395.	1.4	15
563	Current challenges and best-practice protocols for microbiome analysis. <i>Briefings in Bioinformatics</i> , 2021, 22, 178-193.	3.2	268



#	ARTICLE	IF	CITATIONS
564	The spatial variation of soil bacterial community assembly processes affects the accuracy of source tracking in ten major Chinese cities. <i>Science China Life Sciences</i> , 2021, 64, 1546-1559.	2.3	14
565	Microbial communities in mangrove sediments. , 2021, , 141-175.		2
566	Signatures of landscape and captivity in the gut microbiota of Southern Hairy-nosed Wombats ( <i>Lasiorhinus latifrons</i> ). <i>Animal Microbiome</i> , 2021, 3, 4.	1.5	9
567	Robust aggregation of compositional and interval-valued data: The mode on the unit simplex. <i>Fuzzy Sets and Systems</i> , 2022, 446, 124-143.	1.6	2
568	Development of Biofertilizers and Microbial Consortium an Approach to Sustainable Agriculture Practices. <i>Rhizosphere Biology</i> , 2021, , 315-348.	0.4	1
569	Impacts of Invasive Australian Acacias on Soil Bacterial Community Composition, Microbial Enzymatic Activities, and Nutrient Availability in Fynbos Soils. <i>Microbial Ecology</i> , 2021, 82, 704-721.	1.4	19
570	The Apple Microbiome: Structure, Function, and Manipulation for Improved Plant Health. <i>Compendium of Plant Genomes</i> , 2021, , 341-382.	0.3	8
571	Methods for studying the forest tree microbiome. , 2021, , 35-58.		1
572	Antarctic Water Tracks: Microbial Community Responses to Variation in Soil Moisture, pH, and Salinity. <i>Frontiers in Microbiology</i> , 2021, 12, 616730.	1.5	11
573	<i>Enterocytozoon bienersi</i> of animalsâ€™ With an â€™Australian twistâ€™™. <i>Advances in Parasitology</i> , 2021, 111, 1-73.	1.4	26
574	Microbiome structure and functional potential in permafrost soils of the Western Canadian Arctic. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	9
575	Identifying the Alterations in the Microbiome Using Classification and Clustering Analysis: A Path Towards Microbiome Bio-Tech Innovations. <i>Lecture Notes in Networks and Systems</i> , 2021, , 997-1006.	0.5	0
576	<i>Hierarchical Meta-Storms</i> enables comprehensive and rapid comparison of microbiome functional profiles on a large scale using hierarchical dissimilarity metrics and parallel computing. <i>Bioinformatics Advances</i> , 2021, 1, .	0.9	7
577	Feasibility of using alternative swabs and storage solutions for paired SARS-CoV-2 detection and microbiome analysis in the hospital environment. <i>Microbiome</i> , 2021, 9, 25.	4.9	13
578	Polarization of microbial communities between competitive and cooperative metabolism. <i>Nature Ecology and Evolution</i> , 2021, 5, 195-203.	3.4	131
579	Symbiosis in a Rapidly Changing World. <i>Advances in Environmental Microbiology</i> , 2021, , 263-296.	0.1	1
580	Characterization of cerebrospinal fluid (CSF) microbiota from patients with CSF shunt infection and reinfection using high throughput sequencing of 16S ribosomal RNAs. <i>PLoS ONE</i> , 2021, 16, e0244643.	1.1	5
581	The confluence of big data and evolutionary genome mining for the discovery of natural products. <i>Natural Product Reports</i> , 2021, 38, 2024-2040.	5.2	30

#	ARTICLE	IF	CITATIONS
582	Composition and Potential Function of Fecal Bacterial Microbiota from Six Bird Species. <i>Birds</i> , 2021, 2, 42-59.	0.6	3
583	Function-driven microbial genomics for ecofriendly agriculture. , 2021, , 389-431.		2
585	Associations between the indoor microbiome, environmental characteristics and respiratory infections in junior high school students of Johor Bahru, Malaysia. <i>Environmental Sciences: Processes and Impacts</i> , 2021, 23, 1171-1181.	1.7	10
586	Structured environments foster competitor coexistence by manipulating interspecies interfaces. <i>PLoS Computational Biology</i> , 2021, 17, e1007762.	1.5	6
587	The Ecuadorian Microbiome Project: a plea to strengthen microbial genomic research. <i>Neotropical Biodiversity</i> , 2021, 7, 223-237.	0.2	5
588	An evaluation of biological soil health indicators in four long-term continuous agroecosystems in Canada. , 2021, 4, e20164.		6
589	Evaluation of the Microbiome in Men Taking Pre-exposure Prophylaxis for HIV Prevention. <i>AIDS and Behavior</i> , 2021, 25, 2005-2013.	1.4	9
590	Bacterial biota of forest trees. , 2021, , 161-173.		1
591	Forest microbiome: Challenges and future perspectives. , 2021, , 395-399.		0
592	Host reproductive cycle influences the pouch microbiota of wild southern hairy-nosed wombats ( <i>Lasiorchinus latifrons</i> ). <i>Animal Microbiome</i> , 2021, 3, 13.	1.5	11
593	Shifting Prevalence of Plant-Parasitic Nematodes in Orchards and Vineyards of the Okanagan Valley, British Columbia. <i>Plant Health Progress</i> , 2021, 22, 113-121.	0.8	2
594	Microbiome Analysis Using 16S Amplicon Sequencing: From Samples to ASVs. <i>Methods in Molecular Biology</i> , 2021, 2243, 123-141.	0.4	0
595	Equivolumetric Protocol Generates Library Sizes Proportional to Total Microbial Load in 16S Amplicon Sequencing. <i>Frontiers in Microbiology</i> , 2021, 12, 638231.	1.5	13
596	Reduction of Sb(V) by coupled biotic-abiotic processes under sulfidogenic conditions. <i>Heliyon</i> , 2021, 7, e06275.	1.4	10
597	High-throughput sequencing view on the magnitude of global fungal diversity. <i>Fungal Diversity</i> , 2022, 114, 539-547.	4.7	94
598	Antibiotic-resistant bacteria and gut microbiome communities associated with wild-caught shrimp from the United States versus imported farm-raised retail shrimp. <i>Scientific Reports</i> , 2021, 11, 3356.	1.6	18
601	Viromes outperform total metagenomes in revealing the spatiotemporal patterns of agricultural soil viral communities. <i>ISME Journal</i> , 2021, 15, 1956-1970.	4.4	101
602	Dietary Rice Bran-Modified Human Gut Microbial Consortia Confers Protection against Colon Carcinogenesis Following Fecal Transfaunation. <i>Biomedicine</i> , 2021, 9, 144.	1.4	21

#	ARTICLE	IF	CITATIONS
603	Monitoring the microbiome for food safety and quality using deep shotgun sequencing. <i>Npj Science of Food</i> , 2021, 5, 3.	2.5	22
604	Connecting high-throughput biodiversity inventories: Opportunities for a site-based genomic framework for global integration and synthesis. <i>Molecular Ecology</i> , 2021, 30, 1120-1135.	2.0	26
605	Evaluation of curcumin and copper acetate against <i>Salmonella Typhimurium</i> infection, intestinal permeability, and cecal microbiota composition in broiler chickens. <i>Journal of Animal Science and Biotechnology</i> , 2021, 12, 23.	2.1	25
606	User-friendly bioinformatics pipeline gDAT (graphical downstream analysis tool) for analysing rDNA sequences. <i>Molecular Ecology Resources</i> , 2021, 21, 1380-1392.	2.2	27
607	Quantifying Live Microbial Load in Human Saliva Samples over Time Reveals Stable Composition and Dynamic Load. <i>MSystems</i> , 2021, 6, .	1.7	19
608	Taxonomic and functional analyses of intact microbial communities thriving in extreme, astrobiology-relevant, anoxic sites. <i>Microbiome</i> , 2021, 9, 50.	4.9	14
611	Microbiome Search Engine 2: a Platform for Taxonomic and Functional Search of Global Microbiomes on the Whole-Microbiome Level. <i>MSystems</i> , 2021, 6, .	1.7	14
612	Microscopic and Genetic Characterization of Bacterial Symbionts With Bioluminescent Potential in <i>Pyrosoma atlanticum</i> . <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	7
613	A <i>Sarcina</i> bacterium linked to lethal disease in sanctuary chimpanzees in Sierra Leone. <i>Nature Communications</i> , 2021, 12, 763.	5.8	17
615	A community perspective on the concept of marine holobionts: current status, challenges, and future directions. <i>PeerJ</i> , 2021, 9, e10911.	0.9	44
616	Microbiome Analyses Demonstrate Specific Communities Within Five Shark Species. <i>Frontiers in Microbiology</i> , 2021, 12, 605285.	1.5	12
618	A Statistical Perspective on the Challenges in Molecular Microbial Biology. <i>Journal of Agricultural, Biological, and Environmental Statistics</i> , 2021, 26, 131-160.	0.7	10
619	Comparing different sample collection and storage methods for field-based skin microbiome research. <i>American Journal of Human Biology</i> , 2022, 34, e23584.	0.8	8
620	Gut microbial taxa elevated by dietary sugar disrupt memory function. <i>Translational Psychiatry</i> , 2021, 11, 194.	2.4	50
621	Hawaiian Fungal Amplicon Sequence Variants Reveal Otherwise Hidden Biogeography. <i>Microbial Ecology</i> , 2022, 83, 48-57.	1.4	16
622	Mechanism Across Scales: A Holistic Modeling Framework Integrating Laboratory and Field Studies for Microbial Ecology. <i>Frontiers in Microbiology</i> , 2021, 12, 642422.	1.5	12
623	Interactions of host-associated multispecies bacterial communities. <i>Periodontology 2000</i> , 2021, 86, 14-31.	6.3	3
624	The mineralosphere—interactive zone of microbial colonization and carbon use in grassland soils. <i>Biology and Fertility of Soils</i> , 2021, 57, 587-601.	2.3	11

#	ARTICLE	IF	CITATIONS
625	Motivating data contributions via a distinct career currency. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2021, 288, 20202830.	1.2	6
626	Evaluating a Laboratory Flume Microbiome as a Window Into Natural Riverbed Biogeochemistry. <i>Frontiers in Water</i> , 2021, 3, .	1.0	3
627	Microbiome Composition and Function in Aquatic Vertebrates: Small Organisms Making Big Impacts on Aquatic Animal Health. <i>Frontiers in Microbiology</i> , 2021, 12, 567408.	1.5	107
628	A comparison of DNA/RNA extraction protocols for high-throughput sequencing of microbial communities. <i>BioTechniques</i> , 2021, 70, 149-159.	0.8	17
629	Genetic identity and genotype × genotype interactions between symbionts outweigh species level effects in an insect microbiome. <i>ISME Journal</i> , 2021, 15, 2537-2546.	4.4	14
630	A Review of the Molluscan Microbiome: Ecology, Methodology and Future. <i>Malacologia</i> , 2021, 63, .	0.2	6
632	Association of Loneliness and Wisdom With Gut Microbial Diversity and Composition: An Exploratory Study. <i>Frontiers in Psychiatry</i> , 2021, 12, 648475.	1.3	17
633	The Himalayan Onion ( <i>Allium wallichii</i> Kunth) Harbors Unique Spatially Organized Bacterial Communities. <i>Microbial Ecology</i> , 2021, 82, 909-918.	1.4	8
635	The CALeDNA program: Citizen scientists and researchers inventory California's biodiversity. <i>California Agriculture</i> , 2021, 75, 20-32.	0.5	20
637	Methods for exploring the faecal microbiome of premature infants: a review. <i>Maternal Health, Neonatology and Perinatology</i> , 2021, 7, 11.	1.0	3
638	Phylogenetic Core Groups: a promising concept in search of a consistent methodological framework. <i>Microbiome</i> , 2021, 9, 73.	4.9	3
639	Composition and structure of the skin microbiota of roquas off the Eastern South Pacific. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	4
640	Microbial Community Field Surveys Reveal Abundant <i>Pseudomonas</i> Population in Sorghum Rhizosphere Composed of Many Closely Related Phylotypes. <i>Frontiers in Microbiology</i> , 2021, 12, 598180.	1.5	20
643	The Utility of Macroecological Rules for Microbial Biogeography. <i>Frontiers in Ecology and Evolution</i> , 2021, 9, .	1.1	31
644	Evolutionary stasis of a deep subsurface microbial lineage. <i>ISME Journal</i> , 2021, 15, 2830-2842.	4.4	23
645	Soil microbiome predictability increases with spatial and taxonomic scale. <i>Nature Ecology and Evolution</i> , 2021, 5, 747-756.	3.4	23
646	Mining Synergistic Microbial Interactions: A Roadmap on How to Integrate Multi-Omics Data. <i>Microorganisms</i> , 2021, 9, 840.	1.6	8
648	Evaluation of the Effect of Storage Methods on Fecal, Saliva, and Skin Microbiome Composition. <i>MSystems</i> , 2021, 6, .	1.7	22

#	ARTICLE	IF	CITATIONS
649	CRISPR/Cas9 mutagenesis reveals a role for ABCB1 in gut immune responses to <i>Vibrio diazotrophicus</i> in sea urchin larvae. <i>Journal of Experimental Biology</i> , 2021, 224, .	0.8	15
650	Comparative analysis of the intestinal bacterial communities in mud crab <i>Scylla serrata</i> in South India. <i>MicrobiologyOpen</i> , 2021, 10, e1179.	1.2	9
651	Metabolic pathways inferred from a bacterial marker gene illuminate ecological changes across South Pacific frontal boundaries. <i>Nature Communications</i> , 2021, 12, 2213.	5.8	25
652	Three-Dimensional Molecular Cartography of the Caribbean Reef-Building Coral <i>Orbicella faveolata</i> . <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	11
656	Assessment of the microbiome during bacteriophage therapy in combination with systemic antibiotics to treat a case of staphylococcal device infection. <i>Microbiome</i> , 2021, 9, 92.	4.9	40
657	Calf Diarrhea Caused by Prolonged Expansion of Autochthonous Gut Enterobacteriaceae and Their Lytic Bacteriophages. <i>MSystems</i> , 2021, 6, .	1.7	15
658	Genome-Resolved Metagenomics Is Essential for Unlocking the Microbial Black Box of the Soil. <i>Trends in Microbiology</i> , 2021, 29, 279-282.	3.5	11
659	Rethinking restoration indicators and end-points for post-mining landscapes in light of novel ecosystems. <i>Geoderma</i> , 2021, 387, 114944.	2.3	28
661	A comprehensive metagenomics framework to characterize organisms relevant for planetary protection. <i>Microbiome</i> , 2021, 9, 82.	4.9	15
662	<i>C. difficile</i> exploits a host metabolite produced during toxin-mediated disease. <i>Nature</i> , 2021, 593, 261-265.	13.7	48
663	EMPress Enables Tree-Guided, Interactive, and Exploratory Analyses of Multi-omic Data Sets. <i>MSystems</i> , 2021, 6, .	1.7	36
664	Molecular diversity and abundance of the microbial community associated to an offshore oil field on the southeast of Brazil. <i>International Biodeterioration and Biodegradation</i> , 2021, 160, 105215.	1.9	12
665	Responses of Soil Fungal Communities to Lime Application in Wheat Fields in the Pacific Northwest. <i>Frontiers in Microbiology</i> , 2021, 12, 576763.	1.5	7
667	FERONIA restricts <i>Pseudomonas</i> in the rhizosphere microbiome via regulation of reactive oxygen species. <i>Nature Plants</i> , 2021, 7, 644-654.	4.7	102
668	Molecular analysis of a fungal disease in the habitat-forming brown macroalga <i>Phyllospora comosa</i> (Fucales) along a latitudinal gradient. <i>Journal of Phycology</i> , 2021, 57, 1504-1516.	1.0	5
669	Habitats and seasons differentiate the assembly of bacterial communities along a trophic gradient of freshwater lakes. <i>Freshwater Biology</i> , 2021, 66, 1515-1529.	1.2	16
670	Metagenomic analysis reveals the shared and distinct features of the soil resistome across tundra, temperate prairie, and tropical ecosystems. <i>Microbiome</i> , 2021, 9, 108.	4.9	60
671	Phylogeny- and Abundance-Based Metrics Allow for the Consistent Comparison of Core Gut Microbiome Diversity Indices Across Host Species. <i>Frontiers in Microbiology</i> , 2021, 12, 659918.	1.5	14

#	ARTICLE	IF	CITATIONS
672	Differential Impacts of Water Table and Temperature on Bacterial Communities in Pore Water From a Subalpine Peatland, Central China. <i>Frontiers in Microbiology</i> , 2021, 12, 649981.	1.5	9
673	Strategies for Natural Products Discovery from Uncultured Microorganisms. <i>Molecules</i> , 2021, 26, 2977.	1.7	8
674	Soil metaphenomics: a step forward in metagenomics. <i>Archives of Agronomy and Soil Science</i> , 2022, 68, 1645-1663.	1.3	5
675	Evaluation of the Potential of Sewage Sludge Mycobiome to Degrade High Diclofenac and Bisphenol-A Concentrations. <i>Toxics</i> , 2021, 9, 115.	1.6	11
676	All together now: Limitations and recommendations for the simultaneous analysis of all eukaryotic soil sequences. <i>Molecular Ecology Resources</i> , 2021, 21, 1759-1771.	2.2	9
677	Design of synthetic human gut microbiome assembly and butyrate production. <i>Nature Communications</i> , 2021, 12, 3254.	5.8	83
678	Influence of ecological and edaphic factors on biodiversity of soil nematodes. <i>Saudi Journal of Biological Sciences</i> , 2021, 28, 3049-3059.	1.8	45
679	Utilizing stability criteria in choosing feature selection methods yields reproducible results in microbiome data. <i>Biometrics</i> , 2022, 78, 1155-1167.	0.8	4
680	The chosen fewâ€™ variations in common and rare soil bacteria across biomes. <i>ISME Journal</i> , 2021, 15, 3315-3325.	4.4	22
683	The impact of cross-kingdom molecular forensics on genetic privacy. <i>Microbiome</i> , 2021, 9, 114.	4.9	8
684	Impacts of the Marine Hatchery Built Environment, Water and Feed on Mucosal Microbiome Colonization Across Ontogeny in Yellowtail Kingfish, <i>Seriola lalandi</i> . <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	13
685	Energy landscape analysis elucidates the multistability of ecological communities across environmental gradients. <i>Ecological Monographs</i> , 2021, 91, e01469.	2.4	15
688	Host Species and Geography Differentiate Honeybee Gut Bacterial Communities by Changing the Relative Contribution of Community Assembly Processes. <i>MBio</i> , 2021, 12, e0075121.	1.8	29
690	Simulation study and comparative evaluation of viral contiguous sequence identification tools. <i>BMC Bioinformatics</i> , 2021, 22, 329.	1.2	18
691	Coffee Consumption Modulates Amoxicillin-Induced Dysbiosis in the Murine Gut Microbiome. <i>Frontiers in Microbiology</i> , 2021, 12, 637282.	1.5	5
692	A global overview of the trophic structure within microbiomes across ecosystems. <i>Environment International</i> , 2021, 151, 106438.	4.8	48
693	Emergent â€™core communitiesâ€™ of microbes, meiofauna and macrofauna at hydrothermal vents. <i>ISME Communications</i> , 2021, 1, .	1.7	9
694	Beating Naive Bayes at Taxonomic Classification of 16S rRNA Gene Sequences. <i>Frontiers in Microbiology</i> , 2021, 12, 644487.	1.5	12

#	ARTICLE	IF	CITATIONS
695	Diversity and composition of gut microbiome of cervical cancer patients: Do results of 16S rRNA sequencing and whole genome sequencing approaches align?. <i>Journal of Microbiological Methods</i> , 2021, 185, 106213.	0.7	8
696	Intestinal microbiota in health and disease – seeding multidisciplinary research in Germany. <i>International Journal of Medical Microbiology</i> , 2021, 311, 151514.	1.5	0
697	Interactive exploratory data analysis of Integrative Human Microbiome Project data using Metaviz. <i>F1000Research</i> , 2020, 9, 601.	0.8	0
700	Longitudinal Changes in Diet Cause Repeatable and Largely Reversible Shifts in Gut Microbial Communities of Laboratory Mice and Are Observed across Segments of the Entire Intestinal Tract. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5981.	1.8	10
701	KAUST Metagenomic Analysis Platform (KMAP), enabling access to massive analytics of re-annotated metagenomic data. <i>Scientific Reports</i> , 2021, 11, 11511.	1.6	4
702	Systems Analysis of Gut Microbiome Influence on Metabolic Disease in HIV-Positive and High-Risk Populations. <i>MSystems</i> , 2021, 6, .	1.7	7
703	Network Properties of Local Fungal Communities Reveal the Anthropogenic Disturbance Consequences of Farming Practices in Vineyard Soils. <i>MSystems</i> , 2021, 6, .	1.7	16
704	Detection of cell-free microbial DNA using a contaminant-controlled analysis framework. <i>Genome Biology</i> , 2021, 22, 187.	3.8	22
705	Open challenges for microbial network construction and analysis. <i>ISME Journal</i> , 2021, 15, 3111-3118.	4.4	116
706	A global metagenomic map of urban microbiomes and antimicrobial resistance. <i>Cell</i> , 2021, 184, 3376-3393.e17.	13.5	164
708	Bacterial Communities in Concrete Reflect Its Composite Nature and Change with Weathering. <i>MSystems</i> , 2021, 6, .	1.7	11
709	Ammonia-oxidizing archaea are integral to nitrogen cycling in a highly fertile agricultural soil. <i>ISME Communications</i> , 2021, 1, .	1.7	35
710	A globally ubiquitous symbiont can drive experimental host evolution. <i>Molecular Ecology</i> , 2021, 30, 3882-3892.	2.0	6
711	Predictable and host-specific humanization of the gut microbiota in captive primates. <i>Molecular Ecology</i> , 2021, 30, 3677-3687.	2.0	24
712	Carbonate-hosted microbial communities are prolific and pervasive methane oxidizers at geologically diverse marine methane seep sites. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	8
713	Exploring the Boundaries of Microbial Habitability in Soil. <i>Journal of Geophysical Research G: Biogeosciences</i> , 2021, 126, e2020JG006052.	1.3	18
715	SARS-CoV-2 detection status associates with bacterial community composition in patients and the hospital environment. <i>Microbiome</i> , 2021, 9, 132.	4.9	37
717	Assembly of the <i>Populus</i> Microbiome Is Temporally Dynamic and Determined by Selective and Stochastic Factors. <i>MSphere</i> , 2021, 6, e0131620.	1.3	25



#	ARTICLE	IF	CITATIONS
718	Indoor bacterial, fungal and viral species and functional genes in urban and rural schools in Shanxi Province, China—association with asthma, rhinitis and rhinoconjunctivitis in high school students. <i>Microbiome</i> , 2021, 9, 138.	4.9	34
719	Assessing biogeographic survey gaps in bacterial diversity knowledge: A global synthesis of freshwaters. <i>Freshwater Biology</i> , 2021, 66, 1595-1605.	1.2	5
720	MiMiC: a bioinformatic approach for generation of synthetic communities from metagenomes. <i>Microbial Biotechnology</i> , 2021, 14, 1757-1770.	2.0	12
721	Structure of Chimpanzee Gut Microbiomes across Tropical Africa. <i>MSystems</i> , 2021, 6, e0126920.	1.7	8
722	Evaluating and Improving Small Subunit rRNA PCR Primer Coverage for Bacteria, Archaea, and Eukaryotes Using Metagenomes from Global Ocean Surveys. <i>MSystems</i> , 2021, 6, e0056521.	1.7	35
724	MolDiscovery: learning mass spectrometry fragmentation of small molecules. <i>Nature Communications</i> , 2021, 12, 3718.	5.8	44
725	A Comparison of Primers in 16S rRNA Gene Surveys of Bacteria and Archaea from Volcanic Caves. <i>Geomicrobiology Journal</i> , 2021, 38, 741-754.	1.0	8
726	Nutrient-Limited Enrichments of Nitrifiers From Soil Yield Consortia of Nitrosocosmicus-Affiliated AOA and Nitrospira-Affiliated NOB. <i>Frontiers in Microbiology</i> , 2021, 12, 671480.	1.5	4
727	Habitats Are More Important Than Seasons in Shaping Soil Bacterial Communities on the Qinghai-Tibetan Plateau. <i>Microorganisms</i> , 2021, 9, 1595.	1.6	9
728	Linking historical vegetation to bacterial succession under the contrasting climates of the Tibetan Plateau. <i>Ecological Indicators</i> , 2021, 126, 107625.	2.6	6
729	Desiccation time and rainfall control gaseous carbon fluxes in an intermittent stream. <i>Biogeochemistry</i> , 2021, 155, 381-400.	1.7	12
730	Culture-enriched community profiling improves resolution of the vertebrate gut microbiota. <i>Molecular Ecology Resources</i> , 2022, 22, 122-136.	2.2	12
732	Characterization of the gut microbiome in wild rocky mountainsnails ( <i>Oreohelix strigosa</i> ). <i>Animal Microbiome</i> , 2021, 3, 49.	1.5	5
736	Impact of water quality variations on the microbial metagenome across coastal waters in Shenzhen, south China. <i>Ocean and Coastal Management</i> , 2021, 208, 105612.	2.0	4
737	Inventory of the benthic eukaryotic diversity in the oldest European lake. <i>Ecology and Evolution</i> , 2021, 11, 11207-11215.	0.8	2
739	SOIL-INSECT toolbox: A new chamber for analysing the behaviour of herbivorous insects and tri-trophic interactions in soil. <i>European Journal of Entomology</i> , 0, 118, 200-209.	1.2	0
740	Variations in the oral microbiome are associated with depression in young adults. <i>Scientific Reports</i> , 2021, 11, 15009.	1.6	44
741	Swarm v3: towards tera-scale amplicon clustering. <i>Bioinformatics</i> , 2021, 38, 267-269.	1.8	40



#	ARTICLE	IF	CITATIONS
742	Accelerating Key Bioinformatics Tasks 100-fold by Improving Memory Access. , 2021, , .		0
743	Spatial Variability of Abyssal Nitrifying Microbes in the North-Eastern Clarion-Clipperton Zone. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	8
744	Historical contingency impacts on community assembly and ecosystem function in chemosynthetic marine ecosystems. <i>Scientific Reports</i> , 2021, 11, 13994.	1.6	1
747	Wastewater effluents cause microbial community shifts and change trophic status. <i>Water Research</i> , 2021, 200, 117206.	5.3	53
748	Function is a better predictor of plant rhizosphere community membership than <scp>16S</scp> phylogeny. <i>Environmental Microbiology</i> , 2021, 23, 6089-6103.	1.8	3
752	OMICs, Epigenetics, and Genome Editing Techniques for Food and Nutritional Security. <i>Plants</i> , 2021, 10, 1423.	1.6	15
753	Nutrient resource availability mediates niche differentiation and temporal co-occurrence of soil bacterial communities. <i>Applied Soil Ecology</i> , 2021, 163, 103965.	2.1	13
754	Microbiome Structure of the Aphid <i>Myzus persicae</i> (Sulzer) Is Shaped by Different Solanaceae Plant Diets. <i>Frontiers in Microbiology</i> , 2021, 12, 667257.	1.5	16
755	Landscape analyses using eDNA metabarcoding and Earth observation predict community biodiversity in California. <i>Ecological Applications</i> , 2021, 31, e02379.	1.8	23
756	Host-associated microbe PCR (hamPCR) enables convenient measurement of both microbial load and community composition. <i>ELife</i> , 2021, 10, .	2.8	24
758	Disturbance triggers non-linear microbeâ€“environment feedbacks. <i>Biogeosciences</i> , 2021, 18, 4773-4789.	1.3	8
759	Elucidating the Beta-Diversity of the Microbiome: from Global Alignment to Local Alignment. <i>MSystems</i> , 2021, 6, e0036321.	1.7	17
760	Gut microbiome is affected by gut region but robust to host physiological changes in captive active-season ground squirrels. <i>Animal Microbiome</i> , 2021, 3, 56.	1.5	5
761	Evaluation of DNA extraction protocols from liquid-based cytology specimens for studying cervical microbiota. <i>PLoS ONE</i> , 2021, 16, e0237556.	1.1	4
762	The role of soils in habitat creation, maintenance and restoration. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2021, 376, 20200170.	1.8	23
764	How the Physical Environment Shapes the Microbiota. <i>MSystems</i> , 2021, 6, e0067521.	1.7	10
765	A Scale-Free, Fully Connected Global Transition Network Underlies Known Microbiome Diversity. <i>MSystems</i> , 2021, 6, e0039421.	1.7	5
766	Gut microbiota in psychiatric disorders: Better understanding or more complexity to be resolved?. <i>Progress in Neuro-Psychopharmacology and Biological Psychiatry</i> , 2021, 110, 110302.	2.5	0

#	ARTICLE	IF	CITATIONS
767	DAnIEL: A User-Friendly Web Server for Fungal ITS Amplicon Sequencing Data. <i>Frontiers in Microbiology</i> , 2021, 12, 720513.	1.5	10
768	Aboveground and belowground responses to cyanobacterial biofertilizer supplement in a semi-arid, perennial bioenergy cropping system. <i>GCB Bioenergy</i> , 2021, 13, 1908-1923.	2.5	4
769	Consensus Guidelines for Advancing Coral Holobiont Genome and Specimen Voucher Deposition. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	23
770	Response to "Vast (but avoidable) underestimation of global biodiversity". <i>PLoS Biology</i> , 2021, 19, e3001362.	2.6	2
771	Towards the sustainable discovery and development of new antibiotics. <i>Nature Reviews Chemistry</i> , 2021, 5, 726-749.	13.8	439
772	Functional strain redundancy and persistent phage infection in Swiss hard cheese starter cultures. <i>ISME Journal</i> , 2022, 16, 388-399.	4.4	24
773	Spatially resolved correlative microscopy and microbial identification reveal dynamic depth- and mineral-dependent anabolic activity in salt marsh sediment. <i>Environmental Microbiology</i> , 2021, 23, 4756-4777.	1.8	8
776	Do host-associated microbes show a contrarian latitudinal diversity gradient? Insights from <i>Mytilus californianus</i> , an intertidal foundation host. <i>Journal of Biogeography</i> , 2021, 48, 2839-2852.	1.4	6
777	Determining the novel pathogen <i>Neodothiora populina</i> as the causal agent of the aspen running canker disease in Alaska. <i>Canadian Journal of Plant Pathology</i> , 2022, 44, 103-114.	0.8	1
778	Topological Data Analysis Highlights Novel Geographical Signatures of the Human Gut Microbiome. <i>Frontiers in Artificial Intelligence</i> , 2021, 4, 680564.	2.0	3
779	Multiple thresholds and trajectories of microbial biodiversity predicted across browning gradients by neural networks and decision tree learning. <i>ISME Communications</i> , 2021, 1, .	1.7	3
780	The Future of (Soil) Microbiome Studies: Current Limitations, Integration, and Perspectives. <i>MSystems</i> , 2021, 6, e0061321.	1.7	10
781	Metagenomes, metatranscriptomes and microbiomes of naturally decomposing deadwood. <i>Scientific Data</i> , 2021, 8, 198.	2.4	6
782	Naturalization of the microbiota developmental trajectory of Cesarean-born neonates after vaginal seeding. <i>Med</i> , 2021, 2, 951-964.e5.	2.2	37
783	Elucidating biofilm diversity on water lily leaves through 16S rRNA amplicon analysis: Comparison of four DNA extraction kits. <i>Applications in Plant Sciences</i> , 2021, 9, e11444.	0.8	3
784	Forming Consensus To Advance Urobiome Research. <i>MSystems</i> , 2021, 6, e0137120.	1.7	42
785	Dominance of comammox <i>Nitrospira</i> in soil nitrification. <i>Science of the Total Environment</i> , 2021, 780, 146558.	3.9	59
786	A Pilot Study of Microbial Succession in Human Rib Skeletal Remains during Terrestrial Decomposition. <i>MSphere</i> , 2021, 6, e0045521.	1.3	12

#	ARTICLE	IF	CITATIONS
787	The Rhizobial Microbiome from the Tropical Savannah Zones in Northern Côte d'Ivoire. <i>Microorganisms</i> , 2021, 9, 1842.	1.6	7
788	<i>Geomesophilobacter sediminis</i> gen. nov., sp. nov., <i>Geomonas propionica</i> sp. nov. and <i>Geomonas anaerohicana</i> sp. nov., three novel members in the family Geobacteraceae isolated from river sediment and paddy soil. <i>Systematic and Applied Microbiology</i> , 2021, 44, 126233.	1.2	20
789	Gut microbiota alterations in response to sleep length among African-origin adults. <i>PLoS ONE</i> , 2021, 16, e0255323.	1.1	18
791	Towards sustainable agriculture: rhizosphere microbiome engineering. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 7141-7160.	1.7	28
792	Deciphering Succession and Assembly Patterns of Microbial Communities in a Two-Stage Solid-State Fermentation System. <i>Microbiology Spectrum</i> , 2021, 9, e0071821.	1.2	23
794	Performance of Multiple Metagenomics Pipelines in Understanding Microbial Diversity of a Low-Biomass Spacecraft Assembly Facility. <i>Frontiers in Microbiology</i> , 2021, 12, 685254.	1.5	9
795	Macroecological distributions of gene variants highlight the functional organization of soil microbial systems. <i>ISME Journal</i> , 2022, 16, 726-737.	4.4	8
796	Comparative genomic analysis reveals metabolic flexibility of Woesearchaeota. <i>Nature Communications</i> , 2021, 12, 5281.	5.8	25
797	Integrating perspectives in actinomycete research: an ActinoBase review of 2020-21. <i>Microbiology (United Kingdom)</i> , 2021, 167, .	0.7	4
798	The nasal mutualist <i>Dolosigranulum pigrum</i> AMBR11 supports homeostasis via multiple mechanisms. <i>IScience</i> , 2021, 24, 102978.	1.9	15
801	Dysregulation of ILC3s unleashes progression and immunotherapy resistance in colon cancer. <i>Cell</i> , 2021, 184, 5015-5030.e16.	13.5	102
802	Global Geographic Diversity and Distribution of the Myxobacteria. <i>Microbiology Spectrum</i> , 2021, 9, e0001221.	1.2	15
803	Environmental fluctuations reshape an unexpected diversity-disturbance relationship in a microbial community. <i>ELife</i> , 2021, 10, .	2.8	25
804	Metagenomic analysis of microbial communities across a transect from low to highly hydrocarbon-contaminated soils in King George Island, Maritime Antarctica. <i>Geobiology</i> , 2022, 20, 98-111.	1.1	9
805	Changes in soil physicochemical properties and bacterial communities at different soil depths after long-term straw mulching under a no-till system. <i>Soil</i> , 2021, 7, 595-609.	2.2	11
807	Efficient computation of Faith's phylogenetic diversity with applications in characterizing microbiomes. <i>Genome Research</i> , 2021, 31, 2131-2137.	2.4	16
808	Conspicuous Smooth and White Egg-Shaped Sulfur Structures on a Deep-Sea Hydrothermal Vent Formed by Sulfide-Oxidizing Bacteria. <i>Microbiology Spectrum</i> , 2021, 9, e0095521.	1.2	1
810	Exploring how microbiome signatures change across inflammatory bowel disease conditions and disease locations. <i>Scientific Reports</i> , 2021, 11, 18699.	1.6	9

#	ARTICLE	IF	CITATIONS
812	Coming of age for COI metabarcoding of whole organism community DNA: Towards bioinformatic harmonisation. <i>Molecular Ecology Resources</i> , 2022, 22, 847-861.	2.2	22
814	Microbial river-to-sea continuum: gradients in benthic and planktonic diversity, osmoregulation and nutrient cycling. <i>Microbiome</i> , 2021, 9, 190.	4.9	29
815	Decomposition of peatland DOC affected by root exudates is driven by specific r and K strategic bacterial taxa. <i>Scientific Reports</i> , 2021, 11, 18677.	1.6	10
816	Probiotics Modulate Mouse Gut Microbiota and Influence Intestinal Immune and Serotonergic Gene Expression in a Site-Specific Fashion. <i>Frontiers in Microbiology</i> , 2021, 12, 706135.	1.5	18
817	Corpse decomposition increases the diversity and abundance of antibiotic resistance genes in different soil types in a fish model. <i>Environmental Pollution</i> , 2021, 286, 117560.	3.7	19
818	Evolutionary ecology theory “microbial population structure. <i>Current Opinion in Microbiology</i> , 2021, 63, 216-220.	2.3	1
819	Prospects for multi-omics in the microbial ecology of water engineering. <i>Water Research</i> , 2021, 205, 117608.	5.3	26
820	Introduction to Cell Biosensors Through 55 Years of Scientific Production. , 2022, , 3-40.		0
821	Bio-based resources, bioprocesses and bioproducts in value creation architectures for bioeconomy markets and beyond “What really matters. <i>EFB Bioeconomy Journal</i> , 2021, 1, 100009.	1.1	7
822	Seasonal dynamics of soil microbial diversity and functions along elevations across the treeline. <i>Science of the Total Environment</i> , 2021, 794, 148644.	3.9	22
823	Surveillance and prevalence of antimicrobial resistant bacteria from public settings within urban built environments: Challenges and opportunities for hygiene and infection control. <i>Environment International</i> , 2021, 157, 106836.	4.8	28
824	Threshold effects of soil pH on microbial co-occurrence structure in acidic and alkaline arable lands. <i>Science of the Total Environment</i> , 2021, 800, 149592.	3.9	23
825	Late Holocene climate anomaly concurrent with fire activity and ecosystem shifts in the eastern Australian Highlands. <i>Science of the Total Environment</i> , 2022, 802, 149542.	3.9	14
826	The plant microbiota: composition, functions, and engineering. <i>Current Opinion in Biotechnology</i> , 2022, 73, 135-142.	3.3	52
827	Robust regression with compositional covariates. <i>Computational Statistics and Data Analysis</i> , 2022, 165, 107315.	0.7	11
828	The metagenomic approach in myxomycete research. , 2022, , 125-151.		0
831	Exploring the global metagenome for plastic-degrading enzymes. <i>Methods in Enzymology</i> , 2021, 648, 137-157.	0.4	16
832	Habitat heterogeneity induced by pyrogenic organic matter in wildfire-perturbed soils mediates bacterial community assembly processes. <i>ISME Journal</i> , 2021, 15, 1943-1955.	4.4	23

#	ARTICLE	IF	CITATIONS
833	The role of microbiota in allogeneic hematopoietic stem cell transplantation. Expert Opinion on Biological Therapy, 2021, 21, 1121-1131.	1.4	5
834	Global Scenario of Soil Microbiome Research: Current Trends and Future Prospects. Sustainable Development and Biodiversity, 2021, , 573-603.	1.4	1
835	Machine learning applications in microbial ecology, human microbiome studies, and environmental monitoring. Computational and Structural Biotechnology Journal, 2021, 19, 1092-1107.	1.9	111
838	The starlet sea anemone, <i>Nematostella vectensis</i> , possesses body region-specific bacterial associations with spirochetes dominating the capitulum. FEMS Microbiology Letters, 2021, 368, .	0.7	7
839	Are recently deglaciated areas at both poles colonised by the same bacteria?. FEMS Microbiology Letters, 2021, 368, .	0.7	3
840	Effects of aging on the skin and gill microbiota of farmed seabass and seabream. Animal Microbiome, 2021, 3, 10.	1.5	23
841	Impact of Different Exercise Modalities on the Human Gut Microbiome. Sports, 2021, 9, 14.	0.7	48
842	Methanotroph Ecology, Environmental Distribution and Functioning. Microbiology Monographs, 2019, , 1-38.	0.3	6
843	Microbial Consortium as Biofertilizers for Crops Growing Under the Extreme Habitats. Sustainable Development and Biodiversity, 2020, , 381-424.	1.4	12
844	Fungal Biofertilizers for Sustainable Agricultural Productivity. Fungal Biology, 2020, , 199-225.	0.3	8
845	Oxic Methane Cycling: New Evidence for Methane Formation in Oxic Lake Water. , 2019, , 379-400.		6
846	Advancements in Microbial Genome Sequencing and Microbial Community Characterization. , 2019, , 87-113.		1
847	Biodegradation of Pesticides in Brazil and Other Tropical Countries: Experimental and InSilico Studies. Microorganisms for Sustainability, 2019, , 277-304.	0.4	1
848	Experimental and computational approaches to unravel microbial community assembly. Computational and Structural Biotechnology Journal, 2020, 18, 4071-4081.	1.9	14
849	Measuring the microbiome: Best practices for developing and benchmarking microbiomics methods. Computational and Structural Biotechnology Journal, 2020, 18, 4048-4062.	1.9	37
850	Trait-Based Comparison of Coral and Sponge Microbiomes. Scientific Reports, 2020, 10, 2340.	1.6	15
851	Soil microbiomes mediate degradation of vinyl ester-based polymer composites. Communications Materials, 2020, 1, .	2.9	25
852	Dadasnake, a Snakemake implementation of DADA2 to process amplicon sequencing data for microbial ecology. GigaScience, 2020, 9, .	3.3	39

#	ARTICLE	IF	CITATIONS
853	Tepidiforma bonchosmolovskayae gen. nov., sp. nov., a moderately thermophilic Chloroflexi bacterium from a Chukotka hot spring (Arctic, Russia), representing a novel class, Tepidiformia, which includes the previously uncultivated lineage OLB14. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 1192-1202.	0.8	44
854	Microbial genomics amidst the Arctic crisis. Microbial Genomics, 2020, 6, .	1.0	18
855	Metagenomic approaches in microbial ecology: an update on whole-genome and marker gene sequencing analyses. Microbial Genomics, 2020, 6, .	1.0	69
936	Association between algal productivity and phycosphere composition in an outdoor <i>Chlorella sorokiniana</i> reactor based on multiple longitudinal analyses. Microbial Biotechnology, 2020, 13, 1546-1561.	2.0	17
937	Oxygen metabolism shapes microbial settlement on photosynthetic kelp blades compared to artificial kelp substrates. Environmental Microbiology Reports, 2021, 13, 176-184.	1.0	15
938	Spatiotemporal dynamics of molecular messaging in bacterial co-cultures studied by multimodal chemical imaging. , 2019, 10863, .		5
939	Protein tyrosine phosphatase non-receptor type 22 modulates colitis in a microbiota-dependent manner. Journal of Clinical Investigation, 2019, 129, 2527-2541.	3.9	15
940	The Microbe Directory: An annotated, searchable inventory of microbesâ€™ characteristics. Gates Open Research, 2018, 2, 3.	2.0	15
941	CoMA â€™ an intuitive and user-friendly pipeline for amplicon-sequencing data analysis. PLoS ONE, 2020, 15, e0243241.	1.1	15
942	The Amphibian Skin Microbiome and Its Protective Role Against Chytridiomycosis. Herpetologica, 2020, 76, 167.	0.2	60
944	The Microbiome: A Reservoir to Discover New Antimicrobials Agents. Current Topics in Medicinal Chemistry, 2020, 20, 1291-1299.	1.0	4
945	Hydrocarbon-Degrading Bacteria Alcanivorax and Marinobacter Associated With Microalgae Pavlova lutheri and Nannochloropsis oculata. Frontiers in Microbiology, 2020, 11, 572931.	1.5	35
946	Dolomite and Compost Amendments Enhance Cu Phytostabilization and Increase Microbiota of the Leachates from a Cu-Contaminated Soil. Agronomy, 2020, 10, 719.	1.3	6
948	Does diversity beget diversity in microbiomes?. ELife, 2020, 9, .	2.8	33
949	Different analysis strategies of 16S rRNA gene data from rodent studies generate contrasting views of gut bacterial communities associated with diet, health and obesity. PeerJ, 2020, 8, e10372.	0.9	8
950	Fine grained compositional analysis of Port Everglades Inlet microbiome using high throughput DNA sequencing. PeerJ, 2018, 6, e4671.	0.9	4
951	Kelpie: generating full-length â€™ ampliconsâ€™ from whole-metagenome datasets. PeerJ, 2019, 6, e6174.	0.9	11
952	Phytobiomes are compositionally nested from the ground up. PeerJ, 2019, 7, e6609.	0.9	31

#	ARTICLE	IF	CITATIONS
953	Long-read viral metagenomics captures abundant and microdiverse viral populations and their niche-defining genomic islands. PeerJ, 2019, 7, e6800.	0.9	109
954	DISCo-microbe: design of an identifiable synthetic community of microbes. PeerJ, 2020, 8, e8534.	0.9	7
955	Probabilistic model based on circular statistics for quantifying coverage depth dynamics originating from DNA replication. PeerJ, 2020, 8, e8722.	0.9	4
956	Microbiome analysis of healthy and diseased sponges <i>Lubomirskia baicalensis</i> by using cell cultures of primmorphs. PeerJ, 2020, 8, e9080.	0.9	17
957	Needles in haystacks: reevaluating old paradigms for the discovery of bacterial secondary metabolites. Natural Product Reports, 2021, 38, 2083-2099.	5.2	14
958	Enabling microbiome research on personal devices. , 2021, , .		1
959	Temporal turnover of the soil microbiome composition is guild-specific. Ecology Letters, 2021, 24, 2726-2738.	3.0	21
960	High-Throughput Sequencing for Examining Salmonella Prevalence and Pathogen-Microbiota Relationships in Barn Swallows. Frontiers in Ecology and Evolution, 2021, 9, .	1.1	3
961	Functions predict horizontal gene transfer and the emergence of antibiotic resistance. Science Advances, 2021, 7, eabj5056.	4.7	44
962	Global Patterns and Climatic Controls of Dust-Associated Microbial Communities. Microbiology Spectrum, 2021, 9, e0144721.	1.2	8
963	Temporal metabolite responsiveness of microbiota in the tea plant phyllosphere promotes continuous suppression of fungal pathogens. Journal of Advanced Research, 2022, 39, 49-60.	4.4	24
965	Differential Fecal Microbiome Dysbiosis after Equivalent Traumatic Brain Injury in Aged Versus Young Adult Mice. , 2021, 2, 120-130.		3
966	Fine-Scale Spatial Structure of Soil Microbial Communities in Burrows of a Keystone Rodent Following Mass Mortality. Frontiers in Ecology and Evolution, 2021, 9, .	1.1	2
967	Biochar dose determines methane uptake and methanotroph abundance in Haplic Luvisol. Science of the Total Environment, 2022, 806, 151259.	3.9	16
968	Intimate ecosystems: the microbiome and the ecological determinants of health. Canadian Journal of Public Health, 2021, 112, 1004-1007.	1.1	2
969	Evaluation of the Effects of Library Preparation Procedure and Sample Characteristics on the Accuracy of Metagenomic Profiles. MSystems, 2021, 6, e0044021.	1.7	5
970	An integrative study of the microbiome gut-brain-axis and hippocampal inflammation in psychosis: Persistent effects from mode of birth. Schizophrenia Research, 2022, 247, 101-115.	1.1	7
971	Largely invariant communities of bacterial endophytes in the nonphotosynthetic mycoheterotrophic plant <i>Pterospira andromeda</i> . American Journal of Botany, 2021, 108, 2208-2219.	0.8	0



#	ARTICLE	IF	CITATIONS
972	App-SpaM: phylogenetic placement of short reads without sequence alignment. <i>Bioinformatics Advances</i> , 2021, 1, .	0.9	5
973	Microbial diversity in tropical marine sediments assessed using cultureâ€dependent and cultureâ€independent techniques. <i>Environmental Microbiology</i> , 2021, 23, 6859-6875.	1.8	8
974	Toward a Global Public Repository of Community Protocols to Encourage Best Practices in Biomolecular Ocean Observing and Research. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	12
975	A metabolic modeling platform for the computation of microbial ecosystems in time and space (COMETS). <i>Nature Protocols</i> , 2021, 16, 5030-5082.	5.5	70
976	Networked collective microbiomes and the rise of subcellular 'units of life'. <i>Trends in Microbiology</i> , 2022, 30, 112-119.	3.5	5
977	Advancing Equity and Inclusion in Microbiome Research and Training. <i>MSystems</i> , 2021, 6, e0115121.	1.7	9
979	A comprehensive evaluation of single-end sequencing data analyses for environmental microbiome research. <i>Archives of Microbiology</i> , 2021, 203, 6295-6302.	1.0	7
980	Metagenomic Sequencing of Multiple Soil Horizons and Sites in Close Vicinity Revealed Novel Secondary Metabolite Diversity. <i>MSystems</i> , 2021, 6, e0101821.	1.7	16
981	Fast and accurate distanceâ€based phylogenetic placement using divide and conquer. <i>Molecular Ecology Resources</i> , 2022, 22, 1213-1227.	2.2	25
982	Comparative analysis of microbial communities between water and sediment in Laoshan Bay marine ranching with varied aquaculture activities. <i>Marine Pollution Bulletin</i> , 2021, 173, 112990.	2.3	15
1017	Effect of changes of gut microbiota in constipation on lipid metabolism. <i>World Chinese Journal of Digestology</i> , 2020, 28, 341-346.	0.0	0
1020	The hidden layers of microbial community structure: extracting the concealed diversity dimensions from our sequencing data. <i>FEMS Microbiology Letters</i> , 2020, 367, .	0.7	1
1022	Interactive exploratory data analysis of Integrative Human Microbiome Project data using Metaviz. <i>F1000Research</i> , 2020, 9, 601.	0.8	1
1024	Physicochemical and Antibacterial Screening of Coconut Oil on some Clinical Bacteria Isolates. <i>UMYU Journal of Microbiology Research</i> , 2020, 5, 54-59.	0.1	0
1029	Responses of the Soil Microbial Community to Salinity Stress in Maize Fields. <i>Biology</i> , 2021, 10, 1114.	1.3	25
1030	Habitat geometry in artificial microstructure affects bacterial and fungal growth, interactions, and substrate degradation. <i>Communications Biology</i> , 2021, 4, 1226.	2.0	14
1031	Bathyarchaeia occurrence in rich methane sediments from a Brazilian rÃa. <i>Estuarine, Coastal and Shelf Science</i> , 2021, 263, 107631.	0.9	16
1032	The microbiome of a shell mound: ancient anthropogenic waste as a source of <i>Streptomyces</i> degrading recalcitrant polysaccharides. <i>World Journal of Microbiology and Biotechnology</i> , 2021, 37, 210.	1.7	1

#	ARTICLE	IF	CITATIONS
1034	Uncovering host-microbiome interactions in global systems with collaborative programming: a novel approach integrating social and data sciences. <i>F1000Research</i> , 0, 9, 1478.	0.8	0
1035	Putting microbial interactions back into community contexts. <i>Current Opinion in Microbiology</i> , 2022, 65, 56-63.	2.3	24
1037	Harnessing Soil Microbiomes for Creating Healthy and Functional Urban Landscapes. , 2020, , 325-338.		1
1043	RESCRIPT: Reproducible sequence taxonomy reference database management. <i>PLoS Computational Biology</i> , 2021, 17, e1009581.	1.5	277
1044	<i>Candida albicans</i> Isolates 529L and CHN1 Exhibit Stable Colonization of the Murine Gastrointestinal Tract. <i>MBio</i> , 2021, 12, e0287821.	1.8	21
1045	Spatial and temporal comparisons of salt marsh soil fungal communities following the deepwater horizon spill. <i>Wetlands Ecology and Management</i> , 0, , 1.	0.7	0
1046	The Future Is Big and Small: Remote Sensing Enables Cross-Scale Comparisons of Microbiome Dynamics and Ecological Consequences. <i>MSystems</i> , 2021, 6, e0110621.	1.7	4
1048	Expanded analyses of the functional correlations within structural classifications of glycoside hydrolases. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 5931-5942.	1.9	9
1050	Sculpting the soil microbiota. <i>Plant Journal</i> , 2022, 109, 508-522.	2.8	28
1053	Porting and optimizing UniFrac for GPUs. , 2020, , .		3
1057	Harmonising the fields of invasion science and forest pathology. <i>NeoBiota</i> , 0, 62, 301-332.	1.0	16
1061	Studying Seed Microbiomes. <i>Methods in Molecular Biology</i> , 2021, 2232, 1-21.	0.4	5
1062	La milpa como modelo para el estudio de la biodiversidad e interacciones planta-bacteria. <i>TIP Revista Especializada En Ciencias Químico-Biológicas</i> , 0, 23, .	0.3	3
1063	The microbiome: an emerging key player in aging and longevity. <i>Translational Medicine of Aging</i> , 2020, 4, 103-116.	0.6	23
1064	Assessing the efficacy of antibiotic treatment to produce earthworms with a suppressed microbiome. <i>European Journal of Soil Biology</i> , 2022, 108, 103366.	1.4	2
1065	Implications of bacterial mineralisation in aquatic ecosystem response models. <i>Water Research</i> , 2022, 209, 117888.	5.3	3
1066	Technical note: overcoming host contamination in bovine vaginal metagenomic samples with nanopore adaptive sequencing. <i>Journal of Animal Science</i> , 2022, 100, .	0.2	10
1067	Environmental DNA metabarcoding for benthic monitoring: A review of sediment sampling and DNA extraction methods. <i>Science of the Total Environment</i> , 2022, 818, 151783.	3.9	62

#	ARTICLE	IF	CITATIONS
1071	Toward a functional first framework to make soil microbial ecology predictive. <i>Ecology</i> , 2022, 103, e03594.	1.5	19
1072	A primer and discussion on DNA-based microbiome data and related bioinformatics analyses. , 0, 1, .		6
1073	Usefulness of Microbiome for Forensic Geolocation: A Review. <i>Life</i> , 2021, 11, 1322.	1.1	6
1074	Inconsistent Patterns of Microbial Diversity and Composition Between Highly Similar Sequencing Protocols: A Case Study With Reef-Building Corals. <i>Frontiers in Microbiology</i> , 2021, 12, 740932.	1.5	8
1075	High viral abundance and low diversity are associated with increased CRISPR-Cas prevalence across microbial ecosystems. <i>Current Biology</i> , 2022, 32, 220-227.e5.	1.8	23
1076	Minnesota peat viromes reveal terrestrial and aquatic niche partitioning for local and global viral populations. <i>Microbiome</i> , 2021, 9, 233.	4.9	53
1077	Interactive effects of biochar amendment and lead toxicity on soil microbial community. <i>Journal of Hazardous Materials</i> , 2022, 425, 127921.	6.5	23
1078	From DNA sequences to microbial ecology: Wrangling NEON soil microbe data with the neonMicrobe R package. <i>Ecosphere</i> , 2021, 12, e03842.	1.0	3
1079	Water and soil contaminated by arsenic: the use of microorganisms and plants in bioremediation. <i>Environmental Science and Pollution Research</i> , 2022, 29, 9462-9489.	2.7	6
1080	Clean room microbiome complexity impacts planetary protection bioburden. <i>Microbiome</i> , 2021, 9, 238.	4.9	11
1082	Contrasting Effects of Local Environmental and Biogeographic Factors on the Composition and Structure of Bacterial Communities in Arid Monospecific Mangrove Soils. <i>Microbiology Spectrum</i> , 2022, 10, e0090321.	1.2	11
1083	Nutrient supply controls the linkage between species abundance and ecological interactions in marine bacterial communities. <i>Nature Communications</i> , 2022, 13, 175.	5.8	95
1084	A three-dimensional (3D) printing approach to fabricate an isolation chip for high throughput <i>in situ</i> cultivation of environmental microbes. <i>Lab on A Chip</i> , 2022, 22, 387-402.	3.1	3
1086	Age-Associated Gut Dysbiosis, Marked by Loss of Butyrogenic Potential, Correlates With Altered Plasma Tryptophan Metabolites in Older People Living With HIV. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2022, 89, S56-S64.	0.9	7
1087	Indoor Microbiome and The Rising Asthma Prevalence. <i>EMJ Microbiology &amp; Infectious Diseases</i> , 0, , 51-56.	0.0	0
1088	Microbial ecology of the South Atlantic Subtropical Gyre: a state-of-the-art review of an understudied ocean region. <i>Ocean and Coastal Research</i> , 0, 69, .	0.3	4
1089	Genomics Tools and Microbiota: Applications to Response in Coastal Ecosystems. <i>International Oil Spill Conference Proceedings</i> , 2021, 2021, .	0.1	0
1090	Microbial Community Response to Polysaccharide Amendment in Anoxic Hydrothermal Sediments of the Guaymas Basin. <i>Frontiers in Microbiology</i> , 2021, 12, 763971.	1.5	2

#	ARTICLE	IF	CITATIONS
1091	Environmental paleomicrobiology: using <sc>DNA</sc> preserved in aquatic sediments to its full potential. <i>Environmental Microbiology</i> , 2022, 24, 2201-2209.	1.8	27
1093	Multi-omics analyses of the ulcerative colitis gut microbiome link <i>Bacteroides vulgatus</i> proteases with disease severity. <i>Nature Microbiology</i> , 2022, 7, 262-276.	5.9	110
1094	Exploring the role of soil microbiome in global climatic changes. , 2022, , 353-370.		0
1095	Robust host source tracking building on the divergent and non-stochastic assembly of gut microbiomes in wild and farmed large yellow croaker. <i>Microbiome</i> , 2022, 10, 18.	4.9	9
1096	Fine-Scale Adaptations to Environmental Variation and Growth Strategies Drive Phyllosphere <i>Methylobacterium</i> Diversity. <i>MBio</i> , 2022, 13, e0317521.	1.8	7
1097	Scientific concepts and methods for moving persistence assessments into the 21st century. <i>Integrated Environmental Assessment and Management</i> , 2022, 18, 1454-1487.	1.6	24
1100	New Insight Into the Mechanism of Ecological Effects of Artificial Habitats: Elucidating the Relationship Between Protists Associated With Artificial Reefs and Adjacent Seawater. <i>Frontiers in Marine Science</i> , 2022, 8, .	1.2	2
1101	Forest tree growth is linked to mycorrhizal fungal composition and function across Europe. <i>ISME Journal</i> , 2022, 16, 1327-1336.	4.4	62
1102	Small investments with big returns: environmental genomic bioprospecting of microbial life. <i>Critical Reviews in Microbiology</i> , 2022, 48, 641-655.	2.7	7
1103	<i>Bifidobacterium longum</i> Subspecies <i>infantis</i> Strain EVC001 Decreases Neonatal Murine Necrotizing Enterocolitis. <i>Nutrients</i> , 2022, 14, 495.	1.7	8
1104	Generalised mutagenesis with transposon Tn5. A laboratory procedure for the identification of genes responsible for a bacterial phenotype and its regulation, illustrated with phenazine production in <i>Pseudomonas chlororaphis</i> . <i>Journal of Biological Education</i> , 0, , 1-19.	0.8	1
1105	Deep-sea wooden shipwrecks influence sediment microbiome diversity. <i>Limnology and Oceanography</i> , 2022, 67, 482-497.	1.6	7
1106	Ontology-aware neural network: a general framework for pattern mining from microbiome data. <i>Briefings in Bioinformatics</i> , 2022, , .	3.2	1
1107	Advances, challenges, and opportunities in DNA sequencing technology. , 2022, , 31-43.		0
1108	Global diversity and distribution of mushroom-inhabiting bacteria. <i>Environmental Microbiology Reports</i> , 2022, 14, 254-264.	1.0	13
1109	Phylogenetically and functionally diverse microorganisms reside under the Ross Ice Shelf. <i>Nature Communications</i> , 2022, 13, 117.	5.8	17
1110	Metagenomic Sequencing Reveals that the Assembly of Functional Genes and Taxa Varied Highly and Lacked Redundancy in the Earthworm Gut Compared with Soil under Vanadium Stress. <i>MSystems</i> , 2022, 7, e0125321.	1.7	10
1111	Conceptual Exchanges for Understanding Free-Living and Host-Associated Microbiomes. <i>MSystems</i> , 2022, 7, e0137421.	1.7	3

#	ARTICLE	IF	CITATIONS
1112	Effect of climate change and soil dynamics on soil microbes and fertility of soil. , 2022, , 437-468.		3
1113	Uses of molecular taxonomy in identifying phytoplankton communities from the Continuous Plankton Recorder Survey. , 2022, , 47-79.		2
1114	Rare genera differentiate urban green space soil bacterial communities in three cities across the world. Access Microbiology, 2022, 4, 000320.	0.2	2
1116	Host-specific epibiomes of distinct <i>Acropora cervicornis</i> genotypes persist after field transplantation. Coral Reefs, 2022, 41, 265-276.	0.9	8
1117	Considerations and best practices in animal science 16S ribosomal RNA gene sequencing microbiome studies. Journal of Animal Science, 2022, 100, .	0.2	36
1118	Unboxing the black box“one step forward to understand the soil microbiome: A systematic review. Microbial Ecology, 2023, 85, 669-683.	1.4	26
1120	Microbial biogeography of acid mine drainage sediments at a regional scale across southern China. FEMS Microbiology Ecology, 2022, 98, .	1.3	2
1121	Determinants and Interactions of Oral Bacterial and Fungal Microbiota in Healthy Chinese Adults. Microbiology Spectrum, 2022, 10, e0241021.	1.2	15
1122	Conceptual strategies for characterizing interactions in microbial communities. IScience, 2022, 25, 103775.	1.9	12
1123	Polar soils exhibit distinct patterns in microbial diversity and dominant phylotypes. Soil Biology and Biochemistry, 2022, 166, 108550.	4.2	19
1124	Biogeographic patterns of soil microbe communities in the deserts of the Hexi Corridor, northern China. Catena, 2022, 211, 106026.	2.2	14
1125	Recent advances in microbial community analysis from machine learning of multiparametric flow cytometry data. Current Opinion in Biotechnology, 2022, 75, 102688.	3.3	6
1126	Influence of 16S rRNA reference databases in amplicon-based environmental microbiome research. Biotechnology Letters, 2022, 44, 523-533.	1.1	8
1128	Diversity, activity, and abundance of benthic microbes in the Southeastern Mediterranean Sea. FEMS Microbiology Ecology, 2022, 98, .	1.3	13
1129	Soil health, soil genetic horizons and biodiversity<sup>#</sup>. Journal of Plant Nutrition and Soil Science, 2022, 185, 24-34.	1.1	16
1130	High-throughput qPCR and 16S rRNA gene amplicon sequencing as complementary methods for the investigation of the cheese microbiota. BMC Microbiology, 2022, 22, 48.	1.3	21
1131	DNA coding and GÃ¶del numbering. Physica A: Statistical Mechanics and Its Applications, 2022, 594, 127053.	1.2	0
1132	Indoor microbiome, air pollutants and asthma, rhinitis and eczema in preschool children â€“ A repeated cross-sectional study. Environment International, 2022, 161, 107137.	4.8	33

#	ARTICLE	IF	CITATIONS
1133	Fast and flexible analysis of linked microbiome data with mako. <i>Nature Methods</i> , 2022, 19, 51-54.	9.0	7
1134	Decoding the link of microbiome niches with homologous sequences enables accurately targeted protein structure prediction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	12
1135	Soil under stress: The importance of soil life and how it is influenced by (micro)plastic pollution. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 1554-1566.	1.9	30
1136	Advanced Analytical, Chemometric, and Genomic Tools to Identify Polymer's Degradation Products and Potential Microbial Consumers in Wastewater Environments. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
1137	Applying enzymatic biomarkers of the in situ microbial community to assess the risk of coastal sediment. , 2022, , 305-335.		0
1140	Applications and Comparison of Dimensionality Reduction Methods for Microbiome Data. <i>Frontiers in Bioinformatics</i> , 2022, 2, .	1.0	10
1141	High-throughput identification and quantification of single bacterial cells in the microbiota. <i>Nature Communications</i> , 2022, 13, 863.	5.8	8
1142	Plant-Microbe Interaction in Sustainable Agriculture: The Factors That May Influence the Efficacy of PGPM Application. <i>Sustainability</i> , 2022, 14, 2253.	1.6	23
1143	Microbial biogeography of the wombat gastrointestinal tract. <i>PeerJ</i> , 2022, 10, e12982.	0.9	2
1144	Microbial Functional Diversity Correlates with Species Diversity along a Temperature Gradient. <i>MSystems</i> , 2022, 7, e0099121.	1.7	14
1145	Trends in Microbial Community Composition and Function by Soil Depth. <i>Microorganisms</i> , 2022, 10, 540.	1.6	62
1146	A Closer Examination of the "Abundant-Center"™ for Ectomycorrhizal Fungal Community Associated With <i>Picea crassifolia</i> in China. <i>Frontiers in Plant Science</i> , 2022, 13, 759801.	1.7	2
1148	Relationships Between Migration and Microbiome Composition and Diversity in Urban Canada Geese. <i>Frontiers in Ecology and Evolution</i> , 2022, 10, .	1.1	5
1150	From diversity to complexity: Microbial networks in soils. <i>Soil Biology and Biochemistry</i> , 2022, 169, 108604.	4.2	67
1151	Antibiotics Alter the Expression of Genes Related to Behavioral Development in Honey Bees (Hymenoptera: Apidae). <i>Journal of Insect Science</i> , 2022, 22, .	0.6	3
1152	Microbiome structure in large pelagic sharks with distinct feeding ecologies. <i>Animal Microbiome</i> , 2022, 4, 17.	1.5	11
1153	How much metagenome data is needed for protein structure prediction: The advantages of targeted approach from the ecological and evolutionary perspectives. , 2022, 1, .		3
1155	Emergent Diversity and Persistent Turnover in Evolving Microbial Cross-Feeding Networks. <i>Frontiers in Network Physiology</i> , 2022, 2, .	0.8	2

#	ARTICLE	IF	CITATIONS
1156	Microbiome Variation Across Populations of Desert Halophyte <i>Zygophyllum qatarensis</i> . <i>Frontiers in Plant Science</i> , 2022, 13, 841217.	1.7	3
1159	Microbial community succession of submerged bones in an aquatic habitat. <i>Journal of Forensic Sciences</i> , 2022, , .	0.9	5
1161	Biocementation for All, Anywhere: A New Experiment for Introductory Soil Mechanics Courses. , 2022, , .		0
1162	Life stage and proximity to roads shape the skin microbiota of eastern newts ( <i>Notophthalmus</i> ) Tj ETQq1 1 0.784314 rgBT <sub>3</sub> /Overlo	1.8	3
1163	Genome and proteome analyses show the gaseous alkane degrader <i>Desulfosarcina</i> sp. strain <i>BuS5</i> as an extreme metabolic specialist. <i>Environmental Microbiology</i> , 2022, 24, 1964-1976.	1.8	10
1165	Toward understanding the genetic bases underlying plant-mediated cry for help to the microbiota. , 2022, 1, .		29
1166	Microbial communities form rich extracellular metabolomes that foster metabolic interactions and promote drug tolerance. <i>Nature Microbiology</i> , 2022, 7, 542-555.	5.9	58
1167	Pairing litter decomposition with microbial community structures using the Tea Bag Index (TBI). <i>Soil</i> , 2022, 8, 163-176.	2.2	10
1168	Reproducible Propagation of Species-Rich Soil Bacterial Communities Suggests Robust Underlying Deterministic Principles of Community Formation. <i>MSystems</i> , 2022, 7, e0016022.	1.7	10
1171	MicrobioSee: A Web-Based Visualization Toolkit for Multi-Omics of Microbiology. <i>Frontiers in Genetics</i> , 2022, 13, 853612.	1.1	2
1173	Climate-Driven Legacies in Simulated Microbial Communities Alter Litter Decomposition Rates. <i>Frontiers in Ecology and Evolution</i> , 2022, 10, .	1.1	4
1174	MiDAS 4: A global catalogue of full-length 16S rRNA gene sequences and taxonomy for studies of bacterial communities in wastewater treatment plants. <i>Nature Communications</i> , 2022, 13, 1908.	5.8	114
1175	Meta-analysis of diazotrophic signatures across terrestrial ecosystems at the continental scale. <i>Environmental Microbiology</i> , 2022, 24, 2013-2028.	1.8	9
1176	The stochastic logistic model with correlated carrying capacities reproduces beta-diversity metrics of microbial communities. <i>PLoS Computational Biology</i> , 2022, 18, e1010043.	1.5	7
1177	The Right Place at the Right Time: Seasonal Variation of Bacterial Communities in Arid <i>Avicennia marina</i> Soils in the Red Sea Is Specific to Its Position in the Intertidal. <i>Frontiers in Ecology and Evolution</i> , 2022, 10, .	1.1	3
1178	Impact of ozonated water disinfection on soil fungal community composition in continuous ginger field. <i>PLoS ONE</i> , 2022, 17, e0266619.	1.1	0
1179	Dietary fat promotes antibiotic-induced <i>Clostridioides difficile</i> mortality in mice. <i>Npj Biofilms and Microbiomes</i> , 2022, 8, 15.	2.9	6
1180	Microbial communities in sandy beaches from the three domains of life differ by microhabitat and intertidal location. <i>Molecular Ecology</i> , 2022, 31, 3210-3227.	2.0	6



#	ARTICLE	IF	CITATIONS
1181	Shifts in benthic bacterial communities associated with farming stages and a microbiological proxy for assessing sulfidic sediment conditions at fish farms. <i>Marine Pollution Bulletin</i> , 2022, 178, 113603.	2.3	7
1182	Nationwide biogeography and health implications of bacterial communities in household drinking water. <i>Water Research</i> , 2022, 215, 118238.	5.3	7
1183	Petrochemical and municipal wastewater treatment plants activated sludge each own distinct core bacteria driven by their specific incoming wastewater. <i>Science of the Total Environment</i> , 2022, 826, 153962.	3.9	19
1184	A meta-analysis of the effect of organic and mineral fertilizers on soil microbial diversity. <i>Applied Soil Ecology</i> , 2022, 175, 104450.	2.1	34
1185	Advanced analytical, chemometric, and genomic tools to identify polymer degradation products and potential microbial consumers in wastewater environments. <i>Chemical Engineering Journal</i> , 2022, 442, 136175.	6.6	10
1186	Class Ib MHCs Mediated Immune Interactions Play a Critical Role in Maintaining Mucosal Homeostasis in the Mammalian Large Intestine. <i>ImmunoHorizons</i> , 2021, 5, 953-971.	0.8	0
1187	Genome-Scale Metabolic Modeling Enables In-Depth Understanding of Big Data. <i>Metabolites</i> , 2022, 12, 14.	1.3	37
1188	Bacterial Microbiomes in the Sediments of Lotic Systems Ecologic Drivers and Role: A Case Study from the MureÅ River, Transylvania, Romania. <i>Water (Switzerland)</i> , 2021, 13, 3518.	1.2	8
1190	Depth dependence of climatic controls on soil microbial community activity and composition. <i>ISME Communications</i> , 2021, 1, .	1.7	16
1191	PAAR Proteins Are Versatile Clips That Enrich the Antimicrobial Weapon Arsenals of Prokaryotes. <i>MSystems</i> , 2021, 6, e0095321.	1.7	10
1192	Intergenerational effects of a paternal Western diet during adolescence on offspring gut microbiota, stress reactivity, and social behavior. <i>FASEB Journal</i> , 2022, 36, e21981.	0.2	8
1194	Streptozotocin-induced hyperglycemia alters the cecal metabolome and exacerbates antibiotic-induced dysbiosis. <i>Cell Reports</i> , 2021, 37, 110113.	2.9	11
1195	Evaluating replicability in microbiome data. <i>Biostatistics</i> , 2022, 23, 1099-1114.	0.9	12
1197	The Lack of Knowledge on the Microbiome of Golf Turfgrasses Impedes the Development of Successful Microbial Products. <i>Agronomy</i> , 2022, 12, 71.	1.3	2
1198	Evolution-Informed Neural Networks for Microbiome Data Analysis. , 2021, , .		1
1200	Dissecting the dominant hot spring microbial populations based on community-wide sampling at single-cell genomic resolution. <i>ISME Journal</i> , 2022, 16, 1337-1347.	4.4	15
1202	<tt>met v1</tt>: expanding on old estimations of biodiversity from eDNA with a new database framework. <i>Database: the Journal of Biological Databases and Curation</i> , 2022, 2022, .	1.4	0
1203	Trans-Generational Symbiont Transmission Reduced at High Temperatures in a West Nile Virus Vector Mosquito <i>Culex quinquefasciatus</i> . <i>Frontiers in Tropical Diseases</i> , 2022, 3, .	0.5	1

#	ARTICLE	IF	CITATIONS
1206	Menopause Is Associated with an Altered Gut Microbiome and Estrobolome, with Implications for Adverse Cardiometabolic Risk in the Hispanic Community Health Study/Study of Latinos. <i>MSystems</i> , 2022, 7, .	1.7	16
1207	Complex impacts of hydraulic fracturing return fluids on soil microbial community respiration, structure and functional potentials. <i>Environmental Microbiology</i> , 2022, 24, 4108-4123.	1.8	2
1208	A legacy of fire emerges from multiple disturbances to most shape microbial and nitrogen dynamics in a deciduous forest. <i>Soil Biology and Biochemistry</i> , 2022, , 108672.	4.2	3
1209	Early microbial markers of periodontal and cardiometabolic diseases in ORIGINS. <i>Npj Biofilms and Microbiomes</i> , 2022, 8, 30.	2.9	7
1210	Diversity and Metabolism of Microbial Communities in a Hypersaline Lake along a Geochemical Gradient. <i>Biology</i> , 2022, 11, 605.	1.3	4
1328	Bacterial Assemblage in Mediterranean Salt Marshes: Disentangling the Relative Importance of Seasonality, Zonation and Halophytes. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
1331	The Soil Microbiota Recovery in the Agroecosystem: Minimal Information and a New Framework for Sustainable Agriculture. <i>International Journal of Environmental Research and Public Health</i> , 2022, 19, 5423.	1.2	1
1332	Ontology-aware deep learning enables ultrafast and interpretable source tracking among sub-million microbial community samples from hundreds of niches. <i>Genome Medicine</i> , 2022, 14, 43.	3.6	9
1333	Reproducibility of Bacterial Cellulose Nanofibers Over Sub-Cultured Generations for the Development of Novel Textiles. <i>Frontiers in Bioengineering and Biotechnology</i> , 2022, 10, 876822.	2.0	4
1334	Soil <scp>DNA</scp> chronosequence analysis shows bacterial community reâ€assembly following postâ€mining forest rehabilitation. <i>Restoration Ecology</i> , 2023, 31, .	1.4	3
1335	Gut microbiota of ring-tailed lemurs ( <i>Lemur catta</i> ) vary across natural and captive populations and correlate with environmental microbiota. <i>Animal Microbiome</i> , 2022, 4, 29.	1.5	24
1336	Microbial Dark Matter: from Discovery to Applications. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 867-881.	3.0	20
1337	Streptozotocin-Induced Hyperglycemia Is Associated with Unique Microbiome Metabolomic Signatures in Response to Ciprofloxacin Treatment. <i>Antibiotics</i> , 2022, 11, 585.	1.5	0
1338	Ingestion of remediated lead-contaminated soils affects the fecal microbiome of mice. <i>Science of the Total Environment</i> , 2022, 837, 155797.	3.9	3
1339	Maize associated bacterial microbiome linked mitigation of heavy metal stress: A multidimensional detoxification approach. <i>Environmental and Experimental Botany</i> , 2022, 200, 104911.	2.0	24
1340	Microbiomes and Planctomycete diversity in large-scale aquaria habitats. <i>PLoS ONE</i> , 2022, 17, e0267881.	1.1	4
1341	Turning the tide on sex and the microbiota in aquatic animals. <i>Hydrobiologia</i> , 2023, 850, 3823-3835.	1.0	2
1342	Variation in Root Exudate Composition Influences Soil Microbiome Membership and Function. <i>Applied and Environmental Microbiology</i> , 2022, 88, e0022622.	1.4	30

#	ARTICLE	IF	CITATIONS
1343	Evaluating Spatial and Temporal Dynamics of River-Floodplain Surface Water Connectivity Using Hydrometric, Geochemical and Microbial Indicators. <i>Water Resources Research</i> , 2022, 58, .	1.7	5
1344	Comparative Analysis of Metagenomics and Metataxonomics for the Characterization of Vermicompost Microbiomes. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	3
1345	Gut modulatory effects of flaxseed derived Maillard reaction products in Sprague-Dawley rats during sub-chronic toxicity. <i>Food and Chemical Toxicology</i> , 2022, 165, 113115.	1.8	2
1347	Complexity-stability trade-off in empirical microbial ecosystems. <i>Nature Ecology and Evolution</i> , 2022, 6, 693-700.	3.4	29
1348	Microbiomes respond predictably to built habitats on the seafloor. <i>Molecular Ecology</i> , 2023, 32, 6686-6695.	2.0	5
1349	Primer Choice and Xylem-Microbiome-Extraction Method Are Important Determinants in Assessing Xylem Bacterial Community in Olive Trees. <i>Plants</i> , 2022, 11, 1320.	1.6	4
1350	Context-dependent role of abiotic and biotic factors structuring nematode communities along two environmental gradients. <i>Molecular Ecology</i> , 2022, 31, 3903-3916.	2.0	5
1352	It Takes a Village: Using a Crowdsourced Approach to Investigate Organic Matter Composition in Global Rivers Through the Lens of Ecological Theory. <i>Frontiers in Water</i> , 2022, 4, .	1.0	3
1353	Diversity in the soil virosphere: to infinity and beyond?. <i>Trends in Microbiology</i> , 2022, 30, 1025-1035.	3.5	35
1354	Unveiling the egg microbiota of the loggerhead sea turtle <i>Caretta caretta</i> in nesting beaches of the Mediterranean Sea. <i>PLoS ONE</i> , 2022, 17, e0268345.	1.1	6
1356	Metabolic interactions shape a community's phenotype. <i>Trends in Microbiology</i> , 2022, 30, 609-611.	3.5	6
1357	Microbial Communities in Underground Gas Reservoirs Offer Promising Biotechnological Potential. <i>Fermentation</i> , 2022, 8, 251.	1.4	6
1358	Effects of captivity and rewilding on amphibian skin microbiomes. <i>Biological Conservation</i> , 2022, 271, 109576.	1.9	25
1359	Microbiome Diversity Analysis of the Bacterial Community in Idah River, Kogi State, Nigeria. <i>Advances in Microbiology</i> , 2022, 12, 343-362.	0.3	3
1360	Microbiological Analysis and Metagenomic Profiling of the Bacterial Community of an Anthropogenic Soil Modified from Typic Haploxererts. <i>Land</i> , 2022, 11, 748.	1.2	2
1361	Spatial compositional turnover varies with trophic level and body size in marine assemblages of micro- and macroorganisms. <i>Global Ecology and Biogeography</i> , 2022, 31, 1556-1570.	2.7	2
1362	Moroccan Lagoon Microbiomes. <i>Water (Switzerland)</i> , 2022, 14, 1715.	1.2	1
1363	Earth Biogenome Project: present status and future plans. <i>Trends in Genetics</i> , 2022, 38, 811-820.	2.9	7

#	ARTICLE	IF	CITATIONS
1364	Longitudinal urinary microbiome characteristics in women with urgency urinary incontinence undergoing sacral neuromodulation. <i>International Urogynecology Journal</i> , 2023, 34, 517-525.	0.7	2
1365	Optimizing UniFrac with OpenACC Yields Greater Than One Thousand Times Speed Increase. <i>MSystems</i> , 2022, 7, .	1.7	2
1367	High-throughput, single-microbe genomics with strain resolution, applied to a human gut microbiome. <i>Science</i> , 2022, 376, .	6.0	100
1368	Multitomic Analyses of Nascent Preterm Infant Microbiomes Differentiation Suggest Opportunities for Targeted Intervention. <i>Advanced Biology</i> , 2022, 6, .	1.4	4
1369	The microbiome of cryospheric ecosystems. <i>Nature Communications</i> , 2022, 13, .	5.8	20
1370	Near-neutral pH increased n-caprylate production in a microbiome with product inhibition of methanogenesis. <i>Chemical Engineering Journal</i> , 2022, 446, 137170.	6.6	13
1372	The effect of COVID-19 lockdown on mental health, gut microbiota composition and serum cortisol levels. <i>Stress</i> , 2022, 25, 246-257.	0.8	8
1373	A comparison of six DNA extraction protocols for 16S, ITS and shotgun metagenomic sequencing of microbial communities. <i>BioTechniques</i> , 2022, 73, 34-46.	0.8	25
1374	MarkerMAG: linking metagenome-assembled genomes (MAGs) with 16S rRNA marker genes using paired-end short reads. <i>Bioinformatics</i> , 2022, 38, 3684-3688.	1.8	6
1375	Mutual Exclusion of <i>Methanobrevibacter</i> Species in the Human Gut Microbiota Facilitates Directed Cultivation of a <i>Candidatus</i> <i>Methanobrevibacter Intestini</i> Representative. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	6
1376	Identifying plant genes shaping microbiota composition in the barley rhizosphere. <i>Nature Communications</i> , 2022, 13, .	5.8	44
1377	Recurrent neural networks enable design of multifunctional synthetic human gut microbiome dynamics. <i>ELife</i> , 0, 11, .	2.8	18
1379	Culturable Bacterial Diversity from the Basaltic Subsurface of the Young Volcanic Island of Surtsey, Iceland. <i>Microorganisms</i> , 2022, 10, 1177.	1.6	1
1380	The molecular impact of life in an indoor environment. <i>Science Advances</i> , 2022, 8, .	4.7	3
1381	Growth rate determines prokaryote-provirus network modulated by temperature and host genetic traits. <i>Microbiome</i> , 2022, 10, .	4.9	0
1382	Diversity and Biogeography of Human Oral Saliva Microbial Communities Revealed by the Earth Microbiome Project. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5
1383	Microbiome assembly in thawing permafrost and its feedbacks to climate. <i>Global Change Biology</i> , 2022, 28, 5007-5026.	4.2	34
1384	On the effect of inheritance of microbes in commensal microbiomes. <i>Bmc Ecology and Evolution</i> , 2022, 22, .	0.7	0

#	ARTICLE	IF	CITATIONS
1385	A Comprehensive Insight of Current and Future Challenges in Large-Scale Soil Microbiome Analyses. <i>Microbial Ecology</i> , 0, , .	1.4	0
1386	Microbiome and -omics application in food industry. <i>International Journal of Food Microbiology</i> , 2022, 377, 109781.	2.1	10
1387	Interaction of the rhizosphere microbiome and crops under climate change. , 2022, , 235-258.		0
1388	Host Age Prediction from Fecal Microbiota Composition in Male C57BL/6J Mice. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	7
1389	Characterising the Gut Microbiomes in Wild and Captive Short-Beaked Echidnas Reveals Diet-Associated Changes. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	8
1390	Composition and Biogeography of Planktonic Pro- and Eukaryotic Communities in the Atlantic Ocean: Primer Choice Matters. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5
1391	Development of Specific DNA Barcodes for the Dinophyceae Family Kareniaceae and Their Application in the South China Sea. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	0
1392	Priorities for ocean microbiome research. <i>Nature Microbiology</i> , 2022, 7, 937-947.	5.9	27
1393	Gut microbiome of century-old snail specimens stable across time in preservation. <i>Microbiome</i> , 2022, 10, .	4.9	7
1394	specificity: an R package for analysis of feature specificity to environmental and higher dimensional variables, applied to microbiome species data. <i>Environmental Microbiomes</i> , 2022, 17, .	2.2	7
1395	Ecosystem-specific microbiota and microbiome databases in the era of big data. <i>Environmental Microbiomes</i> , 2022, 17, .	2.2	9
1398	A consensus protocol for the recovery of mercury methylation genes from metagenomes. <i>Molecular Ecology Resources</i> , 2023, 23, 190-204.	2.2	10
1399	Watershedâ€scale liming reveals the shortâ€and longâ€term effects of <sc>pH</sc> on the forest soil microbiome and carbon cycling. <i>Environmental Microbiology</i> , 2022, 24, 6184-6199.	1.8	10
1400	The Native Microbial Community of Gastropod-Associated Phasmarhabditis Species Across Central and Southern California. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
1401	Global Meta-analysis of Airborne Bacterial Communities and Associations with Anthropogenic Activities. <i>Environmental Science &amp; Technology</i> , 2022, 56, 9891-9902.	4.6	18
1402	Uncovering Hidden Members and Functions of the Soil Microbiome Using <i>De Novo</i> Metaproteomics. <i>Journal of Proteome Research</i> , 2022, 21, 2023-2035.	1.8	6
1404	Enhancing untargeted metabolomics using metadata-based source annotation. <i>Nature Biotechnology</i> , 2022, 40, 1774-1779.	9.4	25
1405	<sc>metaPR<sup>2</sup></sc>: A database of eukaryotic <sc>18S rRNA</sc> metabarcodes with an emphasis on protists. <i>Molecular Ecology Resources</i> , 2022, 22, 3188-3201.	2.2	24

#	ARTICLE	IF	CITATIONS
1406	Co-Occurrence Relationship and Stochastic Processes Affect Sedimentary Archaeal and Bacterial Community Assembly in Estuarineâ€Coastal Margins. <i>Microorganisms</i> , 2022, 10, 1339.	1.6	7
1407	Exploring the diversity and potential interactions of bacterial and fungal endophytes associated with different cultivars of olive ( <i>Olea europaea</i> ) in Brazil. <i>Microbiological Research</i> , 2022, 263, 127128.	2.5	4
1408	Depth induced assembly discrepancy of multitrophic microbial communities affect microbial nitrogen transformation processes in river cross-sections. <i>Environmental Research</i> , 2022, 214, 113913.	3.7	2
1409	Bioaerosols in the atmosphere at two sites in Northern Europe in spring 2021: Outline of an experimental campaign. <i>Environmental Research</i> , 2022, 214, 113798.	3.7	1
1411	Disentangling the assembly mechanisms of bacterial communities in a transition zone between the alpine steppe and alpine meadow ecosystems on the Tibetan Plateau. <i>Science of the Total Environment</i> , 2022, 847, 157446.	3.9	5
1412	A Specialized Polythioamideâ€Binding Protein Confers Antibiotic Selfâ€Resistance in Anaerobic Bacteria. <i>Angewandte Chemie - International Edition</i> , 2022, 61, .	7.2	2
1414	Hair Microbiome Diversity within and across Primate Species. <i>MSystems</i> , 0, , .	1.7	0
1415	Bacterial assemblage in Mediterranean salt marshes: Disentangling the relative importance of seasonality, zonation and halophytes. <i>Science of the Total Environment</i> , 2022, 846, 157514.	3.9	2
1416	Microbiota succession throughout life from the cradle to the grave. <i>Nature Reviews Microbiology</i> , 2022, 20, 707-720.	13.6	66
1417	Characteristic of the material deposits, microclimate profile, epiphyte abundance, and bacteria populations in the above-ground ecosystem of oil palm. <i>Biodiversitas</i> , 2022, 23, .	0.2	0
1418	microTrait: A Toolset for a Trait-Based Representation of Microbial Genomes. <i>Frontiers in Bioinformatics</i> , 0, 2, .	1.0	8
1420	Characterizing the chicken gut colonization ability of a diverse group of bacteria. <i>Poultry Science</i> , 2022, 101, 102136.	1.5	5
1421	Differences in intestinal microflora of birds among different ecological types. <i>Frontiers in Ecology and Evolution</i> , 0, 10, .	1.1	2
1422	A Pilot Study: the Development of a Facility-Associated Microbiome and Its Association with the Presence of <i>Listeria</i> Spp. in One Small Meat Processing Facility. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	5
1424	Soil Metabolomics Predict Microbial Taxa as Biomarkers of Moisture Status in Soils from a Tidal Wetland. <i>Microorganisms</i> , 2022, 10, 1653.	1.6	3
1426	A ridge-to-reef ecosystem microbial census reveals environmental reservoirs for animal and plant microbiomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	8
1427	Cecal microbiota of feedlot cattle fed a four-species <i>Bacillus</i> supplement. <i>Journal of Animal Science</i> , 2022, 100, .	0.2	4
1428	A Specialized Polythioamideâ€Binding Protein Confers Antibiotic Selfâ€Resistance in Anaerobic Bacteria. <i>Angewandte Chemie</i> , 2022, 134, .	1.6	0

#	ARTICLE	IF	CITATIONS
1429	DSF-family quorum sensing signal-mediated intraspecies, interspecies, and inter-kingdom communication. <i>Trends in Microbiology</i> , 2023, 31, 36-50.	3.5	23
1430	Faecalibaculum rodentium remodels retinoic acid signaling to govern eosinophil-dependent intestinal epithelial homeostasis. <i>Cell Host and Microbe</i> , 2022, 30, 1295-1310.e8.	5.1	32
1431	Toward FAIR Representations of Microbial Interactions. <i>MSystems</i> , 2022, 7, .	1.7	7
1432	Interrelated Effects of Zinc Deficiency and the Microbiome on Group B Streptococcal Vaginal Colonization. <i>MSphere</i> , 2022, 7, .	1.3	6
1433	A Case Study for the Recovery of Authentic Microbial Ancient DNA from Soil Samples. <i>Microorganisms</i> , 2022, 10, 1623.	1.6	6
1434	Experimental methods modestly impact interpretation of the effect of environmental exposures on the larval zebrafish gut microbiome. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
1435	SCNIC: Sparse correlation network investigation for compositional data. <i>Molecular Ecology Resources</i> , 2023, 23, 312-325.	2.2	13
1436	Genome analysis of the candidate phylum MBNT15 bacterium from a boreal peatland predicted its respiratory versatility and dissimilatory iron metabolism. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	9
1437	<scp>FreshOmics</scp>: A manually curated and standardized "omics database for investigating freshwater microbiomes. <i>Molecular Ecology Resources</i> , 2023, 23, 222-232.	2.2	1
1439	Nitrogen fertilization weakens the linkage between soil carbon and microbial diversity: A global meta-analysis. <i>Global Change Biology</i> , 2022, 28, 6446-6461.	4.2	71
1440	Chemical and microbial characterization of sugarcane mill mud for soil applications. <i>PLoS ONE</i> , 2022, 17, e0272013.	1.1	7
1441	Distance-Based Phylogenetic Placement with Statistical Support. <i>Biology</i> , 2022, 11, 1212.	1.3	0
1442	Mapping the relative abundance of soil microbiome biodiversity from eDNA and remote sensing. <i>Science of Remote Sensing</i> , 2022, 6, 100065.	2.2	2
1446	The streamwater microbiome encodes hydrologic data across scales. <i>Science of the Total Environment</i> , 2022, 849, 157911.	3.9	3
1447	Microbial carbon, sulfur, iron, and nitrogen cycling linked to the potential remediation of a meromictic acidic pit lake. <i>ISME Journal</i> , 2022, 16, 2666-2679.	4.4	11
1448	STENSL: Microbial Source Tracking with ENvironment SeLection. <i>MSystems</i> , 0, , .	1.7	3
1449	Responses of soil fungal communities and functional guilds to ~160 years of natural revegetation in the Loess Plateau of China. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
1450	Aerobiology over the Southern Ocean " Implications for bacterial colonization of Antarctica. <i>Environment International</i> , 2022, 169, 107492.	4.8	6



#	ARTICLE	IF	CITATIONS
1451	Meta-Prism 2.0: Enabling algorithm and web server for ultra-fast, memory-efficient, and accurate analysis among millions of microbial community samples. <i>GigaScience</i> , 2022, 11, .	3.3	0
1453	Manure Amendment Sustains Soil Biodiversity by Mitigating Acidification Induced by Chemical N Fertilization. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
1454	Tourmaline: A containerized workflow for rapid and iterable amplicon sequence analysis using QIIME 2 and Snakemake. <i>GigaScience</i> , 2022, 11, .	3.3	5
1455	Fungal communities in soils under global change. <i>Studies in Mycology</i> , 2022, 103, 1-24.	4.5	13
1456	Comprehensive Evaluation of Shotgun Metagenomics, Amplicon Sequencing and Harmonization of Said Platforms for Epidemiological Studies Using the Large Multi-Center HCHS/SOL Cohort. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
1457	Reproducible acquisition, management and meta-analysis of nucleotide sequence (meta)data using q2-fondue. <i>Bioinformatics</i> , 2022, 38, 5081-5091.	1.8	2
1458	Biotransformation of 8:2 Fluorotelomer Alcohol in Soil from Aqueous Film-Forming Foams (AFFFs)-Impacted Sites under Nitrate-, Sulfate-, and Iron-Reducing Conditions. <i>Environmental Science &amp; Technology</i> , 2022, 56, 13728-13739.	4.6	11
1459	Deciphering the Microbiome: Integrating Theory, New Technologies, and Inclusive Science. <i>MSystems</i> , 2022, 7, .	1.7	6
1460	Climate mitigation potential and soil microbial response of cyanobacteria- <i>€</i> fertilized bioenergy crops in a cool semi- <i>€</i> arid cropland. <i>GCB Bioenergy</i> , 2022, 14, 1303-1320.	2.5	2
1461	Comparison of 16S rRNA Gene Primers on Studying Microbial Community Composition in Bottom Water and Sediment of Artificial Reefs in Laoshan Bay, China. <i>Journal of Ocean University of China</i> , 2022, 21, 1313-1322.	0.6	0
1462	Current Challenges and Pitfalls in Soil Metagenomics. <i>Microorganisms</i> , 2022, 10, 1900.	1.6	6
1463	A meta-analysis of acetogenic and methanogenic microbiomes in microbial electrosynthesis. <i>Npj Biofilms and Microbiomes</i> , 2022, 8, .	2.9	6
1464	Biodiversity, environmental drivers, and sustainability of the global deep-sea sponge microbiome. <i>Nature Communications</i> , 2022, 13, .	5.8	21
1465	Review of the Current State of Freely Accessible Web Tools for the Analysis of 16S rRNA Sequencing of the Gut Microbiome. <i>International Journal of Molecular Sciences</i> , 2022, 23, 10865.	1.8	2
1466	Overview of the Nomenclature and Network of Contributors to the Development of Bioreactors for Human Gut Simulation Using Bibliometric Tools: A Fragmented Landscape. <i>Journal of Agricultural and Food Chemistry</i> , 2022, 70, 11458-11467.	2.4	2
1467	Nutrient management and bioaugmentation interactively shape plant- <i>€</i> microbe interactions in <i>Miscanthus</i> - <i>€</i> <i>giganteus</i> . <i>GCB Bioenergy</i> , 2022, 14, 1235-1249.	2.5	6
1468	More than just hitchhikers: a survey of bacterial communities associated with diatoms originating from sea turtles. <i>FEMS Microbiology Ecology</i> , 2022, 98, .	1.3	2
1469	EXPERT: transfer learning-enabled context-aware microbial community classification. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	3

#	ARTICLE	IF	CITATIONS
1470	Microbes Contribute to Chemopreventive Efficacy, Intestinal Tumorigenesis, and the Metabolome. <i>Cancer Prevention Research</i> , 2022, 15, 803-814.	0.7	3
1472	Limited microbiome differences in captive and semi-wild primate populations consuming similar diets. <i>FEMS Microbiology Ecology</i> , 2022, 98, .	1.3	6
1473	Even allocation of benefits stabilizes microbial community engaged in metabolic division of labor. <i>Cell Reports</i> , 2022, 40, 111410.	2.9	19
1474	Antarctic biodiversity predictions through substrate qualities and environmental <scp>DNA</scp>. <i>Frontiers in Ecology and the Environment</i> , 2022, 20, 550-557.	1.9	6
1475	Different Distribution of Core Microbiota in Upper Soil Layer in Two Places of North China Plain. <i>Open Microbiology Journal</i> , 2022, 16, .	0.2	1
1476	The presence of silver nanoparticles reduces demand for dissolved phosphorus to the benefit of biological nitrogen fixation in the coastal eastern Mediterranean Sea. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	2
1477	Source and acquisition of rhizosphere microbes in Antarctic vascular plants. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	6
1478	Complete metamorphosis and microbiota turnover in insects. <i>Molecular Ecology</i> , 2023, 32, 6543-6551.	2.0	10
1479	Effects of source sample amount on biodiversity surveys of bacteria, fungi, and nematodes in soil ecosystems. <i>Frontiers in Ecology and Evolution</i> , 0, 10, .	1.1	2
1480	Concepts and conjectures concerning predatory performance of myxobacteria. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	12
1482	Random sampling associated with microbial profiling leads to overestimated stochasticity inference in community assembly. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
1483	Benchmarking Community-Wide Estimates of Growth Potential from Metagenomes Using Codon Usage Statistics. <i>MSystems</i> , 2022, 7, .	1.7	4
1485	Environmental microbiology going computational “ predictive ecology and unpredicted discoveries. <i>Environmental Microbiology</i> , 0, , .	1.8	1
1488	An ancient respiratory system in the widespread sedimentary archaea Thermopfundales. <i>Molecular Biology and Evolution</i> , 0, , .	3.5	2
1489	Cross-biome metagenomic analyses of the impact of pollutants on taxonomic and functional diversity of bacterial communities from different geographical regions. <i>Gene Reports</i> , 2022, 29, 101690.	0.4	1
1490	The Porifera microeukaryome: Addressing the neglected associations between sponges and protists. <i>Microbiological Research</i> , 2022, 265, 127210.	2.5	3
1491	Applying meta-data of soybean grain in origin trace and quarantine inspection. <i>Food Research International</i> , 2022, 162, 111998.	2.9	2
1492	The Promises, Challenges, and Opportunities of Omics for Studying the Plant Holobiont. <i>Microorganisms</i> , 2022, 10, 1013.	1.6	2

#	ARTICLE	IF	CITATIONS
1493	High-resolution phylogenetic and population genetic analysis of microbial communities with RoC-ITS. ISME Communications, 2022, 2, .	1.7	0
1494	Technology-driven surrogates and the perils of epistemic misalignment: an analysis in contemporary microbiome science. Synthese, 2022, 200, .	0.6	2
1495	PAT: a comprehensive database of prokaryotic antimicrobial toxins. Nucleic Acids Research, 2023, 51, D452-D459.	6.5	3
1496	Screening Salamanders for Symbionts. Methods in Molecular Biology, 2023, , 425-442.	0.4	0
1497	The role of macrophyte-associated microbiomes in lacustrine wetlands: an example of the littoral zone of lake Atitlan, Guatemala. Hydrobiologia, 0, , .	1.0	1
1499	Soil viruses: Understudied agents of soil ecology. Environmental Microbiology, 2023, 25, 143-146.	1.8	7
1500	Helichrysum italicum (Roth) G. Don and Helichrysum arenarium (L.) Moench Infusion Consumption Affects the Inflammatory Status and the Composition of Human Gut Microbiota in Patients with Traits of Metabolic Syndrome: A Randomized Comparative Study. Foods, 2022, 11, 3277.	1.9	3
1502	Deciphering the core seed endo-bacteriome of the highland barley in Tibet plateau. Frontiers in Plant Science, 0, 13, .	1.7	2
1503	Can heavy metal pollution induce soil bacterial community resistance to antibiotics in boreal forests?. Journal of Applied Ecology, 0, , .	1.9	0
1504	Characterization of the GU microbiome in women with self-perceived bladder health over the life course. Neurourology and Urodynamics, 2023, 42, 133-145.	0.8	2
1505	Global airborne bacterial community interactions with Earth's microbiomes and anthropogenic activities. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	29
1506	The Cynomolgus Macaque Intestinal Mycobiont Is Dominated by the Kazachstania Genus and K. pintolopesii Species. Journal of Fungi (Basel, Switzerland), 2022, 8, 1054.	1.5	6
1508	Year-around survey and manipulation experiments reveal differential sensitivities of soil prokaryotic and fungal communities to saltwater intrusion in Florida Everglades wetlands. Science of the Total Environment, 2023, 858, 159865.	3.9	1
1509	Twenty-five years of Genomes OnLine Database (GOLD): data updates and new features in v.9. Nucleic Acids Research, 2023, 51, D957-D963.	6.5	31
1510	Uneven response of microbial communities to intense dust deposition across the coastal transition zone off Mauritania. Frontiers in Marine Science, 0, 9, .	1.2	1
1511	Spatial turnover of soil viral populations and genotypes overlain by cohesive responses to moisture in grasslands. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	27
1512	Microbial communities associated with kelp detritus in temperate and subantarctic intertidal sediments. Science of the Total Environment, 2023, 857, 159392.	3.9	5
1513	Microbiomes. , 2022, , .		0

#	ARTICLE	IF	CITATIONS
1514	Distinct Changes in Abundance of Culturable Microbial Community and Respiration Activities in Response to Mineralâ€“Organic Mixture Application in Contaminated Soil. Sustainability, 2022, 14, 15004.	1.6	1
1515	Diet-derived metabolites and mucus link the gut microbiome to fever after cytotoxic cancer treatment. Science Translational Medicine, 2022, 14, .	5.8	13
1516	Longitudinal analysis of the Five Sisters hot springs in Yellowstone National Park reveals a dynamic thermoalkaline environment. Scientific Reports, 2022, 12, .	1.6	4
1518	Steelhead trout ( <i>Oncorhynchus mykiss</i> ) fed probiotic during the earliest developmental stages have enhanced growth rates and intestinal microbiome bacterial diversity. Frontiers in Marine Science, 0, 9, .	1.2	5
1519	Decrypting phytomicrobiome of the neurotoxic actinorhizal species, <i>Coriaria myrtifolia</i> , and dispersal boundary of <i>Frankia</i> cluster 2 in soil outward compatible host rhizosphere. Frontiers in Microbiology, 0, 13, .	1.5	2
1520	High throughput method of 16S rRNA gene sequencing library preparation for plant root microbial community profiling. Scientific Reports, 2022, 12, .	1.6	2
1521	Principles for quorum sensing-based exogeneous denitrifier enhancement of nitrogen removal in biofilm: a review. Critical Reviews in Environmental Science and Technology, 2023, 53, 1404-1429.	6.6	3
1522	Anaerobic Fermentation of Silage from the Above-Ground Biomass of Jerusalem Artichoke ( <i>Helianthus</i> ) Tj ETQq1 1 0.784314 rgBT /Over Production. Applied Sciences (Switzerland), 2022, 12, 11417.	1.3	1
1523	Mineralogy affects prokaryotic community composition in an acidic metal mine. Microbiological Research, 2023, 266, 127257.	2.5	3
1524	The bacteriome of the halophyte <i>Atriplex nummularia</i> (old man saltbush) in salt-affected soils - an ecological model. FEMS Microbiology Ecology, 2022, 98, .	1.3	2
1525	Host biology, ecology and the environment influence microbial biomass and diversity in 101 marine fish species. Nature Communications, 2022, 13, .	5.8	21
1526	&lt;b&gt;Evaluation of Environmental Hygiene in Railway Vehicles Using Microbiome Analysis&lt;/b&gt;. Quarterly Report of RTRI (Railway Technical Research Institute) (Japan), 2022, 63, 283-288.	0.1	1
1527	The Kitty Microbiome Project: Defining the Healthy Fecal â€œCore Microbiomeâ€“in Pet Domestic Cats. Veterinary Sciences, 2022, 9, 635.	0.6	6
1528	Dietary lead modulates the mouse intestinal microbiome: Subacute exposure to lead acetate and lead contaminated soil. Ecotoxicology and Environmental Safety, 2023, 249, 114430.	2.9	4
1529	Presence and distribution of triazine herbicides and their effects on microbial communities in the Laizhou Bay, Northern China. Marine Pollution Bulletin, 2023, 186, 114460.	2.3	7
1530	Universal drivers of cheese microbiomes. IScience, 2023, 26, 105744.	1.9	3
1531	A core epiphytic bacterial consortia synergistically protect citrus from postharvest disease. Food Chemistry, 2023, 407, 135103.	4.2	5
1532	Distinct distribution patterns of the abundant and rare bacteria in high plateau hot spring sediments. Science of the Total Environment, 2023, 863, 160832.	3.9	2

#	ARTICLE	IF	CITATIONS
1534	Latent functional diversity may accelerate microbial community responses to temperature fluctuations. <i>ELife</i> , 0, 11, .	2.8	5
1535	Standardized multi-omics of Earth's microbiomes reveals microbial and metabolite diversity. <i>Nature Microbiology</i> , 2022, 7, 2128-2150.	5.9	48
1536	Gut microbiota suppress feeding induced by palatable foods. <i>Current Biology</i> , 2023, 33, 147-157.e7.	1.8	10
1537	proGenomes3: approaching one million accurately and consistently annotated high-quality prokaryotic genomes. <i>Nucleic Acids Research</i> , 2023, 51, D760-D766.	6.5	15
1538	Microbial infection risk predicts antimicrobial potential of avian symbionts. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
1539	Bioinformatic Approaches for Describing the Oral Microbiota. <i>Methods in Molecular Biology</i> , 2023, , 105-130.	0.4	0
1541	Assessing aerobic biotransformation of 8:2 fluorotelomer alcohol in aqueous film-forming foam (AFFF)-impacted soils: Pathways and microbial community dynamics. <i>Journal of Hazardous Materials</i> , 2023, 446, 130629.	6.5	6
1542	A Reproducible and Tunable Synthetic Soil Microbial Community Provides New Insights into Microbial Ecology. <i>MSystems</i> , 2022, 7, .	1.7	12
1543	Metabarcoding Approaches for Soil Eukaryotes, Protists, and Microfauna. <i>Methods in Molecular Biology</i> , 2023, , 1-16.	0.4	2
1546	Reply to: Erroneous predictions of auxotrophies by CarveMe. <i>Nature Ecology and Evolution</i> , 0, , .	3.4	0
1547	Global Distribution of Carbohydrate Utilization Potential in the Prokaryotic Tree of Life. <i>MSystems</i> , 2022, 7, .	1.7	7
1548	Alterations in the cutaneous microbiome of patients with psoriasis and psoriatic arthritis reveal similarities between non-lesional and lesional skin. <i>Annals of the Rheumatic Diseases</i> , 2023, 82, 507-514.	0.5	6
1549	Î²-Carotene suppresses cancer cachexia by regulating the adipose tissue metabolism and gut microbiota dysregulation. <i>Journal of Nutritional Biochemistry</i> , 2023, 114, 109248.	1.9	1
1550	Let's end taxonomic blank slates with molecular morphology. <i>Frontiers in Ecology and Evolution</i> , 0, 10, .	1.1	2
1551	Healthy dietary patterns are associated with the gut microbiome in the Hispanic Community Health Study/Study of Latinos. <i>American Journal of Clinical Nutrition</i> , 2023, 117, 540-552.	2.2	7
1553	Estimate of the degradation potentials of cellulose, xylan, and chitin across global prokaryotic communities. <i>Environmental Microbiology</i> , 2023, 25, 397-409.	1.8	2
1554	Soil Microbial Biochemical Activity and Influence of Climate Change. <i>Climate Change Management</i> , 2023, , 137-155.	0.6	0
1555	The need for an integrated multi-OMICS approach in microbiome science in the food system. <i>Comprehensive Reviews in Food Science and Food Safety</i> , 2023, 22, 1082-1103.	5.9	12

#	ARTICLE	IF	CITATIONS
1557	A minimum suite of soil health indicators for North American agriculture. <i>Soil Security</i> , 2023, 10, 100084.	1.2	19
1558	Integrating pH into the metabolic theory of ecology to predict bacterial diversity in soil. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	3.3	17
1560	Ecological insights into soil health according to the genomic traits and environment-wide associations of bacteria in agricultural soils. <i>ISME Communications</i> , 2023, 3, .	1.7	12
1561	Soil Microbial Community and Climate Change Drivers. <i>Climate Change Management</i> , 2023, , 111-120.	0.6	1
1562	Origins of scaling laws in microbial dynamics. <i>Physical Review Research</i> , 2023, 5, .	1.3	2
1563	Cell-cell metabolite exchange creates a pro-survival metabolic environment that extends lifespan. <i>Cell</i> , 2023, 186, 63-79.e21.	13.5	14
1565	Capturing marine microbiomes and environmental DNA: A field sampling guide. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	6
1566	<i>Streptomyces</i> development is involved in the efficient containment of viral infections. <i>MicroLife</i> , 2023, 4, .	1.0	8
1567	Change and stasis of distinct sediment microbiomes across Port Everglades Inlet (PEI) and the adjacent coral reefs. <i>PeerJ</i> , 0, 11, e14288.	0.9	2
1568	Current Progress of Bioinformatics for Human Health. <i>Translational Bioinformatics</i> , 2023, , 145-162.	0.0	0
1569	Adverse impacts of Roundup on soil bacteria, soil chemistry and mycorrhizal fungi during restoration of a Colorado grassland. <i>Applied Soil Ecology</i> , 2023, 185, 104778.	2.1	4
1570	Long-Term Manure Amendment Sustains Black Soil Biodiversity by Mitigating Acidification Induced by Chemical N Fertilization. <i>Microorganisms</i> , 2023, 11, 64.	1.6	2
1571	Functional metagenomics profiling of symbiotic microbiome. , 2023, , 691-713.		1
1572	Thermal acclimation of methanotrophs from the genus <i>Methylobacter</i> . <i>ISME Journal</i> , 2023, 17, 502-513.	4.4	4
1573	Omnicrobe, an open-access database of microbial habitats and phenotypes using a comprehensive text mining and data fusion approach. <i>PLoS ONE</i> , 2023, 18, e0272473.	1.1	1
1574	Comprehensive evaluation of shotgun metagenomics, amplicon sequencing, and harmonization of these platforms for epidemiological studies. <i>Cell Reports Methods</i> , 2023, 3, 100391.	1.4	5
1575	How does heat stress affect sponge microbiomes? Structure and resilience of microbial communities of marine sponges from different habitats. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	5
1576	Local-scale soil nematode diversity in a subtropical forest depends on the phylogenetic and functional diversity of neighbor trees. <i>Plant and Soil</i> , 0, , .	1.8	0

#	ARTICLE	IF	CITATIONS
1577	Bacterial diversity in the aquatic system in India based on metagenome analysis—a critical review. <i>Environmental Science and Pollution Research</i> , 2023, 30, 28383-28406.	2.7	2
1579	Status of urban ecology in Africa: A systematic review. <i>Landscape and Urban Planning</i> , 2023, 233, 104707.	3.4	6
1580	Best practice for wildlife gut microbiome research: A comprehensive review of methodology for 16S rRNA gene investigations. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	5
1581	Metabarcoding inventory of an arctic tundra soil ecosystem reveals highly heterogeneous communities at a small scale. <i>Polar Biology</i> , 2023, 46, 461-471.	0.5	2
1582	Contribution of soil bacteria to the atmosphere across biomes. <i>Science of the Total Environment</i> , 2023, 871, 162137.	3.9	3
1583	Decoding dissolved information: environmental DNA sequencing at global scale to monitor a changing ocean. <i>Current Opinion in Biotechnology</i> , 2023, 81, 102936.	3.3	5
1585	Indoor Microbiome and The Rising Asthma Prevalence. <i>EMJ Microbiology &amp; Infectious Diseases</i> , 0, , 51-56.	0.0	0
1586	The Molecular Effect of Wearing Silver-Threaded Clothing on the Human Skin. <i>MSystems</i> , 2023, 8, .	1.7	1
1587	Metagenomic Analysis of the Abundance and Composition of Antibiotic Resistance Genes in Hospital Wastewater in Benin, Burkina Faso, and Finland. <i>MSphere</i> , 2023, 8, .	1.3	11
1588	An Environmental DNA Primer for Microbial and Restoration Ecology. <i>Microbial Ecology</i> , 0, , .	1.4	3
1589	Host phylogeny and functional traits differentiate gut microbiomes in a diverse natural community of small mammals. <i>Molecular Ecology</i> , 2023, 32, 2320-2334.	2.0	3
1590	Will free-living microbial community composition drive biogeochemical responses to global change?. <i>Biogeochemistry</i> , 2023, 162, 285-307.	1.7	2
1592	Diverse Microbial Hot Spring Mat Communities at Black Canyon of the Colorado River. <i>Microbial Ecology</i> , 0, , .	1.4	1
1594	Cloacal microbiota are biogeographically structured in larks from desert, tropical and temperate areas. <i>BMC Microbiology</i> , 2023, 23, .	1.3	0
1595	Environmental DNA metabarcoding reveals the influence of human activities on microeukaryotic plankton along the Chinese coastline. <i>Water Research</i> , 2023, 233, 119730.	5.3	12
1597	Can Satellite Remote Sensing Assist in the Characterization of Yeasts Related to Biogeographical Origin?. <i>Sensors</i> , 2023, 23, 2059.	2.1	1
1598	Transmission mode and dispersal traits correlate with host specificity in mammalian gut microbes. <i>Molecular Ecology</i> , 2024, 33, .	2.0	6
1599	Plasma, urine, and stool metabolites in response to dietary rice bran and navy bean supplementation in adults at high-risk for colorectal cancer. , 0, 2, .		2



#	ARTICLE	IF	CITATIONS
1600	Small Spatial Scale Drivers of Secondary Metabolite Biosynthetic Diversity in Environmental Microbiomes. <i>MSystems</i> , 0, , .	1.7	1
1601	Optimization of Molecular Methods for Detecting Duckweed-Associated Bacteria. <i>Plants</i> , 2023, 12, 872.	1.6	2
1602	Reliability of species detection in 16S microbiome analysis: Comparison of five widely used pipelines and recommendations for a more standardized approach. <i>PLoS ONE</i> , 2023, 18, e0280870.	1.1	6
1603	Unravelling microalgal-bacterial interactions in aquatic ecosystems through 16S rRNA gene-based co-occurrence networks. <i>Scientific Reports</i> , 2023, 13, .	1.6	8
1604	Insights into the Methodological, Biotic and Abiotic Factors Influencing the Characterization of Xylem-Inhabiting Microbial Communities of Olive Trees. <i>Plants</i> , 2023, 12, 912.	1.6	5
1605	Diversity of protist genera in periphyton of tufa-depositing karstic river. <i>Annals of Microbiology</i> , 2023, 73, .	1.1	0
1606	Microbiome response in an urban river system is dominated by seasonality over wastewater treatment upgrades. <i>Environmental Microbiomes</i> , 2023, 18, .	2.2	0
1607	Strong restructuration of skin microbiota during captivity challenges ex-situ conservation of amphibians. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
1608	Diversity of Microbial Communities, PAHs, and Metals in Road and Leaf Dust of Functional Zones of Moscow and Murmansk. <i>Microorganisms</i> , 2023, 11, 526.	1.6	1
1609	Effect of fabric mulch ground covers on lemon trees rhizosphere microbiome in Florida flatwood soils. <i>Frontiers in Soil Science</i> , 0, 3, .	0.8	1
1610	The Impact of IMTA on the Spatial and Temporal Distribution of the Surface Planktonic Bacteria Community in the Surrounding Sea Area of Xiasanhengshan Island of the East China Sea. <i>Journal of Marine Science and Engineering</i> , 2023, 11, 476.	1.2	5
1611	Fine-scale evaluation of two standard 16S rRNA gene amplicon primer pairs for analysis of total prokaryotes and archaeal nitrifiers in differently managed soils. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	2
1612	Getting to the root of tree soil microbiome sampling. <i>Phytobiomes Journal</i> , 0, , .	1.4	0
1613	Knowledge Gaps, Research Needs, and Opportunities in Plant Disease Diagnostics Assay Development and Validation. <i>PhytoFrontiers</i> , 0, , .	0.8	2
1614	Microbial Virulence Factors, Antimicrobial Resistance Genes, Metabolites, and Synthetic Chemicals in Cabins of Commercial Aircraft. <i>Metabolites</i> , 2023, 13, 343.	1.3	1
1615	<sc>Prenatal</sc> household size and composition are associated with infant fecal bacterial diversity in <sc>C</sc>ebu, <sc>P</sc>hilippines. <i>American Journal of Biological Anthropology</i> , 2023, 181, 45-58.	0.6	2
1616	<tt>SCRAPT:</tt>an iterative algorithm for clustering large 16S rRNA gene data sets. <i>Nucleic Acids Research</i> , 0, , .	6.5	0
1617	Exploring Microbial Diversity of Arid Regions of Globe for Agricultural Sustainability: A Revisit. , 2023, , 1-25.		0

#	ARTICLE	IF	CITATIONS
1618	Analysis of an Indian colorectal cancer faecal microbiome collection demonstrates universal colorectal cancer-associated patterns, but closest correlation with other Indian cohorts. <i>BMC Microbiology</i> , 2023, 23, .	1.3	0
1619	Australian soil microbiome: A first sightseeing regional prediction driven by cycles of soil temperature and pedogenic variations. <i>Molecular Ecology</i> , 2023, 32, 6243-6259.	2.0	5
1620	Polybacterial shift in benthic river biofilms attributed to organic pollution – a prospect of a new biosentinel?. <i>Hydrology Research</i> , 2023, 54, 348-359.	1.1	1
1621	Exploring microbial functional biodiversity at the protein family level – From metagenomic sequence reads to annotated protein clusters. <i>Frontiers in Bioinformatics</i> , 0, 3, .	1.0	2
1625	Association of the gut microbiome with kidney function and damage in the Hispanic Community Health Study/Study of Latinos (HCHS/SOL). <i>Gut Microbes</i> , 2023, 15, .	4.3	3
1627	Integrated multiomic wastewater-based epidemiology can elucidate population-level dietary behaviour and inform public health nutrition assessments. <i>Nature Food</i> , 2023, 4, 257-266.	6.2	4
1628	Uncovering Bacterial Hosts of Class 1 Integrons in an Urban Coastal Aquatic Environment with a Single-Cell Fusion-Polymerase Chain Reaction Technology. <i>Environmental Science &amp; Technology</i> , 2023, 57, 4870-4879.	4.6	3
1629	Microbiota metabolites in the female reproductive system: Focused on the short-chain fatty acids. <i>Heliyon</i> , 2023, 9, e14562.	1.4	6
1631	Temporal dynamics of geothermal microbial communities in Aotearoa-New Zealand. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
1633	Hyperactive nanobacteria with host-dependent traits pervade Omnitrophota. <i>Nature Microbiology</i> , 2023, 8, 727-744.	5.9	9
1634	Spatial profiling of microbial communities by sequential FISH with error-robust encoding. <i>Nature Communications</i> , 2023, 14, .	5.8	12
1635	Garden soil bacteria transiently colonize gardeners' skin after direct soil contact. <i>Urban Agriculture &amp; Regional Food Systems</i> , 2023, 8, .	0.6	1
1636	The analysis of gut microbiota in patients with bile acid diarrhoea treated with colesevelam. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	2
1637	The biogeography of host-associated bacterial microbiomes: Revisiting classic biodiversity patterns. <i>Global Ecology and Biogeography</i> , 2023, 32, 931-944.	2.7	6
1639	More is Different: Metabolic Modeling of Diverse Microbial Communities. <i>MSystems</i> , 2023, 8, .	1.7	4
1641	Differences in gut bacterial community composition between modern and slower-growing broiler breeder lines: Implications of growth selection on microbiome composition. <i>Frontiers in Physiology</i> , 0, 14, .	1.3	0
1642	Flex Meta-Storms elucidates the microbiome local beta-diversity under specific phenotypes. <i>Bioinformatics</i> , 2023, 39, .	1.8	2
1643	Realising respiratory microbiomic meta-analyses: time for a standardised framework. <i>Microbiome</i> , 2023, 11, .	4.9	5

#	ARTICLE	IF	CITATIONS
1644	Diversity and function of methyl-coenzyme M reductase-encoding archaea in Yellowstone hot springs revealed by metagenomics and mesocosm experiments. <i>ISME Communications</i> , 2023, 3, .	1.7	10
1646	The contrasting effects of fluctuating temperature on bacterial diversity and performances in temperate and subtropical soils. <i>Molecular Ecology</i> , 2023, 32, 3686-3701.	2.0	0
1647	Forest microbiome and global change. <i>Nature Reviews Microbiology</i> , 2023, 21, 487-501.	13.6	33
1648	Mock community as an in situ positive control for amplicon sequencing of microbiotas from the same ecosystem. <i>Scientific Reports</i> , 2023, 13, .	1.6	2
1649	Systematic Evaluation of the Viable Microbiome in the Human Oral and Gut Samples with Spike-in Gram+/â€“ Bacteria. <i>MSystems</i> , 2023, 8, .	1.7	4
1650	The microbial dark matter and â€œwanted listâ€•in worldwide wastewater treatment plants. <i>Microbiome</i> , 2023, 11, .	4.9	10
1651	Testing the stress gradient hypothesis in soil bacterial communities associated with vegetation belts in the Andean Atacama Desert. <i>Environmental Microbiomes</i> , 2023, 18, .	2.2	3
1652	Reducing bias in microbiome research: Comparing methods from sample collection to sequencing. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
1653	Neotropical Frog Foam Nestâ€™s Microbiomes. <i>Microorganisms</i> , 2023, 11, 900.	1.6	0
1654	Soil depth and geographic distance modulate bacterial Î²â€™diversity in deep soil profiles throughout the U.S. Corn Belt. <i>Molecular Ecology</i> , 2023, 32, 3718-3732.	2.0	2
1656	Composition and function of the Galapagos penguin gut microbiome vary with age, location, and a putative bacterial pathogen. <i>Scientific Reports</i> , 2023, 13, .	1.6	5
1657	A social niche breadth score reveals niche range strategies of generalists and specialists. <i>Nature Ecology and Evolution</i> , 2023, 7, 768-781.	3.4	15
1658	Big Data for a Small World: A Review on Databases and Resources for Studying Microbiomes. <i>Journal of the Indian Institute of Science</i> , 0, , .	0.9	2
1659	Evolving approaches to profiling the microbiome in skin disease. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	4
1660	Selecting 16S rRNA Primers for Microbiome Analysis in a Hostâ€™Microbe System: The Case of the Jellyfish <i>Rhopilema nomadica</i> . <i>Microorganisms</i> , 2023, 11, 955.	1.6	2
1662	Microbiome-based enrichment pattern mining has enabled a deeper understanding of the biomeâ€™speciesâ€™function relationship. <i>Communications Biology</i> , 2023, 6, .	2.0	0
1663	Body Size Poorly Predicts Host-Associated Microbial Diversity in Wild Birds. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	3
1664	Gut Microbiota Dysbiosis in Suspected Food Protein Induced Proctocolitisâ€™A Prospective Comparative Cohort Trial. <i>Journal of Pediatric Gastroenterology and Nutrition</i> , 2023, 77, 31-38.	0.9	2

#	ARTICLE	IF	CITATIONS
1665	Thermophilic <i>Dehalococcoidia</i> with unusual traits shed light on an unexpected past. ISME Journal, 2023, 17, 952-966.	4.4	5
1666	More Than Dirt: Soil Health Needs to Be Emphasized in Stream and Floodplain Restorations. Soil Systems, 2023, 7, 36.	1.0	2
1668	A lncRNA from an inflammatory bowel disease risk locus maintains intestinal host-commensal homeostasis. Cell Research, 2023, 33, 372-388.	5.7	4
1669	Network Model with Scale-Free, High Clustering Coefficients, and Small-World Properties. Journal of Applied Mathematics, 2023, 2023, 1-11.	0.4	1
1671	Reconstructing the landscape of gut microbial species across 29,000 diverse individuals. Nucleic Acids Research, 0, , .	6.5	0
1672	Maternal Bacterial Engraftment in Multiple Body Sites of Cesarean Section Born Neonates after Vaginal Seeding—a Randomized Controlled Trial. MBio, 2023, 14, .	1.8	7
1673	Challenges for Plant Growth Promoting Microorganism Transfer from Science to Industry: A Case Study from Chile. Microorganisms, 2023, 11, 1061.	1.6	1
1674	SAG-RAD: A Method for Single-Cell Population Genomics of Unicellular Eukaryotes. Molecular Biology and Evolution, 2023, 40, .	3.5	2
1684	Mushroom Metagenome: Tool to Unravel Interaction Network of Plant, Mycorrhiza, and Bacteria. Rhizosphere Biology, 2023, , 497-520.	0.4	0
1698	Species-specific relationships between deep sea sponges and their symbiotic <i>Nitrosopumilaceae</i> . ISME Journal, 2023, 17, 1517-1519.	4.4	1
1717	Microbial applications for sustainable space exploration beyond low Earth orbit. Npj Microgravity, 2023, 9, .	1.9	7
1727	Island Digital Ecosystem Avatars (IDEA) Consortium: Infrastructure for Democratic Ecological Action. Social and Ecological Interactions in the Galapagos Islands, 2023, , 439-452.	0.4	0
1730	Basic Data Processing in QIIME 2. , 2023, , 65-94.		0
1745	Microbiomic Profiling of Food Processing Environments and Foods for Food Safety and Quality. , 2024, , 335-347.		0
1751	Microorganisms, climate change, and the Sustainable Development Goals: progress and challenges. Nature Reviews Microbiology, 2023, 21, 622-623.	13.6	2
1790	Global Fungal Diversity Estimated from High-Throughput Sequencing. , 2023, , 227-238.		0
1796	Challenges and opportunities in sharing microbiome data and analyses. Nature Microbiology, 2023, 8, 1960-1970.	5.9	5
1811	Microbiome biodiversity—current advancement and applications. , 2023, , 143-165.		0

#	ARTICLE	IF	CITATIONS
1835	Soil microbiome engineering for sustainability in a changing environment. <i>Nature Biotechnology</i> , 2023, 41, 1716-1728.	9.4	6
1839	A global catalogue of plant-beneficial bacteria. <i>Nature Food</i> , 2023, 4, 933-934.	6.2	0
1857	Responses of Soil Bacterial Communities to Invasive Australian <i>Acacia</i> Species Over Large Spatial Scales. , 2023, , 382-398.		0
1870	Bacterial and Archaeal DNA from Lake Sediments. <i>Developments in Paleoenvironmental Research</i> , 2023, , 85-151.	7.5	0
1890	One Health Perspectives for Addressing Antimicrobial Resistance. , 2024, , 1-21.		0
1897	Possible solutions for the conservation of benthic habitats and organisms. , 2024, , 191-236.		0
1899	Soil bacteria and archaea. , 2024, , 41-74.		0
1901	Multiple approaches to understanding the benthos. , 2024, , 75-130.		0
1921	Host-pathogen interactions with special reference to microbiota analysis and integration of systems biology approaches. , 2024, , 191-211.		0
1924	Use Cases and Future Aspects of Intelligent Techniques in Microbial Data Analysis. <i>Microorganisms for Sustainability</i> , 2024, , 259-280.	0.4	0