

Unusual biology across a group comprising more than 1

Nature

523, 208-211

DOI: [10.1038/nature14486](https://doi.org/10.1038/nature14486)

Citation Report

#	ARTICLE	IF	CITATIONS
2	Metagenome-assembled genomes uncover a global brackish microbiome. <i>Genome Biology</i> , 2015, 16, 279.	3.8	186
3	Back to Basics – The Influence of DNA Extraction and Primer Choice on Phylogenetic Analysis of Activated Sludge Communities. <i>PLoS ONE</i> , 2015, 10, e0132783.	1.1	437
4	Prediction of microbial phenotypes based on comparative genomics. <i>BMC Bioinformatics</i> , 2015, 16, S1.	1.2	38
5	Evaluation of shotgun metagenomics sequence classification methods using in silico and in vitro simulated communities. <i>BMC Bioinformatics</i> , 2015, 16, 363.	1.2	145
6	Highly divergent ancient gene families in metagenomic samples are compatible with additional divisions of life. <i>Biology Direct</i> , 2015, 10, 64.	1.9	14
7	Shedding light on microbial dark matter: a <i>TM6</i> bacterium as natural endosymbiont of a free-living amoeba. <i>Environmental Microbiology Reports</i> , 2015, 7, 970-978.	1.0	48
8	Small genomes and the difficulty to define minimal translation and metabolic machineries. <i>Frontiers in Ecology and Evolution</i> , 2015, 3, .	1.1	9
9	Groundwater Isolation Governs Chemistry and Microbial Community Structure along Hydrologic Flowpaths. <i>Frontiers in Microbiology</i> , 2015, 6, 1457.	1.5	93
10	Insights into the life of an oxygenic phototroph. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 14747-14748.	3.3	1
12	Mechanosensitive channel MSL8 regulates osmotic forces during pollen hydration and germination. <i>Science</i> , 2015, 350, 438-441.	6.0	184
13	Ten Years of Maintaining and Expanding a Microbial Genome and Metagenome Analysis System. <i>Trends in Microbiology</i> , 2015, 23, 730-741.	3.5	20
14	Methane metabolism in the archaeal phylum Bathyarchaeota revealed by genome-centric metagenomics. <i>Science</i> , 2015, 350, 434-438.	6.0	677
15	Beyond known methanogens. <i>Science</i> , 2015, 350, 384-384.	6.0	17
16	Microbial Malaise: How Can We Classify the Microbiome?. <i>Trends in Microbiology</i> , 2015, 23, 671-679.	3.5	36
18	From cultured to uncultured genome sequences: metagenomics and modeling microbial ecosystems. <i>Cellular and Molecular Life Sciences</i> , 2015, 72, 4287-4308.	2.4	114
19	Twenty years of bacterial genome sequencing. <i>Nature Reviews Microbiology</i> , 2015, 13, 787-794.	13.6	246
20	Snowmelt Induced Hydrologic Perturbations Drive Dynamic Microbiological and Geochemical Behaviors across a Shallow Riparian Aquifer. <i>Frontiers in Earth Science</i> , 2016, 4, .	0.8	24
21	Protist-Bacteria Associations: Gammaproteobacteria and Alphaproteobacteria Are Prevalent as Digestion-Resistant Bacteria in Ciliated Protozoa. <i>Frontiers in Microbiology</i> , 2016, 7, 498.	1.5	88

#	ARTICLE	IF	CITATIONS
22	Carbon and Sulfur Cycling below the Chemocline in a Meromictic Lake and the Identification of a Novel Taxonomic Lineage in the FCB Superphylum, Candidatus Aegiribacteria. <i>Frontiers in Microbiology</i> , 2016, 7, 598.	1.5	51
23	Single-Cell (Meta-)Genomics of a Dimorphic Candidatus <i>Thiomargarita nelsonii</i> Reveals Genomic Plasticity. <i>Frontiers in Microbiology</i> , 2016, 7, 603.	1.5	36
24	Co-occurrence Analysis of Microbial Taxa in the Atlantic Ocean Reveals High Connectivity in the Free-Living Bacterioplankton. <i>Frontiers in Microbiology</i> , 2016, 7, 649.	1.5	152
25	Large Differences in Bacterial Community Composition among Three Nearby Extreme Waterbodies of the High Andean Plateau. <i>Frontiers in Microbiology</i> , 2016, 7, 976.	1.5	54
26	Bacterial Active Community Cycling in Response to Solar Radiation and Their Influence on Nutrient Changes in a High-Altitude Wetland. <i>Frontiers in Microbiology</i> , 2016, 7, 1823.	1.5	43
27	Genomic and Transcriptomic Evidence for Carbohydrate Consumption among Microorganisms in a Cold Seep Brine Pool. <i>Frontiers in Microbiology</i> , 2016, 7, 1825.	1.5	29
28	Molecular Ecology of Hypersaline Microbial Mats: Current Insights and New Directions. <i>Microorganisms</i> , 2016, 4, 6.	1.6	43
29	Molecular Approaches to Studying Microbial Communities: Targeting the 16S Ribosomal RNA Gene. <i>Journal of UOEH</i> , 2016, 38, 223-232.	0.3	39
30	Genome-centric resolution of microbial diversity, metabolism and interactions in anaerobic digestion. <i>Environmental Microbiology</i> , 2016, 18, 3144-3158.	1.8	123
31	Genomic and metagenomic challenges and opportunities for bioleaching: a mini-review. <i>Research in Microbiology</i> , 2016, 167, 529-538.	1.0	61
32	Enhancing metaproteomics – The value of models and defined environmental microbial systems. <i>Proteomics</i> , 2016, 16, 783-798.	1.3	62
33	Functional metagenomic selection of ribulose 1, 5-bisphosphate carboxylase/oxygenase from uncultivated bacteria. <i>Environmental Microbiology</i> , 2016, 18, 1187-1199.	1.8	26
34	Reconstructing single genomes from complex microbial communities. <i>IT - Information Technology</i> , 2016, 58, 133-139.	0.6	7
35	ConsPred: a rule-based (re-)annotation framework for prokaryotic genomes. <i>Bioinformatics</i> , 2016, 32, 3327-3329.	1.8	10
36	Cultivating microbial dark matter in benzene-degrading methanogenic consortia. <i>Environmental Microbiology</i> , 2016, 18, 2923-2936.	1.8	54
37	HydDB: A web tool for hydrogenase classification and analysis. <i>Scientific Reports</i> , 2016, 6, 34212.	1.6	372
38	Genomics-informed isolation and characterization of a symbiotic Nanoarchaeota system from a terrestrial geothermal environment. <i>Nature Communications</i> , 2016, 7, 12115.	5.8	154
39	Direct 16S rRNA-seq from bacterial communities: a PCR-independent approach to simultaneously assess microbial diversity and functional activity potential of each taxon. <i>Scientific Reports</i> , 2016, 6, 32165.	1.6	90

#	ARTICLE	IF	CITATIONS
40	From Genomes to Phenotypes: Traitair, the Microbial Trait Analyzer. <i>MSystems</i> , 2016, 1, .	1.7	102
41	A catalogue of 136 microbial draft genomes from Red Sea metagenomes. <i>Scientific Data</i> , 2016, 3, 160050.	2.4	47
42	Genomic insights into members of the candidate phylum Hyd24-12 common in mesophilic anaerobic digesters. <i>ISME Journal</i> , 2016, 10, 2352-2364.	4.4	62
43	Toward a Predictive Understanding of Earth's Microbiomes to Address 21st Century Challenges. <i>MBio</i> , 2016, 7, .	1.8	124
44	Genome-Resolved Metagenomic Analysis Reveals Roles for Candidate Phyla and Other Microbial Community Members in Biogeochemical Transformations in Oil Reservoirs. <i>MBio</i> , 2016, 7, e01669-15.	1.8	151
45	Permafrost Meta-Omics and Climate Change. <i>Annual Review of Earth and Planetary Sciences</i> , 2016, 44, 439-462.	4.6	82
46	High definition for systems biology of microbial communities: metagenomics gets genome-centric and strain-resolved. <i>Current Opinion in Biotechnology</i> , 2016, 39, 174-181.	3.3	30
47	Scaling laws predict global microbial diversity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 5970-5975.	3.3	857
48	MeCorS: Metagenome-enabled error correction of single cell sequencing reads. <i>Bioinformatics</i> , 2016, 32, 2199-2201.	1.8	8
49	Geomicrobiology and Metagenomics of Terrestrial Deep Subsurface Microbiomes. <i>Advances in Applied Microbiology</i> , 2016, 94, 1-77.	1.3	47
50	Microbial Metagenomics Reveals Climate-Relevant Subsurface Biogeochemical Processes. <i>Trends in Microbiology</i> , 2016, 24, 600-610.	3.5	35
51	RubisCO of a nucleoside pathway known from Archaea is found in diverse uncultivated phyla in bacteria. <i>ISME Journal</i> , 2016, 10, 2702-2714.	4.4	98
52	Their World: A Diversity of Microbial Environments. <i>Advances in Environmental Microbiology</i> , 2016, , .	0.1	10
53	Microbes and the Arctic Ocean. <i>Advances in Environmental Microbiology</i> , 2016, , 341-381.	0.1	5
54	Metagenomic analysis of rapid gravity sand filter microbial communities suggests novel physiology of <i>Nitrospira</i> spp.. <i>ISME Journal</i> , 2016, 10, 2569-2581.	4.4	213
55	Microbiology: the road to strain-level identification. <i>Nature Methods</i> , 2016, 13, 401-404.	9.0	34
56	Bipartite graph analyses reveal interdomain LGT involving ultrasmall prokaryotes and their divergent, membrane-related proteins. <i>Environmental Microbiology</i> , 2016, 18, 5072-5081.	1.8	12
57	Grad-seq guides the discovery of ProQ as a major small RNA-binding protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 11591-11596.	3.3	267

#	ARTICLE	IF	CITATIONS
58	The changing view of eukaryogenesis – fossils, cells, lineages and how they all come together. <i>Journal of Cell Science</i> , 2016, 129, 3695-3703.	1.2	77
59	Microbial bioinformatics 2020. <i>Microbial Biotechnology</i> , 2016, 9, 681-686.	2.0	16
60	Metagenomic signatures of a tropical mining-impacted stream reveal complex microbial and metabolic networks. <i>Chemosphere</i> , 2016, 161, 266-273.	4.2	39
61	Metagenomics and Bioinformatics in Microbial Ecology: Current Status and Beyond. <i>Microbes and Environments</i> , 2016, 31, 204-212.	0.7	76
62	Systematic improvement of amplicon marker gene methods for increased accuracy in microbiome studies. <i>Nature Biotechnology</i> , 2016, 34, 942-949.	9.4	623
63	MetaG: a graph-based metagenomic gene analysis for big DNA data. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2016, 5, 1.	1.2	7
64	The Modern Synthesis in the Light of Microbial Genomics. <i>Annual Review of Microbiology</i> , 2016, 70, 279-297.	2.9	58
65	Uncovering oral <i>Neisseria</i> tropism and persistence using metagenomic sequencing. <i>Nature Microbiology</i> , 2016, 1, 16070.	5.9	68
66	Shedding light on cell compartmentation in the candidate phylum Poribacteria by high resolution visualisation and transcriptional profiling. <i>Scientific Reports</i> , 2016, 6, 35860.	1.6	31
67	Genome-based microbial ecology of anammox granules in a full-scale wastewater treatment system. <i>Nature Communications</i> , 2016, 7, 11172.	5.8	373
68	Measurement of bacterial replication rates in microbial communities. <i>Nature Biotechnology</i> , 2016, 34, 1256-1263.	9.4	342
69	Thousands of microbial genomes shed light on interconnected biogeochemical processes in an aquifer system. <i>Nature Communications</i> , 2016, 7, 13219.	5.8	994
70	Microbial metabolisms in a 2.5-km-deep ecosystem created by hydraulic fracturing in shales. <i>Nature Microbiology</i> , 2016, 1, 16146.	5.9	207
71	Metagenomics uncovers gaps in amplicon-based detection of microbial diversity. <i>Nature Microbiology</i> , 2016, 1, 15032.	5.9	207
72	A new view of the tree of life. <i>Nature Microbiology</i> , 2016, 1, 16048.	5.9	1,823
73	The Underestimation of Global Microbial Diversity. <i>MBio</i> , 2016, 7, .	1.8	23
74	Single sample resolution of rare microbial dark matter in a marine invertebrate metagenome. <i>Scientific Reports</i> , 2016, 6, 34362.	1.6	34
75	Microbial diversity: The tree of life comes of age. <i>Nature Microbiology</i> , 2016, 1, 16056.	5.9	14

#	ARTICLE	IF	CITATIONS
76	Recovering complete and draft population genomes from metagenome datasets. <i>Microbiome</i> , 2016, 4, 8.	4.9	254
77	Status of the Archaeal and Bacterial Census: an Update. <i>MBio</i> , 2016, 7, .	1.8	118
78	Machine Learning for Microbial Phenotype Prediction. , 2016, , .		2
79	Constructing and Analyzing Metabolic Flux Models of Microbial Communities. <i>Springer Protocols</i> , 2016, , 247-273.	0.1	8
80	Sporulation, bacterial cell envelopes and the origin of life. <i>Nature Reviews Microbiology</i> , 2016, 14, 535-542.	13.6	88
81	The bright side of microbial dark matter: lessons learned from the uncultivated majority. <i>Current Opinion in Microbiology</i> , 2016, 31, 217-226.	2.3	241
82	Long-Term Field Study of Microbial Community and Dechlorinating Activity Following Carboxymethyl Cellulose-Stabilized Nanoscale Zero-Valent Iron Injection. <i>Environmental Science & Technology</i> , 2016, 50, 7658-7670.	4.6	97
83	Bacterial Electron Transfer Chains Primed by Proteomics. <i>Advances in Microbial Physiology</i> , 2016, 68, 219-352.	1.0	5
84	Proposal of fifteen new species of <i>Parasynecococcus</i> based on genomic, physiological and ecological features. <i>Archives of Microbiology</i> , 2016, 198, 973-986.	1.0	10
85	Building genetic containment. <i>Nature Chemical Biology</i> , 2016, 12, 55-56.	3.9	3
86	Computational approaches to predict bacteriophage–host relationships. <i>FEMS Microbiology Reviews</i> , 2016, 40, 258-272.	3.9	394
87	Shotgun proteomics of bacterial pathogens: advances, challenges and clinical implications. <i>Expert Review of Proteomics</i> , 2016, 13, 139-156.	1.3	20
88	Beating the odds. <i>Nature Chemical Biology</i> , 2016, 12, 54-55.	3.9	19
89	Genome-Based Microbial Taxonomy Coming of Age. <i>Cold Spring Harbor Perspectives in Biology</i> , 2016, 8, a018085.	2.3	69
90	Critical biogeochemical functions in the subsurface are associated with bacteria from new phyla and little studied lineages. <i>Environmental Microbiology</i> , 2016, 18, 159-173.	1.8	164
91	Major bacterial lineages are essentially devoid of CRISPR-Cas viral defence systems. <i>Nature Communications</i> , 2016, 7, 10613.	5.8	224
92	Microbial diversity in European alpine permafrost and active layers. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw018.	1.3	266
93	Marine mammals harbor unique microbiotas shaped by and yet distinct from the sea. <i>Nature Communications</i> , 2016, 7, 10516.	5.8	196

#	ARTICLE	IF	CITATIONS
94	Global metagenomic survey reveals a new bacterial candidate phylum in geothermal springs. <i>Nature Communications</i> , 2016, 7, 10476.	5.8	189
95	Coevolution mechanisms that adapt viruses to genetic code variations implemented in their hosts. <i>Journal of Genetics</i> , 2016, 95, 3-12.	0.4	3
96	Comparative Genomics of Candidate Phylum TM6 Suggests That Parasitism Is Widespread and Ancestral in This Lineage. <i>Molecular Biology and Evolution</i> , 2016, 33, 915-927.	3.5	119
97	Phenotypic and Physiological Characterization of the Epibiotic Interaction Between TM7x and Its Basibiont Actinomyces. <i>Microbial Ecology</i> , 2016, 71, 243-255.	1.4	68
98	Phylogenomic analysis of lipid biosynthetic genes of Archaea shed light on the "lipid divide"™. <i>Environmental Microbiology</i> , 2017, 19, 54-69.	1.8	77
99	Genomic resolution of a cold subsurface aquifer community provides metabolic insights for novel microbes adapted to high CO ₂ concentrations. <i>Environmental Microbiology</i> , 2017, 19, 459-474.	1.8	212
100	Ecology of the Oral Microbiome: Beyond Bacteria. <i>Trends in Microbiology</i> , 2017, 25, 362-374.	3.5	222
101	Genome-Resolved Meta-Omics Ties Microbial Dynamics to Process Performance in Biotechnology for Thiocyanate Degradation. <i>Environmental Science & Technology</i> , 2017, 51, 2944-2953.	4.6	51
102	Where less may be more: how the rare biosphere pulls ecosystems strings. <i>ISME Journal</i> , 2017, 11, 853-862.	4.4	857
103	Asgard archaea illuminate the origin of eukaryotic cellular complexity. <i>Nature</i> , 2017, 541, 353-358.	13.7	882
104	The Source and Evolutionary History of a Microbial Contaminant Identified Through Soil Metagenomic Analysis. <i>MBio</i> , 2017, 8, .	1.8	17
105	A novel archaeal species belonging to <i>Methanoculleus</i> genus identified via de-novo assembly and metagenomic binning process in biogas reactors. <i>Anaerobe</i> , 2017, 46, 23-32.	1.0	63
106	C21orf57 is a human homologue of bacterial YbeY proteins. <i>Biochemical and Biophysical Research Communications</i> , 2017, 484, 612-617.	1.0	15
107	Microbial strain-level population structure and genetic diversity from metagenomes. <i>Genome Research</i> , 2017, 27, 626-638.	2.4	540
108	Water Table Dynamics and Biogeochemical Cycling in a Shallow, Variably-Saturated Floodplain. <i>Environmental Science & Technology</i> , 2017, 51, 3307-3317.	4.6	100
109	Origin of microbial biomineralization and magnetotaxis during the Archean. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 2171-2176.	3.3	98
111	Poorly known microbial taxa dominate the microbiome of permafrost thaw ponds. <i>ISME Journal</i> , 2017, 11, 1938-1941.	4.4	32
112	Unveiling microbial interactions in stratified mat communities from a warm saline shallow pond. <i>Environmental Microbiology</i> , 2017, 19, 2405-2421.	1.8	35

#	ARTICLE	IF	CITATIONS
113	The state of rhizospheric science in the era of multi-omics: A practical guide to omics technologies. <i>Rhizosphere</i> , 2017, 3, 212-221.	1.4	66
114	Metal homeostasis in bacteria: the role of ArsR&SmtB family of transcriptional repressors in combating varying metal concentrations in the environment. <i>BioMetals</i> , 2017, 30, 459-503.	1.8	40
115	The metabolic potential of the single cell genomes obtained from the Challenger Deep, <sc>M</sc>ariana <sc>T</sc>rench within the candidate superphylum <sc>P</sc>arcubacteria (<sc>OD</sc>1). <i>Environmental Microbiology</i> , 2017, 19, 2769-2784.	1.8	88
116	Resilience of the prokaryotic microbial community of <i>Acropora digitifera</i> to elevated temperature. <i>MicrobiologyOpen</i> , 2017, 6, e00478.	1.2	35
117	Comparative genomics of the DNA damage&inducible network in the Patescibacteria. <i>Environmental Microbiology</i> , 2017, 19, 3465-3474.	1.8	51
118	Novel Antibiotic Resistance Determinants from Agricultural Soil Exposed to Antibiotics Widely Used in Human Medicine and Animal Farming. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	62
119	Reference standards for next-generation sequencing. <i>Nature Reviews Genetics</i> , 2017, 18, 473-484.	7.7	194
120	Unusual respiratory capacity and nitrogen metabolism in a Parcubacterium (OD1) of the Candidate Phyla Radiation. <i>Scientific Reports</i> , 2017, 7, 40101.	1.6	119
121	Plant community reassembly on restored semi-natural grasslands lags behind the assembly of the arbuscular mycorrhizal fungal communities. <i>Biological Conservation</i> , 2017, 212, 196-208.	1.9	12
122	Novel approaches in function-driven single-cell genomics. <i>FEMS Microbiology Reviews</i> , 2017, 41, 538-548.	3.9	24
123	RNA-Dependent Cysteine Biosynthesis in Bacteria and Archaea. <i>MBio</i> , 2017, 8, .	1.8	20
124	Diversity and ecology of and biomineralization by magnetotactic bacteria. <i>Environmental Microbiology Reports</i> , 2017, 9, 345-356.	1.0	83
125	Potential for microbial H2 and metal transformations associated with novel bacteria and archaea in deep terrestrial subsurface sediments. <i>ISME Journal</i> , 2017, 11, 1915-1929.	4.4	137
126	Retroelement-guided protein diversification abounds in vast lineages of Bacteria and Archaea. <i>Nature Microbiology</i> , 2017, 2, 17045.	5.9	62
127	Exploring the under-investigated µbial dark matter&of drinking water treatment plants. <i>Scientific Reports</i> , 2017, 7, 44350.	1.6	41
128	Global Distribution Patterns and Pangenomic Diversity of the Candidate Phylum &Latescibacteria& (WS3). <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	107
129	Ecogenomics of Deep-Ocean Microbial Bathotypes. , 2017, , 7-50.		8
130	New CRISPR&Cas systems from uncultivated microbes. <i>Nature</i> , 2017, 542, 237-241.	13.7	471

#	ARTICLE	IF	CITATIONS
131	A decade of irrigation transforms the soil microbiome of a semi-arid pine forest. <i>Molecular Ecology</i> , 2017, 26, 1190-1206.	2.0	163
132	Hydrocarbon and Lipid Microbiology Protocols. <i>Springer Protocols</i> , 2017, , .	0.1	1
133	SandTraps are efficient, scalable, and mild systems for harvesting, washing and concentrating cells. <i>Journal of Microbiological Methods</i> , 2017, 132, 106-111.	0.7	7
134	Gaia and her microbiome. <i>FEMS Microbiology Ecology</i> , 2017, 93, fiw247.	1.3	29
135	Relic DNA is abundant in soil and obscures estimates of soil microbial diversity. <i>Nature Microbiology</i> , 2017, 2, 16242.	5.9	660
136	Finding life's missing pieces. <i>Nature Microbiology</i> , 2017, 2, 1458-1459.	5.9	0
137	The trajectory of microbial single-cell sequencing. <i>Nature Methods</i> , 2017, 14, 1045-1054.	9.0	120
138	In it for the long haul: evolutionary consequences of persistent endosymbiosis. <i>Current Opinion in Genetics and Development</i> , 2017, 47, 83-90.	1.5	31
139	Stochastic Community Assembly: Does It Matter in Microbial Ecology?. <i>Microbiology and Molecular Biology Reviews</i> , 2017, 81, .	2.9	1,291
140	Metabolic Roles of Uncultivated Bacterioplankton Lineages in the Northern Gulf of Mexico "Dead Zone". <i>MBio</i> , 2017, 8, .	1.8	80
141	Searching for Life on Mars Before It Is Too Late. <i>Astrobiology</i> , 2017, 17, 962-970.	1.5	61
142	Recovery of nearly 8,000 metagenome-assembled genomes substantially expands the tree of life. <i>Nature Microbiology</i> , 2017, 2, 1533-1542.	5.9	1,465
143	Shotgun metagenomics, from sampling to analysis. <i>Nature Biotechnology</i> , 2017, 35, 833-844.	9.4	1,196
144	Unusual metabolic diversity of hyperalkaliphilic microbial communities associated with subterranean serpentinization at The Cedars. <i>ISME Journal</i> , 2017, 11, 2584-2598.	4.4	95
145	Present and Future of Culturing Bacteria. <i>Annual Review of Microbiology</i> , 2017, 71, 711-730.	2.9	192
146	Diversity and dynamics of the DNA- and cDNA-derived compost fungal communities throughout the commercial cultivation process for <i>Agaricus bisporus</i> . <i>Mycologia</i> , 2017, 109, 475-484.	0.8	20
147	Improved genome recovery and integrated cell-size analyses of individual uncultured microbial cells and viral particles. <i>Nature Communications</i> , 2017, 8, 84.	5.8	169
148	New insights into biodrying mechanism associated with tryptophan and tyrosine degradations during sewage sludge biodrying. <i>Bioresource Technology</i> , 2017, 244, 132-141.	4.8	21

#	ARTICLE	IF	CITATIONS
149	Response of Microbial Community Function to Fluctuating Geochemical Conditions within a Legacy Radioactive Waste Trench Environment. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	12
150	The growing tree of Archaea: new perspectives on their diversity, evolution and ecology. <i>ISME Journal</i> , 2017, 11, 2407-2425.	4.4	320
151	Minimum information about a single amplified genome (MISAG) and a metagenome-assembled genome (MIMAG) of bacteria and archaea. <i>Nature Biotechnology</i> , 2017, 35, 725-731.	9.4	1,512
153	Archaea and the origin of eukaryotes. <i>Nature Reviews Microbiology</i> , 2017, 15, 711-723.	13.6	388
154	Strain-resolved analysis of hospital rooms and infants reveals overlap between the human and room microbiome. <i>Nature Communications</i> , 2017, 8, 1814.	5.8	162
155	Novel Microbial Diversity and Functional Potential in the Marine Mammal Oral Microbiome. <i>Current Biology</i> , 2017, 27, 3752-3762.e6.	1.8	82
156	Methanogenesis in oxygenated soils is a substantial fraction of wetland methane emissions. <i>Nature Communications</i> , 2017, 8, 1567.	5.8	195
157	Sulfide Generation by Dominant <i>Halanaerobium</i> Microorganisms in Hydraulically Fractured Shales. <i>MSphere</i> , 2017, 2, .	1.3	62
158	Evolutionary Genomics of Defense Systems in Archaea and Bacteria. <i>Annual Review of Microbiology</i> , 2017, 71, 233-261.	2.9	256
159	Migrating SSU rRNA gene surveys to the metagenomics era. <i>Environmental Microbiology Reports</i> , 2017, 9, 23-24.	1.0	9
160	Gifted microbes for genome mining and natural product discovery. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2017, 44, 573-588.	1.4	200
161	High-resolution characterization of the human microbiome. <i>Translational Research</i> , 2017, 179, 7-23.	2.2	55
162	Geochemical and microbial community determinants of reductive dechlorination at a site biostimulated with glycerol. <i>Environmental Microbiology</i> , 2017, 19, 968-981.	1.8	47
163	It's the song, not the singer: an exploration of holobiosis and evolutionary theory. <i>Biology and Philosophy</i> , 2017, 32, 5-24.	0.7	155
164	Microbial Biodiversity: Straight from the Dolphin's Mouth. <i>Current Biology</i> , 2017, 27, R1307-R1309.	1.8	0
165	9. Assessing metabolic activity at methane seeps: a testing ground for slow growing environmental systems. , 2017, , 223-260.		0
166	Towards a balanced view of the bacterial tree of life. <i>Microbiome</i> , 2017, 5, 140.	4.9	102
167	Bioinformatic Analysis Reveals Archaeal tRNATyr and tRNATrp Identities in Bacteria. <i>Life</i> , 2017, 7, 8.	1.1	13

#	ARTICLE	IF	CITATIONS
168	Complete 4.55-Megabase-Pair Genome of <i>Candidatus</i> <i>Fluviicola riflensis</i> , Curated from Short-Read Metagenomic Sequences. <i>Genome Announcements</i> , 2017, 5, .	0.8	7
169	Metatranscriptomic Analysis Reveals Unexpectedly Diverse Microbial Metabolism in a Biogeochemical Hot Spot in an Alluvial Aquifer. <i>Frontiers in Microbiology</i> , 2017, 8, 40.	1.5	14
170	Technological Microbiology: Development and Applications. <i>Frontiers in Microbiology</i> , 2017, 8, 827.	1.5	68
171	Temporal Dynamics of Soil Microbial Communities below the Seedbed under Two Contrasting Tillage Regimes. <i>Frontiers in Microbiology</i> , 2017, 8, 1127.	1.5	124
172	Nutrient and Rainfall Additions Shift Phylogenetically Estimated Traits of Soil Microbial Communities. <i>Frontiers in Microbiology</i> , 2017, 8, 1271.	1.5	25
173	Editorial: Virus Discovery by Metagenomics: The (Im)possibilities. <i>Frontiers in Microbiology</i> , 2017, 8, 1710.	1.5	32
174	Ecogenomics and Taxonomy of Cyanobacteria Phylum. <i>Frontiers in Microbiology</i> , 2017, 8, 2132.	1.5	99
175	Rokubacteria: Genomic Giants among the Uncultured Bacterial Phyla. <i>Frontiers in Microbiology</i> , 2017, 8, 2264.	1.5	142
176	Review of Molecular Techniques for the Identification of Bacterial Communities in Biological Effluent Treatment Facilities at Pulp and Paper Mills. <i>BioResources</i> , 2017, 12, .	0.5	11
177	Assessing biosynthetic potential of agricultural groundwater through metagenomic sequencing: A diverse anammox community dominates nitrate-rich groundwater. <i>PLoS ONE</i> , 2017, 12, e0174930.	1.1	26
178	Comparing and Evaluating Metagenome Assembly Tools from a Microbiologist's Perspective - Not Only Size Matters!. <i>PLoS ONE</i> , 2017, 12, e0169662.	1.1	186
179	Assembling metagenomes, one community at a time. <i>BMC Genomics</i> , 2017, 18, 521.	1.2	89
180	DESMAN: a new tool for de novo extraction of strains from metagenomes. <i>Genome Biology</i> , 2017, 18, 181.	3.8	152
181	Phylogenomics of Cas4 family nucleases. <i>BMC Evolutionary Biology</i> , 2017, 17, 232.	3.2	61
182	Phylogenetic analysis of the core histone doublet and DNA topo II genes of <i>Marseilleviridae</i> : evidence of proto-eukaryotic provenance. <i>Epigenetics and Chromatin</i> , 2017, 10, 55.	1.8	33
183	Members of the Candidate Phyla Radiation are functionally differentiated by carbon- and nitrogen-cycling capabilities. <i>Microbiome</i> , 2017, 5, 112.	4.9	118
184	Bottled aqua incognita: microbiota assembly and dissolved organic matter diversity in natural mineral waters. <i>Microbiome</i> , 2017, 5, 126.	4.9	26
185	Interpreting Microbial Biosynthesis in the Genomic Age: Biological and Practical Considerations. <i>Marine Drugs</i> , 2017, 15, 165.	2.2	21

#	ARTICLE	IF	CITATIONS
186	Higher recall in metagenomic sequence classification exploiting overlapping reads. BMC Genomics, 2017, 18, 917.	1.2	14
187	Expanded diversity of microbial groups that shape the dissimilatory sulfur cycle. ISME Journal, 2018, 12, 1715-1728.	4.4	347
188	Major New Microbial Groups Expand Diversity and Alter our Understanding of the Tree of Life. Cell, 2018, 172, 1181-1197.	13.5	498
189	Genome-resolved metagenomics identifies genetic mobility, metabolic interactions, and unexpected diversity in perchlorate-reducing communities. ISME Journal, 2018, 12, 1568-1581.	4.4	82
190	Extreme halophilic archaea derive from two distinct methanogen Class II lineages. Molecular Phylogenetics and Evolution, 2018, 127, 46-54.	1.2	52
191	The activity of nitrifying microorganisms in a high-altitude Andean wetland. FEMS Microbiology Ecology, 2018, 94, .	1.3	15
192	Dynamic bacterial community changes in the autothermal thermophilic aerobic digestion process with cell lysis activities, shaking and temperature increase. Journal of Bioscience and Bioengineering, 2018, 126, 196-204.	1.1	12
193	Cultivation and genomics of the first freshwater SAR11 (LD12) isolate. ISME Journal, 2018, 12, 1846-1860.	4.4	123
194	Metabolic potential and <i>in situ</i> transcriptomic profiles of previously uncharacterized key microbial groups involved in coupled carbon, nitrogen and sulfur cycling in anoxic marine zones. Environmental Microbiology, 2018, 20, 2727-2742.	1.8	18
195	Methodological Strategies in Microbiome Research and their Explanatory Implications. Perspectives on Science, 2018, 26, 239-265.	0.3	14
196	Getting Momentum: From Biocatalysis to Advanced Synthetic Biology. Trends in Biochemical Sciences, 2018, 43, 180-198.	3.7	70
197	Microbial Dark Matter Investigations: How Microbial Studies Transform Biological Knowledge and Empirically Sketch a Logic of Scientific Discovery. Genome Biology and Evolution, 2018, 10, 707-715.	1.1	82
198	Abditibacterium utsteinense sp. nov., the first cultivated member of candidate phylum FBP, isolated from ice-free Antarctic soil samples. Systematic and Applied Microbiology, 2018, 41, 279-290.	1.2	58
199	Differential depth distribution of microbial function and putative symbionts through sediment-hosted aquifers in the deep terrestrial subsurface. Nature Microbiology, 2018, 3, 328-336.	5.9	227
200	Bacterial RNA Biology on a Genome Scale. Molecular Cell, 2018, 70, 785-799.	4.5	201
201	Application of molecular tools to elucidate the microbiota of seafood. Journal of Applied Microbiology, 2018, 124, 1347-1365.	1.4	7
202	Phylogenetic clustering of small low nucleic acid-content bacteria across diverse freshwater ecosystems. ISME Journal, 2018, 12, 1344-1359.	4.4	84
203	Host and symbiont intraspecific variability: The case of Paramecium calkinsi and <i>Candidatus Trichorickettsia mobilis</i> . European Journal of Protistology, 2018, 62, 79-94.	0.5	44

#	ARTICLE	IF	CITATIONS
204	Retrieval of a million high-quality, full-length microbial 16S and 18S rRNA gene sequences without primer bias. <i>Nature Biotechnology</i> , 2018, 36, 190-195.	9.4	165
205	How Much Do rRNA Gene Surveys Underestimate Extant Bacterial Diversity?. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	47
207	Diversity-generating retroelements: natural variation, classification and evolution inferred from a large-scale genomic survey. <i>Nucleic Acids Research</i> , 2018, 46, 11-24.	6.5	102
208	GraftM: a tool for scalable, phylogenetically informed classification of genes within metagenomes. <i>Nucleic Acids Research</i> , 2018, 46, e59-e59.	6.5	130
209	The generality of Constructive Neutral Evolution. <i>Biology and Philosophy</i> , 2018, 33, 1.	0.7	20
210	The multi-omics promise in context: from sequence to microbial isolate. <i>Critical Reviews in Microbiology</i> , 2018, 44, 212-229.	2.7	158
211	Predicted microbial secretomes and their target substrates in marine sediment. <i>Nature Microbiology</i> , 2018, 3, 32-37.	5.9	85
212	Effects of different C/N ratios on bacterial compositions and processes in an organically managed soil. <i>Biology and Fertility of Soils</i> , 2018, 54, 137-147.	2.3	15
213	The fourth wave of biocatalysis is approaching. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2018, 376, 20170063.	1.6	108
214	Metabolic versatility of small archaea Micrarchaeota and Parvarchaeota. <i>ISME Journal</i> , 2018, 12, 756-775.	4.4	91
215	Bacterial Flagellins: Does Size Matter?. <i>Trends in Microbiology</i> , 2018, 26, 575-581.	3.5	13
216	A novel Chromatiales bacterium is a potential sulfide oxidizer in multiple orders of marine sponges. <i>Environmental Microbiology</i> , 2018, 20, 800-814.	1.8	27
217	Discovery of an expansive bacteriophage family that includes the most abundant viruses from the human gut. <i>Nature Microbiology</i> , 2018, 3, 38-46.	5.9	245
218	Diversity and community structure of marine microbes around the Benham Rise underwater plateau, northeastern Philippines. <i>PeerJ</i> , 2018, 6, e4781.	0.9	19
220	Parallel Evolution of Genome Streamlining and Cellular Bioenergetics across the Marine Radiation of a Bacterial Phylum. <i>MBio</i> , 2018, 9, .	1.8	27
221	Visualization-assisted binning of metagenome assemblies reveals potential new pathogenic profiles in idiopathic travelers' diarrhea. <i>Microbiome</i> , 2018, 6, 201.	4.9	20
222	Coral-associated bacteria demonstrate phyllosymbiosis and cophylogeny. <i>Nature Communications</i> , 2018, 9, 4921.	5.8	264
223	Changes in the Drinking Water Microbiome: Effects of Water Treatments Along the Flow of Two Drinking Water Treatment Plants in a Urbanized Area, Milan (Italy). <i>Frontiers in Microbiology</i> , 2018, 9, 2557.	1.5	45

#	ARTICLE	IF	CITATIONS
224	Acetate Activates Deep Subsurface Fracture Fluid Microbial Communities in Olkiluoto, Finland. <i>Geosciences (Switzerland)</i> , 2018, 8, 399.	1.0	13
225	Rapid evolution of decreased host susceptibility drives a stable relationship between ultrasmall parasite TM7x and its bacterial host. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 12277-12282.	3.3	59
226	Genomic and in-situ Transcriptomic Characterization of the Candidate Phylum NPL-UPL2 From Highly Alkaline Highly Reducing Serpentinized Groundwater. <i>Frontiers in Microbiology</i> , 2018, 9, 3141.	1.5	31
227	Giant flagellins form thick flagellar filaments in two species of marine $\hat{3}$ -proteobacteria. <i>PLoS ONE</i> , 2018, 13, e0206544.	1.1	10
228	Occurrence and Fate of Ultramicrobacteria in a Full-Scale Drinking Water Treatment Plant. <i>Frontiers in Microbiology</i> , 2018, 9, 2922.	1.5	8
229	Microbiome characterization by high-throughput transfer RNA sequencing and modification analysis. <i>Nature Communications</i> , 2018, 9, 5353.	5.8	48
230	Members of <i>Marinobacter</i> and <i>Arcobacter</i> Influence System Biogeochemistry During Early Production of Hydraulically Fractured Natural Gas Wells in the Appalachian Basin. <i>Frontiers in Microbiology</i> , 2018, 9, 2646.	1.5	33
231	Widespread Antibiotic, Biocide, and Metal Resistance in Microbial Communities Inhabiting a Municipal Waste Environment and Anthropogenically Impacted River. <i>MSphere</i> , 2018, 3, .	1.3	12
232	Impact of hydrologic boundaries on microbial planktonic and biofilm communities in shallow terrestrial subsurface environments. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	49
233	Sizing Up the Uncultured Microbial Majority. <i>MSystems</i> , 2018, 3, .	1.7	13
234	The East River, Colorado, Watershed: A Mountainous Community Testbed for Improving Predictive Understanding of Multiscale Hydrological and Biogeochemical Dynamics. <i>Vadose Zone Journal</i> , 2018, 17, 1-25.	1.3	115
235	Monitoring of microbial dynamics in a drinking water distribution system using the culture-free, user-friendly, MYcrobiota platform. <i>Scientific Reports</i> , 2018, 8, 14727.	1.6	12
236	A metagenomics roadmap to the uncultured genome diversity in hypersaline soda lake sediments. <i>Microbiome</i> , 2018, 6, 168.	4.9	120
237	Discovering novel hydrolases from hot environments. <i>Biotechnology Advances</i> , 2018, 36, 2077-2100.	6.0	38
238	Microbiome Analysis. <i>Methods in Molecular Biology</i> , 2018, , .	0.4	13
239	Subsampled Assemblies and Hybrid Nucleotide Composition/Differential Coverage Binning for Genome-Resolved Metagenomics. <i>Methods in Molecular Biology</i> , 2018, 1849, 215-225.	0.4	2
240	Quorum Sensing Modulates the Epibiotic-Parasitic Relationship Between <i>Actinomyces odontolyticus</i> and Its <i>Saccharibacteria</i> epibiont, a <i>Nanosynbacter lyticus</i> Strain, TM7x. <i>Frontiers in Microbiology</i> , 2018, 9, 2049.	1.5	32
241	The Tree of Life. <i>Grand Challenges in Biology and Biotechnology</i> , 2018, , 55-99.	2.4	8

#	ARTICLE	IF	CITATIONS
242	High-quality genome sequences of uncultured microbes by assembly of read clouds. <i>Nature Biotechnology</i> , 2018, 36, 1067-1075.	9.4	103
243	Programmed DNA destruction by miniature CRISPR-Cas14 enzymes. <i>Science</i> , 2018, 362, 839-842.	6.0	757
244	G3 PhyloChip Analysis Confirms the Promise of Plant-Based Culture Media for Unlocking the Composition and Diversity of the Maize Root Microbiome and for Recovering Unculturable Candidate Divisions/Phyla. <i>Microbes and Environments</i> , 2018, 33, 317-325.	0.7	21
245	Genomic Description of "Candidatus Abyssubacteria," a Novel Subsurface Lineage Within the Candidate Phylum Hydrogenedentes. <i>Frontiers in Microbiology</i> , 2018, 9, 1993.	1.5	36
246	Online flow cytometric monitoring of microbial water quality in a full-scale water treatment plant. <i>Npj Clean Water</i> , 2018, 1, .	3.1	48
247	Phylogenetic Diversity. , 2018, , .		9
248	Metagenomic analysis with strain-level resolution reveals fine-scale variation in the human pregnancy microbiome. <i>Genome Research</i> , 2018, 28, 1467-1480.	2.4	117
249	Single-cell genomics of co-sorted Nanoarchaeota suggests novel putative host associations and diversification of proteins involved in symbiosis. <i>Microbiome</i> , 2018, 6, 161.	4.9	44
250	Environmental microbiology and metagenomics: the Brave New World is here, what's next?. <i>Environmental Microbiology</i> , 2018, 20, 4210-4212.	1.8	5
251	Biodiversity, the Tree of Life, and Science Communication. , 2018, , 41-71.		14
252	Biosynthetic capacity, metabolic variety and unusual biology in the CPR and DPANN radiations. <i>Nature Reviews Microbiology</i> , 2018, 16, 629-645.	13.6	314
254	Recovery of genomes from metagenomes via a dereplication, aggregation and scoring strategy. <i>Nature Microbiology</i> , 2018, 3, 836-843.	5.9	906
255	Fast and Sensitive Classification of Short Metagenomic Reads with SKraken. <i>Communications in Computer and Information Science</i> , 2018, , 212-226.	0.4	9
256	Analysis of Microbial Diversity: Regarding the (Paradoxical) Difficulty of Seeing Big in Metagenomics. , 2018, , 63-87.		0
257	Analytic Methods in Microbiome Studies. , 2018, , 29-42.		0
258	Selective successional transport of bacterial populations from rooted agricultural topsoil to deeper layers upon extreme precipitation events. <i>Soil Biology and Biochemistry</i> , 2018, 124, 168-178.	4.2	16
259	It Takes a Village: Microbial Communities Thrive through Interactions and Metabolic Handoffs. <i>MSystems</i> , 2018, 3, .	1.7	34
260	Vertically distinct microbial communities in the Mariana and Kermadec trenches. <i>PLoS ONE</i> , 2018, 13, e0195102.	1.1	62

#	ARTICLE	IF	CITATIONS
261	Complex Evolutionary History of Translation Elongation Factor 2 and Diphthamide Biosynthesis in Archaea and Parabasalids. <i>Genome Biology and Evolution</i> , 2018, 10, 2380-2393.	1.1	37
262	Specificities and Efficiencies of Primers Targeting Candidatus Phylum Saccharibacteria in Activated Sludge. <i>Materials</i> , 2018, 11, 1129.	1.3	22
263	<i>The Helicobacter pylori</i> cell shape promoting protein Csd5 interacts with the cell wall, MurF, and the bacterial cytoskeleton. <i>Molecular Microbiology</i> , 2018, 110, 114-127.	1.2	26
264	Agulhas Current properties shape microbial community diversity and potential functionality. <i>Scientific Reports</i> , 2018, 8, 10542.	1.6	12
265	Insights into the ecology, evolution, and metabolism of the widespread Woese archaeotal lineages. <i>Microbiome</i> , 2018, 6, 102.	4.9	181
266	Microbial Community Cohesion Mediates Community Turnover in Unperturbed Aquifers. <i>MSystems</i> , 2018, 3, .	1.7	63
267	Stable isotope informed genome-resolved metagenomics reveals that Saccharibacteria utilize microbially-processed plant-derived carbon. <i>Microbiome</i> , 2018, 6, 122.	4.9	156
268	A microbial community snapshot of windrows from a commercial composting facility. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 8069-8077.	1.7	14
269	Electrical Signal Reporter, Pore-Forming Protein, for Rapid, Miniaturized, and Universal Identification of Microorganisms. <i>Analytical Chemistry</i> , 2018, 90, 9853-9858.	3.2	5
270	Genomic inference of the metabolism and evolution of the archaeal phylum Aigarchaeota. <i>Nature Communications</i> , 2018, 9, 2832.	5.8	108
271	Profiling microbial strains in urban environments using metagenomic sequencing data. <i>Biology Direct</i> , 2018, 13, 9.	1.9	29
272	The last universal common ancestor between ancient Earth chemistry and the onset of genetics. <i>PLoS Genetics</i> , 2018, 14, e1007518.	1.5	120
273	Metagenomic Approaches for Understanding New Concepts in Microbial Science. <i>International Journal of Genomics</i> , 2018, 2018, 1-15.	0.8	100
274	A standardized bacterial taxonomy based on genome phylogeny substantially revises the tree of life. <i>Nature Biotechnology</i> , 2018, 36, 996-1004.	9.4	2,615
275	Ideas and perspectives: Strengthening the biogeosciences in environmental research networks. <i>Biogeosciences</i> , 2018, 15, 4815-4832.	1.3	24
276	Novel Autotrophic Organisms Contribute Significantly to the Internal Carbon Cycling Potential of a Boreal Lake. <i>MBio</i> , 2018, 9, .	1.8	18
277	New Biological Insights Into How Deforestation in Amazonia Affects Soil Microbial Communities Using Metagenomics and Metagenome-Assembled Genomes. <i>Frontiers in Microbiology</i> , 2018, 9, 1635.	1.5	51
278	On the Origin of Isoprenoid Biosynthesis. <i>Molecular Biology and Evolution</i> , 2018, 35, 2185-2197.	3.5	54

#	ARTICLE	IF	CITATIONS
282	Novel prosthecate bacteria from the candidate phylum Acetothermia. ISME Journal, 2018, 12, 2225-2237.	4.4	75
283	Novel soil bacteria possess diverse genes for secondary metabolite biosynthesis. Nature, 2018, 558, 440-444.	13.7	321
284	A distinct abundant group of microbial rhodopsins discovered using functional metagenomics. Nature, 2018, 558, 595-599.	13.7	190
285	Karst Water Environment. Handbook of Environmental Chemistry, 2019, , .	0.2	5
287	The importance of designating type material for uncultured taxa. Systematic and Applied Microbiology, 2019, 42, 15-21.	1.2	149
288	Genomes From Uncultivated Microorganisms. , 2019, , .		4
289	High proportions of bacteria and archaea across most biomes remain uncultured. ISME Journal, 2019, 13, 3126-3130.	4.4	264
290	Mode and Structure of the Bacterial Community on Human Scalp Hair. Microbes and Environments, 2019, 34, 252-259.	0.7	17
291	Comparison of Microbiomes and Resistomes in Two Karst Groundwater Sites in Chongqing, China. Ground Water, 2019, 57, 807-818.	0.7	8
292	Contrasting Winter Versus Summer Microbial Communities and Metabolic Functions in a Permafrost Thaw Lake. Frontiers in Microbiology, 2019, 10, 1656.	1.5	65
293	The Methodology Behind Network Thinking: Graphs to Analyze Microbial Complexity and Evolution. Methods in Molecular Biology, 2019, 1910, 271-308.	0.4	4
294	Predominance of Cand. Patescibacteria in Groundwater Is Caused by Their Preferential Mobilization From Soils and Flourishing Under Oligotrophic Conditions. Frontiers in Microbiology, 2019, 10, 1407.	1.5	160
295	Passage and community changes of filterable bacteria during microfiltration of a surface water supply. Environment International, 2019, 131, 104998.	4.8	16
296	Phytoremediation of cadmium-contaminated soil by Sorghum bicolor and the variation of microbial community. Chemosphere, 2019, 235, 985-994.	4.2	44
297	General Geochemistry and Microbiology Techniques. , 2019, , 3-60.		2
298	PhyloMagnet: fast and accurate screening of short-read meta-omics data using gene-centric phylogenetics. Bioinformatics, 2020, 36, 1718-1724.	1.8	7
299	Microbial assembly, interaction, functioning, activity and diversification: a review derived from community compositional data. Marine Life Science and Technology, 2019, 1, 112-128.	1.8	104
300	Putative Mixotrophic Nitrifying-Denitrifying Gammaproteobacteria Implicated in Nitrogen Cycling Within the Ammonia/Oxygen Transition Zone of an Oil Sands Pit Lake. Frontiers in Microbiology, 2019, 10, 2435.	1.5	42

#	ARTICLE	IF	CITATIONS
301	Culturing the uncultured. <i>Nature Biotechnology</i> , 2019, 37, 1278-1279.	9.4	8
302	A Bioinformatics Guide to Plant Microbiome Analysis. <i>Frontiers in Plant Science</i> , 2019, 10, 1313.	1.7	54
303	Current Status and Potential Applications of Underexplored Prokaryotes. <i>Microorganisms</i> , 2019, 7, 468.	1.6	17
304	Genome-resolved viral and cellular metagenomes revealed potential key virus-host interactions in a deep freshwater lake. <i>Environmental Microbiology</i> , 2019, 21, 4740-4754.	1.8	49
305	Robust taxonomic classification of uncharted microbial sequences and bins with CAT and BAT. <i>Genome Biology</i> , 2019, 20, 217.	3.8	269
306	<i>Aedes</i> spp. and Their Microbiota: A Review. <i>Frontiers in Microbiology</i> , 2019, 10, 2036.	1.5	90
307	Bacterial Diversity in the Metal-Rich Terrestrial Deep Subsurface Sediments of Krishna Godavari Basin, India. <i>Geomicrobiology Journal</i> , 2019, 36, 917-932.	1.0	4
308	Genomic signatures and co-occurrence patterns of the ultra-small <i>Saccharimonadia</i> (phylum) Tj ETQq1 1 0.784314 rgBT /Overlock 101	2.0	101
309	Current and Promising Approaches to Identify Horizontal Gene Transfer Events in Metagenomes. <i>Genome Biology and Evolution</i> , 2019, 11, 2750-2766.	1.1	70
310	History of the Hadean "Living Microfossil" OD1 and Ultra-reducing Environments. <i>Journal of Geography (Chigaku Zasshi)</i> , 2019, 128, 571-596.	0.1	13
311	The distinction of CPR bacteria from other bacteria based on protein family content. <i>Nature Communications</i> , 2019, 10, 4173.	5.8	112
312	Biogeography, Ecology, and Evolution of Deep Life. , 2019, , 524-555.		6
313	Megaphages infect <i>Prevotella</i> and variants are widespread in gut microbiomes. <i>Nature Microbiology</i> , 2019, 4, 693-700.	5.9	141
314	Uncovering the Uncultivated Majority in Antarctic Soils: Toward a Synergistic Approach. <i>Frontiers in Microbiology</i> , 2019, 10, 242.	1.5	51
315	Genomic and metagenomic insights into the microbial community of a thermal spring. <i>Microbiome</i> , 2019, 7, 8.	4.9	40
316	Metagenomics a modern approach to reveal the secrets of unculturable microbes. , 2019, , 177-195.		1
317	Selection of a Microbial Community in the Course of Formation of Acid Mine Drainage. <i>Microbiology</i> , 2019, 88, 292-299.	0.5	10
318	The Pedological Context Modulates the Response of Soil Microbial Communities to Agroecological Management. <i>Frontiers in Ecology and Evolution</i> , 2019, 7, .	1.1	13

#	ARTICLE	IF	CITATIONS
319	Chromulinavorax destructans, a pathogen of microzooplankton that provides a window into the enigmatic candidate phylum Dependistia. PLoS Pathogens, 2019, 15, e1007801.	2.1	59
320	Composite Metagenome-Assembled Genomes Reduce the Quality of Public Genome Repositories. MBio, 2019, 10, .	1.8	76
321	Microbial communities across a hillslope-riparian transect shaped by proximity to the stream, groundwater table, and weathered bedrock. Ecology and Evolution, 2019, 9, 6869-6900.	0.8	24
322	Multiple levels of the unknown in microbiome research. BMC Biology, 2019, 17, 48.	1.7	101
323	The endolithic bacterial diversity of shallow bedrock ecosystems. Science of the Total Environment, 2019, 679, 35-44.	3.9	34
324	Divergent microbial communities in groundwater and overlying soils exhibit functional redundancy for plant-polysaccharide degradation. PLoS ONE, 2019, 14, e0212937.	1.1	30
325	Metagenomic recovery of two distinct comammox <i>Nitrospira</i> from the terrestrial subsurface. Environmental Microbiology, 2019, 21, 3627-3637.	1.8	69
326	The Water Microbiome Through a Pilot Scale Advanced Treatment Facility for Direct Potable Reuse. Frontiers in Microbiology, 2019, 10, 993.	1.5	36
327	Microbiome: Current Status and Future Applications. Success in Academic Surgery, 2019, , 213-232.	0.1	1
328	The trouble with oxygen: The ecophysiology of extant phototrophs and implications for the evolution of oxygenic photosynthesis. Free Radical Biology and Medicine, 2019, 140, 233-249.	1.3	38
329	Candidate Phyla Radiation Roizmanbacteria From Hot Springs Have Novel and Unexpectedly Abundant CRISPR-Cas Systems. Frontiers in Microbiology, 2019, 10, 928.	1.5	36
330	Culturomics of the plant prokaryotic microbiome and the dawn of plant-based culture media – A review. Journal of Advanced Research, 2019, 19, 15-27.	4.4	102
331	The cooling tower water microbiota: Seasonal dynamics and co-occurrence of bacterial and protist phylotypes. Water Research, 2019, 159, 464-479.	5.3	51
333	Sulfur-Oxidizing Bacteria Dominate in the Water from a Flooded Coal Mine Shaft in Kuzbass. Microbiology, 2019, 88, 120-123.	0.5	8
334	Saccharibacteria (TM7) in the Human Oral Microbiome. Journal of Dental Research, 2019, 98, 500-509.	2.5	123
335	Carbon Fixation by Marine Ultrasmall Prokaryotes. Genome Biology and Evolution, 2019, 11, 1166-1177.	1.1	24
336	Genomic Characterization of Candidate Division LCP-89 Reveals an Atypical Cell Wall Structure, Microcompartment Production, and Dual Respiratory and Fermentative Capacities. Applied and Environmental Microbiology, 2019, 85, .	1.4	14
337	Understanding and overcoming the pitfalls and biases of next-generation sequencing (NGS) methods for use in the routine clinical microbiological diagnostic laboratory. European Journal of Clinical Microbiology and Infectious Diseases, 2019, 38, 1059-1070.	1.3	154

#	ARTICLE	IF	CITATIONS
338	Virus Genomes from Deep Sea Sediments Expand the Ocean Megavirome and Support Independent Origins of Viral Gigantism. <i>MBio</i> , 2019, 10, .	1.8	85
339	MetaCHIP: community-level horizontal gene transfer identification through the combination of best-match and phylogenetic approaches. <i>Microbiome</i> , 2019, 7, 36.	4.9	69
340	Autometa: automated extraction of microbial genomes from individual shotgun metagenomes. <i>Nucleic Acids Research</i> , 2019, 47, e57-e57.	6.5	69
341	Genome-resolved metagenomics of an autotrophic thiocyanate-remediating microbial bioreactor consortium. <i>Water Research</i> , 2019, 158, 106-117.	5.3	11
342	A census-based estimate of Earth's bacterial and archaeal diversity. <i>PLoS Biology</i> , 2019, 17, e3000106.	2.6	139
344	Source Community and Assembly Processes Affect the Efficiency of Microbial Microcystin Degradation on Drinking Water Filtration Membranes. <i>Frontiers in Microbiology</i> , 2019, 10, 843.	1.5	4
345	New insights from uncultivated genomes of the global human gut microbiome. <i>Nature</i> , 2019, 568, 505-510.	13.7	505
346	Microbial diversity of an Antarctic subglacial community and high-resolution replicate sampling inform hydrological connectivity in a polar desert. <i>Environmental Microbiology</i> , 2019, 21, 2290-2306.	1.8	20
347	An Instrumental Environment for Metagenomic Analysis. <i>Springer Proceedings in Earth and Environmental Sciences</i> , 2019, , 151-158.	0.2	1
348	Marker genes as predictors of shared genomic function. <i>BMC Genomics</i> , 2019, 20, 268.	1.2	11
349	Spring Water of an Alpine Karst Aquifer Is Dominated by a Taxonomically Stable but Discharge-Responsive Bacterial Community. <i>Frontiers in Microbiology</i> , 2019, 10, 28.	1.5	23
350	Simultaneous Bayesian inference of phylogeny and molecular coevolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 5027-5036.	3.3	9
351	Effect of the extraction and purification of soil DNA and pooling of PCR amplification products on the description of bacterial and archaeal communities. <i>Journal of Applied Microbiology</i> , 2019, 126, 1454-1467.	1.4	26
352	Wide Distribution of Phage That Infect Freshwater SAR11 Bacteria. <i>MSystems</i> , 2019, 4, .	1.7	11
353	Complete Genome Sequence of Strain AC001, a Novel Cultured Member of the Human Oral Microbiome from the Candidate Phylum <i>Saccharibacteria</i> (TM7). <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	11
354	Unusual Metabolism and Hypervariation in the Genome of a Gracilibacterium (BD1-5) from an Oil-Degrading Community. <i>MBio</i> , 2019, 10, .	1.8	43
356	Genome-Resolved Metagenomics Extends the Environmental Distribution of the <i>Verrucomicrobia</i> Phylum to the Deep Terrestrial Subsurface. <i>MSphere</i> , 2019, 4, .	1.3	38
357	Ecology and Evolution of Rhizobia. , 2019, , .		38

#	ARTICLE	IF	CITATIONS
358	Phylogenomics of 10,575 genomes reveals evolutionary proximity between domains Bacteria and Archaea. <i>Nature Communications</i> , 2019, 10, 5477.	5.8	197
359	Discovery of High Abundances of Aster-Like Nanoparticles in Pelagic Environments: Characterization and Dynamics. <i>Frontiers in Microbiology</i> , 2019, 10, 2376.	1.5	8
361	Metatranscriptomic reconstruction reveals RNA viruses with the potential to shape carbon cycling in soil. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 25900-25908.	3.3	165
362	The Emergence of Life. <i>Space Science Reviews</i> , 2019, 215, 1.	3.7	53
363	Targeted isolation and cultivation of uncultivated bacteria by reverse genomics. <i>Nature Biotechnology</i> , 2019, 37, 1314-1321.	9.4	231
364	Relevance of phenotypic information for the taxonomy of not-yet-cultured microorganisms. <i>Systematic and Applied Microbiology</i> , 2019, 42, 22-29.	1.2	34
365	Biogeochemical Regimes in Shallow Aquifers Reflect the Metabolic Coupling of the Elements Nitrogen, Sulfur, and Carbon. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	47
366	Lateral Gene Transfer Shapes the Distribution of RuBisCO among Candidate Phyla Radiation Bacteria and DPANN Archaea. <i>Molecular Biology and Evolution</i> , 2019, 36, 435-446.	3.5	54
367	A qualitative criterion for identifying the root of the tree of life. <i>Journal of Theoretical Biology</i> , 2019, 464, 126-131.	0.8	11
368	<i>Candidatus Krumholzbacterium zodletense</i> gen. nov., sp nov, the first representative of the candidate phylum Krumholzbacteriota phyl. nov. recovered from an anoxic sulfidic spring using genome resolved metagenomics. <i>Systematic and Applied Microbiology</i> , 2019, 42, 85-93.	1.2	39
369	Exploring the Human Microbiome: The Potential Future Role of Next-Generation Sequencing in Disease Diagnosis and Treatment. <i>Frontiers in Immunology</i> , 2018, 9, 2868.	2.2	207
370	Towards a systematic understanding of differences between archaeal and bacterial diversity. <i>Environmental Microbiology Reports</i> , 2019, 11, 9-12.	1.0	3
371	Uneven distribution of cobamide biosynthesis and dependence in bacteria predicted by comparative genomics. <i>ISME Journal</i> , 2019, 13, 789-804.	4.4	162
372	Genomes OnLine database (GOLD) v.7: updates and new features. <i>Nucleic Acids Research</i> , 2019, 47, D649-D659.	6.5	169
373	Crystal structure of a <i>Thermus aquaticus</i> diversity-generating retroelement variable protein. <i>PLoS ONE</i> , 2019, 14, e0205618.	1.1	5
374	The Prodigal Compound: Return of Ribosyl 1,5-Bisphosphate as an Important Player in Metabolism. <i>Microbiology and Molecular Biology Reviews</i> , 2019, 83, .	2.9	2
375	The Ecological Role of Micro-organisms in the Antarctic Environment. <i>Springer Polar Sciences</i> , 2019, , .	0.0	11
376	Patterns of Microorganisms Inhabiting Antarctic Freshwater Lakes with Special Reference to Aquatic Moss Pillars. <i>Springer Polar Sciences</i> , 2019, , 25-43.	0.0	2

#	ARTICLE	IF	CITATIONS
377	Natural Products from Mammalian Gut Microbiota. Trends in Biotechnology, 2019, 37, 492-504.	4.9	54
378	The universal ancestor, the deeper nodes of the tree of life, and the fundamental types of primary cells (cellular domains). Journal of Theoretical Biology, 2019, 460, 142-143.	0.8	15
379	Giant mimiviruses escape many canonical criteria of the virus definition. Clinical Microbiology and Infection, 2019, 25, 147-154.	2.8	17
380	Microbial Diversity of Thermophiles Through the Lens of Next Generation Sequencing. , 2019, , 217-226.		6
381	A review of methods and databases for metagenomic classification and assembly. Briefings in Bioinformatics, 2019, 20, 1125-1136.	3.2	368
382	Microbial genomes retrieved from High Arctic lake sediments encode for adaptation to cold and oligotrophic environments. Limnology and Oceanography, 2020, 65, S233.	1.6	20
383	Complex food webs coincide with high genetic potential for chemolithoautotrophy in fractured bedrock groundwater. Water Research, 2020, 170, 115306.	5.3	28
384	Microaerobic conditions caused the overwhelming dominance of Acinetobacter spp. and the marginalization of Rhodococcus spp. in diesel fuel/crude oil mixture-amended enrichment cultures. Archives of Microbiology, 2020, 202, 329-342.	1.0	33
385	Unlinked rRNA genes are widespread among bacteria and archaea. ISME Journal, 2020, 14, 597-608.	4.4	30
386	Groundwater cable bacteria conserve energy by sulfur disproportionation. ISME Journal, 2020, 14, 623-634.	4.4	64
387	CAMITAX: Taxon labels for microbial genomes. GigaScience, 2020, 9, .	3.3	6
388	A diverse uncultivated microbial community is responsible for organic matter degradation in the Black Sea sulphidic zone. Environmental Microbiology, 2021, 23, 2709-2728.	1.8	47
389	Genome-inferred spatio-temporal resolution of an uncultivated Roizman bacterium reveals its ecological preferences in groundwater. Environmental Microbiology, 2020, 22, 726-737.	1.8	31
390	Linking metagenomics to aquatic microbial ecology and biogeochemical cycles. Limnology and Oceanography, 2020, 65, S2.	1.6	82
391	Ultra-small and abundant: Candidate phyla radiation bacteria are potential catalysts of carbon transformation in a thermokarst lake ecosystem. Limnology and Oceanography Letters, 2020, 5, 212-220.	1.6	38
392	Metabolic relationships of uncultured bacteria associated with the microalgae <i>Gambierdiscus</i> . Environmental Microbiology, 2020, 22, 1764-1783.	1.8	28
393	A brief history of periodontics in the United States of America: Pioneers and thought leaders of the past, and current challenges. Periodontology 2000, 2020, 82, 12-25.	6.3	12
394	Spatio-temporal insights into microbiology of the freshwater-to-hypersaline, oxic-to-hypoxic euxinic waters of Ursu Lake. Environmental Microbiology, 2021, 23, 3523-3540.	1.8	25

#	ARTICLE	IF	CITATIONS
395	Fibrillar evolution through the Tree of Life: Comparative genomics and microsynteny network analyses provide new insights into the evolutionary history of Fibrillar. PLoS Computational Biology, 2020, 16, e1008318.	1.5	8
397	Relationship between the bacterial community structures on human hair and scalp. Bioscience, Biotechnology and Biochemistry, 2020, 84, 2585-2596.	0.6	5
398	Single-virus genomics and beyond. Nature Reviews Microbiology, 2020, 18, 705-716.	13.6	18
399	Traversing the "Omic" landscape of microbial halotolerance for key molecular processes and new insights. Critical Reviews in Microbiology, 2020, 46, 631-653.	2.7	10
400	Methane oxidation and methylotroph population dynamics in groundwater mesocosms. Environmental Microbiology, 2020, 22, 1222-1237.	1.8	18
401	Metagenomic analysis of gut microbiome and resistome of diarrheal fecal samples from Kolkata, India, reveals the core and variable microbiota including signatures of microbial dark matter. Gut Pathogens, 2020, 12, 32.	1.6	34
402	Groundwater <i>Elusimicrobia</i> are metabolically diverse compared to gut microbiome <i>Elusimicrobia</i> and some have a novel nitrogenase paralog. ISME Journal, 2020, 14, 2907-2922.	4.4	51
403	Utilization of marigold (<i>Tagetes erecta</i>) flower fermentation wastewater as a fertilizer and its effect on microbial community structure in maize rhizosphere and non-rhizosphere soil. Biotechnology and Biotechnological Equipment, 2020, 34, 522-531.	0.5	1
404	Biogeochemical Implications of N ₂ O-Reducing Thermophilic Campylobacteria in Deep-Sea Vent Fields, and the Description of <i>Nitratiruptor labii</i> sp. nov.. IScience, 2020, 23, 101462.	1.9	16
405	Overlooked Diversity of Ultramicrobacterial Minorities at the Air-Sea Interface. Atmosphere, 2020, 11, 1214.	1.0	9
408	Inclusion of Oxford Nanopore long reads improves all microbial and viral metagenome-assembled genomes from a complex aquifer system. Environmental Microbiology, 2020, 22, 4000-4013.	1.8	42
409	Undinarchaeota illuminate DPANN phylogeny and the impact of gene transfer on archaeal evolution. Nature Communications, 2020, 11, 3939.	5.8	102
410	Evaluating metagenomics tools for genome binning with real metagenomic datasets and CAMI datasets. BMC Bioinformatics, 2020, 21, 334.	1.2	53
411	Diverse Microorganisms in Sediment and Groundwater Are Implicated in Extracellular Redox Processes Based on Genomic Analysis of Bioanode Communities. Frontiers in Microbiology, 2020, 11, 1694.	1.5	9
412	Acquisition and Adaptation of Ultra-small Parasitic Reduced Genome Bacteria to Mammalian Hosts. Cell Reports, 2020, 32, 107939.	2.9	152
413	Emergence of Metabolite Provisioning as a By-Product of Evolved Biological Functions. MSystems, 2020, 5, .	1.7	15
414	Microbial Communities in Permafrost Soils of Larsemann Hills, Eastern Antarctica: Environmental Controls and Effect of Human Impact. Microorganisms, 2020, 8, 1202.	1.6	17
415	Spatial and Temporal Dynamics in Attached and Suspended Bacterial Communities in Three Drinking Water Distribution Systems with Variable Biological Stability. Environmental Science & Technology, 2020, 54, 14535-14546.	4.6	22

#	ARTICLE	IF	CITATIONS
416	Atribacteria Reproducing over Millions of Years in the Atlantic Abyssal Subseafloor. <i>MBio</i> , 2020, 11, .	1.8	23
417	Isolation and cultivation of candidate phyla radiation <i>Saccharibacteria</i> (TM7) bacteria in coculture with bacterial hosts. <i>Journal of Oral Microbiology</i> , 2020, 12, 1814666.	1.2	36
418	State of the Art in the Culture of the Human Microbiota: New Interests and Strategies. <i>Clinical Microbiology Reviews</i> , 2020, 34, .	5.7	33
419	Expanding magnetic organelle biogenesis in the domain Bacteria. <i>Microbiome</i> , 2020, 8, 152.	4.9	44
420	The saccharibacterium TM7x elicits differential responses across its host range. <i>ISME Journal</i> , 2020, 14, 3054-3067.	4.4	35
421	Complete Genome Sequence of Strain BB001, a Novel Epibiont Bacterium from the Candidate Phylum Saccharibacteria (TM7). <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	4
422	Microbial Processes and Microbial Communities in the Water Column of the Polar Meromictic Lake Bolshie Khruslomeny at the White Sea Coast. <i>Frontiers in Microbiology</i> , 2020, 11, 1945.	1.5	14
423	Femtoplankton: What's New?. <i>Viruses</i> , 2020, 12, 881.	1.5	4
424	Ancestral Absence of Electron Transport Chains in Patescibacteria and DPANN. <i>Frontiers in Microbiology</i> , 2020, 11, 1848.	1.5	62
425	Microbial dark matter filling the niche in hypersaline microbial mats. <i>Microbiome</i> , 2020, 8, 135.	4.9	35
426	Microbiomes in a manganese oxide producing ecosystem in the Ytterby mine, Sweden: impact on metal mobility. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	14
427	Metagenome assembled genomes reveal similar functional profiles of <i>CPR</i> /Patescibacteria phyla in soils. <i>Environmental Microbiology Reports</i> , 2020, 12, 651-655.	1.0	27
428	Chitinases Encoded in the Genomes of Acidobacteria: Origin and Evolution. <i>Microbiology</i> , 2020, 89, 379-386.	0.5	0
429	Large freshwater phages with the potential to augment aerobic methane oxidation. <i>Nature Microbiology</i> , 2020, 5, 1504-1515.	5.9	66
430	Functional and genetic markers of niche partitioning among enigmatic members of the human oral microbiome. <i>Genome Biology</i> , 2020, 21, 292.	3.8	132
431	Discovery of Novel Biosynthetic Gene Cluster Diversity From a Soil Metagenomic Library. <i>Frontiers in Microbiology</i> , 2020, 11, 585398.	1.5	16
432	Saccharibacteria as Organic Carbon Sinks in Hydrocarbon-Fueled Communities. <i>Frontiers in Microbiology</i> , 2020, 11, 587782.	1.5	22
433	Isolation of a member of the candidate phylum Atribacteria reveals a unique cell membrane structure. <i>Nature Communications</i> , 2020, 11, 6381.	5.8	62

#	ARTICLE	IF	CITATIONS
434	Diversity, ecology and evolution of Archaea. <i>Nature Microbiology</i> , 2020, 5, 887-900.	5.9	262
435	Precise phylogenetic analysis of microbial isolates and genomes from metagenomes using PhyloPhlAn 3.0. <i>Nature Communications</i> , 2020, 11, 2500.	5.8	368
436	An evolutionary path to altered cofactor specificity in a metalloenzyme. <i>Nature Communications</i> , 2020, 11, 2738.	5.8	22
437	Microbial Ecosystems in Central Andes Extreme Environments. , 2020, , .		9
438	<i>Vermamoeba vermiformis</i> CDC-19 draft genome sequence reveals considerable gene trafficking including with candidate phyla radiation and giant viruses. <i>Scientific Reports</i> , 2020, 10, 5928.	1.6	20
439	Characterisation of fungal and bacterial dynamics in an active green wall used for indoor air pollutant removal. <i>Building and Environment</i> , 2020, 179, 106987.	3.0	24
440	Iterative subtractive binning of freshwater chronoserics metagenomes identifies over 400 novel species and their ecologic preferences. <i>Environmental Microbiology</i> , 2020, 22, 3394-3412.	1.8	69
441	Size Matters: Ultra-small and Filterable Microorganisms in the Environment. <i>Microbes and Environments</i> , 2020, 35, n/a.	0.7	45
442	Consistent Metagenome-Derived Metrics Verify and Delineate Bacterial Species Boundaries. <i>MSystems</i> , 2020, 5, .	1.7	135
443	Microbial Nitrogen Metabolism in Chloraminated Drinking Water Reservoirs. <i>MSphere</i> , 2020, 5, .	1.3	28
444	Enhancing degradation and biogas production during anaerobic digestion of food waste using alkali pretreatment. <i>Environmental Research</i> , 2020, 188, 109743.	3.7	44
445	Roadmap for naming uncultivated Archaea and Bacteria. <i>Nature Microbiology</i> , 2020, 5, 987-994.	5.9	115
446	Accurate and complete genomes from metagenomes. <i>Genome Research</i> , 2020, 30, 315-333.	2.4	263
447	Lipid analysis of CO ₂ -rich subsurface aquifers suggests an autotrophy-based deep biosphere with lysolipids enriched in CPR bacteria. <i>ISME Journal</i> , 2020, 14, 1547-1560.	4.4	29
448	The Influence of O ₂ on the Enrichment and Activities of Acidophilic Fe(III) Reducing Bacteria. <i>Geomicrobiology Journal</i> , 2020, 37, 564-571.	1.0	0
449	The rise of diversity in metabolic platforms across the Candidate Phyla Radiation. <i>BMC Biology</i> , 2020, 18, 69.	1.7	54
450	Adaptation of Carbon Source Utilization Patterns of <i>Geobacter metallireducens</i> During Sessile Growth. <i>Frontiers in Microbiology</i> , 2020, 11, 1271.	1.5	3
451	Metagenomics: Applications of functional and structural approaches and meta-omics. , 2020, , 471-505.		4

#	ARTICLE	IF	CITATIONS
452	A scoutRNA Is Required for Some Type V CRISPR-Cas Systems. <i>Molecular Cell</i> , 2020, 79, 416-424.e5.	4.5	49
453	Advantages and Limits of Metagenomic Assembly and Binning of a Giant Virus. <i>MSystems</i> , 2020, 5, .	1.7	14
454	Phylum-level diversity of the microbiome of the extremophilic basidiomycete fungus <i>Pisolithus arhizus</i> (Scop.) Rauschert: An island of biodiversity in a thermal soil desert. <i>MicrobiologyOpen</i> , 2020, 9, e1062.	1.2	9
455	Microbial Diversity, Interventions and Scope. , 2020, , .		4
456	Linkage of antibiotic resistance genes, associated bacteria communities and metabolites in the wheat rhizosphere from chlorpyrifos-contaminated soil. <i>Science of the Total Environment</i> , 2020, 741, 140457.	3.9	41
457	Design of targeted primers based on 16S rRNA sequences in meta-transcriptomic datasets and identification of a novel taxonomic group in the Asgard archaea. <i>BMC Microbiology</i> , 2020, 20, 25.	1.3	13
458	Complete Genome of a Member of a New Bacterial Lineage in the Microgenomates Group Reveals an Unusual Nucleotide Composition Disparity Between Two Strands of DNA and Limited Metabolic Potential. <i>Microorganisms</i> , 2020, 8, 320.	1.6	23
459	The Link Between the Ecology of the Prokaryotic Rare Biosphere and Its Biotechnological Potential. <i>Frontiers in Microbiology</i> , 2020, 11, 231.	1.5	37
460	FeGenie: A Comprehensive Tool for the Identification of Iron Genes and Iron Gene Neighborhoods in Genome and Metagenome Assemblies. <i>Frontiers in Microbiology</i> , 2020, 11, 37.	1.5	195
461	Insights Obtained by Culturing Saccharibacteria With Their Bacterial Hosts. <i>Journal of Dental Research</i> , 2020, 99, 685-694.	2.5	62
462	Bacterial Origin and Reductive Evolution of the CPR Group. <i>Genome Biology and Evolution</i> , 2020, 12, 103-121.	1.1	11
463	Tree of motility " A proposed history of motility systems in the tree of life. <i>Genes To Cells</i> , 2020, 25, 6-21.	0.5	108
464	Aerobic biodegradation in freshwater and marine environments of textile microfibers generated in clothes laundering: Effects of cellulose and polyester-based microfibers on the microbiome. <i>Marine Pollution Bulletin</i> , 2020, 151, 110826.	2.3	62
465	Increased replication of dissimilatory nitrate-reducing bacteria leads to decreased anammox bioreactor performance. <i>Microbiome</i> , 2020, 8, 7.	4.9	42
466	Hiding in Plain Sight: The Globally Distributed Bacterial Candidate Phylum PAUC34f. <i>Frontiers in Microbiology</i> , 2020, 11, 376.	1.5	5
467	Small and mighty: adaptation of superphylum Patescibacteria to groundwater environment drives their genome simplicity. <i>Microbiome</i> , 2020, 8, 51.	4.9	205
468	A genomic catalog of Earth's microbiomes. <i>Nature Biotechnology</i> , 2021, 39, 499-509.	9.4	457
469	Centennial glacier retreat increases sedimentation and eutrophication in Subantarctic periglacial lakes: A study case of Lake Uruguay. <i>Science of the Total Environment</i> , 2021, 754, 142066.	3.9	14

#	ARTICLE	IF	CITATIONS
470	Ecogenomics and metabolic potential of the South Atlantic Ocean microbiome. <i>Science of the Total Environment</i> , 2021, 765, 142758.	3.9	16
471	Innovations to culturing the uncultured microbial majority. <i>Nature Reviews Microbiology</i> , 2021, 19, 225-240.	13.6	254
472	Evidence for non- ϵ -methanogenic metabolisms in globally distributed archaeal clades basal to the <i>Methanomassiliicoccales</i> . <i>Environmental Microbiology</i> , 2021, 23, 340-357.	1.8	19
473	Physical connections: prokaryotes parasitizing their kin. <i>Environmental Microbiology Reports</i> , 2021, 13, 54-61.	1.0	9
474	The microbial rare biosphere: current concepts, methods and ecological principles. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	61
475	Role of Recombinant DNA Technology in Biofertilizer Production. , 2021, , 143-163.		0
476	An emerging view of the diversity, ecology and function of Archaea in alkaline hydrothermal environments. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	6
477	High temperatures enhance the microbial genetic potential to recycle C and N from necromass in high- ϵ mountain soils. <i>Global Change Biology</i> , 2021, 27, 1365-1386.	4.2	49
479	Epipelagic microbiome of the Small Aral Sea: Metagenomic structure and ecological diversity. <i>MicrobiologyOpen</i> , 2021, 10, e1142.	1.2	3
480	An Unexpectedly Complex Mitochondrion in <i>Andalucia godoyi</i> , a Protist with the Most Bacteria-like Mitochondrial Genome. <i>Molecular Biology and Evolution</i> , 2021, 38, 788-804.	3.5	8
481	Archaeal roots of intramembrane aspartyl protease siblings signal peptide peptidase and presenilin. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 232-241.	1.5	7
483	Nanopore sequencing and its application to the study of microbial communities. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 1497-1511.	1.9	106
485	Mixotrophic chemosynthesis in a deep-sea anemone from hydrothermal vents in the Pescadero Basin, Gulf of California. <i>BMC Biology</i> , 2021, 19, 8.	1.7	14
486	Genome-resolved metagenomics reveals site-specific diversity of episymbiotic CPR bacteria and DPANN archaea in groundwater ecosystems. <i>Nature Microbiology</i> , 2021, 6, 354-365.	5.9	109
487	Archaea as components of forest microbiome. , 2021, , 357-370.		0
488	MicrobeAnnotator: a user-friendly, comprehensive functional annotation pipeline for microbial genomes. <i>BMC Bioinformatics</i> , 2021, 22, 11.	1.2	61
490	Exploring Changes in the Microbiota of <i>Aedes albopictus</i> : Comparison Among Breeding Site Water, Larvae, and Adults. <i>Frontiers in Microbiology</i> , 2021, 12, 624170.	1.5	24
492	Gulf of Mexico blue hole harbors high levels of novel microbial lineages. <i>ISME Journal</i> , 2021, 15, 2206-2232.	4.4	13

#	ARTICLE	IF	CITATIONS
493	Acetylene-Fueled Trichloroethene Reductive Dechlorination in a Groundwater Enrichment Culture. <i>MBio</i> , 2021, 12, .	1.8	6
495	New Insights into the Role of Oral Microbiota Dysbiosis in the Pathogenesis of Inflammatory Bowel Disease. <i>Digestive Diseases and Sciences</i> , 2022, 67, 42-55.	1.1	21
496	Metagenomic tools in microbial ecology research. <i>Current Opinion in Biotechnology</i> , 2021, 67, 184-191.	3.3	77
497	The microbial dimension of submarine groundwater discharge: current challenges and future directions. <i>FEMS Microbiology Reviews</i> , 2021, 45, .	3.9	38
498	Biodegradation of Lindane (γ -Hexachlorocyclohexane) To Nontoxic End Products by Sequential Treatment with Three Mixed Anaerobic Microbial Cultures. <i>Environmental Science & Technology</i> , 2021, 55, 2968-2979.	4.6	11
500	Diversity and Molecular Characterization of Marine Halophilic Bacteria from Southeast Coast of India. <i>Geomicrobiology Journal</i> , 2021, 38, 524-531.	1.0	3
501	Methanogens and Their Syntrophic Partners Dominate Zones of Enhanced Magnetic Susceptibility at a Petroleum Contaminated Site. <i>Frontiers in Earth Science</i> , 2021, 9, .	0.8	10
502	Different Effects of Mineral Versus Vegetal Granular Activated Carbon Filters on the Microbial Community Composition of a Drinking Water Treatment Plant. <i>Frontiers in Ecology and Evolution</i> , 2021, 9, .	1.1	3
503	Resilience of the oral microbiome. <i>Periodontology 2000</i> , 2021, 86, 113-122.	6.3	91
505	Reductive evolution and unique predatory mode in the CPR bacterium <i>Vampirococcus lugosii</i> . <i>Nature Communications</i> , 2021, 12, 2454.	5.8	64
506	Thiocyanate and Organic Carbon Inputs Drive Convergent Selection for Specific Autotrophic <i>Azotobacter</i> and <i>Thiobacillus</i> Strains Within Complex Microbiomes. <i>Frontiers in Microbiology</i> , 2021, 12, 643368.	1.5	10
507	Evolutionary stasis of a deep subsurface microbial lineage. <i>ISME Journal</i> , 2021, 15, 2830-2842.	4.4	23
508	The tree of life describes a tripartite cellular world. <i>BioEssays</i> , 2021, 43, 2000343.	1.2	8
511	Cocultivation of an ultrasmall environmental parasitic bacterium with lytic ability against bacteria associated with wastewater foams. <i>Nature Microbiology</i> , 2021, 6, 703-711.	5.9	43
512	The History of Microbiology—A Personal Interpretation. <i>Annual Review of Microbiology</i> , 2021, 75, 1-17.	2.9	7
513	A method for achieving complete microbial genomes and improving bins from metagenomics data. <i>PLoS Computational Biology</i> , 2021, 17, e1008972.	1.5	22
514	Microbial Hotspots in Lithic Microhabitats Inferred from DNA Fractionation and Metagenomics in the Atacama Desert. <i>Microorganisms</i> , 2021, 9, 1038.	1.6	19
515	Meanders as a scaling motif for understanding of floodplain soil microbiome and biogeochemical potential at the watershed scale. <i>Microbiome</i> , 2021, 9, 121.	4.9	11

#	ARTICLE	IF	CITATIONS
517	A rooted phylogeny resolves early bacterial evolution. <i>Science</i> , 2021, 372, .	6.0	128
518	A human respiratory tract-associated bacterium with an extremely small genome. <i>Communications Biology</i> , 2021, 4, 628.	2.0	3
519	Interdomain horizontal gene transfer of nickel-binding superoxide dismutase. <i>Geobiology</i> , 2021, 19, 450-459.	1.1	11
522	Rhizomal Reclassification of Living Organisms. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5643.	1.8	16
523	Phylogenetic analysis of mutational robustness based on codon usage supports that the standard genetic code does not prefer extreme environments. <i>Scientific Reports</i> , 2021, 11, 10963.	1.6	3
525	Nonessential Ribosomal Proteins in Bacteria and Archaea Identified Using Clusters of Orthologous Genes. <i>Journal of Bacteriology</i> , 2021, 203, .	1.0	14
526	Microbial Taxonomy Run Amok. <i>Trends in Microbiology</i> , 2021, 29, 394-404.	3.5	38
527	Printing Microbial Dark Matter: Using Single Cell Dispensing and Genomics to Investigate the Patescibacteria/Candidate Phyla Radiation. <i>Frontiers in Microbiology</i> , 2021, 12, 635506.	1.5	14
528	Expanded Diversity and Phylogeny of mer Genes Broadens Mercury Resistance Paradigms and Reveals an Origin for MerA Among Thermophilic Archaea. <i>Frontiers in Microbiology</i> , 2021, 12, 682605.	1.5	37
529	Biogeochemical Mobility of Contaminants from a Replica Radioactive Waste Trench in Response to Rainfall-Induced Redox Oscillations. <i>Environmental Science & Technology</i> , 2021, 55, 8793-8805.	4.6	9
530	Complete Genome Sequence of Strain JB001, a Member of Saccharibacteria Clade G6 (â€œ Candidatus) Tj ETQq0 0.0 rgBT /Overlock 10	0.3	3
531	GUNC: detection of chimerism and contamination in prokaryotic genomes. <i>Genome Biology</i> , 2021, 22, 178.	3.8	94
533	Dissecting and tuning primer editing by proofreading polymerases. <i>Nucleic Acids Research</i> , 2021, 49, e87-e87.	6.5	9
534	Analysis of Bacterial Communities on North Sea Macroalgae and Characterization of the Isolated Planctomycetes <i>Adhaeritor mobilis</i> gen. nov., sp. nov., <i>Roseimaritima multifibrata</i> sp. nov., <i>Rosistilla ulvae</i> sp. nov. and <i>Rubripirellula lacrimiformis</i> sp. nov.. <i>Microorganisms</i> , 2021, 9, 1494.	1.6	34
535	Functional diversity of microbial communities in inactive seafloor sulfide deposits. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	16
536	Pathogenic and Indigenous Denitrifying Bacteria are Transcriptionally Active and Key Multi-Antibiotic-Resistant Players in Wastewater Treatment Plants. <i>Environmental Science & Technology</i> , 2021, 55, 10862-10874.	4.6	60
539	STRONG: metagenomics strain resolution on assembly graphs. <i>Genome Biology</i> , 2021, 22, 214.	3.8	59
542	Culture-independent assessment of the diazotrophic Bradyrhizobium communities in the Pampa and Atlantic Forest Biomes localities in southern Brazil. <i>Systematic and Applied Microbiology</i> , 2021, 44, 126228.	1.2	9

#	ARTICLE	IF	CITATIONS
545	Carbon sources of benthic fauna in temperate lakes across multiple trophic states. <i>Biogeosciences</i> , 2021, 18, 4369-4388.	1.3	7
547	Microbial biodiversity: A newly isolated cyanobacterium sheds light on the evolution of photosynthesis. <i>Current Biology</i> , 2021, 31, R843-R845.	1.8	3
548	Features of the Microbial Composition of the Belozersky Group Soda Lakes (Republic of Buryatia). <i>Inland Water Biology</i> , 2021, 14, 368-376.	0.2	0
549	Evolution of Microbial Genomics: Conceptual Shifts over a Quarter Century. <i>Trends in Microbiology</i> , 2021, 29, 582-592.	3.5	33
551	Cross-Shore and Depth Zonations in Bacterial Diversity Are Linked to Age and Source of Dissolved Organic Matter across the Intertidal Area of a Sandy Beach. <i>Microorganisms</i> , 2021, 9, 1720.	1.6	4
552	Patterns of Gene Content and Co-occurrence Constrain the Evolutionary Path toward Animal Association in Candidate Phyla Radiation Bacteria. <i>MBio</i> , 2021, 12, e0052121.	1.8	30
553	Genome-Resolved Meta-Analysis of the Microbiome in Oil Reservoirs Worldwide. <i>Microorganisms</i> , 2021, 9, 1812.	1.6	10
554	Complete Genomes of Clade G6 <i>Saccharibacteria</i> Suggest a Divergent Ecological Niche and Lifestyle. <i>MSphere</i> , 2021, 6, e0053021.	1.3	9
555	Post-weaning shifts in microbiome composition and metabolism revealed by over 25,000 pig gut metagenome-assembled genomes. <i>Microbial Genomics</i> , 2021, 7, .	1.0	9
556	Bacterial communities at a groundwater-surface water ecotone: gradual change or abrupt transition points along a contamination gradient?. <i>Environmental Microbiology</i> , 2021, 23, 6694-6706.	1.8	5
557	Reconstruction of Metagenome-Assembled Genomes from Aquaria. <i>Microbiology Resource Announcements</i> , 2021, 10, e0055721.	0.3	1
560	Soil Candidate Phyla Radiation Bacteria Encode Components of Aerobic Metabolism and Co-occur with Nanoarchaea in the Rare Biosphere of Rhizosphere Grassland Communities. <i>MSystems</i> , 2021, 6, e0120520.	1.7	24
561	Plant-Microbe Interaction: Aboveground to Belowground, from the Good to the Bad. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10388.	1.8	27
564	Host factors that shape the bacterial community structure on scalp hair shaft. <i>Scientific Reports</i> , 2021, 11, 17711.	1.6	7
565	MetaPlatanus: a metagenome assembler that combines long-range sequence links and species-specific features. <i>Nucleic Acids Research</i> , 2021, 49, e130-e130.	6.5	6
567	The Clinical Relevance of the Microbiome in Hidradenitis Suppurativa: A Systematic Review. <i>Vaccines</i> , 2021, 9, 1076.	2.1	8
568	Survival of the fittest: Prokaryotic communities within a SWRO desalination plant. <i>Desalination</i> , 2021, 514, 115152.	4.0	6
569	Description and functional testing of four species of the novel phototrophic genus <i>Chioneia</i> gen. nov., isolated from different East Antarctic environments. <i>Systematic and Applied Microbiology</i> , 2021, 44, 126250.	1.2	26

#	ARTICLE	IF	CITATIONS
570	Exploring the global vaginal microbiome and its impact on human health. <i>Microbial Pathogenesis</i> , 2021, 160, 105172.	1.3	21
572	Cometabolism of the Superphylum Patescibacteria with Anammox Bacteria in a Long-Term Freshwater Anammox Column Reactor. <i>Water (Switzerland)</i> , 2021, 13, 208.	1.2	51
573	Metagenomics: A powerful lens viewing the microbial world. , 2021, , 309-339.		4
574	Microbial Communities Composition, Activity, and Dynamics at Salar de Huasco: A Polyextreme Environment in the Chilean Altiplano. , 2020, , 123-139.		6
575	Bacteria in Indoor and Occupational Settings. , 2017, , 35-55.		2
576	History of Rhizobial Taxonomy. , 2019, , 23-39.		3
577	Endosymbiosis before eukaryotes: mitochondrial establishment in protoeukaryotes. <i>Cellular and Molecular Life Sciences</i> , 2020, 77, 3503-3523.	2.4	34
578	Modest proposals to expand the type material for naming of prokaryotes. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 2108-2112.	0.8	84
579	Metagenome-assembled genome binning methods with short reads disproportionately fail for plasmids and genomic Islands. <i>Microbial Genomics</i> , 2020, 6, .	1.0	67
649	Complete Genome Sequence of Strain PM004, a Novel Cultured Member of the Human Oral Microbiome from the Candidate Phylum <i>Saccharibacteria</i> (TM7). <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	9
650	Individuality, phenotypic differentiation, dormancy and "persistence"™ in culturable bacterial systems: commonalities shared by environmental, laboratory, and clinical microbiology. <i>F1000Research</i> , 2015, 4, 179.	0.8	46
651	Individuality, phenotypic differentiation, dormancy and "persistence"™ in culturable bacterial systems: commonalities shared by environmental, laboratory, and clinical microbiology. <i>F1000Research</i> , 2015, 4, 179.	0.8	49
652	What Is the Tree of Life?. <i>PLoS Genetics</i> , 2016, 12, e1005912.	1.5	35
653	Highly active rubiscos discovered by systematic interrogation of natural sequence diversity. <i>EMBO Journal</i> , 2020, 39, e104081.	3.5	72
655	Metagenomic Approaches Unearth Methanotroph Phylogenetic and Metabolic Diversity. <i>Current Issues in Molecular Biology</i> , 2019, 33, 57-84.	1.0	39
656	Microfluidic-based mini-metagenomics enables discovery of novel microbial lineages from complex environmental samples. <i>ELife</i> , 2017, 6, .	2.8	69
657	Metabolic network percolation quantifies biosynthetic capabilities across the human oral microbiome. <i>ELife</i> , 2019, 8, .	2.8	24
658	Single-amino acid variants reveal evolutionary processes that shape the biogeography of a global SAR11 subclade. <i>ELife</i> , 2019, 8, .	2.8	89

#	ARTICLE	IF	CITATIONS
659	Structure of the bacterial ribosome at 2 Å... resolution. <i>ELife</i> , 2020, 9, .	2.8	151
660	Biases in genome reconstruction from metagenomic data. <i>PeerJ</i> , 2020, 8, e10119.	0.9	32
661	Analysis of five complete genome sequences for members of the class Peribacteria in the recently recognized Peregrinibacteria bacterial phylum. <i>PeerJ</i> , 2016, 4, e1607.	0.9	57
662	Identifying contamination with advanced visualization and analysis practices: metagenomic approaches for eukaryotic genome assemblies. <i>PeerJ</i> , 2016, 4, e1839.	0.9	91
663	Towards quantitative viromics for both double-stranded and single-stranded DNA viruses. <i>PeerJ</i> , 2016, 4, e2777.	0.9	185
664	Metagenomic identification of active methanogens and methanotrophs in serpentinite springs of the Voltri Massif, Italy. <i>PeerJ</i> , 2017, 5, e2945.	0.9	91
665	Characterization of shifts of koala (<i>Phascolarctos cinereus</i>) intestinal microbial communities associated with antibiotic treatment. <i>PeerJ</i> , 2018, 6, e4452.	0.9	30
666	Identifying accurate metagenome and amplicon software via a meta-analysis of sequence to taxonomy benchmarking studies. <i>PeerJ</i> , 2019, 7, e6160.	0.9	34
667	Active virus-host interactions at sub-freezing temperatures in Arctic peat soil. <i>Microbiome</i> , 2021, 9, 208.	4.9	52
670	Annotating unknown species of urban microorganisms on a global scale unveils novel functional diversity and local environment association. <i>Environmental Research</i> , 2022, 207, 112183.	3.7	7
671	Episymbiotic Saccharibacteria suppresses gingival inflammation and bone loss in mice through host bacterial modulation. <i>Cell Host and Microbe</i> , 2021, 29, 1649-1662.e7.	5.1	39
672	Biosynthetic CdS-Thiobacillus thioparus hybrid for solar-driven carbon dioxide fixation. <i>Nano Research</i> , 2023, 16, 4531-4538.	5.8	10
674	Genome-resolved metagenomics reveals how soil bacterial communities respond to elevated H ₂ availability. <i>Soil Biology and Biochemistry</i> , 2021, 163, 108464.	4.2	12
701	Extremophile Microorganisms and Their Industrial Applications. , 2020, , 137-156.		1
702	Genetically Modified Microbes as Biofertilizers. , 2020, , 275-293.		3
711	Utilization of low-molecular-weight organic compounds by the filterable fraction of a lotic microbiome. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	0
712	Importance of Candidate Phyla Radiation (CPR) Bacteria for the Origin of Life. <i>Journal of Geography (Chigaku Zasshi)</i> , 2020, 129, 881-898.	0.1	5
714	Marine Ultrasmall Prokaryotes Likely Affect the Cycling of Carbon, Methane, Nitrogen, and Sulfur. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	6

#	ARTICLE	IF	CITATIONS
715	Fast and persistent responses of alpine permafrost microbial communities to in situ warming. <i>Science of the Total Environment</i> , 2022, 807, 150720.	3.9	18
716	Metagenome Mining. , 2020, , 50-89.		0
717	Surface Water Intrusion, Land Use Impacts, and Bacterial Community Composition in Shallow Groundwater Wells Supplying Potable Water in Sparsely Populated Areas of a Boreal Region. <i>Microbiology Spectrum</i> , 2021, 9, e0017921.	1.2	7
718	Cultivation of a vampire: <i>Candidatus</i> <i>Absconditicoccus praedator</i> ™. <i>Environmental Microbiology</i> , 2022, 24, 30-49.	1.8	30
719	Evaluating <i>de Novo</i> Assembly and Binning Strategies for Time Series Drinking Water Metagenomes. <i>Microbiology Spectrum</i> , 2021, 9, e0143421.	1.2	16
720	Multiple energy sources and metabolic strategies sustain microbial diversity in Antarctic desert soils. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	68
721	Microbial diversity in extreme environments. <i>Nature Reviews Microbiology</i> , 2022, 20, 219-235.	13.6	153
722	Heme auxotrophy in abundant aquatic microbial lineages. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	20
723	The Deep Rocky Biosphere: New Geomicrobiological Insights and Prospects. <i>Frontiers in Microbiology</i> , 2021, 12, 785743.	1.5	3
724	Leave no stone unturned: individually adapted xerotolerant Thaumarchaeota sheltered below the boulders of the Atacama Desert hyperarid core. <i>Microbiome</i> , 2021, 9, 234.	4.9	18
725	Genome-centric metagenomics provides new insights into the microbial community and metabolic potential of landfill leachate microbiota. <i>Science of the Total Environment</i> , 2022, 816, 151635.	3.9	7
727	The Mouse Gastrointestinal Bacteria Catalogue enables translation between the mouse and human gut microbiotas via functional mapping. <i>Cell Host and Microbe</i> , 2022, 30, 124-138.e8.	5.1	59
728	Genome-resolved evidence for functionally redundant communities and novel nitrogen fixers in the deyin-1 hydrothermal field, Mid-Atlantic Ridge. <i>Microbiome</i> , 2022, 10, 8.	4.9	5
729	Hybrid, ultra-deep metagenomic sequencing enables genomic and functional characterization of low-abundance species in the human gut microbiome. <i>Gut Microbes</i> , 2022, 14, 2021790.	4.3	27
731	Deep distributed computing to reconstruct extremely large lineage trees. <i>Nature Biotechnology</i> , 2022, 40, 566-575.	9.4	14
732	Acquisition of the arginine deiminase system benefits epiparasitic Saccharibacteria and their host bacteria in a mammalian niche environment. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	30
734	Genomic insights into versatile lifestyle of three new bacterial candidate phyla. <i>Science China Life Sciences</i> , 2022, 65, 1547-1562.	2.3	8
735	Genome Sequence of a New <i>Candidatus</i> <i>Phylum</i> <i>Dependentiae</i> Isolate from Chiba, Japan. <i>Microbiology Resource Announcements</i> , 2022, 11, e0112321.	0.3	3

#	ARTICLE	IF	CITATIONS
736	Evolving Perspective on the Origin and Diversification of Cellular Life and the Virosphere. <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	13
737	Inferring the Contribution of Microbial Taxa and Organic Matter Molecular Formulas to Ecological Assembly. <i>Frontiers in Microbiology</i> , 2022, 13, 803420.	1.5	5
738	An estimate of the deepest branches of the tree of life from ancient vertically evolving genes. <i>ELife</i> , 2022, 11, .	2.8	43
741	Reverse Genomics: Design of Universal Epitope Sets to Isolate All Saccharibacteria Members from the Human Oral Cavity. <i>Microorganisms</i> , 2022, 10, 602.	1.6	3
742	Strain-Level Variation and Diverse Host Bacterial Responses in Episymbiotic Saccharibacteria. <i>MSystems</i> , 2022, 7, e0148821.	1.7	6
743	<i>Methanosaeta</i> and <i>Candidatus Velamenicoccus archaeovorus</i> : Applied and Environmental Microbiology, 2022, 88, e0240721.	1.4	7
744	Occurrence and Seasonal Dynamics of ALNs in Freshwater Lakes Are Influenced by Their Biological Environment. <i>Microbial Ecology</i> , 2022, , 1.	1.4	0
746	Dataset for Genome Sequencing and De Novo Assembly of the Candidate Phyla Radiation in Supragingival Plaque. <i>Canadian Journal of Infectious Diseases and Medical Microbiology</i> , 2022, 2022, 1-10.	0.7	0
747	Unifying the known and unknown microbial coding sequence space. <i>ELife</i> , 2022, 11, .	2.8	41
749	From legacy contamination to watershed systems science: a review of scientific insights and technologies developed through DOE-supported research in water and energy security. <i>Environmental Research Letters</i> , 2022, 17, 043004.	2.2	12
750	Polyethylene terephthalate microplastic fibers increase the release of extracellular antibiotic resistance genes during sewage sludge anaerobic digestion. <i>Water Research</i> , 2022, 217, 118426.	5.3	29
751	CPR-C4 is a highly conserved novel protease from the Candidate Phyla Radiation with remote structural homology to human vasohibins. <i>Journal of Biological Chemistry</i> , 2022, 298, 101919.	1.6	2
752	Recovering metagenome-assembled genomes from shotgun metagenomic sequencing data: Methods, applications, challenges, and opportunities. <i>Microbiological Research</i> , 2022, 260, 127023.	2.5	17
753	Dissimilatory microbial sulfur and methane metabolism in the water column of a shallow meromictic lake. <i>Systematic and Applied Microbiology</i> , 2022, 45, 126320.	1.2	7
754	Quantifying Microbial Activity <i>In Situ</i> : the Link between Cells and Cycles. <i>MSystems</i> , 2021, 6, e0075821.	1.7	0
756	Adapted Protocol for <i>Saccharibacteria</i> Cocultivation: Two New Members Join the Club of Candidate Phyla Radiation. <i>Microbiology Spectrum</i> , 2021, 9, e0106921.	1.2	8
757	Interplay between microbial community composition and chemodiversity of dissolved organic matter throughout the Black Sea water column redox gradient. <i>Limnology and Oceanography</i> , 2022, 67, 329-347.	1.6	8
759	Small and Equipped: the Rich Repertoire of Antibiotic Resistance Genes in Candidate Phyla Radiation Genomes. <i>MSystems</i> , 2021, 6, e0089821.	1.7	13

#	ARTICLE	IF	CITATIONS
760	The economical lifestyle of CPR bacteria in groundwater allows little preference for environmental drivers. <i>Environmental Microbiomes</i> , 2021, 16, 24.	2.2	36
761	Adapting Macroecology to Microbiology: Using Occupancy Modeling To Assess Functional Profiles across Metagenomes. <i>MSystems</i> , 2021, 6, e0079021.	1.7	1
762	Above- and below-ground biodiversity responses to the prolonged flood pulse in central-western Amazonia, Brazil. <i>Environmental DNA</i> , 2022, 4, 533-548.	3.1	1
763	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
764	How clear is our current view on microbial dark matter? (Re-)assessing public MAG & SAG datasets with MDMcleaner. <i>Nucleic Acids Research</i> , 2022, 50, e76-e76.	6.5	19
765	Saccharibacteria harness light energy using type-1 rhodopsins that may rely on retinal sourced from microbial hosts. <i>ISME Journal</i> , 2022, 16, 2056-2059.	4.4	13
766	DNA sequence and taxonomic gap analyses to quantify the coverage of aquatic cyanobacteria and eukaryotic microalgae in reference databases: Results of a survey in the Alpine region. <i>Science of the Total Environment</i> , 2022, 834, 155175.	3.9	18
768	Complete Genome Sequence of <i>Candidatus</i> Nanosynbacter Strain HMT-348_TM7c-JB, a Member of <i>Saccharibacteria</i> Clade G1. <i>Microbiology Resource Announcements</i> , 2022, , e0002322.	0.3	2
876	Opportunities and challenges of using metagenomic data to bring uncultured microbes into cultivation. <i>Microbiome</i> , 2022, 10, 76.	4.9	59
877	New Beta-lactamases in Candidate Phyla Radiation: Owing Pleiotropic Enzymes Is a Smart Paradigm for Microorganisms with a Reduced Genome. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5446.	1.8	5
878	Patterns and ecological drivers of viral communities in acid mine drainage sediments across Southern China. <i>Nature Communications</i> , 2022, 13, 2389.	5.8	25
880	Holistic approach to chemical and microbiological quality of aquatic ecosystems impacted by wastewater effluent discharges. <i>Science of the Total Environment</i> , 2022, 835, 155388.	3.9	6
882	Community Structure and Microbial Associations in Sediment-Free Methanotrophic Enrichment Cultures from a Marine Methane Seep. <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	8
883	Accelerated Evolution by Diversity-Generating Retroelements. <i>Annual Review of Microbiology</i> , 2022, 76, 389-411.	2.9	12
884	Ecogenomics sheds light on diverse lifestyle strategies in freshwater CPR. <i>Microbiome</i> , 2022, 10, .	4.9	22
885	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
886	<i>Mycolicibacter acidiphilus</i> sp. nov., an extremely acid-tolerant member of the genus <i>Mycolicibacter</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	8
887	Bacterial Necromass Is Rapidly Metabolized by Heterotrophic Bacteria and Supports Multiple Trophic Levels of the Groundwater Microbiome. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	5

#	ARTICLE	IF	CITATIONS
888	Features of smaller ribosomes in candidate phyla radiation (CPR) bacteria revealed with a molecular evolutionary analysis. <i>Rna</i> , 2022, 28, 1041-1057.	1.6	5
889	Unique pool of carbohydrate-degrading enzymes in novel bacteria assembled from cow and buffalo rumen metagenomes. <i>Applied Microbiology and Biotechnology</i> , 2022, 106, 4643-4654.	1.7	4
890	Candidate Phyla Radiation, an Underappreciated Division of the Human Microbiome, and Its Impact on Health and Disease. <i>Clinical Microbiology Reviews</i> , 2022, 35, .	5.7	19
891	Metabolic Potential of the Superphylum <i>Patescibacteria</i> ; Reconstructed from Activated Sludge Samples from a Municipal Wastewater Treatment Plant. <i>Microbes and Environments</i> , 2022, 37, n/a.	0.7	11
892	It's a Long Way to the Tap: Microbiome and DNA-Based Omics at the Core of Drinking Water Quality. <i>International Journal of Environmental Research and Public Health</i> , 2022, 19, 7940.	1.2	9
893	Carbon fixation rates in groundwater similar to those in oligotrophic marine systems. <i>Nature Geoscience</i> , 2022, 15, 561-567.	5.4	28
894	PCycDB: a comprehensive and accurate database for fast analysis of phosphorus cycling genes. <i>Microbiome</i> , 2022, 10, .	4.9	30
895	Substrate-restricted methanogenesis and limited volatile organic compound degradation in highly diverse and heterogeneous municipal landfill microbial communities. <i>ISME Communications</i> , 2022, 2, .	1.7	8
897	Trawling the ocean virome. <i>Nature Methods</i> , 2022, 19, 928-931.	9.0	1
899	Microbial paracetamol degradation involves a high diversity of novel amidase enzyme candidates. <i>Water Research X</i> , 2022, 16, 100152.	2.8	22
900	Investigation of Antibiotic Resistome in Hospital Wastewater during the COVID-19 Pandemic: Is the Initial Phase of the Pandemic Contributing to Antimicrobial Resistance?. <i>Environmental Science & Technology</i> , 2022, 56, 15007-15018.	4.6	24
902	Transcriptome of Epibiont <i>Saccharibacteria</i> <i>Nanosynbacter lyticus</i> Strain TM7x During the Establishment of Symbiosis. <i>Journal of Bacteriology</i> , 2022, 204, .	1.0	4
903	Long-Read-Resolved, Ecosystem-Wide Exploration of Nucleotide and Structural Microdiversity of Lake Bacterioplankton Genomes. <i>MSystems</i> , 2022, 7, .	1.7	11
904	The overlooked role of a biotin precursor for marine bacteria - desthiobiotin as an escape route for biotin auxotrophy. <i>ISME Journal</i> , 2022, 16, 2599-2609.	4.4	9
905	Water Physicochemical Parameters and Microbial Composition Distinguish <i>Anopheles</i> and <i>Culex</i> Mosquito Breeding Sites: Potential as Ecological Markers for Larval Source Surveillance. <i>Journal of Medical Entomology</i> , 0, , .	0.9	3
906	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
907	Characterization of chlorinated paraffin-degrading bacteria from marine estuarine sediments. <i>Journal of Hazardous Materials</i> , 2022, 440, 129699.	6.5	12
908	High spatial heterogeneity and low connectivity of bacterial communities along a Mediterranean subterranean estuary. <i>Molecular Ecology</i> , 2022, 31, 5745-5764.	2.0	11

#	ARTICLE	IF	CITATIONS
909	Community and shotgun metagenomic analysis of Alligator mississippiensis oral cavity and GI tracts reveal complex ecosystems and potential reservoirs of antibiotic resistance. Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology, 2022, 274, 111319.	0.8	1
910	Assembling a Reference Phylogenomic Tree of Bacteria and Archaea by Summarizing Many Gene Phylogenies. Methods in Molecular Biology, 2022, , 137-165.	0.4	1
911	Progress and Challenges in Studying the Ecophysiology of Archaea. Methods in Molecular Biology, 2022, , 469-486.	0.4	0
912	Reconstruction of Archaeal Genomes from Short-Read Metagenomes. Methods in Molecular Biology, 2022, , 487-527.	0.4	0
913	Functional characterization of prokaryotic dark matter: the road so far and what lies ahead. Current Research in Microbial Sciences, 2022, 3, 100159.	1.4	2
914	Symbiosis between <i>Candidatus</i> Patescibacteria and Archaea Discovered in Wastewater-Treating Bioreactors. MBio, 2022, 13, .	1.8	28
915	Long-term excessive application of K ₂ SO ₄ fertilizer alters bacterial community and functional pathway of tobacco-planting soil. Frontiers in Plant Science, 0, 13, .	1.7	7
916	The dark side of the ribosome life cycle. RNA Biology, 2022, 19, 1045-1049.	1.5	2
917	Critical assessment of pan-genomic analysis of metagenome-assembled genomes. Briefings in Bioinformatics, 2022, 23, .	3.2	6
918	Metagenomic and metatranscriptomic insights into sulfate-reducing bacteria in a revegetated acidic mine wasteland. Npj Biofilms and Microbiomes, 2022, 8, .	2.9	2
920	Assessing the performance and microbial structure of biofilms in membrane aerated biofilm reactor for high p-nitrophenol concentration treatment. Journal of Environmental Chemical Engineering, 2022, 10, 108635.	3.3	6
924	Electrochemical Enrichment and Isolation of Electrogenic Bacteria from 0.22 µm Filtrate. Microorganisms, 2022, 10, 2051.	1.6	1
925	Microbial assembly and co-occurrence network in an aquifer under press perturbation. Annals of Microbiology, 2022, 72, .	1.1	2
927	<i>binny</i> : an automated binning algorithm to recover high-quality genomes from complex metagenomic datasets. Briefings in Bioinformatics, 2022, 23, .	3.2	5
928	Novel Cross-domain Symbiosis between <i>Candidatus</i> Patescibacteria and Hydrogenotrophic Methanogenic Archaea <i>Methanospirillum</i> Discovered in a Methanogenic Ecosystem. Microbes and Environments, 2022, 37, n/a.	0.7	3
929	Widespread but Poorly Understood Bacteria: Candidate Phyla Radiation. Microorganisms, 2022, 10, 2232.	1.6	9
932	A survey of the biosynthetic potential and specialized metabolites of archaea and understudied bacteria. Current Research in Biotechnology, 2023, 5, 100117.	1.9	5
933	A comparative analysis employing a gene- and genome-centric metagenomic approach reveals changes in composition, function, and activity in waterworks with different treatment processes and source water in Finland. Water Research, 2023, 229, 119495.	5.3	7

#	ARTICLE	IF	CITATIONS
934	Ecological landscape explains aquifers microbial structure. <i>Science of the Total Environment</i> , 2023, 862, 160822.	3.9	0
935	Ancient origin and constrained evolution of the division and cell wall gene cluster in Bacteria. <i>Nature Microbiology</i> , 2022, 7, 2114-2127.	5.9	19
936	Unexpected absence of ribosomal protein genes from metagenome-assembled genomes. <i>ISME Communications</i> , 2022, 2, .	1.7	13
937	Comparison of Metagenomics and Metatranscriptomics Tools: A Guide to Making the Right Choice. <i>Genes</i> , 2022, 13, 2280.	1.0	9
938	Adaptive genetic traits in pelagic freshwater microbes. <i>Environmental Microbiology</i> , 2023, 25, 606-641.	1.8	12
939	Diverse Methylmercury (MeHg) Producers and Degradars Inhabit Acid Mine Drainage Sediments, but Few Taxa Correlate with MeHg Accumulation. <i>MSystems</i> , 2023, 8, .	1.7	1
940	Type IV pili trigger episymbiotic association of Saccharibacteria with its bacterial host. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	18
941	Occurrence, Diversity, and Genomes of <i>Candidatus</i> Patescibacteria along the Early Diagenesis of Marine Sediments. <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	2
942	Here, there and everywhere: Ecology and biology of the Dependientiae phylum. <i>Environmental Microbiology</i> , 2023, 25, 597-605.	1.8	0
943	The response of rumen pH, fermentation parameters and rumen bacteria to feeds of different concentrate to roughage ratios in buffalos. , 0, 1, .		2
944	Culture-based approaches to studying "microbial dark matter". <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	3.3	2
945	Into the darkness of the microbial dark matter in situ activities through expression profiles of Patescibacteria populations. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5
946	Comparative Analysis of Metagenomic (Amplicon and Shotgun) DNA Sequencing to Characterize Microbial Communities in Household On-Site Wastewater Treatment Systems. <i>Water (Switzerland)</i> , 2023, 15, 271.	1.2	1
947	MetaBinner: a high-performance and stand-alone ensemble binning method to recover individual genomes from complex microbial communities. <i>Genome Biology</i> , 2023, 24, .	3.8	14
948	Antibiotic resistance genes and taxa analysis from mat and planktonic microbiomes of Antarctic perennial ice-covered Lake Fryxell and Lake Bonney. <i>Antarctic Science</i> , 2022, 34, 408-422.	0.5	1
949	Variable impact of geochemical gradients on the functional potential of bacteria, archaea, and phages from the permanently stratified Lac Pavin. <i>Microbiome</i> , 2023, 11, .	4.9	4
950	The Structure of Evolutionary Model Space for Proteins across the Tree of Life. <i>Biology</i> , 2023, 12, 282.	1.3	2
951	Proposal to include the categories kingdom and domain in the International Code of Nomenclature of Prokaryotes. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2023, 73, .	0.8	6

#	ARTICLE	IF	CITATIONS
952	Single-cell amplified genomes reveal most streamlined free-living marine bacteria. <i>Environmental Microbiology</i> , 2023, 25, 1136-1154.	1.8	5
953	A first insight into the Polish Bochnia Salt Mine metagenome. <i>Environmental Science and Pollution Research</i> , 2023, 30, 49551-49566.	2.7	1
954	Scientific novelty beyond the experiment. <i>Microbial Biotechnology</i> , 2023, 16, 1131-1173.	2.0	30
955	Ultra-small bacteria and archaea exhibit genetic flexibility towards groundwater oxygen content, and adaptations for attached or planktonic lifestyles. <i>ISME Communications</i> , 2023, 3, .	1.7	3
956	A novel and diverse group of Candidatus Patescibacteria from bathypelagic Lake Baikal revealed through long-read metagenomics. <i>Environmental Microbiomes</i> , 2023, 18, .	2.2	2
958	Two treatment methods on <i>Ulva prolifera</i> bloom result in distinctively different ecological effects in coastal environment. <i>Frontiers in Marine Science</i> , 0, 10, .	1.2	2
960	From the Mountain to the Valley: Drivers of Groundwater Prokaryotic Communities along an Alpine River Corridor. <i>Microorganisms</i> , 2023, 11, 779.	1.6	2
961	Genome-centric metagenomics reveals the host-driven dynamics and ecological role of CPR bacteria in an activated sludge system. <i>Microbiome</i> , 2023, 11, .	4.9	11
962	Linking prokaryotic genome size variation to metabolic potential and environment. <i>ISME Communications</i> , 2023, 3, .	1.7	1
963	Detection of specific uncultured bacteriophages by fluorescence in situ hybridisation in pig microbiome. <i>PLoS ONE</i> , 2023, 18, e0283676.	1.1	2
964	Metagenomic analyses of a microbial assemblage in a subglacial lake beneath the Vatnajökull ice cap, Iceland. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
965	O ₂ partitioning of sulfur oxidizing bacteria drives acidity and thiosulfate distributions in mining waters. <i>Nature Communications</i> , 2023, 14, .	5.8	2
967	Previously uncharacterized rectangular bacterial structures in the dolphin mouth. <i>Nature Communications</i> , 2023, 14, .	5.8	1
968	Structure and Seasonal Variability of Microbial Communities of Groundwater in the City of Moscow. <i>Microbiology</i> , 2023, 92, 192-203.	0.5	0
1000	The oral microbiome: diversity, biogeography and human health. <i>Nature Reviews Microbiology</i> , 2024, 22, 89-104.	13.6	18
1015	Machine learning for microbiologists. <i>Nature Reviews Microbiology</i> , 2024, 22, 191-205.	13.6	6
1016	Populations and Communities. , 2023, , 415-589.		1
1036	Molecular taxonomy. , 2024, , 503-510.		0

#	ARTICLE	IF	CITATIONS
1043	Candidatus Enterousia, Bacteria with Reduced Genomes from the Intestines of Farm Animals. <i>Microbiology</i> , 2023, 92, S50-S55.	0.5	0