

Fast and sensitive protein alignment using DIAMOND

Nature Methods

12, 59-60

DOI: [10.1038/nmeth.3176](https://doi.org/10.1038/nmeth.3176)

Citation Report

#	ARTICLE	IF	CITATIONS
6	Pathosphere.org: pathogen detection and characterization through a web-based, open-source informatics platform. BMC Bioinformatics, 2015, 16, 416.	2.6	16
7	Entropy-Scaling Search of Massive Biological Data. Cell Systems, 2015, 1, 130-140.	6.2	64
8	Spatially extensive microbial biogeography of the Indian Ocean provides insights into the unique community structure of a pristine coral atoll. Scientific Reports, 2015, 5, 15383.	3.3	28
9	Evaluation of shotgun metagenomics sequence classification methods using in silico and in vitro simulated communities. BMC Bioinformatics, 2015, 16, 363.	2.6	145
10	The role of biofilms as environmental reservoirs of antibiotic resistance. Frontiers in Microbiology, 2015, 6, 1216.	3.5	321
11	Similar Microbial Communities Found on Two Distant Seafloor Basalts. Frontiers in Microbiology, 2015, 6, 1409.	3.5	14
12	FCMM: A comparative metagenomic approach for functional characterization of multiple metagenome samples. Journal of Microbiological Methods, 2015, 115, 121-128.	1.6	2
13	High speed BLASTN: an accelerated MegaBLAST search tool. Nucleic Acids Research, 2015, 43, 7762-7768.	14.5	322
14	Clinical metagenomic identification of Balamuthia mandrillaris encephalitis and assembly of the draft genome: the continuing case for reference genome sequencing. Genome Medicine, 2015, 7, 113.	8.2	102
15	Roles of Thermophiles and Fungi in Bitumen Degradation in Mostly Cold Oil Sands Outcrops. Applied and Environmental Microbiology, 2015, 81, 6825-6838.	3.1	41
16	antiSMASH 3.0—a comprehensive resource for the genome mining of biosynthetic gene clusters. Nucleic Acids Research, 2015, 43, W237-W243.	14.5	1,764
17	ALP & FALP: C++ libraries for pairwise local alignment <i>E</i>-values. Bioinformatics, 2016, 32, 304-305.	4.1	7
18	Topological characterization of neuronal arbor morphology via sequence representation: II - global alignment. BMC Bioinformatics, 2015, 16, 209.	2.6	31
19	Experimental Design and Bioinformatics Analysis for the Application of Metagenomics in Environmental Sciences and Biotechnology. Environmental Science & Technology, 2015, 49, 12628-12640.	10.0	72
20	SANSParallel: interactive homology search against Uniprot. Nucleic Acids Research, 2015, 43, W24-W29.	14.5	38
21	From cultured to uncultured genome sequences: metagenomics and modeling microbial ecosystems. Cellular and Molecular Life Sciences, 2015, 72, 4287-4308.	5.4	114
22	Antibiotic Selection Pressure Determination through Sequence-Based Metagenomics. Antimicrobial Agents and Chemotherapy, 2015, 59, 7335-7345.	3.2	61
23	Complete nitrification by a single microorganism. Nature, 2015, 528, 555-559.	27.8	1,336

#	ARTICLE	IF	CITATIONS
24	Global analysis of gene expression dynamics within the marine microbial community during the VAHINE mesocosm experiment in the southwest Pacific. <i>Biogeosciences</i> , 2016, 13, 4135-4149.	3.3	17
25	Expanding the view on the evolution of the nematode dauer signalling pathways: refinement through gene gain and pathway co-option. <i>BMC Genomics</i> , 2016, 17, 476.	2.8	35
26	Tsetse fly tolerance to <i>T. brucei</i> infection: transcriptome analysis of trypanosome-associated changes in the tsetse fly salivary gland. <i>BMC Genomics</i> , 2016, 17, 971.	2.8	38
27	The Common Gut Microbe <i>Eubacterium hallii</i> also Contributes to Intestinal Propionate Formation. <i>Frontiers in Microbiology</i> , 2016, 7, 713.	3.5	224
28	Functional Metagenomics of Spacecraft Assembly Cleanrooms: Presence of Virulence Factors Associated with Human Pathogens. <i>Frontiers in Microbiology</i> , 2016, 7, 1321.	3.5	24
29	Metagenome and Metatranscriptome Analyses Using Protein Family Profiles. <i>PLoS Computational Biology</i> , 2016, 12, e1004991.	3.2	21
30	GPU-Acceleration of Sequence Homology Searches with Database Subsequence Clustering. <i>PLoS ONE</i> , 2016, 11, e0157338.	2.5	8
31	MetaStorm: A Public Resource for Customizable Metagenomics Annotation. <i>PLoS ONE</i> , 2016, 11, e0162442.	2.5	59
32	Microbial Potential for Ecosystem N Loss Is Increased by Experimental N Deposition. <i>PLoS ONE</i> , 2016, 11, e0164531.	2.5	13
34	Novel Strategies for Applied Metagenomics. <i>Inflammatory Bowel Diseases</i> , 2016, 22, 709-718.	1.9	25
35	Changes in the Functional Potential of the Gut Microbiome Following Probiotic Supplementation during <i>Helicobacter Pylori</i> Treatment. <i>Helicobacter</i> , 2016, 21, 493-503.	3.5	27
36	Methanogenic paraffin degradation proceeds via alkane addition to fumarate by <i>Smithella</i> spp. mediated by a syntrophic coupling with hydrogenotrophic methanogens. <i>Environmental Microbiology</i> , 2016, 18, 2604-2619.	3.8	71
37	Phosphorus depletion in forest soils shapes bacterial communities towards phosphorus recycling systems. <i>Environmental Microbiology</i> , 2016, 18, 1988-2000.	3.8	212
38	Metagenomic Comparison of Antibiotic Resistance Genes Associated with Liquid and Dewatered Biosolids. <i>Journal of Environmental Quality</i> , 2016, 45, 463-470.	2.0	9
39	GRASPx: efficient homolog-search of short peptide metagenome database through simultaneous alignment and assembly. <i>BMC Bioinformatics</i> , 2016, 17, 283.	2.6	5
40	Insights from the draft genome of the subsection V (Stigonematales) cyanobacterium <i>Hapalosiphon</i> sp. Strain MRB220 associated with 2-MIB production. <i>Standards in Genomic Sciences</i> , 2016, 11, 58.	1.5	8
41	A new method for decontamination of <i>de novo</i> transcriptomes using a hierarchical clustering algorithm. <i>Bioinformatics</i> , 2017, 33, 1293-1300.	4.1	26
42	Disentangling the influence of earthworms in sugarcane rhizosphere. <i>Scientific Reports</i> , 2016, 6, 38923.	3.3	38

#	ARTICLE	IF	CITATIONS
43	The venom gland transcriptome of the parasitoid wasp <i>Nasonia vitripennis</i> highlights the importance of novel genes in venom function. <i>BMC Genomics</i> , 2016, 17, 571.	2.8	18
44	FAST: Fast annotation with synchronized threads. , 2016, , .		2
45	Comparing genome versus proteome-based identification of clinical bacterial isolates. <i>Briefings in Bioinformatics</i> , 2018, 19, bbw122.	6.5	7
46	Ionic Liquids Impact the Bioenergy Feedstock-Degrading Microbiome and Transcription of Enzymes Relevant to Polysaccharide Hydrolysis. <i>MSystems</i> , 2016, 1, .	3.8	15
47	k-SLAM: accurate and ultra-fast taxonomic classification and gene identification for large metagenomic data sets. <i>Nucleic Acids Research</i> , 2017, 45, gkw1248.	14.5	50
48	Metagenomic profiling of historic Colorado Front Range flood impact on distribution of riverine antibiotic resistance genes. <i>Scientific Reports</i> , 2016, 6, 38432.	3.3	55
49	Identification and genome reconstruction of abundant distinct taxa in microbiomes from one thermophilic and three mesophilic production-scale biogas plants. <i>Biotechnology for Biofuels</i> , 2016, 9, 156.	6.2	120
50	Challenges in the analysis of viral metagenomes. <i>Virus Evolution</i> , 2016, 2, vew022.	4.9	83
51	Computational prospecting the great viral unknown. <i>FEMS Microbiology Letters</i> , 2016, 363, fnw077.	1.8	56
52	Evaluating techniques for metagenome annotation using simulated sequence data. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw095.	2.7	61
53	The information science of microbial ecology. <i>Current Opinion in Microbiology</i> , 2016, 31, 209-216.	5.1	26
54	AC-DIAMOND: Accelerating Protein Alignment via Better SIMD Parallelization and Space-Efficient Indexing. <i>Lecture Notes in Computer Science</i> , 2016, , 426-433.	1.3	1
55	MOCAT2: a metagenomic assembly, annotation and profiling framework. <i>Bioinformatics</i> , 2016, 32, 2520-2523.	4.1	172
56	Soil biochar amendment shapes the composition of N ₂ O-reducing microbial communities. <i>Science of the Total Environment</i> , 2016, 562, 379-390.	8.0	117
57	Graph mining for next generation sequencing: leveraging the assembly graph for biological insights. <i>BMC Genomics</i> , 2016, 17, 340.	2.8	2
58	Single-Cell Genome and Group-Specific <i>dsrAB</i> Sequencing Implicate Marine Members of the Class <i>Dehalococcoidia</i> (Phylum <i>Chloroflexi</i>) in Sulfur Cycling. <i>MBio</i> , 2016, 7, .	4.1	78
59	Comparative transcriptome analysis of <i>Gastrodia elata</i> (Orchidaceae) in response to fungus symbiosis to identify gastrodin biosynthesis-related genes. <i>BMC Genomics</i> , 2016, 17, 212.	2.8	39
60	Novel oligonucleotide primers reveal a high diversity of microbes which drive phosphorous turnover in soil. <i>Journal of Microbiological Methods</i> , 2016, 125, 91-97.	1.6	80

#	ARTICLE	IF	CITATIONS
61	High Throughput Analysis of Integron Gene Cassettes in Wastewater Environments. Environmental Science & Technology, 2016, 50, 11825-11836.	10.0	68
62	Reading the Underlying Information From Massive Metagenomic Sequencing Data. Proceedings of the IEEE, 2016, , 1-15.	21.3	12
63	SAR11 bacteria linked to ocean anoxia and nitrogen loss. Nature, 2016, 536, 179-183.	27.8	160
64	Computational biology in the 21st century. Communications of the ACM, 2016, 59, 72-80.	4.5	56
65	Elucidating and mining the Tulipa and Lilium transcriptomes. Plant Molecular Biology, 2016, 92, 249-261.	3.9	16
66	Fast and sensitive taxonomic classification for metagenomics with Kaiju. Nature Communications, 2016, 7, 11257.	12.8	1,406
67	SWORDâ€”a highly efficient protein database search. Bioinformatics, 2016, 32, i680-i684.	4.1	21
68	COMAN: a web server for comprehensive metatranscriptomics analysis. BMC Genomics, 2016, 17, 622.	2.8	34
69	Reprint of â€œNovel mycoviruses discovered from metatranscriptomics survey of soybean phyllosphere phytobiomesâ€•. Virus Research, 2016, 219, 11-21.	2.2	13
70	A Bayesian inference method for the analysis of transcriptional regulatory networks in metagenomic data. Algorithms for Molecular Biology, 2016, 11, 19.	1.2	11
71	Comparative metagenomics unveils functions and genome features of microbialite-associated communities along a depth gradient. Environmental Microbiology, 2016, 18, 4990-5004.	3.8	30
72	An evaluation of the accuracy and speed of metagenome analysis tools. Scientific Reports, 2016, 6, 19233.	3.3	278
73	FMAP: Functional Mapping and Analysis Pipeline for metagenomics and metatranscriptomics studies. BMC Bioinformatics, 2016, 17, 420.	2.6	98
74	Draft Genome Sequence of a Tropical Freshwater Cyanobacterium, <i>Limnothrix</i> sp. Strain P13C2. Genome Announcements, 2016, 4, .	0.8	3
75	Isolation and genomic characterization of Culex theileri flaviviruses in field-collected mosquitoes from Turkey. Infection, Genetics and Evolution, 2016, 46, 138-147.	2.3	13
76	MetaTrans: an open-source pipeline for metatranscriptomics. Scientific Reports, 2016, 6, 26447.	3.3	87
77	Integrative microbial community analysis reveals full-scale enhanced biological phosphorus removal under tropical conditions. Scientific Reports, 2016, 6, 25719.	3.3	61
78	Novel highly divergent reassortant bat rotaviruses in Cameroon, without evidence of zoonosis. Scientific Reports, 2016, 6, 34209.	3.3	44

#	ARTICLE	IF	CITATIONS
79	A metagenomic-based survey of microbial (de)halogenation potential in a German forest soil. <i>Scientific Reports</i> , 2016, 6, 28958.	3.3	51
80	ROcker: accurate detection and quantification of target genes in short-read metagenomic data sets by modeling sliding-window bitscores. <i>Nucleic Acids Research</i> , 2017, 45, gkw900.	14.5	37
81	The Gut Microbiome of Pediatric Crohn's Disease Patients Differs from Healthy Controls in Genes That Can Influence the Balance Between a Healthy and Dysregulated Immune Response. <i>Inflammatory Bowel Diseases</i> , 2016, 22, 2607-2618.	1.9	33
82	Molecular analysis of the Sydney rock oyster (<i>Saccostrea glomerata</i>) CO2 stress response. <i>Climate Change Responses</i> , 2016, 3, .	2.6	9
83	Proteomic Stable Isotope Probing Reveals Taxonomically Distinct Patterns in Amino Acid Assimilation by Coastal Marine Bacterioplankton. <i>MSystems</i> , 2016, 1, .	3.8	43
84	Metagenomic analysis reveals that bacteriophages are reservoirs of antibiotic resistance genes. <i>International Journal of Antimicrobial Agents</i> , 2016, 48, 163-167.	2.5	121
85	The evolution of genome mining in microbes – a review. <i>Natural Product Reports</i> , 2016, 33, 988-1005.	10.3	538
86	The MG-RAST metagenomics database and portal in 2015. <i>Nucleic Acids Research</i> , 2016, 44, D590-D594.	14.5	187
87	Taxonomer: an interactive metagenomics analysis portal for universal pathogen detection and host mRNA expression profiling. <i>Genome Biology</i> , 2016, 17, 111.	8.8	152
88	An integrated metagenome and -proteome analysis of the microbial community residing in a biogas production plant. <i>Journal of Biotechnology</i> , 2016, 231, 268-279.	3.8	33
89	Environmental Breviatea harbour mutualistic <i>Arcobacter</i> epibionts. <i>Nature</i> , 2016, 534, 254-258.	27.8	68
90	The genome of the yellow potato cyst nematode, <i>Globodera rostochiensis</i> , reveals insights into the basis of parasitism and virulence. <i>Genome Biology</i> , 2016, 17, 124.	8.8	156
91	MetaPro-IQ: a universal metaproteomic approach to studying human and mouse gut microbiota. <i>Microbiome</i> , 2016, 4, 31.	11.1	154
92	Time- and Oil-Dependent Transcriptomic and Physiological Responses to <i>Deepwater Horizon</i> Oil in Mahi-Mahi (<i>Coryphaena hippurus</i>) Embryos and Larvae. <i>Environmental Science & Technology</i> , 2016, 50, 7842-7851.	10.0	123
93	Novel mycoviruses discovered from metatranscriptomics survey of soybean phyllosphere phytobiomes. <i>Virus Research</i> , 2016, 213, 332-342.	2.2	136
94	Potential and pitfalls of eukaryotic metagenome skimming: a test case for lichens. <i>Molecular Ecology Resources</i> , 2016, 16, 511-523.	4.8	24
95	Defining the microbial transcriptional response to colitis through integrated host and microbiome profiling. <i>ISME Journal</i> , 2016, 10, 2389-2404.	9.8	40
96	MMseqs software suite for fast and deep clustering and searching of large protein sequence sets. <i>Bioinformatics</i> , 2016, 32, 1323-1330.	4.1	131

#	ARTICLE	IF	CITATIONS
97	Assessment of k-mer spectrum applicability for metagenomic dissimilarity analysis. BMC Bioinformatics, 2016, 17, 38.	2.6	57
98	SUPER-FOCUS: a tool for agile functional analysis of shotgun metagenomic data. Bioinformatics, 2016, 32, 354-361.	4.1	161
99	A simple statistical test of taxonomic or functional homogeneity using replicated microbiome sequencing samples. Journal of Biotechnology, 2017, 250, 45-50.	3.8	1
100	Gut microbiota dysbiosis contributes to the development of hypertension. Microbiome, 2017, 5, 14.	11.1	1,086
101	An optimistic protein assembly from sequence reads salvaged an uncharacterized segment of mouse picobirnavirus. Scientific Reports, 2017, 7, 40447.	3.3	2
102	Soil microbial communities and elk foraging intensity: implications for soil biogeochemical cycling in the sagebrush steppe. Ecology Letters, 2017, 20, 202-211.	6.4	21
103	A fast and robust protocol for metataxonomic analysis using RNAseq data. Microbiome, 2017, 5, 7.	11.1	25
104	Fast and simple protein-alignment-guided assembly of orthologous gene families from microbiome sequencing reads. Microbiome, 2017, 5, 11.	11.1	31
105	Differential sharing and distinct co-occurrence networks among spatially close bacterial microbiota of bark, mosses and lichens. Molecular Ecology, 2017, 26, 2826-2838.	3.9	79
106	Genome of a giant bacteriophage from a decaying Trichodesmium bloom. Marine Genomics, 2017, 33, 21-25.	1.1	7
107	The transcriptome of the avian malaria parasite <i>Plasmodium ashfordi</i> displays host-specific gene expression. Molecular Ecology, 2017, 26, 2939-2958.	3.9	41
108	Shotgun metagenomic sequencing reveals freshwater beach sands as reservoir of bacterial pathogens. Water Research, 2017, 115, 360-369.	11.3	41
109	Neanderthal behaviour, diet, and disease inferred from ancient DNA in dental calculus. Nature, 2017, 544, 357-361.	27.8	398
110	Association of the Intestinal Microbiome with the Development of Neovascular Age-Related Macular Degeneration. Scientific Reports, 2017, 7, 40826.	3.3	149
111	Comparative analysis of metagenomes of Italian top soil improvers. Environmental Research, 2017, 155, 108-115.	7.5	5
112	Rapid protein alignment in the cloud: HAMOND combines fast DIAMOND alignments with Hadoop parallelism. Journal of Biotechnology, 2017, 257, 58-60.	3.8	5
113	Microbial potential for carbon and nutrient cycling in a geogenic supercritical carbon dioxide reservoir. Environmental Microbiology, 2017, 19, 2228-2245.	3.8	25
114	Advances in the application of high-throughput sequencing in invertebrate virology. Journal of Invertebrate Pathology, 2017, 147, 145-156.	3.2	12

#	ARTICLE	IF	CITATIONS
115	Microbial Respiration and Formate Oxidation as Metabolic Signatures of Inflammation-Associated Dysbiosis. <i>Cell Host and Microbe</i> , 2017, 21, 208-219.	11.0	239
116	Diversity and functions of the sheep faecal microbiota: a multi-omic characterization. <i>Microbial Biotechnology</i> , 2017, 10, 541-554.	4.2	51
117	Validation of Metagenomic Next-Generation Sequencing Tests for Universal Pathogen Detection. <i>Archives of Pathology and Laboratory Medicine</i> , 2017, 141, 776-786.	2.5	404
118	Blubber transcriptome response to acute stress axis activation involves transient changes in adipogenesis and lipolysis in a fasting-adapted marine mammal. <i>Scientific Reports</i> , 2017, 7, 42110.	3.3	40
119	Origins and challenges of viral dark matter. <i>Virus Research</i> , 2017, 239, 136-142.	2.2	167
120	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.	7.1	98
121	Ancient <scp>DNA</scp> analysis identifies marine mollusc shells as new metagenomic archives of the past. <i>Molecular Ecology Resources</i> , 2017, 17, 835-853.	4.8	62
122	Soda pans of the Pannonian steppe harbor unique bacterial communities adapted to multiple extreme conditions. <i>Extremophiles</i> , 2017, 21, 639-649.	2.3	44
123	Arsenic metabolism in high altitude modern stromatolites revealed by metagenomic analysis. <i>Scientific Reports</i> , 2017, 7, 1024.	3.3	75
124	A submarine volcanic eruption leads to a novel microbial habitat. <i>Nature Ecology and Evolution</i> , 2017, 1, 144.	7.8	42
125	Massive horizontal transfer of transposable elements in insects. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 4721-4726.	7.1	184
126	RNA-seq analysis of the salt stress-induced transcripts in fast-growing bioenergy tree, <i>Paulownia elongata</i>. <i>Journal of Plant Interactions</i> , 2017, 12, 128-136.	2.1	12
127	Metagenomics analysis of red blood cell and fresh-frozen plasma units. <i>Transfusion</i> , 2017, 57, 1787-1800.	1.6	24
128	From data to knowledge: The future of multi-omics data analysis for the rhizosphere. <i>Rhizosphere</i> , 2017, 3, 222-229.	3.0	30
129	Diversity of bacteria and archaea from two shallow marine hydrothermal vents from Vulcano Island. <i>Extremophiles</i> , 2017, 21, 733-742.	2.3	48
130	Gut Microbiome Function Predicts Response to Anti-integrin Biologic Therapy in Inflammatory Bowel Diseases. <i>Cell Host and Microbe</i> , 2017, 21, 603-610.e3.	11.0	306
131	Bioinformatics tools for quantitative and functional metagenome and metatranscriptome data analysis in microbes. <i>Briefings in Bioinformatics</i> , 2018, 19, 1415-1429.	6.5	34
132	A high-coverage draft genome of the mycalesine butterfly <i>Bicyclus anynana</i> . <i>GigaScience</i> , 2017, 6, 1-7.	6.4	55

#	ARTICLE	IF	CITATIONS
133	Fast Genome-Wide Functional Annotation through Orthology Assignment by eggNOG-Mapper. <i>Molecular Biology and Evolution</i> , 2017, 34, 2115-2122.	8.9	2,156
134	GHOSTX: A Fast Sequence Homology Search Tool for Functional Annotation of Metagenomic Data. <i>Methods in Molecular Biology</i> , 2017, 1611, 15-25.	0.9	8
135	From Gene Annotation to Function Prediction for Metagenomics. <i>Methods in Molecular Biology</i> , 2017, 1611, 27-34.	0.9	12
136	Functional association prediction by community profiling. <i>Methods</i> , 2017, 129, 8-17.	3.8	5
137	antiSMASH 4.0â€”improvements in chemistry prediction and gene cluster boundary identification. <i>Nucleic Acids Research</i> , 2017, 45, W36-W41.	14.5	1,196
138	A Robust Framework for Microbial Archaeology. <i>Annual Review of Genomics and Human Genetics</i> , 2017, 18, 321-356.	6.2	144
139	The metabolic potential of the single cell genomes obtained from the Challenger Deep, <scp>M</scp>ariana <scp>T</scp>rench within the candidate superphylum <scp>P</scp>arcubacteria (<scp>OD</scp>1). <i>Environmental Microbiology</i> , 2017, 19, 2769-2784.	3.8	88
140	Functional implications of microbial and viral gut metagenome changes in early stage L-DOPA-naÃ“ve Parkinsonâ€™s disease patients. <i>Genome Medicine</i> , 2017, 9, 39.	8.2	420
141	Random sequences are an abundant source of bioactive RNAs or peptides. <i>Nature Ecology and Evolution</i> , 2017, 1, 0217.	7.8	76
142	Landâ€™use influences phosphatase gene microdiversity in soils. <i>Environmental Microbiology</i> , 2017, 19, 2740-2753.	3.8	115
143	Viral gut metagenomics of sympatric wild and domestic canids, and monitoring of viruses: Insights from an endangered wolf population. <i>Ecology and Evolution</i> , 2017, 7, 4135-4146.	1.9	28
144	Stormwater loadings of antibiotic resistance genes in an urban stream. <i>Water Research</i> , 2017, 123, 144-152.	11.3	101
145	Dysbiosis in chronic periodontitis: Key microbial players and interactions with the human host. <i>Scientific Reports</i> , 2017, 7, 3703.	3.3	174
146	SANDPUMA: ensemble predictions of nonribosomal peptide chemistry reveal biosynthetic diversity across <i>Actinobacteria</i>. <i>Bioinformatics</i> , 2017, 33, 3202-3210.	4.1	89
147	Effects of uranium concentration on microbial community structure and functional potential. <i>Environmental Microbiology</i> , 2017, 19, 3323-3341.	3.8	38
148	The Role of Denitrification in Stormwater Detention Basin Treatment of Nitrogen. <i>Environmental Science & Technology</i> , 2017, 51, 7928-7935.	10.0	52
149	plantiSMASH: automated identification, annotation and expression analysis of plant biosynthetic gene clusters. <i>Nucleic Acids Research</i> , 2017, 45, W55-W63.	14.5	193
150	Novel highly divergent sapoviruses detected by metagenomics analysis in straw-colored fruit bats in Cameroon. <i>Emerging Microbes and Infections</i> , 2017, 6, 1-7.	6.5	44

#	ARTICLE	IF	CITATIONS
151	Epibionts dominate metabolic functional potential of <i>Trichodesmium</i> colonies from the oligotrophic ocean. <i>ISME Journal</i> , 2017, 11, 2090-2101.	9.8	65
152	Genome Sequence of a Bovine Rhinitis B Virus Identified in Cattle in Sweden. <i>Genome Announcements</i> , 2017, 5, .	0.8	5
153	A six-gene phylogenetic overview of Basidiomycota and allied phyla with estimated divergence times of higher taxa and a phyloproteomics perspective. <i>Fungal Diversity</i> , 2017, 84, 43-74.	12.3	124
154	Predation by <i>Bdellovibrio bacteriovorus</i> significantly reduces viability and alters the microbial community composition of activated sludge flocs and granules. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	2.7	45
155	Evolutionary Transcriptomics and Proteomics: Insight into Plant Adaptation. <i>Trends in Plant Science</i> , 2017, 22, 462-471.	8.8	51
156	H-BLAST: a fast protein sequence alignment toolkit on heterogeneous computers with GPUs. <i>Bioinformatics</i> , 2017, 33, 1130-1138.	4.1	18
157	Giant viruses with an expanded complement of translation system components. <i>Science</i> , 2017, 356, 82-85.	12.6	234
158	Factors influencing ruminal bacterial community diversity and composition and microbial fibrolytic enzyme abundance in lactating dairy cows with a focus on the role of active dry yeast. <i>Journal of Dairy Science</i> , 2017, 100, 4377-4393.	3.4	53
159	Electrochemical and genomic analysis of novel electroactive isolates obtained via potentiostatic enrichment from tropical sediment. <i>Journal of Power Sources</i> , 2017, 356, 539-548.	7.8	26
160	A novel rhabdovirus, related to Merida virus, in field-collected mosquitoes from Anatolia and Thrace. <i>Archives of Virology</i> , 2017, 162, 1903-1911.	2.1	18
161	Selective Isolation of a <i>Eucalyptus</i> spp. Woodchip Bacterial Community and Its Taxonomic and Metabolic Profiling. <i>Bioenergy Research</i> , 2017, 10, 547-565.	3.9	4
162	A review of microscopy and comparative molecular-based methods to characterize "Plastisphere" communities. <i>Analytical Methods</i> , 2017, 9, 2132-2143.	2.7	76
163	Candidate new rotavirus species in Schreiber's bats, Serbia. <i>Infection, Genetics and Evolution</i> , 2017, 48, 19-26.	2.3	155
164	Metagenomic profiling of gut microbial communities in both wild and artificially reared Bar-headed goose (<i>Anser indicus</i>). <i>MicrobiologyOpen</i> , 2017, 6, e00429.	3.0	39
165	Protracted Regional Dissemination of GIM-1-Producing <i>Serratia marcescens</i> in Western Germany. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	3.2	6
166	Loeffler 4.0: Diagnostic Metagenomics. <i>Advances in Virus Research</i> , 2017, 99, 17-37.	2.1	14
167	Metagenomic and metatranscriptomic analysis of saliva reveals disease-associated microbiota in patients with periodontitis and dental caries. <i>Npj Biofilms and Microbiomes</i> , 2017, 3, 23.	6.4	109
168	Diatoms dominate the eukaryotic metatranscriptome during spring in coastal "dead zone" sediments. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20171617.	2.6	15

#	ARTICLE	IF	CITATIONS
169	Analysis of the bacterial microbiome in the small octopus, <i>Octopus variabilis</i> , from South Korea to detect the potential risk of foodborne illness and to improve product management. Food Research International, 2017, 102, 51-60.	6.2	11
170	The making of a miscreant: tobacco smoke and the creation of pathogen-rich biofilms. Npj Biofilms and Microbiomes, 2017, 3, 26.	6.4	33
171	Sequencing genomes from mixed DNA samples - evaluating the metagenome skimming approach in lichenized fungi. Scientific Reports, 2017, 7, 14881.	3.3	41
172	Bioinformatics for Microbiome Research: Concepts, Strategies, and Advances. , 2017, , 111-123.		3
173	Microbial Community Composition and Functions Through Metagenomics. , 2017, , 633-657.		0
174	Functional Analysis in Metagenomics Using MEGAN 6. , 2017, , 65-74.		12
175	Metagenome Assembly and Functional Annotation. , 2017, , 151-159.		0
176	MMseqs2 enables sensitive protein sequence searching for the analysis of massive data sets. Nature Biotechnology, 2017, 35, 1026-1028.	17.5	1,879
177	Genomic diversification of giant enteric symbionts reflects host dietary lifestyles. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E7592-E7601.	7.1	64
178	Bioinformatics for NGS-based metagenomics and the application to biogas research. Journal of Biotechnology, 2017, 261, 10-23.	3.8	84
179	Towards a Universal Molecular Microbiological Test. Journal of Clinical Microbiology, 2017, 55, 3175-3182.	3.9	18
180	Supplemental thymol and carvacrol increases ileum <i>Lactobacillus</i> population and reduces effect of necrotic enteritis caused by <i>Clostridium perfringens</i> in chickens. Scientific Reports, 2017, 7, 7334.	3.3	56
181	De novo transcriptome assembly for the spiny mouse (<i>Acomys cahirinus</i>). Scientific Reports, 2017, 7, 8996.	3.3	37
182	Intermittent Fasting Promotes White Adipose Browning and Decreases Obesity by Shaping the Gut Microbiota. Cell Metabolism, 2017, 26, 672-685.e4.	16.2	427
183	Metagenomic insight into the microbial networks and metabolic mechanism in anaerobic digesters for food waste by incorporating activated carbon. Scientific Reports, 2017, 7, 11293.	3.3	53
184	Genome characteristics and environmental distribution of the first phage that infects the LD28 clade, a freshwater methylotrophic bacterial group. Environmental Microbiology, 2017, 19, 4714-4727.	3.8	26
186	Deep Sequencing of RNA from Blood and Oral Swab Samples Reveals the Presence of Nucleic Acid from a Number of Pathogens in Patients with Acute Ebola Virus Disease and Is Consistent with Bacterial Translocation across the Gut. MSphere, 2017, 2, .	2.9	30
187	Ninety-nine <i>de novo</i> assembled genomes from the moose (<i>Alces alces</i>) rumen microbiome provide new insights into microbial plant biomass degradation. ISME Journal, 2017, 11, 2538-2551.	9.8	120

#	ARTICLE	IF	CITATIONS
188	The core transcriptome of mammalian placentas and the divergence of expression with placental shape. <i>Placenta</i> , 2017, 57, 71-78.	1.5	62
189	Cryptic oxygen cycling in anoxic marine zones. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 8319-8324.	7.1	116
190	Contamination of the Arctic reflected in microbial metagenomes from the Greenland ice sheet. <i>Environmental Research Letters</i> , 2017, 12, 074019.	5.2	41
191	Multi-omics Analysis of Periodontal Pocket Microbial Communities Pre- and Posttreatment. <i>MSystems</i> , 2017, 2, .	3.8	47
192	Soil nutritional status and biogeography influence rhizosphere microbial communities associated with the invasive tree <i>Acacia dealbata</i> . <i>Scientific Reports</i> , 2017, 7, 6472.	3.3	54
193	Metagenomic Analysis of Silage. <i>Journal of Visualized Experiments</i> , 2017, , .	0.3	7
194	Characterization of <i>Legionella</i> Species from Watersheds in British Columbia, Canada. <i>MSphere</i> , 2017, 2, .	2.9	32
196	Legume crop rotation suppressed nitrifying microbial community in a sugarcane cropping soil. <i>Scientific Reports</i> , 2017, 7, 16707.	3.3	42
197	Major role of nitrite-oxidizing bacteria in dark ocean carbon fixation. <i>Science</i> , 2017, 358, 1046-1051.	12.6	229
198	Increased Biosynthetic Gene Dosage in a Genome-Reduced Defensive Bacterial Symbiont. <i>MSystems</i> , 2017, 2, .	3.8	46
199	Assessing species biomass contributions in microbial communities via metaproteomics. <i>Nature Communications</i> , 2017, 8, 1558.	12.8	211
200	Total Lipopolysaccharide from the Human Gut Microbiome Silences Toll-Like Receptor Signaling. <i>MSystems</i> , 2017, 2, .	3.8	202
201	Virioplankton Assemblage Structure in the Lower River and Ocean Continuum of the Amazon. <i>MSphere</i> , 2017, 2, .	2.9	10
202	Soil biochar amendment affects the diversity of <i>nosZ</i> transcripts: Implications for N ₂ O formation. <i>Scientific Reports</i> , 2017, 7, 3338.	3.3	55
203	Microbial survival strategies in ancient permafrost: insights from metagenomics. <i>ISME Journal</i> , 2017, 11, 2305-2318.	9.8	149
204	Marine viruses discovered via metagenomics shed light on viral strategies throughout the oceans. <i>Nature Communications</i> , 2017, 8, 15955.	12.8	231
205	ARMAN [™] archaea depend on association with euryarchaeal host in culture and in situ. <i>Nature Communications</i> , 2017, 8, 60.	12.8	116
206	Challenges and perspectives of metaproteomic data analysis. <i>Journal of Biotechnology</i> , 2017, 261, 24-36.	3.8	195

#	ARTICLE	IF	CITATIONS
207	Fast and accurate HLA typing from short-read next-generation sequence data with xHLA. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 8059-8064.	7.1	118
208	Best hits of 11110110111: model-free selection and parameter-free sensitivity calculation of spaced seeds. Algorithms for Molecular Biology, 2017, 12, 1.	1.2	27
209	Co-circulation of West Nile virus and distinct insect-specific flaviviruses in Turkey. Parasites and Vectors, 2017, 10, 149.	2.5	24
210	Using metagenomics to investigate human and environmental resistomes. Journal of Antimicrobial Chemotherapy, 2017, 72, 2690-2703.	3.0	87
211	Candidate Brocadiales dominates C, N and S cycling in anoxic groundwater of a pristine limestone-fracture aquifer. Journal of Proteomics, 2017, 152, 153-160.	2.4	36
212	Severe Gut Microbiota Dysbiosis Is Associated With Poor Growth in Patients With Short Bowel Syndrome. Journal of Parenteral and Enteral Nutrition, 2017, 41, 1202-1212.	2.6	58
213	Identification of a Lineage D Betacoronavirus in Cave Nectar Bats (<i>Eonycteris spelaea</i>) in Singapore and an Overview of Lineage D Reservoir Ecology in SE Asian Bats. Transboundary and Emerging Diseases, 2017, 64, 1790-1800.	3.0	22
214	Antimicrobial resistance surveillance in the genomic age. Annals of the New York Academy of Sciences, 2017, 1388, 78-91.	3.8	71
215	Acute Liver Failure Due to Echovirus 9 Associated With Persistent B-Cell Depletion From Rituximab. Open Forum Infectious Diseases, 2017, 4, ofx174.	0.9	11
216	Functional gene networks based on the gene neighborhood in metagenomes. Animal Cells and Systems, 2017, 21, 301-306.	2.2	10
217	Identification of an enterovirus recombinant with a torovirus-like gene insertion during a diarrhea outbreak in fattening pigs. Virus Evolution, 2017, 3, vex024.	4.9	30
218	Bioinformatics in Microbiome Analysis. Methods in Microbiology, 2017, 44, 1-18.	0.8	4
219	Enhanced Desiccation Tolerance in Mature Cultures of the Streptophytic Green Alga <i>Zygnema circumcarinatum</i> Revealed by Transcriptomics. Plant and Cell Physiology, 2017, 58, 2067-2084.	3.1	95
220	Scaling bioinformatics applications on HPC. BMC Bioinformatics, 2017, 18, 501.	2.6	9
221	Whole metagenome profiles of particulates collected from the International Space Station. Microbiome, 2017, 5, 81.	11.1	54
222	Bayes ANOVA <i>Euglena gracilis</i>		
223	Efficient Distributed Smith-Waterman Algorithm Based on Apache Spark. , 2017, , .		9
224	A Dramatic Difference in Global Gene Expression between TCDD-Treated Atlantic Tomcod Larvae from the Resistant Hudson River and a Nearby Sensitive Population. Genome Biology and Evolution, 2017, 9, 2251-2264.	2.5	2

#	ARTICLE	IF	CITATIONS
225	Analysis of Plant Pan-Genomes and Transcriptomes with GET_HOMOLOGUES-EST, a Clustering Solution for Sequences of the Same Species. <i>Frontiers in Plant Science</i> , 2017, 8, 184.	3.6	63
226	RNA-seq: Applications and Best Practices. , 0, , .		17
227	Multi-Omic Biogeography of the Gastrointestinal Microbiota of a Pre-Weaned Lamb. <i>Proteomes</i> , 2017, 5, 36.	3.5	10
228	Optimisation of 16S rRNA gut microbiota profiling of extremely low birth weight infants. <i>BMC Genomics</i> , 2017, 18, 841.	2.8	47
229	The All-Rounder Sodalis: A New Bacteriome-Associated Endosymbiont of the Lygaeoid Bug <i>Henestaris halophilus</i> (Heteroptera: Henestariinae) and a Critical Examination of Its Evolution. <i>Genome Biology and Evolution</i> , 2017, 9, 2893-2910.	2.5	65
230	Comparative Pan-Genome Analysis of <i>Piscirickettsia salmonis</i> Reveals Genomic Divergences within Genogroups. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 459.	3.9	52
231	Draft of Zucchini (<i>Cucurbita pepo</i> L.) Proteome: A Resource for Genetic and Genomic Studies. <i>Frontiers in Genetics</i> , 2017, 8, 181.	2.3	18
232	Metagenomic Binning Recovers a Transcriptionally Active Gammaproteobacterium Linking Methanotrophy to Partial Denitrification in an Anoxic Oxygen Minimum Zone. <i>Frontiers in Marine Science</i> , 2017, 4, .	2.5	44
233	Diversity and Transcriptional Levels of RuBisCO Form II of Sulfur-Oxidizing γ -Proteobacteria in Coastal-Upwelling Waters with Seasonal Anoxia. <i>Frontiers in Marine Science</i> , 2017, 4, .	2.5	4
234	Metatranscriptomics Reveals the Active Bacterial and Eukaryotic Fibrolytic Communities in the Rumen of Dairy Cow Fed a Mixed Diet. <i>Frontiers in Microbiology</i> , 2017, 8, 67.	3.5	131
235	Trophic Interactions of Infant <i>Bifidobacteria</i> and <i>Eubacterium hallii</i> during L-Fucose and Fucosyllactose Degradation. <i>Frontiers in Microbiology</i> , 2017, 8, 95.	3.5	131
236	Metagenomic Sequencing for Surveillance of Food- and Waterborne Viral Diseases. <i>Frontiers in Microbiology</i> , 2017, 8, 230.	3.5	57
237	Metaproteogenomics Reveals Taxonomic and Functional Changes between Cecal and Fecal Microbiota in Mouse. <i>Frontiers in Microbiology</i> , 2017, 8, 391.	3.5	66
238	Untangling Genomes of Novel Planctomycetal and Verrucomicrobial Species from Monterey Bay Kelp Forest Metagenomes by Refined Binning. <i>Frontiers in Microbiology</i> , 2017, 8, 472.	3.5	70
239	Structure and Function of the Fecal Microbiota in Diarrheic Neonatal Piglets. <i>Frontiers in Microbiology</i> , 2017, 8, 502.	3.5	103
240	Toward a Metagenomic Understanding on the Bacterial Composition and Resistome in Hong Kong Banknotes. <i>Frontiers in Microbiology</i> , 2017, 8, 632.	3.5	21
241	Comparative Genomic Analysis of the Class Epsilonproteobacteria and Proposed Reclassification to Epsilonbacteraeota (phyl. nov.). <i>Frontiers in Microbiology</i> , 2017, 8, 682.	3.5	409
242	Conserved Transcriptional Responses to Nutrient Stress in Bloom-Forming Algae. <i>Frontiers in Microbiology</i> , 2017, 8, 1279.	3.5	31

#	ARTICLE	IF	CITATIONS
243	Unraveling Core Functional Microbiota in Traditional Solid-State Fermentation by High-Throughput Amplicons and Metatranscriptomics Sequencing. <i>Frontiers in Microbiology</i> , 2017, 8, 1294.	3.5	181
244	Unraveling the Microbial Interactions and Metabolic Potentials in Pre- and Post-treated Sludge from a Wastewater Treatment Plant Using Metagenomic Studies. <i>Frontiers in Microbiology</i> , 2017, 8, 1382.	3.5	27
245	Environmental Pollutant Benzo[a]Pyrene Impacts the Volatile Metabolome and Transcriptome of the Human Gut Microbiota. <i>Frontiers in Microbiology</i> , 2017, 8, 1562.	3.5	48
246	Alternative Growth Promoters Modulate Broiler Gut Microbiome and Enhance Body Weight Gain. <i>Frontiers in Microbiology</i> , 2017, 8, 2088.	3.5	88
247	Microbial Community Composition and Functional Capacity in a Terrestrial Ferruginous, Sulfate-Depleted Mud Volcano. <i>Frontiers in Microbiology</i> , 2017, 8, 2137.	3.5	32
248	PALADIN: protein alignment for functional profiling whole metagenome shotgun data. <i>Bioinformatics</i> , 2017, 33, 1473-1478.	4.1	38
249	The Influence of Age and Sex on Ocular Surface Microbiota in Healthy Adults. , 2017, 58, 6030.		107
250	Taxonomic differences of gut microbiomes drive cellulolytic enzymatic potential within hind-gut fermenting mammals. <i>PLoS ONE</i> , 2017, 12, e0189404.	2.5	22
251	Comparing and Evaluating Metagenome Assembly Tools from a Microbiologist's Perspective - Not Only Size Matters!. <i>PLoS ONE</i> , 2017, 12, e0169662.	2.5	186
252	Comparative genomics of the tardigrades <i>Hypsibius dujardini</i> and <i>Ramazzottius varieornatus</i> . <i>PLoS Biology</i> , 2017, 15, e2002266.	5.6	170
253	Multidomain analyses of a longitudinal human microbiome intestinal cleanout perturbation experiment. <i>PLoS Computational Biology</i> , 2017, 13, e1005706.	3.2	64
254	Comprehensive benchmarking and ensemble approaches for metagenomic classifiers. <i>Genome Biology</i> , 2017, 18, 182.	8.8	260
255	Temporal dynamics in microbial soil communities at anthrax carcass sites. <i>BMC Microbiology</i> , 2017, 17, 206.	3.3	12
256	Isolation and characterization of the fall Chinook aquareovirus. <i>Virology Journal</i> , 2017, 14, 170.	3.4	8
257	Metagenomic mining pectinolytic microbes and enzymes from an apple pomace-adapted compost microbial community. <i>Biotechnology for Biofuels</i> , 2017, 10, 198.	6.2	27
258	Generic amplification and next generation sequencing reveal Crimean-Congo hemorrhagic fever virus AP92-like strain and distinct tick phleboviruses in Anatolia, Turkey. <i>Parasites and Vectors</i> , 2017, 10, 335.	2.5	37
259	VirFinder: a novel k-mer based tool for identifying viral sequences from assembled metagenomic data. <i>Microbiome</i> , 2017, 5, 69.	11.1	433
260	Environmental drivers of viral community composition in Antarctic soils identified by viromics. <i>Microbiome</i> , 2017, 5, 83.	11.1	94

#	ARTICLE	IF	CITATIONS
261	Deciphering functional diversification within the lichen microbiota by meta-omics. <i>Microbiome</i> , 2017, 5, 82.	11.1	91
262	Huanglongbing impairs the rhizosphere-to-rhizoplane enrichment process of the citrus root-associated microbiome. <i>Microbiome</i> , 2017, 5, 97.	11.1	177
263	Perilipin-2 modulates dietary fat-induced microbial global gene expression profiles in the mouse intestine. <i>Microbiome</i> , 2017, 5, 117.	11.1	17
264	More than 2500 years of oil exposure shape sediment microbiomes with the potential for syntrophic degradation of hydrocarbons linked to methanogenesis. <i>Microbiome</i> , 2017, 5, 118.	11.1	31
265	The gut mycobiome of the Human Microbiome Project healthy cohort. <i>Microbiome</i> , 2017, 5, 153.	11.1	609
266	Potential and active functions in the gut microbiota of a healthy human cohort. <i>Microbiome</i> , 2017, 5, 79.	11.1	123
267	Complete genome sequence of the marine <i>Rhodococcus</i> sp. H-CA8f isolated from Comau fjord in Northern Patagonia, Chile. <i>Marine Genomics</i> , 2018, 40, 13-17.	1.1	9
268	Filling the Gaps in the Kirromycin Biosynthesis: Deciphering the Role of Genes Involved in Ethylmalonyl-CoA Supply and Tailoring Reactions. <i>Scientific Reports</i> , 2018, 8, 3230.	3.3	17
270	Bioinformatics Tools for Shotgun Metagenomic Data Analysis. , 2018, , 91-110.		4
272	Horizontal gene cluster transfer increased hallucinogenic mushroom diversity. <i>Evolution Letters</i> , 2018, 2, 88-101.	3.3	73
273	Assembly of 913 microbial genomes from metagenomic sequencing of the cow rumen. <i>Nature Communications</i> , 2018, 9, 870.	12.8	405
274	Transcriptional patterns identify resource controls on the diazotroph <i>Trichodesmium</i> in the Atlantic and Pacific oceans. <i>ISME Journal</i> , 2018, 12, 1486-1495.	9.8	17
275	Effects of timber harvesting on the genetic potential for carbon and nitrogen cycling in five North American forest ecozones. <i>Scientific Reports</i> , 2018, 8, 3142.	3.3	17
276	Enhanced phytoremediation of <i>Robinia pseudoacacia</i> in heavy metal-contaminated soils with rhizobia and the associated bacterial community structure and function. <i>Chemosphere</i> , 2018, 197, 729-740.	8.2	64
277	The first <i>Taxus</i> rhizosphere microbiome revealed by shotgun metagenomic sequencing. <i>Journal of Basic Microbiology</i> , 2018, 58, 501-512.	3.3	9
278	Application of metagenome analysis to characterize the molecular diversity and saxitoxin-producing potentials of a cyanobacterial community: a case study in the North Han River, Korea. <i>Applied Biological Chemistry</i> , 2018, 61, 153-161.	1.9	16
279	Fecal microbiota transplantation reverses antibiotic and chemotherapy-induced gut dysbiosis in mice. <i>Scientific Reports</i> , 2018, 8, 6219.	3.3	99
280	ViDiTâ€“CACTUS: an inexpensive and versatile library preparation and sequence analysis method for virus discovery and other microbiology applications. <i>Canadian Journal of Microbiology</i> , 2018, 64, 761-773.	1.7	12

#	ARTICLE	IF	CITATIONS
281	A Blast implementation in Hadoop MapReduce using low cost commodity hardware. <i>Procedia Computer Science</i> , 2018, 127, 69-75.	2.0	5
282	Detection and characterization of a rhabdovirus causing mortality in black bullhead catfish, <i>Ameiurus melas</i> . <i>Journal of Fish Diseases</i> , 2018, 41, 1063-1075.	1.9	4
283	Transcriptome of the bivalve <i>Limecola balthica</i> L. from Western Pacific: A new resource for studies of European populations. <i>Marine Genomics</i> , 2018, 40, 58-63.	1.1	4
284	Transcriptome analysis of <i>Pinus halepensis</i> under drought stress and during recovery. <i>Tree Physiology</i> , 2018, 38, 423-441.	3.1	96
285	Genome-by-genome approach for fast bacterial genealogical relationship evaluation. <i>Bioinformatics</i> , 2018, 34, 3025-3027.	4.1	25
286	RNA Sequencing of Stentor Cell Fragments Reveals Transcriptional Changes during Cellular Regeneration. <i>Current Biology</i> , 2018, 28, 1281-1288.e3.	3.9	21
287	Analysis of the genomic basis of functional diversity in dinoflagellates using a transcriptome-based sequence similarity network. <i>Molecular Ecology</i> , 2018, 27, 2365-2380.	3.9	12
288	Microbial activity during a coastal phytoplankton bloom on the Western Antarctic Peninsula in late summer. <i>FEMS Microbiology Letters</i> , 2018, 365, .	1.8	24
289	A resource for sustainable management: De novo assembly and annotation of the liver transcriptome of the Atlantic chub mackerel, <i>Scomber colias</i> . <i>Data in Brief</i> , 2018, 18, 276-284.	1.0	7
290	Mapping the virome in wild-caught <i>Aedes aegypti</i> from Cairns and Bangkok. <i>Scientific Reports</i> , 2018, 8, 4690.	3.3	84
291	GO FEAT: a rapid web-based functional annotation tool for genomic and transcriptomic data. <i>Scientific Reports</i> , 2018, 8, 1794.	3.3	99
292	DNA stable-isotope probing identifies uncultivated members of <i>Pseudonocardia</i> associated with biodegradation of pyrene in agricultural soil. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	2.7	25
293	Hologenomic adaptations underlying the evolution of sanguivory in the common vampire bat. <i>Nature Ecology and Evolution</i> , 2018, 2, 659-668.	7.8	124
294	Biochar affects community composition of nitrous oxide reducers in a field experiment. <i>Soil Biology and Biochemistry</i> , 2018, 119, 143-151.	8.8	46
295	Respiratory disease in ball pythons (<i>Python regius</i>) experimentally infected with ball python nidovirus. <i>Virology</i> , 2018, 517, 77-87.	2.4	35
296	New Insights into the Function and Global Distribution of Polyethylene Terephthalate (PET)-Degrading Bacteria and Enzymes in Marine and Terrestrial Metagenomes. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	259
297	Whole metagenome sequencing reveals links between mosquito microbiota and insecticide resistance in malaria vectors. <i>Scientific Reports</i> , 2018, 8, 2084.	3.3	101
298	ARGs-OAP v2.0 with an expanded SARG database and Hidden Markov Models for enhancement characterization and quantification of antibiotic resistance genes in environmental metagenomes. <i>Bioinformatics</i> , 2018, 34, 2263-2270.	4.1	375

#	ARTICLE	IF	CITATIONS
299	Anaerobic degradation of 1-methylnaphthalene by a member of the Thermoanaerobacteraceae contained in an iron-reducing enrichment culture. <i>Biodegradation</i> , 2018, 29, 23-39.	3.0	35
300	Coordinated gene expression between <i>Trichodesmium</i> and its microbiome over day–night cycles in the North Pacific Subtropical Gyre. <i>ISME Journal</i> , 2018, 12, 997-1007.	9.8	57
301	A model species for agricultural pest genomics: the genome of the Colorado potato beetle, <i>Leptinotarsa decemlineata</i> (Coleoptera: Chrysomelidae). <i>Scientific Reports</i> , 2018, 8, 1931.	3.3	215
302	Genomic insights into metabolic potentials of two simultaneous aerobic denitrification and phosphorus removal bacteria, <i>Achromobacter</i> sp. GAD3 and <i>Agrobacterium</i> sp. LAD9. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	2.7	31
303	Corallivory and the microbial debacle in two branching scleractinians. <i>ISME Journal</i> , 2018, 12, 1109-1126.	9.8	18
304	Significance of dark CO ₂ fixation in arctic soils. <i>Soil Biology and Biochemistry</i> , 2018, 119, 11-21.	8.8	58
305	Investigation on microbial diversity of industrial Zhacai paocai during fermentation using high-throughput sequencing and their functional characterization. <i>LWT - Food Science and Technology</i> , 2018, 91, 460-466.	5.2	86
306	Bipartite Network Analysis of Gene Sharings in the Microbial World. <i>Molecular Biology and Evolution</i> , 2018, 35, 899-913.	8.9	31
307	Temporal and Spatial Distribution of the Acetic Acid Bacterium Communities throughout the Wooden Casks Used for the Fermentation and Maturation of Lambic Beer Underlines Their Functional Role. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	32
308	Community proteogenomics reveals the systemic impact of phosphorus availability on microbial functions in tropical soil. <i>Nature Ecology and Evolution</i> , 2018, 2, 499-509.	7.8	116
309	A global ocean atlas of eukaryotic genes. <i>Nature Communications</i> , 2018, 9, 373.	12.8	297
310	The Long Intergenic Noncoding RNA (LincRNA) Landscape of the Soybean Genome. <i>Plant Physiology</i> , 2018, 176, 2133-2147.	4.8	88
311	A new mechanistic understanding of light-limitation in the seagrass <i>Zostera muelleri</i> . <i>Marine Environmental Research</i> , 2018, 134, 55-67.	2.5	19
312	Direct sequencing of the white spot syndrome virus from Brazil: Genome assembly and new insights on phylogeny. <i>Virus Research</i> , 2018, 245, 52-61.	2.2	9
313	Genomic features of bacterial adaptation to plants. <i>Nature Genetics</i> , 2018, 50, 138-150.	21.4	480
314	Symposium review: Mining metagenomic and metatranscriptomic data for clues about microbial metabolic functions in ruminants. <i>Journal of Dairy Science</i> , 2018, 101, 5605-5618.	3.4	24
315	Comparative Genomics Highlights Symbiotic Capacities and High Metabolic Flexibility of the Marine Genus <i>Pseudovibrio</i> . <i>Genome Biology and Evolution</i> , 2018, 10, 125-142.	2.5	26
316	PLAZA 4.0: an integrative resource for functional, evolutionary and comparative plant genomics. <i>Nucleic Acids Research</i> , 2018, 46, D1190-D1196.	14.5	460

#	ARTICLE	IF	CITATIONS
317	Gamma-aminobutyric Acid Enriched Rice Bran Diet Attenuates Insulin Resistance and Balances Energy Expenditure via Modification of Gut Microbiota and Short-Chain Fatty Acids. <i>Journal of Agricultural and Food Chemistry</i> , 2018, 66, 881-890.	5.2	54
318	Metagenomic and metabolomic analyses unveil dysbiosis of gut microbiota in chronic heart failure patients. <i>Scientific Reports</i> , 2018, 8, 635.	3.3	218
319	Deep sequence analysis reveals the ovine rumen as a reservoir of antibiotic resistance genes. <i>Environmental Pollution</i> , 2018, 235, 571-575.	7.5	26
320	<i>Salmonella enterica</i> genomes from victims of a major sixteenth-century epidemic in Mexico. <i>Nature Ecology and Evolution</i> , 2018, 2, 520-528.	7.8	218
321	Metatranscriptome of human faecal microbial communities in a cohort of adult men. <i>Nature Microbiology</i> , 2018, 3, 356-366.	13.3	168
322	Dynamics of metatranscription in the inflammatory bowel disease gut microbiome. <i>Nature Microbiology</i> , 2018, 3, 337-346.	13.3	408
323	Shared Nearest Neighbor Clustering in a Locality Sensitive Hashing Framework. <i>Journal of Computational Biology</i> , 2018, 25, 236-250.	1.6	6
324	Metagenomic analysis of antibiotic resistance genes in coastal industrial mariculture systems. <i>Bioresource Technology</i> , 2018, 253, 235-243.	9.6	101
325	Functional metagenomics reveals a novel carbapenem-hydrolyzing mobile beta-lactamase from Indian river sediments contaminated with antibiotic production waste. <i>Environment International</i> , 2018, 112, 279-286.	10.0	60
326	Metagenomic exploration reveals a marked change in the river resistome and mobilome after treated wastewater discharges. <i>Environmental Pollution</i> , 2018, 234, 538-542.	7.5	44
327	MetaCherchant: analyzing genomic context of antibiotic resistance genes in gut microbiota. <i>Bioinformatics</i> , 2018, 34, 434-444.	4.1	31
328	Female Mimicry by Sneaker Males Has a Transcriptomic Signature in Both the Brain and the Gonad in a Sex-Changing Fish. <i>Molecular Biology and Evolution</i> , 2018, 35, 225-241.	8.9	29
329	Functional sequencing read annotation for high precision microbiome analysis. <i>Nucleic Acids Research</i> , 2018, 46, e23-e23.	14.5	33
330	Studying microbial functionality within the gut ecosystem by systems biology. <i>Genes and Nutrition</i> , 2018, 13, 5.	2.5	31
331	Flexible metagenome analysis using the MGX framework. <i>Microbiome</i> , 2018, 6, 76.	11.1	29
332	Generic accelerated sequence alignment in SeqAn using vectorization and multi-threading. <i>Bioinformatics</i> , 2018, 34, 3437-3445.	4.1	30
333	CoNekT: an open-source framework for comparative genomic and transcriptomic network analyses. <i>Nucleic Acids Research</i> , 2018, 46, W133-W140.	14.5	81
334	Shifting metabolic priorities among key protistan taxa within and below the euphotic zone. <i>Environmental Microbiology</i> , 2018, 20, 2865-2879.	3.8	32

#	ARTICLE	IF	CITATIONS
335	Phylogenomic analyses reveal extensive gene flow within the magic flowers (<i>Achimenes</i>). American Journal of Botany, 2018, 105, 726-740.	1.7	11
336	Abundance and taxonomic affiliation of molybdenum transport and utilization genes in Tengchong hot springs, China. Environmental Microbiology, 2018, 20, 2397-2409.	3.8	5
337	Bacterial potentials for uptake, solubilization and mineralization of extracellular phosphorus in agricultural soils are highly stable under different fertilization regimes. Environmental Microbiology Reports, 2018, 10, 320-327.	2.4	49
338	A metagenomic survey identifies Tamdy orthonairovirus as well as divergent phlebo-, rhabdo-, chu- and flavi-like viruses in Anatolia, Turkey. Ticks and Tick-borne Diseases, 2018, 9, 1173-1183.	2.7	48
339	The plant hormone abscisic acid regulates the growth and metabolism of endophytic fungus <i>Aspergillus nidulans</i> . Scientific Reports, 2018, 8, 6504.	3.3	34
340	Practical considerations for plant phylogenomics. Applications in Plant Sciences, 2018, 6, e1038.	2.1	165
341	Improving the annotation of the <i>Heterorhabditis bacteriophora</i> genome. GigaScience, 2018, 7, .	6.4	18
342	The consistent differential expression of genetic pathways following exposure of an industrial <i>Pseudomonas aeruginosa</i> strain to preservatives and a laundry detergent formulation. FEMS Microbiology Letters, 2018, 365, .	1.8	10
343	Embryophyte stress signaling evolved in the algal progenitors of land plants. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E3471-E3480.	7.1	164
344	taxMaps: comprehensive and highly accurate taxonomic classification of short-read data in reasonable time. Genome Research, 2018, 28, 751-758.	5.5	25
345	A barnavirus sequence mined from a transcriptome of the Antarctic pearlwort <i>Colobanthus quitensis</i> . Archives of Virology, 2018, 163, 1921-1926.	2.1	15
346	GraftM: a tool for scalable, phylogenetically informed classification of genes within metagenomes. Nucleic Acids Research, 2018, 46, e59-e59.	14.5	130
347	A Metagenome-Based Investigation of Gene Relationships for Non-Substrate-Associated Microbial Phosphorus Cycling in the Water Column of Streams and Rivers. Microbial Ecology, 2018, 76, 856-865.	2.8	5
348	Metagenomic insight into methanogenic reactors promoting direct interspecies electron transfer via granular activated carbon. Bioresource Technology, 2018, 259, 414-422.	9.6	108
349	Microbiome Dynamics in a Large Artificial Seawater Aquarium. Applied and Environmental Microbiology, 2018, 84, .	3.1	33
350	Analysis of culturable and non-culturable bacteria and their potential to form biofilms in a primary treated dairy wastewater system. Environmental Technology (United Kingdom), 2018, 39, 2185-2192.	2.2	11
351	dbCAN-seq: a database of carbohydrate-active enzyme (CAZyme) sequence and annotation. Nucleic Acids Research, 2018, 46, D516-D521.	14.5	224
352	Genomes of Novel Microbial Lineages Assembled from the Sub-Ice Waters of Lake Baikal. Applied and Environmental Microbiology, 2018, 84, .	3.1	91

#	ARTICLE	IF	CITATIONS
353	panX: pan-genome analysis and exploration. <i>Nucleic Acids Research</i> , 2018, 46, e5-e5.	14.5	241
354	Metagenomic insights into zooplankton-associated bacterial communities. <i>Environmental Microbiology</i> , 2018, 20, 492-505.	3.8	57
355	Microbiome dynamics and adaptation of expression signatures during methane production failure and process recovery. <i>Bioresource Technology</i> , 2018, 247, 347-356.	9.6	16
356	Phage hunters: Computational strategies for finding phages in large-scale omics datasets. <i>Virus Research</i> , 2018, 244, 110-115.	2.2	33
357	Feeding strategy shapes gut metagenomic enrichment and functional specialization in captive lemurs. <i>Gut Microbes</i> , 2018, 9, 202-217.	9.8	21
358	An unusual presentation of pseudocowpox associated with an outbreak of pustular ulcerative vulvovaginitis in a Swedish dairy herd. <i>Journal of Veterinary Diagnostic Investigation</i> , 2018, 30, 256-259.	1.1	5
359	Metabolic versatility of small archaea Micrarchaeota and Parvarchaeota. <i>ISME Journal</i> , 2018, 12, 756-775.	9.8	91
360	Metagenomic sequencing of environmental DNA reveals marine faunal assemblages from the West Antarctic Peninsula. <i>Marine Genomics</i> , 2018, 37, 148-160.	1.1	92
361	Diverse replication-associated protein encoding circular DNA viruses in guano samples of Central-Eastern European bats. <i>Archives of Virology</i> , 2018, 163, 671-678.	2.1	14
362	<i>Trichoderma harzianum</i> MTCC 5179 impacts the population and functional dynamics of microbial community in the rhizosphere of black pepper (<i>Piper nigrum</i> L.). <i>Brazilian Journal of Microbiology</i> , 2018, 49, 463-470.	2.0	38
363	Pan-arthropod analysis reveals somatic piRNAs as an ancestral defence against transposable elements. <i>Nature Ecology and Evolution</i> , 2018, 2, 174-181.	7.8	214
364	Metatranscriptomics analysis of cyanobacterial aggregates during cyanobacterial bloom period in Lake Taihu, China. <i>Environmental Science and Pollution Research</i> , 2018, 25, 4811-4825.	5.3	20
365	Comparison of methods for library construction and short read annotation of shellfish viral metagenomes. <i>Genes and Genomics</i> , 2018, 40, 281-288.	1.4	3
366	De novo assembly of the kidney and spleen transcriptomes of the cosmopolitan blue shark, <i>Prionace glauca</i> . <i>Marine Genomics</i> , 2018, 37, 50-53.	1.1	6
367	West Nile virus, <i>Anopheles flavivirus</i> , a novel flavivirus as well as Merida-like rhabdovirus Turkey in field-collected mosquitoes from Thrace and Anatolia. <i>Infection, Genetics and Evolution</i> , 2018, 57, 36-45.	2.3	23
368	Old meets new: most probable number validation of metagenomic and metatranscriptomic datasets in soil. <i>Letters in Applied Microbiology</i> , 2018, 66, 14-18.	2.2	4
369	Molecular Characterization of an Endozoicomonas-Like Organism Causing Infection in the King Scallop (<i>Pecten maximus</i> L.). <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	23
370	Evaluating in Vitro Culture Medium of Gut Microbiome with Orthogonal Experimental Design and a Metaproteomics Approach. <i>Journal of Proteome Research</i> , 2018, 17, 154-163.	3.7	41

#	ARTICLE	IF	CITATIONS
371	Vector-borne viruses and their detection by viral metagenomics. <i>Infection Ecology and Epidemiology</i> , 2018, 8, 1553465.	0.8	3
372	Global transcriptome analysis of the aphelid <i>Paraphelidium tribonemae</i> supports the phagotrophic origin of fungi. <i>Communications Biology</i> , 2018, 1, 231.	4.4	63
373	VirNet: Deep attention model for viral reads identification. , 2018, , .		17
374	MetaFlow: an interactive user-friendly workflow for automated analysis of whole genome shotgun sequencing metagenomic data. , 2018, , .		0
375	Microbial Ecology on Solar Panels in Berkeley, CA, United States. <i>Frontiers in Microbiology</i> , 2018, 9, 3043.	3.5	23
376	Read cloud sequencing elucidates microbiome dynamics in a hematopoietic cell transplant patient. , 2018, 2018, 234-241.		2
377	Complete Genome Sequence of Psittacine Adenovirus 1, Identified from <i>Poicephalus senegalus</i> in Italy. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	8
378	Hidden diversity and evolution of viruses in market fish. <i>Virus Evolution</i> , 2018, 4, vey031.	4.9	54
379	Potential Applications and Challenges of Metagenomics in Human Viral Infections. , 0, , .		2
380	BARM and BalticMicrobeDB, a reference metagenome and interface to meta-omic data for the Baltic Sea. <i>Scientific Data</i> , 2018, 5, 180146.	5.3	54
381	Genetic characterization of extraintestinal <i>Escherichia coli</i> isolates from chicken, cow and swine. <i>AMB Express</i> , 2018, 8, 117.	3.0	10
382	Changes in feeding habits promoted the differentiation of the composition and function of gut microbiotas between domestic dogs (<i>Canis lupus familiaris</i>) and gray wolves (<i>Canis lupus</i>). <i>AMB Express</i> , 2018, 8, 123.	3.0	30
384	Chronic Physical Disturbance Substantially Alters the Response of Biological Soil Crusts to a Wetting Pulse, as Characterized by Metatranscriptomic Sequencing. <i>Frontiers in Microbiology</i> , 2018, 9, 2382.	3.5	40
385	Visualization-assisted binning of metagenome assemblies reveals potential new pathogenic profiles in idiopathic travelersâ€™ diarrhea. <i>Microbiome</i> , 2018, 6, 201.	11.1	20
386	Molecular Investigation of the Ciliate <i>Spirostomum semivirescens</i> , with First Transcriptome and New Geographical Records. <i>Protist</i> , 2018, 169, 875-886.	1.5	22
387	Complete Genome Sequence of <i>Austwickia chelonae</i> LK16-18, Isolated from Crocodile Lizards. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	2
388	Characterisation of the British honey bee metagenome. <i>Nature Communications</i> , 2018, 9, 4995.	12.8	51
389	KrakenUniq: confident and fast metagenomics classification using unique k-mer counts. <i>Genome Biology</i> , 2018, 19, 198.	8.8	283

#	ARTICLE	IF	CITATIONS
390	Hidden diversity of soil giant viruses. <i>Nature Communications</i> , 2018, 9, 4881.	12.8	112
391	Use of Next-Generation Sequencing for Diagnosis of West Nile Virus Infection in Patient Returning to Belgium from Hungary. <i>Emerging Infectious Diseases</i> , 2018, 24, 2380-2382.	4.3	14
392	Disseminated <i>Spiroplasma apis</i> Infection in Patient with Agammaglobulinemia, France. <i>Emerging Infectious Diseases</i> , 2018, 24, 2382-2386.	4.3	13
393	The structure and function of the global citrus rhizosphere microbiome. <i>Nature Communications</i> , 2018, 9, 4894.	12.8	304
394	Microbial Functional Responses to Cholesterol Catabolism in Denitrifying Sludge. <i>MSystems</i> , 2018, 3, .	3.8	12
395	Reevaluating the Salty Divide: Phylogenetic Specificity of Transitions between Marine and Freshwater Systems. <i>MSystems</i> , 2018, 3, .	3.8	37
396	Abundance of Chlorinated Solvent and 1,4-Dioxane Degrading Microorganisms at Five Chlorinated Solvent Contaminated Sites Determined via Shotgun Sequencing. <i>Environmental Science & Technology</i> , 2018, 52, 13914-13924.	10.0	16
397	Succession and persistence of microbial communities and antimicrobial resistance genes associated with International Space Station environmental surfaces. <i>Microbiome</i> , 2018, 6, 204.	11.1	107
398	The gill-associated microbiome is the main source of wood plant polysaccharide hydrolases and secondary metabolite gene clusters in the mangrove shipworm <i>Neoteredo reynei</i> . <i>PLoS ONE</i> , 2018, 13, e0200437.	2.5	18
399	Transcriptionally Active Lung Microbiome and Its Association with Bacterial Biomass and Host Inflammatory Status. <i>MSystems</i> , 2018, 3, .	3.8	58
400	Genome-wide identification and characterization of long non-coding RNAs involved in the early somatic embryogenesis in <i>Dimocarpus longan</i> Lour. <i>BMC Genomics</i> , 2018, 19, 805.	2.8	45
401	Genetic diversity, infection prevalence, and possible transmission routes of <i>Bartonella</i> spp. in vampire bats. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006786.	3.0	46
402	Genome Sequence of the Soybean Cyst Nematode (<i>Heterodera glycines</i>) Endosymbiont <i>Candidatus Cardinium hertigi</i> Strain cHgTN10. <i>Genome Announcements</i> , 2018, 6, .	0.8	6
403	The Gastric Microbiome Is Perturbed in Advanced Gastric Adenocarcinoma Identified Through Shotgun Metagenomics. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 433.	3.9	88
404	Viral diversity of <i>Rhipicephalus microplus</i> parasitizing cattle in southern Brazil. <i>Scientific Reports</i> , 2018, 8, 16315.	3.3	72
405	Genome-Wide Comparison of Carbohydrate-Active Enzymes (CAZymes) Repertoire of <i>Flammulina ononis</i> . <i>Mycobiology</i> , 2018, 46, 349-360.	1.7	14
406	A metatranscriptomic analysis of diseased social wasps (<i>Vespula vulgaris</i>) for pathogens, with an experimental infection of larvae and nests. <i>PLoS ONE</i> , 2018, 13, e0209589.	2.5	13
407	PhageWeb – Web Interface for Rapid Identification and Characterization of Prophages in Bacterial Genomes. <i>Frontiers in Genetics</i> , 2018, 9, 644.	2.3	30

#	ARTICLE	IF	CITATIONS
408	Phylogenomic Analysis of the Gammaproteobacterial Methanotrophs (Order Methylococcales) Calls for the Reclassification of Members at the Genus and Species Levels. <i>Frontiers in Microbiology</i> , 2018, 9, 3162.	3.5	156
409	Draft Genome Sequence of the Extremely Desiccation-Tolerant Cyanobacterium <i>Gloeocapsopsis</i> sp. Strain AAB1. <i>Genome Announcements</i> , 2018, 6, .	0.8	12
410	Communities of Phytoplankton Viruses across the Transition Zone of the St. Lawrence Estuary. <i>Viruses</i> , 2018, 10, 672.	3.3	5
411	Gut microbiota composition and functional changes in inflammatory bowel disease and irritable bowel syndrome. <i>Science Translational Medicine</i> , 2018, 10, .	12.4	351
412	Species Designations Belie Phenotypic and Genotypic Heterogeneity in Oral Streptococci. <i>MSystems</i> , 2018, 3, .	3.8	45
413	Adaptions of Lichen Microbiota Functioning Under Persistent Exposure to Arsenic Contamination. <i>Frontiers in Microbiology</i> , 2018, 9, 2959.	3.5	16
414	Hunters or farmers? Microbiome characteristics help elucidate the diet composition in an aquatic carnivorous plant. <i>Microbiome</i> , 2018, 6, 225.	11.1	29
415	Transcriptome-Stable Isotope Probing Provides Targeted Functional and Taxonomic Insights Into Microaerobic Pollutant-Degrading Aquifer Microbiota. <i>Frontiers in Microbiology</i> , 2018, 9, 2696.	3.5	20
416	A Divergent Hepatitis D-Like Agent in Birds. <i>Viruses</i> , 2018, 10, 720.	3.3	69
417	Carbapenemases on the move: it's good to be on ICEs. <i>Mobile DNA</i> , 2018, 9, 37.	3.6	39
418	The novel EHEC gene <i>asa</i> overlaps the TEGT transporter gene in antisense and is regulated by NaCl and growth phase. <i>Scientific Reports</i> , 2018, 8, 17875.	3.3	31
419	Nanopore-based detection and characterization of yam viruses. <i>Scientific Reports</i> , 2018, 8, 17879.	3.3	57
420	Differential gene expression for carotenoid biosynthesis in a green alga <i>Ulva prolifera</i> based on transcriptome analysis. <i>BMC Genomics</i> , 2018, 19, 916.	2.8	19
421	Pooled whole-genome sequencing of interspecific chestnut (<i>Castanea</i>) hybrids reveals loci associated with differences in caching behavior of fox squirrels (<i>Sciurus niger</i> L.). <i>Ecology and Evolution</i> , 2018, 8, 10638-10654.	1.9	1
422	Nuclear genome sequence of the plastid-lacking cryptomonad <i>Goniomonas avonlea</i> provides insights into the evolution of secondary plastids. <i>BMC Biology</i> , 2018, 16, 137.	3.8	42
423	The chicken gut metagenome and the modulatory effects of plant-derived benzylisoquinoline alkaloids. <i>Microbiome</i> , 2018, 6, 211.	11.1	204
424	High throughput ANI analysis of 90K prokaryotic genomes reveals clear species boundaries. <i>Nature Communications</i> , 2018, 9, 5114.	12.8	2,816
425	Full-length title: NRPPUR database search and in vitro analysis identify an NRPS-PKS biosynthetic gene cluster with a potential antibiotic effect. <i>BMC Bioinformatics</i> , 2018, 19, 463.	2.6	12

#	ARTICLE	IF	CITATIONS
426	Burn injury alters the intestinal microbiome's taxonomic composition and functional gene expression. PLoS ONE, 2018, 13, e0205307.	2.5	27
427	Functional shifts in microbial mats recapitulate early Earth metabolic transitions. Nature Ecology and Evolution, 2018, 2, 1700-1708.	7.8	40
428	Genetic repertoires of anaerobic microbiomes driving generation of biogas. Biotechnology for Biofuels, 2018, 11, 255.	6.2	8
429	Pathogenic functions of host microbiota. Microbiome, 2018, 6, 174.	11.1	70
430	Origin of exon skipping-rich transcriptomes in animals driven by evolution of gene architecture. Genome Biology, 2018, 19, 135.	8.8	61
431	Genomes from uncultivated prokaryotes: a comparison of metagenome-assembled and single-amplified genomes. Microbiome, 2018, 6, 173.	11.1	86
432	Microbial Community and Metabolic Activity in Thiocyanate Degrading Low Temperature Microbial Fuel Cells. Frontiers in Microbiology, 2018, 9, 2308.	3.5	7
433	Considerations for Optimization of High-Throughput Sequencing Bioinformatics Pipelines for Virus Detection. Viruses, 2018, 10, 528.	3.3	21
434	Viable cyanobacteria in the deep continental subsurface. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 10702-10707.	7.1	124
435	In-Depth Venome of the Brazilian Rattlesnake <i>Crotalus durissus terrificus</i> : An Integrative Approach Combining Its Venom Gland Transcriptome and Venom Proteome. Journal of Proteome Research, 2018, 17, 3941-3958.	3.7	24
436	Unveiling the RNA virosphere associated with marine microorganisms. Molecular Ecology Resources, 2018, 18, 1444-1455.	4.8	59
437	The Genomic Potentials of NOB and Comammox Nitrospira in River Sediment Are Impacted by Native Freshwater Mussels. Frontiers in Microbiology, 2018, 9, 2061.	3.5	25
438	Caloric restriction promotes functional changes involving short-chain fatty acid biosynthesis in the rat gut microbiota. Scientific Reports, 2018, 8, 14778.	3.3	57
439	<i>Bifidobacterium primatium</i> sp. nov., <i>Bifidobacterium scaligerum</i> sp. nov., <i>Bifidobacterium felsineum</i> sp. nov. and <i>Bifidobacterium simiarum</i> sp. nov.: Four novel taxa isolated from the faeces of the cotton top tamarin (<i>Saguinus oedipus</i>) and the emperor tamarin (<i>Saguinus imperator</i>). Systematic and Applied Microbiology, 2018, 41, 593-603.	2.8	38
440	Discovering novel hydrolases from hot environments. Biotechnology Advances, 2018, 36, 2077-2100.	11.7	38
441	Analyzing Metabolic Pathways in Microbiomes. Methods in Molecular Biology, 2018, 1849, 291-307.	0.9	0
442	Freshwater Viromes: From Sampling to Evaluation. Methods in Molecular Biology, 2018, 1849, 17-27.	0.9	0
443	Transkingdom Networks: A Systems Biology Approach to Identify Causal Members of Host-Microbiota Interactions. Methods in Molecular Biology, 2018, 1849, 227-242.	0.9	23

#	ARTICLE	IF	CITATIONS
444	Landscape of alternative splicing in <i>Capra hircus</i> . Scientific Reports, 2018, 8, 15128.	3.3	3
445	<i>Trichodesmium</i> physiological ecology and phosphate reduction in the western tropical South Pacific. Biogeosciences, 2018, 15, 5761-5778.	3.3	13
446	Firefly genomes illuminate parallel origins of bioluminescence in beetles. ELife, 2018, 7, .	6.0	108
447	Microbial community and functions associated with digestion of algal polysaccharides in the visceral tract of <i>Haliotis discus hannai</i> : Insights from metagenome and metatranscriptome analysis. PLoS ONE, 2018, 13, e0205594.	2.5	13
448	Protective role of the vulture facial skin and gut microbiomes aid adaptation to scavenging. Acta Veterinaria Scandinavica, 2018, 60, 61.	1.6	40
449	Immune-suppression by OsHV-1 viral infection causes fatal bacteraemia in Pacific oysters. Nature Communications, 2018, 9, 4215.	12.8	217
450	Prevalent reliance of bacterioplankton on exogenous vitamin B1 and precursor availability. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E10447-E10456.	7.1	64
451	To B or Not to B: Comparative Genomics Suggests <i>Arsenophonus</i> as a Source of B Vitamins in Whiteflies. Frontiers in Microbiology, 2018, 9, 2254.	3.5	49
452	The Planktonic Core Microbiome and Core Functions in the Cattle Rumen by Next Generation Sequencing. Frontiers in Microbiology, 2018, 9, 2285.	3.5	62
453	Dynamic and Functional Characteristics of Predominant Species in Industrial Paocai as Revealed by Combined DGGE and Metagenomic Sequencing. Frontiers in Microbiology, 2018, 9, 2416.	3.5	30
454	A most wanted list of conserved microbial protein families with no known domains. PLoS ONE, 2018, 13, e0205749.	2.5	17
455	Growing and cultivating the forest genomics database, TreeGenes. Database: the Journal of Biological Databases and Curation, 2018, 2018, 1-11.	3.0	40
456	Species-level functional profiling of metagenomes and metatranscriptomes. Nature Methods, 2018, 15, 962-968.	19.0	1,125
457	Virus-virus interactions and host ecology are associated with <sc>RNA</sc> virome structure in wild birds. Molecular Ecology, 2018, 27, 5263-5278.	3.9	77
458	Investigation of the viral and bacterial microbiota in intestinal samples from mink (<i>Neovison vison</i>) with pre-weaning diarrhea syndrome using next generation sequencing. PLoS ONE, 2018, 13, e0205890.	2.5	5
459	The chemodiversity of paddy soil dissolved organic matter correlates with microbial community at continental scales. Microbiome, 2018, 6, 187.	11.1	130
460	Biodiversity of cyanobacteria and other aquatic microorganisms across a freshwater to brackish water gradient determined by shotgun metagenomic sequencing analysis in the San Francisco Estuary, USA. PLoS ONE, 2018, 13, e0203953.	2.5	22
461	Bacterial Survival Strategies in an Alkaline Tailing Site and the Physiological Mechanisms of Dominant Phylotypes As Revealed by Metagenomic Analyses. Environmental Science & Technology, 2018, 52, 13370-13380.	10.0	112

#	ARTICLE	IF	CITATIONS
462	Developing specific molecular biomarkers for thermal stress in salmonids. BMC Genomics, 2018, 19, 749.	2.8	105
463	Pan-Parastagonospora Comparative Genome Analysisâ€”Effector Prediction and Genome Evolution. Genome Biology and Evolution, 2018, 10, 2443-2457.	2.5	43
464	GePMI: A statistical model for personal intestinal microbiome identification. Npj Biofilms and Microbiomes, 2018, 4, 20.	6.4	7
465	Shared Transcriptional Control and Disparate Gain and Loss of Aphid Parasitism Genes. Genome Biology and Evolution, 2018, 10, 2716-2733.	2.5	53
466	Cloning and Functional Analysis of SaCLCc1, a Gene Belonging to the Chloride Channel Family (CLC), from the Halophyte Suaeda altissima (L.) Pall.. Doklady Biochemistry and Biophysics, 2018, 481, 186-189.	0.9	8
467	Transcriptome Analysis and In Situ Hybridization for FcaGHV1 in Feline Lymphoma. Viruses, 2018, 10, 464.	3.3	6
468	Utilization of rare codon-rich markers for screening amino acid overproducers. Nature Communications, 2018, 9, 3616.	12.8	28
469	Whole Genome Sequencing of the Pirarucu (<i>Arapaima gigas</i>) Supports Independent Emergence of Major Teleost Clades. Genome Biology and Evolution, 2018, 10, 2366-2379.	2.5	33
470	Expansion of the metazoan virosphere: progress, pitfalls, and prospects. Current Opinion in Virology, 2018, 31, 17-23.	5.4	33
471	Metatranscriptomics reveals a differential temperature effect on the structural and functional organization of the anaerobic food web in rice field soil. Microbiome, 2018, 6, 169.	11.1	54
472	Comparison of Healthy and Dandruff Scalp Microbiome Reveals the Role of Commensals in Scalp Health. Frontiers in Cellular and Infection Microbiology, 2018, 8, 346.	3.9	63
473	Structural and Functional Analysis of the Gut Microbiome for Toxicologists. Current Protocols in Toxicology / Editorial Board, Mahin D Maines (editor-in-chief) [et Al], 2018, 78, e54.	1.1	6
474	Single-cell genomics of co-sorted Nanoarchaeota suggests novel putative host associations and diversification of proteins involved in symbiosis. Microbiome, 2018, 6, 161.	11.1	44
475	Insights into the Evolution of Multicellularity from the Sea Lettuce Genome. Current Biology, 2018, 28, 2921-2933.e5.	3.9	134
476	Diurnal Changes in Active Carbon and Nitrogen Pathways Along the Temperature Gradient in Porcelana Hot Spring Microbial Mat. Frontiers in Microbiology, 2018, 9, 2353.	3.5	36
477	Incipient de novo genes can evolve from frozen accidents that escaped rapid transcript turnover. Nature Ecology and Evolution, 2018, 2, 1626-1632.	7.8	74
478	Distinctive Archaeal Composition of an Artisanal Crystallizer Pond and Functional Insights Into Salt-Saturated Hypersaline Environment Adaptation. Frontiers in Microbiology, 2018, 9, 1800.	3.5	14
479	High Prevalence of Quorum-Sensing and Quorum-Quenching Activity among Cultivable Bacteria and Metagenomic Sequences in the Mediterranean Sea. Genes, 2018, 9, 100.	2.4	37

#	ARTICLE	IF	CITATIONS
480	Profiles of quorum sensing (QS)-related sequences in phycospheric microorganisms during a marine dinoflagellate bloom, as determined by a metagenomic approach. <i>Microbiological Research</i> , 2018, 217, 1-13.	5.3	23
481	Functional Gut Microbiota Remodeling Contributes to the Caloric Restriction-Induced Metabolic Improvements. <i>Cell Metabolism</i> , 2018, 28, 907-921.e7.	16.2	170
482	The Ocean Gene Atlas: exploring the biogeography of plankton genes online. <i>Nucleic Acids Research</i> , 2018, 46, W289-W295.	14.5	126
483	Comparative Transcriptome Profiling Analysis of Red- and White-Fleshed Strawberry (<i>Fragaria</i> — <i>ananassa</i>) Provides New Insight into the Regulation of the Anthocyanin Pathway. <i>Plant and Cell Physiology</i> , 2018, 59, 1844-1859.	3.1	48
484	Short-Term Transcriptional Response of Microbial Communities to Nitrogen Fertilization in a Pine Forest Soil. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	16
485	Bloom of a denitrifying methanotroph, <i>Candidatus</i> <i>Methyloirabilis limnetica</i> ™, in a deep stratified lake. <i>Environmental Microbiology</i> , 2018, 20, 2598-2614.	3.8	87
486	Towards a congruent reclassification and nomenclature of the thermophilic species of the genus <i>Pseudothermotoga</i> within the order Thermotogales. <i>Systematic and Applied Microbiology</i> , 2018, 41, 555-563.	2.8	24
487	Genomic and ecological study of two distinctive freshwater bacteriophages infecting a Comamonadaceae bacterium. <i>Scientific Reports</i> , 2018, 8, 7989.	3.3	19
488	Pan-genomic approach shows insight of genetic divergence and pathogenic-adaptation of <i>Pasteurella multocida</i> . <i>Gene</i> , 2018, 670, 193-206.	2.2	31
489	ASaiM: a Galaxy-based framework to analyze microbiota data. <i>GigaScience</i> , 2018, 7, .	6.4	25
490	dbCAN2: a meta server for automated carbohydrate-active enzyme annotation. <i>Nucleic Acids Research</i> , 2018, 46, W95-W101.	14.5	1,641
491	Recovery of genomes from metagenomes via a dereplication, aggregation and scoring strategy. <i>Nature Microbiology</i> , 2018, 3, 836-843.	13.3	906
492	Metagenomic analysis reveals the prevalence and persistence of antibiotic- and heavy metal-resistance genes in wastewater treatment plant. <i>Journal of Microbiology</i> , 2018, 56, 408-415.	2.8	69
493	Dysbiosis of maternal and neonatal microbiota associated with gestational diabetes mellitus. <i>Gut</i> , 2018, 67, 1614-1625.	12.1	305
494	AC-DIAMOND v1: accelerating large-scale DNA-protein alignment. <i>Bioinformatics</i> , 2018, 34, 3744-3746.	4.1	8
495	The vaginal eukaryotic DNA virome and preterm birth. <i>American Journal of Obstetrics and Gynecology</i> , 2018, 219, 189.e1-189.e12.	1.3	90
496	The impact of <i>Staphylococcus aureus</i> genomic variation on clinical phenotype of children with acute hematogenous osteomyelitis. <i>Heliyon</i> , 2018, 4, e00674.	3.2	10
497	Fern genomes elucidate land plant evolution and cyanobacterial symbioses. <i>Nature Plants</i> , 2018, 4, 460-472.	9.3	391

#	ARTICLE	IF	CITATIONS
498	Genomics of the Uncultivated, Periodontitis-Associated Bacterium <i>Tannerella</i> sp. BU045 (Oral) Tj ETQq0 0 0,rgBT /Overlock 10 Tf	3.8	10
499	Clustering huge protein sequence sets in linear time. Nature Communications, 2018, 9, 2542.	12.8	497
500	Patterns of Conservation and Diversification in the Fungal Polarization Network. Genome Biology and Evolution, 2018, 10, 1765-1782.	2.5	15
501	Comparative genomics of bdelloid rotifers: Insights from desiccating and nondesiccating species. PLoS Biology, 2018, 16, e2004830.	5.6	78
502	Adventitious viruses persistently infect three commonly used mosquito cell lines. Virology, 2018, 521, 175-180.	2.4	29
503	Complete Genome Sequences of Three Related Avian Avulavirus 1 Isolates from Poultry Farmers in Pakistan. Genome Announcements, 2018, 6, .	0.8	5
504	<i>Clostridium difficile</i> Alters the Structure and Metabolism of Distinct Cecal Microbiomes during Initial Infection To Promote Sustained Colonization. MSphere, 2018, 3, .	2.9	73
505	Mantis: A Fast, Small, and Exact Large-Scale Sequence-Search Index. Cell Systems, 2018, 7, 201-207.e4.	6.2	79
506	Assessing the Efficiency of Cultivation Techniques To Recover Natural Product Biosynthetic Gene Populations from Sediment. ACS Chemical Biology, 2018, 13, 2074-2081.	3.4	15
507	Biogeography and environmental conditions shape bacteriophage-bacteria networks across the human microbiome. PLoS Computational Biology, 2018, 14, e1006099.	3.2	45
508	Plant-Microbe Interactions Drive Denitrification Rates, Dissolved Nitrogen Removal, and the Abundance of Denitrification Genes in Stormwater Control Measures. Environmental Science & Technology, 2018, 52, 9320-9329.	10.0	57
509	Expanding the Arterivirus Host Spectrum: Olivier's Shrew Virus 1, A Novel Arterivirus Discovered in African Giant Shrews. Scientific Reports, 2018, 8, 11171.	3.3	6
510	Fast automated reconstruction of genome-scale metabolic models for microbial species and communities. Nucleic Acids Research, 2018, 46, 7542-7553.	14.5	410
511	Cameroonian fruit bats harbor divergent viruses, including rotavirus H, bastroviruses, and picobirnaviruses using an alternative genetic code. Virus Evolution, 2018, 4, vey008.	4.9	90
512	Community dynamics and functional characteristics of naphthalene-degrading populations in contaminated surface sediments and hypoxic/anoxic groundwater. Environmental Microbiology, 2018, 20, 3543-3559.	3.8	22
513	The Environmental Exposures and Inner- and Intercity Traffic Flows of the Metro System May Contribute to the Skin Microbiome and Resistome. Cell Reports, 2018, 24, 1190-1202.e5.	6.4	56
514	Structure and function of the global topsoil microbiome. Nature, 2018, 560, 233-237.	27.8	1,370
515	Specific genetic variation in two non-motile substrains of the model cyanobacterium <i>Synechocystis</i> sp. PCC 6803. Journal of Oceanology and Limnology, 2018, 36, 2322-2332.	1.3	1

#	ARTICLE	IF	CITATIONS
516	A de novo approach to disentangle partner identity and function in holobiont systems. <i>Microbiome</i> , 2018, 6, 105.	11.1	19
517	Conducting metagenomic studies in microbiology and clinical research. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 8629-8646.	3.6	26
518	Mesophilic Sporeformers Identified in Whey Powder by Using Shotgun Metagenomic Sequencing. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	15
519	Characterization of Bathyarchaeota genomes assembled from metagenomes of biofilms residing in mesophilic and thermophilic biogas reactors. <i>Biotechnology for Biofuels</i> , 2018, 11, 167.	6.2	38
520	Gut microbiota, short chain fatty acids, and obesity across the epidemiologic transition: the METS-Microbiome study protocol. <i>BMC Public Health</i> , 2018, 18, 978.	2.9	32
521	Signatures of Selection in the Genomes of Chinese Chestnut (<i>Castanea mollissima</i> Blume): The Roots of Nut Tree Domestication. <i>Frontiers in Plant Science</i> , 2018, 9, 810.	3.6	18
522	Near-future CO2 levels impair the olfactory system of a marine fish. <i>Nature Climate Change</i> , 2018, 8, 737-743.	18.8	97
523	Viromic Analysis of Wastewater Input to a River Catchment Reveals a Diverse Assemblage of RNA Viruses. <i>MSystems</i> , 2018, 3, .	3.8	59
524	Prediction of plant lncRNA by ensemble machine learning classifiers. <i>BMC Genomics</i> , 2018, 19, 316.	2.8	53
525	Diabetes-associated alterations in the cecal microbiome and metabolome are independent of diet or environment in the UC Davis Type 2 Diabetes Mellitus Rat model. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2018, 315, E961-E972.	3.5	18
526	High Quality de Novo Transcriptome Assembly of <i>Croton tiglium</i> . <i>Frontiers in Molecular Biosciences</i> , 2018, 5, 62.	3.5	48
527	Development of a production chain from vegetable biowaste to platform chemicals. <i>Microbial Cell Factories</i> , 2018, 17, 90.	4.0	12
528	Consensus assessment of the contamination level of publicly available cyanobacterial genomes. <i>PLoS ONE</i> , 2018, 13, e0200323.	2.5	41
529	Structural and functional characterization of a novel lipolytic enzyme from a Brazilian Cerrado soil metagenomic library. <i>Biotechnology Letters</i> , 2018, 40, 1395-1406.	2.2	7
530	Association Between Gut Microbiota and CD4 Recovery in HIV-1 Infected Patients. <i>Frontiers in Microbiology</i> , 2018, 9, 1451.	3.5	90
531	Co-Infection Patterns in Individual <i>Ixodes scapularis</i> Ticks Reveal Associations between Viral, Eukaryotic and Bacterial Microorganisms. <i>Viruses</i> , 2018, 10, 388.	3.3	44
532	Network-based genetic investigation of virulence-associated phenotypes in methicillin-resistant <i>Staphylococcus aureus</i> . <i>Scientific Reports</i> , 2018, 8, 10796.	3.3	5
533	A Novel Eukaryotic Denitrification Pathway in Foraminifera. <i>Current Biology</i> , 2018, 28, 2536-2543.e5.	3.9	75

#	ARTICLE	IF	CITATIONS
534	Metagenomic Characterization of the Human Intestinal Microbiota in Fecal Samples from STEC-Infected Patients. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 25.	3.9	47
535	<i>Ostreococcus tauri</i> Luminescent Reporter Lines as Biosensors for Detecting Pollution From Copper-Mine Tailing Effluents in Coastal Environments. <i>Frontiers in Environmental Science</i> , 2018, 6, .	3.3	1
536	Digging Deeper Into the Pyriproxyfen-Response of the Amphipod <i>Gammarus fossarum</i> With a Next-Generation Ultra-High-Field Orbitrap Analyser: New Perspectives for Environmental Toxicoproteomics. <i>Frontiers in Environmental Science</i> , 2018, 6, .	3.3	13
537	Occurrence of Harmful Cyanobacteria in Drinking Water from a Severely Drought-Impacted Semi-arid Region. <i>Frontiers in Microbiology</i> , 2018, 9, 176.	3.5	46
538	Study of the Metatranscriptome of Eight Social and Solitary Wild Bee Species Reveals Novel Viruses and Bee Parasites. <i>Frontiers in Microbiology</i> , 2018, 9, 177.	3.5	60
539	Contrasting the Genetic Patterns of Microbial Communities in Soda Lakes with and without Cyanobacterial Bloom. <i>Frontiers in Microbiology</i> , 2018, 9, 244.	3.5	25
540	Physiological and Metagenomic Characterizations of the Synergistic Relationships between Ammonia- and Nitrite-Oxidizing Bacteria in Freshwater Nitrification. <i>Frontiers in Microbiology</i> , 2018, 9, 280.	3.5	15
541	Metagenomic Insights Into the Microbial Community and Nutrient Cycling in the Western Subarctic Pacific Ocean. <i>Frontiers in Microbiology</i> , 2018, 9, 623.	3.5	42
542	<i>Nitrosospora</i> sp. Govern Nitrous Oxide Emissions in a Tropical Soil Amended With Residues of Bioenergy Crop. <i>Frontiers in Microbiology</i> , 2018, 9, 674.	3.5	41
543	Circadian Disruption Changes Gut Microbiome Taxa and Functional Gene Composition. <i>Frontiers in Microbiology</i> , 2018, 9, 737.	3.5	148
544	A Large-Scale Comparative Metagenomic Study Reveals the Functional Interactions in Six Bloom-Forming <i>Microcystis</i> -Epibiont Communities. <i>Frontiers in Microbiology</i> , 2018, 9, 746.	3.5	72
545	Overview of Virus Metagenomic Classification Methods and Their Biological Applications. <i>Frontiers in Microbiology</i> , 2018, 9, 749.	3.5	99
546	Comparative Metatranscriptomics of Wheat Rhizosphere Microbiomes in Disease Suppressive and Non-suppressive Soils for <i>Rhizoctonia solani</i> AG8. <i>Frontiers in Microbiology</i> , 2018, 9, 859.	3.5	66
547	Taxon-Function Decoupling as an Adaptive Signature of Lake Microbial Metacommunities Under a Chronic Polymetallic Pollution Gradient. <i>Frontiers in Microbiology</i> , 2018, 9, 869.	3.5	19
548	The Oxidative Metabolism of Fossil Hydrocarbons and Sulfide Minerals by the Lithobiontic Microbial Community Inhabiting Deep Subterrestrial Kupferschiefer Black Shale. <i>Frontiers in Microbiology</i> , 2018, 9, 972.	3.5	15
549	Thousands of Novel Endolysins Discovered in Uncultured Phage Genomes. <i>Frontiers in Microbiology</i> , 2018, 9, 1033.	3.5	50
550	Microbial Community Structureâ€“Function Relationships in Yaquina Bay Estuary Reveal Spatially Distinct Carbon and Nitrogen Cycling Capacities. <i>Frontiers in Microbiology</i> , 2018, 9, 1282.	3.5	48
551	Metagenomic Analysis of Cyanobacteria in an Oligotrophic Tropical Estuary, South Atlantic. <i>Frontiers in Microbiology</i> , 2018, 9, 1393.	3.5	17

#	ARTICLE	IF	CITATIONS
552	“Candidatus Aquirickettsiella gammari”™ (Gammaproteobacteria: Legionellales: Coxiellaceae): A bacterial pathogen of the freshwater crustacean Gammarus fossarum (Malacostraca: Amphipoda). Journal of Invertebrate Pathology, 2018, 156, 41-53.	3.2	23
553	Agulhas Current properties shape microbial community diversity and potential functionality. Scientific Reports, 2018, 8, 10542.	3.3	12
554	Disentangling the drivers of functional complexity at the metagenomic level in Shark Bay microbial mat microbiomes. ISME Journal, 2018, 12, 2619-2639.	9.8	94
555	Metatranscriptome Analysis of the Vaginal Microbiota Reveals Potential Mechanisms for Protection against Metronidazole in Bacterial Vaginosis. MSphere, 2018, 3, .	2.9	63
556	MCRiceRepGP: a framework for the identification of genes associated with sexual reproduction in rice. Plant Journal, 2018, 96, 188-202.	5.7	13
557	Disentangling the complexity of permafrost soil by using high resolution profiling of microbial community composition, key functions and respiration rates. Environmental Microbiology, 2018, 20, 4328-4342.	3.8	37
558	Novel Parvoviruses from Wild and Domestic Animals in Brazil Provide New Insights into Parvovirus Distribution and Diversity. Viruses, 2018, 10, 143.	3.3	28
559	A Novel Hepadnavirus Identified in an Immunocompromised Domestic Cat in Australia. Viruses, 2018, 10, 269.	3.3	49
560	Virological Sampling of Inaccessible Wildlife with Drones. Viruses, 2018, 10, 300.	3.3	49
561	Genome-centric view of carbon processing in thawing permafrost. Nature, 2018, 560, 49-54.	27.8	337
562	Metagenomic analysis revealed the effects of goat milk feeding and breast feeding on the gut microbiome of Amur tiger cubs. Biochemical and Biophysical Research Communications, 2018, 503, 2590-2596.	2.1	12
563	SAMSA2: a standalone metatranscriptome analysis pipeline. BMC Bioinformatics, 2018, 19, 175.	2.6	107
564	Arabidopsis thaliana and Pseudomonas Pathogens Exhibit Stable Associations over Evolutionary Timescales. Cell Host and Microbe, 2018, 24, 168-179.e4.	11.0	145
565	Fine metagenomic profile of the Mediterranean stratified and mixed water columns revealed by assembly and recruitment. Microbiome, 2018, 6, 128.	11.1	95
566	Species classifier choice is a key consideration when analysing low-complexity food microbiome data. Microbiome, 2018, 6, 50.	11.1	65
567	Similarity of the dog and human gut microbiomes in gene content and response to diet. Microbiome, 2018, 6, 72.	11.1	211
568	Age and fecal microbial strain-specific differences in patients with spondyloarthritis. Arthritis Research and Therapy, 2018, 20, 14.	3.5	58
569	DeepARG: a deep learning approach for predicting antibiotic resistance genes from metagenomic data. Microbiome, 2018, 6, 23.	11.1	462

#	ARTICLE	IF	CITATIONS
570	MEGAN-LR: new algorithms allow accurate binning and easy interactive exploration of metagenomic long reads and contigs. <i>Biology Direct</i> , 2018, 13, 6.	4.6	141
571	Genome-centric metatranscriptomes and ecological roles of the active microbial populations during cellulosic biomass anaerobic digestion. <i>Biotechnology for Biofuels</i> , 2018, 11, 117.	6.2	29
572	A reservoir of “historical” antibiotic resistance genes in remote pristine Antarctic soils. <i>Microbiome</i> , 2018, 6, 40.	11.1	244
573	PANNZER2: a rapid functional annotation web server. <i>Nucleic Acids Research</i> , 2018, 46, W84-W88.	14.5	328
574	Strategies for Taxonomic and Functional Annotation of Metagenomes. , 2018, , 55-79.		11
575	Ancient hepatitis B viruses from the Bronze Age to the Medieval period. <i>Nature</i> , 2018, 557, 418-423.	27.8	155
576	Taxon-Driven Functional Shifts Associated with Storm Flow in an Urban Stream Microbial Community. <i>MSphere</i> , 2018, 3, .	2.9	20
577	Genome Analyses of the Microalga <i>Picochlorum</i> Provide Insights into the Evolution of Thermotolerance in the Green Lineage. <i>Genome Biology and Evolution</i> , 2018, 10, 2347-2365.	2.5	36
578	Holistic Assessment of Rumen Microbiome Dynamics through Quantitative Metatranscriptomics Reveals Multifunctional Redundancy during Key Steps of Anaerobic Feed Degradation. <i>MSystems</i> , 2018, 3, .	3.8	74
579	Comparative Metagenomic Analysis of Rhizosphere Microbial Community Composition and Functional Potentials under <i>Rehmannia glutinosa</i> Consecutive Monoculture. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2394.	4.1	37
580	Transcriptomic comparison of two barley genotypes differing in arsenic tolerance exposed to arsenate and phosphate treatments. <i>Plant Physiology and Biochemistry</i> , 2018, 130, 589-603.	5.8	14
581	Maximal viral information recovery from sequence data using VirMAP. <i>Nature Communications</i> , 2018, 9, 3205.	12.8	46
582	The genome of the golden apple snail <i>Pomacea canaliculata</i> provides insight into stress tolerance and invasive adaptation. <i>GigaScience</i> , 2018, 7, .	6.4	68
583	Broad Phylogenetic Diversity Associated with Nitrogen Loss through Sulfur Oxidation in a Large Public Marine Aquarium. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	7
584	Metagenomic sequencing suggests a diversity of RNA interference-like responses to viruses across multicellular eukaryotes. <i>PLoS Genetics</i> , 2018, 14, e1007533.	3.5	95
585	Genome Sequencing and Carbohydrate-Active Enzyme (CAZyme) Repertoire of the White Rot Fungus <i>Flammulina elastica</i> . <i>International Journal of Molecular Sciences</i> , 2018, 19, 2379.	4.1	47
586	Defence transcriptome assembly and pathogenesis related gene family analysis in <i>Pinus tecunumanii</i> (low elevation). <i>BMC Genomics</i> , 2018, 19, 632.	2.8	32
587	MetaBinG2: a fast and accurate metagenomic sequence classification system for samples with many unknown organisms. <i>Biology Direct</i> , 2018, 13, 15.	4.6	9

#	ARTICLE	IF	CITATIONS
588	High-Resolution Temporal and Spatial Patterns of Virome in Wastewater Treatment Systems. Environmental Science & Technology, 2018, 52, 10337-10346.	10.0	25
589	Salinity-Aided Selection of Progressive Onset Denitrifiers as a Means of Providing Nitrite for Anammox. Environmental Science & Technology, 2018, 52, 10665-10672.	10.0	64
590	Following the terrestrial tracks of <i>Caulobacter</i> - redefining the ecology of a reputed aquatic oligotroph. ISME Journal, 2018, 12, 3025-3037.	9.8	56
591	TOPAZ: asymmetric suffix array neighbourhood search for massive protein databases. BMC Bioinformatics, 2018, 19, 278.	2.6	4
592	Phylogenomic analysis of 2556 single-copy protein-coding genes resolves most evolutionary relationships for the major clades in the most diverse group of lichen-forming fungi. Fungal Diversity, 2018, 92, 31-41.	12.3	19
593	phylotaR: An Automated Pipeline for Retrieving Orthologous DNA Sequences from GenBank in R. Life, 2018, 8, 20.	2.4	26
594	Characterization of LE3 and LE4, the only lytic phages known to infect the spirochete Leptospira. Scientific Reports, 2018, 8, 11781.	3.3	10
595	Evidence for complete nitrification in enrichment culture of tidal sediments and diversity analysis of clade a comammox Nitrospira in natural environments. Applied Microbiology and Biotechnology, 2018, 102, 9363-9377.	3.6	57
596	Virome of >12 thousand Culex mosquitoes from throughout California. Virology, 2018, 523, 74-88.	2.4	88
597	Adipose transcriptome analysis provides novel insights into molecular regulation of prolonged fasting in northern elephant seal pups. Physiological Genomics, 2018, 50, 495-503.	2.3	15
598	Genomic and Biotechnological Characterization of the Heavy-Metal Resistant, Arsenic-Oxidizing Bacterium Ensifer sp. M14. Genes, 2018, 9, 379.	2.4	25
599	Parallel and Gradual Genome Erosion in the Blattabacterium Endosymbionts of Mastotermes darwiniensis and Cryptocercus Wood Roaches. Genome Biology and Evolution, 2018, 10, 1622-1630.	2.5	14
600	The virome of Drosophila suzukii, an invasive pest of soft fruit. Virus Evolution, 2018, 4, vey009.	4.9	67
601	Current strategies to induce secondary metabolites from microbial biosynthetic cryptic gene clusters. Annals of Microbiology, 2018, 68, 419-432.	2.6	19
602	Computational and Statistical Considerations in the Analysis of Metagenomic Data. , 2018, , 81-102.		10
603	Transient Osmotic Perturbation Causes Long-Term Alteration to the Gut Microbiota. Cell, 2018, 173, 1742-1754.e17.	28.9	171
605	Identification of fungi in shotgun metagenomics datasets. PLoS ONE, 2018, 13, e0192898.	2.5	83
606	Viral Discovery in the Invasive Australian Cane Toad (Rhinella marina) Using Metatranscriptomic and Genomic Approaches. Journal of Virology, 2018, 92, .	3.4	13

#	ARTICLE	IF	CITATIONS
607	Nitrogen-fixing populations of Planctomycetes and Proteobacteria are abundant in surface ocean metagenomes. <i>Nature Microbiology</i> , 2018, 3, 804-813.	13.3	436
608	Investigating the viral ecology of global bee communities with high-throughput metagenomics. <i>Scientific Reports</i> , 2018, 8, 8879.	3.3	58
609	Genomics of Actinobacteria With a Focus on Natural Product Biosynthetic Genes. , 2018, , 325-335.		0
610	Comparative immunological study of the snail <i>Physella acuta</i> (Hydrophila, Pulmonata) reveals shared and unique aspects of gastropod immunobiology. <i>Molecular Immunology</i> , 2018, 101, 108-119.	2.2	17
611	Metagenomic insights into the roles of <i>Proteobacteria</i> in the gastrointestinal microbiomes of healthy dogs and cats. <i>MicrobiologyOpen</i> , 2018, 7, e00677.	3.0	148
612	A distinct abundant group of microbial rhodopsins discovered using functional metagenomics. <i>Nature</i> , 2018, 558, 595-599.	27.8	190
613	Operon-mapper: a web server for precise operon identification in bacterial and archaeal genomes. <i>Bioinformatics</i> , 2018, 34, 4118-4120.	4.1	167
614	The Functional Potential of the Rhizospheric Microbiome of an Invasive Tree Species, <i>Acacia dealbata</i> . <i>Microbial Ecology</i> , 2019, 77, 191-200.	2.8	46
615	Effusion: prediction of protein function from sequence similarity networks. <i>Bioinformatics</i> , 2019, 35, 442-451.	4.1	12
616	SonicParanoid: fast, accurate and easy orthology inference. <i>Bioinformatics</i> , 2019, 35, 149-151.	4.1	103
618	Genome Detective: an automated system for virus identification from high-throughput sequencing data. <i>Bioinformatics</i> , 2019, 35, 871-873.	4.1	254
619	Profiling the Gut Microbiome: Practice and Potential. , 2019, , 200-217.		0
620	Sequence Similarity Searching. <i>Current Protocols in Protein Science</i> , 2019, 95, e71.	2.8	50
621	Dietary specialization in mutualistic acacia ants affects relative abundance but not identity of host-associated bacteria. <i>Molecular Ecology</i> , 2019, 28, 900-916.	3.9	34
622	Accurate multiple alignment of distantly related genome sequences using filtered spaced word matches as anchor points. <i>Bioinformatics</i> , 2019, 35, 211-218.	4.1	11
623	Metagenomic binning through low-density hashing. <i>Bioinformatics</i> , 2019, 35, 219-226.	4.1	21
624	Diversity of Bacteria Exhibiting Bile Acid-inducible β -dehydroxylation Genes in the Human Gut. <i>Computational and Structural Biotechnology Journal</i> , 2019, 17, 1016-1019.	4.1	84
625	Multiple Independent Origins of Apicomplexan-Like Parasites. <i>Current Biology</i> , 2019, 29, 2936-2941.e5.	3.9	84

#	ARTICLE	IF	CITATIONS
626	Identification of Primary Antimicrobial Resistance Drivers in Agricultural Nontyphoidal Salmonella enterica Serovars by Using Machine Learning. <i>MSystems</i> , 2019, 4, .	3.8	21
627	Metagenomic next-generation sequencing aids the diagnosis of viral infections in febrile returning travellers. <i>Journal of Infection</i> , 2019, 79, 383-388.	3.3	45
628	Next generation sequencing, biochemical characterization, metabolic pathway analysis of novel probiotic <i>Pediococcus acidilactici</i> NCDC 252 and its evolutionary relationship with other lactic acid bacteria. <i>Molecular Biology Reports</i> , 2019, 46, 5883-5895.	2.3	20
629	Benchmarking Metagenomics Tools for Taxonomic Classification. <i>Cell</i> , 2019, 178, 779-794.	28.9	364
630	Reduced genetic potential for butyrate fermentation in the gut microbiome of infants who develop allergic sensitization. <i>Journal of Allergy and Clinical Immunology</i> , 2019, 144, 1638-1647.e3.	2.9	95
631	The Oral Mouse Microbiome Promotes Tumorigenesis in Oral Squamous Cell Carcinoma. <i>MSystems</i> , 2019, 4, .	3.8	50
632	Rearing pattern alters porcine myofiber type, fat deposition, associated microbial communities and functional capacity. <i>BMC Microbiology</i> , 2019, 19, 181.	3.3	21
633	Discrepant gene functional potential and cross-feedings of anammox bacteria <i>Ca. Jettenia caeni</i> and <i>Ca. Brocadia sinica</i> in response to acetate. <i>Water Research</i> , 2019, 165, 114974.	11.3	67
634	DeepGOPlus: improved protein function prediction from sequence. <i>Bioinformatics</i> , 2020, 36, 422-429.	4.1	242
635	A first insight into the structure and function of rhizosphere microbiota in Antarctic plants using shotgun metagenomic. <i>Polar Biology</i> , 2019, 42, 1825-1835.	1.2	18
636	A consensus <i>S. cerevisiae</i> metabolic model Yeast8 and its ecosystem for comprehensively probing cellular metabolism. <i>Nature Communications</i> , 2019, 10, 3586.	12.8	217
637	Method Development for DNA and Proteome SIP Analysis of Activated Sludge for Anaerobic Dichloromethane Biodegradation. <i>Methods in Molecular Biology</i> , 2019, 2046, 207-219.	0.9	1
638	The Landscape of Genetic Content in the Gut and Oral Human Microbiome. <i>Cell Host and Microbe</i> , 2019, 26, 283-295.e8.	11.0	207
639	Great Lakes <i>Cladophora</i> harbors phylogenetically diverse nitrogen-fixing microorganisms. <i>Environmental DNA</i> , 2019, 1, 186-195.	5.8	5
640	Potential roles of gut microbiome and metabolites in modulating ALS in mice. <i>Nature</i> , 2019, 572, 474-480.	27.8	454
641	Early-life gut microbiome modulation reduces the abundance of antibiotic-resistant bacteria. <i>Antimicrobial Resistance and Infection Control</i> , 2019, 8, 131.	4.1	63
642	Sequenceserver: A Modern Graphical User Interface for Custom BLAST Databases. <i>Molecular Biology and Evolution</i> , 2019, 36, 2922-2924.	8.9	173
643	Dietary Oligosaccharides Attenuate Stress-Induced Disruptions in Immune Reactivity and Microbial B-Vitamin Metabolism. <i>Frontiers in Immunology</i> , 2019, 10, 1774.	4.8	14

#	ARTICLE	IF	CITATIONS
644	A Species-Wide Inventory of NLR Genes and Alleles in <i>Arabidopsis thaliana</i> . <i>Cell</i> , 2019, 178, 1260-1272.e14.	28.9	265
645	Fecal Metaproteomic Analysis Reveals Unique Changes of the Gut Microbiome Functions After Consumption of Sourdough Carasau Bread. <i>Frontiers in Microbiology</i> , 2019, 10, 1733.	3.5	26
646	Compendium of 4,941 rumen metagenome-assembled genomes for rumen microbiome biology and enzyme discovery. <i>Nature Biotechnology</i> , 2019, 37, 953-961.	17.5	353
647	Microbial diversity analysis and screening for novel xylanase enzymes from the sediment of the Lobios Hot Spring in Spain. <i>Scientific Reports</i> , 2019, 9, 11195.	3.3	37
648	Defining the human gut host-phage network through single-cell viral tagging. <i>Nature Microbiology</i> , 2019, 4, 2192-2203.	13.3	95
649	Assignment of virus and antimicrobial resistance genes to microbial hosts in a complex microbial community by combined long-read assembly and proximity ligation. <i>Genome Biology</i> , 2019, 20, 153.	8.8	66
650	Why does nitrogen addition to forest soils inhibit decomposition?. <i>Soil Biology and Biochemistry</i> , 2019, 137, 107570.	8.8	37
651	Microbiota-derived lantibiotic restores resistance against vancomycin-resistant <i>Enterococcus</i> . <i>Nature</i> , 2019, 572, 665-669.	27.8	176
652	A Comparative Analysis of Biosynthetic Gene Clusters in Lean and Obese Humans. <i>BioMed Research International</i> , 2019, 2019, 1-7.	1.9	4
653	Discrimination power of knowledge-based potential dictated by the dominant energies in native protein structures. <i>Amino Acids</i> , 2019, 51, 1029-1038.	2.7	1
654	Predictive metabolomic profiling of microbial communities using amplicon or metagenomic sequences. <i>Nature Communications</i> , 2019, 10, 3136.	12.8	176
655	Comparative genomics groups phages of Negativicutes and classical Firmicutes despite different Gram-staining properties. <i>Environmental Microbiology</i> , 2019, 21, 3989-4001.	3.8	8
656	In marine <i>Bacteroidetes</i> the bulk of glycan degradation during algae blooms is mediated by few clades using a restricted set of genes. <i>ISME Journal</i> , 2019, 13, 2800-2816.	9.8	125
657	Metatranscriptomics reveals mycoviral populations in the ovine rumen. <i>FEMS Microbiology Letters</i> , 2019, 366, .	1.8	7
658	Subcellular Compartments Interplay for Carbon and Nitrogen Allocation in <i>Chromera velia</i> and <i>Vitrella brassicaformis</i> . <i>Genome Biology and Evolution</i> , 2019, 11, 1765-1779.	2.5	18
659	Effects of microbiota-directed foods in gnotobiotic animals and undernourished children. <i>Science</i> , 2019, 365, .	12.6	305
660	Genomic Analysis Identifies Novel <i>Pseudomonas aeruginosa</i> Resistance Genes under Selection during Inhaled Aztreonam Therapy <i>In Vivo</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	11
661	Revisiting the Phylogenetic History of Helminths Through Genomics, the Case of the New <i>Echinococcus oligarthrus</i> Genome. <i>Frontiers in Genetics</i> , 2019, 10, 708.	2.3	12

#	ARTICLE	IF	CITATIONS
662	iMicrobe: Tools and data-driven discovery platform for the microbiome sciences. GigaScience, 2019, 8, .	6.4	24
663	Whole genome sequencing revealed microbiome in lung adenocarcinomas presented as ground-glass nodules. Translational Lung Cancer Research, 2019, 8, 235-246.	2.8	19
664	Identification of diverse arthropod associated viruses in native Australian fleas. Virology, 2019, 535, 189-199.	2.4	24
665	De novo transcriptome of the newly described phototrophic dinoflagellate Yihiella yeosuensis: comparison between vegetative cells and cysts. Marine Biology, 2019, 166, 1.	1.5	10
666	Highly variable mRNA half-life time within marine bacterial taxa and functional genes. Environmental Microbiology, 2019, 21, 3873-3884.	3.8	21
667	The first clawed lobster virus Homarus gammarus nudivirus (HgNV n. sp.) expands the diversity of the Nudiviridae. Scientific Reports, 2019, 9, 10086.	3.3	15
668	Chromosome-Level Alpaca Reference Genome VicPac3.1 Improves Genomic Insight Into the Biology of New World Camelids. Frontiers in Genetics, 2019, 10, 586.	2.3	19
669	A pollution gradient contributes to the taxonomic, functional, and resistome diversity of microbial communities in marine sediments. Microbiome, 2019, 7, 104.	11.1	100
670	Introduction to the Analysis of Environmental Sequences: Metagenomics with MEGAN. Methods in Molecular Biology, 2019, 1910, 591-604.	0.9	23
671	Multiple Data Analyses and Statistical Approaches for Analyzing Data from Metagenomic Studies and Clinical Trials. Methods in Molecular Biology, 2019, 1910, 605-634.	0.9	8
672	Responses of tundra soil microbial communities to half a decade of experimental warming at two critical depths. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 15096-15105.	7.1	83
673	The Methodology Behind Network Thinking: Graphs to Analyze Microbial Complexity and Evolution. Methods in Molecular Biology, 2019, 1910, 271-308.	0.9	4
674	Distinct Taxonomic and Functional Profiles of the Microbiome Associated With Different Soil Horizons of a Moist Tussock Tundra in Alaska. Frontiers in Microbiology, 2019, 10, 1442.	3.5	26
675	Genome-Wide and Functional View of Proteolytic and Lipolytic Bacteria for Efficient Biogas Production through Enhanced Sewage Sludge Hydrolysis. Molecules, 2019, 24, 2624.	3.8	8
676	Genomic and Seasonal Variations among Aquatic Phages Infecting the Baltic Sea Gammaproteobacterium <i>Rheinheimera</i> sp. Strain BAL341. Applied and Environmental Microbiology, 2019, 85, .	3.1	20
677	Fungiculture in Termites Is Associated with a Mycolytic Gut Bacterial Community. MSphere, 2019, 4, .	2.9	35
678	Darkness-induced effects on gene expression in <i>Cosmarium crenatum</i> (Zygnematophyceae) from a polar habitat. Scientific Reports, 2019, 9, 10559.	3.3	6
679	Recurrent gene co-amplification on <i>Drosophila</i> X and Y chromosomes. PLoS Genetics, 2019, 15, e1008251.	3.5	41

#	ARTICLE	IF	CITATIONS
680	Enzymes of early-diverging, zoosporic fungi. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 6885-6902.	3.6	30
681	Target-independent high-throughput sequencing methods provide evidence that already known human viral pathogens play a main role in respiratory infections with unexplained etiology. <i>Emerging Microbes and Infections</i> , 2019, 8, 1054-1065.	6.5	4
682	Evidence for rapid evolution in a grassland biodiversity experiment. <i>Molecular Ecology</i> , 2019, 28, 4097-4117.	3.9	41
683	The transcriptome of Darwin's bark spider silk glands predicts proteins contributing to dragline silk toughness. <i>Communications Biology</i> , 2019, 2, 275.	4.4	46
684	The effect of quorum sensing on performance of salt-tolerance aerobic granular sludge: linking extracellular polymeric substances and microbial community. <i>Biodegradation</i> , 2019, 30, 447-456.	3.0	10
685	Genome evolution and host-microbiome shifts correspond with intraspecific niche divergence within harmful algal bloom-forming <i>Microcystis aeruginosa</i> . <i>Molecular Ecology</i> , 2019, 28, 3994-4011.	3.9	29
686	T cell-mediated regulation of the microbiota protects against obesity. <i>Science</i> , 2019, 365, .	12.6	236
687	Diversity of tryptophan halogenases in sponges of the genus <i>Aplysina</i> . <i>FEMS Microbiology Ecology</i> , 2019, 95, .	2.7	11
688	Atmospheric carbon monoxide oxidation is a widespread mechanism supporting microbial survival. <i>ISME Journal</i> , 2019, 13, 2868-2881.	9.8	133
689	Flavonoid Biosynthesis Is Likely More Susceptible to Elevation and Tree Age Than Other Branch Pathways Involved in Phenylpropanoid Biosynthesis in Ginkgo Leaves. <i>Frontiers in Plant Science</i> , 2019, 10, 983.	3.6	31
691	De novo transcriptome assembly of the fresh-cut white husk of <i>Juglans cathayensis</i> Dode: Insights for enzymatic browning mechanism of fresh-cut husk of walnut. <i>Scientia Horticulturae</i> , 2019, 257, 108654.	3.6	15
692	Symbiosis, Selection, and Novelty: Freshwater Adaptation in the Unique Sponges of Lake Baikal. <i>Molecular Biology and Evolution</i> , 2019, 36, 2462-2480.	8.9	22
693	Trait-based life-history strategies explain succession scenario for complex bacterial communities under varying disturbance. <i>Environmental Microbiology</i> , 2019, 21, 3751-3764.	3.8	25
694	Cell Wall Enzymes in <i>Zygnema circumcarinatum</i> UTEX 1559 Respond to Osmotic Stress in a Plant-Like Fashion. <i>Frontiers in Plant Science</i> , 2019, 10, 732.	3.6	13
695	Diverse hydrogen production and consumption pathways influence methane production in ruminants. <i>ISME Journal</i> , 2019, 13, 2617-2632.	9.8	132
696	Alternate succession of aggregate-forming cyanobacterial genera correlated with their attached bacteria by co-pathways. <i>Science of the Total Environment</i> , 2019, 688, 867-879.	8.0	32
698	OMA standalone: orthology inference among public and custom genomes and transcriptomes. <i>Genome Research</i> , 2019, 29, 1152-1163.	5.5	111
699	The South American Fruit Fly: An Important Pest Insect With RNAi-Sensitive Larval Stages. <i>Frontiers in Physiology</i> , 2019, 10, 794.	2.8	21

#	ARTICLE	IF	CITATIONS
700	The Genome Sequence of the Anthelmintic-Susceptible New Zealand Haemonchus contortus. <i>Genome Biology and Evolution</i> , 2019, 11, 1965-1970.	2.5	29
701	High-Throughput Sequencing-Based Investigation of Viruses in Human Cancers by Multienrichment Approach. <i>Journal of Infectious Diseases</i> , 2019, 220, 1312-1324.	4.0	13
702	Single Cell Genomics-Based Analysis of Gene Content and Expression of Prophages in a Diffuse-Flow Deep-Sea Hydrothermal System. <i>Frontiers in Microbiology</i> , 2019, 10, 1262.	3.5	14
703	Fecal Short-Chain Fatty Acids Are Not Predictive of Colonic Tumor Status and Cannot Be Predicted Based on Bacterial Community Structure. <i>MBio</i> , 2019, 10, .	4.1	32
704	Characterization and analysis of the transcriptome in <i>Gymnocypris selincuoensis</i> on the Qinghai-Tibetan Plateau using single-molecule long-read sequencing and RNA-seq. <i>DNA Research</i> , 2019, 26, 353-363.	3.4	31
705	PhyloMagnet: fast and accurate screening of short-read meta-omics data using gene-centric phylogenetics. <i>Bioinformatics</i> , 2020, 36, 1718-1724.	4.1	7
706	Complete mitochondrial genomes from transcriptomes: assessing pros and cons of data mining for assembling new mitogenomes. <i>Scientific Reports</i> , 2019, 9, 14806.	3.3	14
707	CSMD: a computational subtraction-based microbiome discovery pipeline for species-level characterization of clinical metagenomic samples. <i>Bioinformatics</i> , 2019, 36, 1577-1583.	4.1	2
708	Reference gene and small RNA data from multiple tissues of <i>Davidia involucrata</i> Baill. <i>Scientific Data</i> , 2019, 6, 181.	5.3	4
709	A high-quality genome assembly from a single, field-collected spotted lanternfly (<i>Lycorma delicatula</i>) using the PacBio Sequel II system. <i>CigaScience</i> , 2019, 8, .	6.4	35
710	The mobile FOX AmpC beta-lactamases originated in <i>Aeromonas allosaccharophila</i> . <i>International Journal of Antimicrobial Agents</i> , 2019, 54, 798-802.	2.5	15
711	Study on cyanidin metabolism in petals of pink-flowered strawberry based on transcriptome sequencing and metabolite analysis. <i>BMC Plant Biology</i> , 2019, 19, 423.	3.6	23
712	Carbohydrate active enzymes are affected by diet transition from milk to solid food in infant gut microbiota. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	2.7	10
713	Influence of Maternal Inulin-Type Prebiotic Intervention on Glucose Metabolism and Gut Microbiota in the Offspring of C57BL Mice. <i>Frontiers in Endocrinology</i> , 2019, 10, 675.	3.5	16
714	Insights into the ecological roles and evolution of methyl-coenzyme M reductase-containing hot spring Archaea. <i>Nature Communications</i> , 2019, 10, 4574.	12.8	90
715	The <i>Prevotella copri</i> Complex Comprises Four Distinct Clades Underrepresented in Westernized Populations. <i>Cell Host and Microbe</i> , 2019, 26, 666-679.e7.	11.0	274
716	BiomeNet: a database for construction and analysis of functional interaction networks for any species with a sequenced genome. <i>Bioinformatics</i> , 2019, 36, 1584-1589.	4.1	6
717	Altered short chain fatty acid profiles induced by dietary fiber intervention regulate AMPK levels and intestinal homeostasis. <i>Food and Function</i> , 2019, 10, 7174-7187.	4.6	43

#	ARTICLE	IF	CITATIONS
718	WASPS: web-assisted symbolic plasmid synteny server. <i>Bioinformatics</i> , 2019, 36, 1629-1631.	4.1	3
719	PIRATE: A fast and scalable pangenomics toolbox for clustering diverged orthologues in bacteria. <i>GigaScience</i> , 2019, 8, .	6.4	152
720	New perspectives on the plant PARP family: Arabidopsis PARP3 is inactive, and PARP1 exhibits predominant poly (ADP-ribose) polymerase activity in response to DNA damage. <i>BMC Plant Biology</i> , 2019, 19, 364.	3.6	24
721	CARD 2020: antibiotic resistome surveillance with the comprehensive antibiotic resistance database. <i>Nucleic Acids Research</i> , 2020, 48, D517-D525.	14.5	1,605
722	Whole Genome Assembly of the Snout Otter Clam, <i>Lutraria rhynchaena</i> , Using Nanopore and Illumina Data, Benchmarked Against Bivalve Genome Assemblies. <i>Frontiers in Genetics</i> , 2019, 10, 1158.	2.3	16
723	Multi-Tissue Transcriptomes Yield Information on High-Altitude Adaptation and Sex-Determination in <i>Scutigera cf. sikimensis</i> . <i>Genes</i> , 2019, 10, 873.	2.4	1
724	MGnify: the microbiome analysis resource in 2020. <i>Nucleic Acids Research</i> , 2020, 48, D570-D578.	14.5	296
725	Distinct Gut Microbiota Induced by Different Fat-to-Sugar-Ratio High-Energy Diets Share Similar Pro-obesity Genetic and Metabolite Profiles in Prediabetic Mice. <i>MSystems</i> , 2019, 4, .	3.8	18
727	Pathogen-induced activation of disease-suppressive functions in the endophytic root microbiome. <i>Science</i> , 2019, 366, 606-612.	12.6	621
728	Filovirus-reactive antibodies in humans and bats in Northeast India imply zoonotic spillover. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007733.	3.0	30
729	Deciphering the Functioning of Microbial Communities: Shedding Light on the Critical Steps in Metaproteomics. <i>Frontiers in Microbiology</i> , 2019, 10, 2395.	3.5	16
730	Potential Correlation between Dietary Fiber-Suppressed Microbial Conversion of Choline to Trimethylamine and Formation of Methylglyoxal. <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 13247-13257.	5.2	13
731	Marine Proteobacteria metabolize glycolate via the β^2 -hydroxyaspartate cycle. <i>Nature</i> , 2019, 575, 500-504.	27.8	71
732	Transcriptomic analysis reveals flavonoid biosynthesis of <i>Syringa oblata</i> Lindl. in response to different light intensity. <i>BMC Plant Biology</i> , 2019, 19, 487.	3.6	21
733	Recovery of the Gut Microbiota after Antibiotics Depends on Host Diet, Community Context, and Environmental Reservoirs. <i>Cell Host and Microbe</i> , 2019, 26, 650-665.e4.	11.0	166
734	Ecological specificity of the metagenome in a set of lower termite species supports contribution of the microbiome to adaptation of the host. <i>Animal Microbiome</i> , 2019, 1, 13.	3.8	21
735	Genomic dissection of an extended phenotype: Oak galling by a cynipid gall wasp. <i>PLoS Genetics</i> , 2019, 15, e1008398.	3.5	44
736	An Integrated Pipeline for Annotation and Visualization of Metagenomic Contigs. <i>Frontiers in Genetics</i> , 2019, 10, 999.	2.3	92

#	ARTICLE	IF	CITATIONS
737	Metagenomics Reveals Seasonal Functional Adaptation of the Gut Microbiome to Host Feeding and Fasting in the Chinese Alligator. <i>Frontiers in Microbiology</i> , 2019, 10, 2409.	3.5	34
738	Complete genome sequencing of <i>Shigella</i> sp. PAMC 28760: Identification of CAZyme genes and analysis of their potential role in glycogen metabolism for cold survival adaptation. <i>Microbial Pathogenesis</i> , 2019, 137, 103759.	2.9	15
739	Emergence of the Ug99 lineage of the wheat stem rust pathogen through somatic hybridisation. <i>Nature Communications</i> , 2019, 10, 5068.	12.8	121
740	Free-living and symbiotic lifestyles of a thermotolerant coral endosymbiont display profoundly distinct transcriptomes under both stable and heat stress conditions. <i>Molecular Ecology</i> , 2019, 28, 5265-5281.	3.9	40
741	Mash Screen: high-throughput sequence containment estimation for genome discovery. <i>Genome Biology</i> , 2019, 20, 232.	8.8	173
742	<i>Didelphis albiventris</i> : an overview of unprecedented transcriptome sequencing of the white-eared opossum. <i>BMC Genomics</i> , 2019, 20, 866.	2.8	0
743	SwiftOrtho: A fast, memory-efficient, multiple genome orthology classifier. <i>GigaScience</i> , 2019, 8, .	6.4	26
744	Retinal artery occlusion is associated with compositional and functional shifts in the gut microbiome and altered trimethylamine-N-oxide levels. <i>Scientific Reports</i> , 2019, 9, 15303.	3.3	19
745	Long Read Single-Molecule Real-Time Sequencing Elucidates Transcriptome-Wide Heterogeneity and Complexity in Esophageal Squamous Cells. <i>Frontiers in Genetics</i> , 2019, 10, 915.	2.3	12
746	Eukaryote Genes Are More Likely than Prokaryote Genes to Be Composites. <i>Genes</i> , 2019, 10, 648.	2.4	2
747	Active Fungal Communities in Asymptomatic <i>Eucalyptus grandis</i> Stems Differ between a Susceptible and Resistant Clone. <i>Microorganisms</i> , 2019, 7, 375.	3.6	6
748	Insights into the Bacterial Profiles and Resistome Structures Following the Severe 2018 Flood in Kerala, South India. <i>Microorganisms</i> , 2019, 7, 474.	3.6	4
749	High Diversity and Novel Enteric Viruses in Fecal Viromes of Healthy Wild and Captive Thai <i>Cynomolgus</i> Macaques (<i>Macaca fascicularis</i>). <i>Viruses</i> , 2019, 11, 971.	3.3	18
750	Characterization and novel Est-SSR marker development of an important Chinese medicinal plant, <i>Morinda officinalis</i> How (Rubiaceae). <i>Biotechnology and Biotechnological Equipment</i> , 2019, 33, 1311-1318.	1.3	7
751	Differential selection pressure exerted by root rot disease on the microbial communities in the rhizosphere of avocado (<i>Persea americana</i> Mill.). <i>Annals of Applied Biology</i> , 2019, 175, 376-387.	2.5	11
752	Robust taxonomic classification of uncharted microbial sequences and bins with CAT and BAT. <i>Genome Biology</i> , 2019, 20, 217.	8.8	269
753	Trophic Status Is Associated With Community Structure and Metabolic Potential of Planktonic Microbiota in Plateau Lakes. <i>Frontiers in Microbiology</i> , 2019, 10, 2560.	3.5	39
754	Genomic Insights into the Fungal Lignocellulolytic Machinery of <i>Flammulina rossica</i> . <i>Microorganisms</i> , 2019, 7, 421.	3.6	5

#	ARTICLE	IF	CITATIONS
755	Greater genetic and regulatory plasticity of retained duplicates in <i>Epichloa</i> endophytic fungi. <i>Molecular Ecology</i> , 2019, 28, 5103-5114.	3.9	6
756	High-throughput DNA sequencing technologies for water and wastewater analysis. <i>Science Progress</i> , 2019, 102, 351-376.	1.9	16
757	Expression Patterns, Molecular Characterization, and Response to Host Stress of CYP Genes from <i>Phenacoccus solenopsis</i> (Hemiptera: Pseudococcidae). <i>Insects</i> , 2019, 10, 264.	2.2	2
758	Prevalence and proliferation of antibiotic resistance genes in the subtropical mangrove wetland ecosystem of South China Sea. <i>MicrobiologyOpen</i> , 2019, 8, e871.	3.0	27
759	Transcriptome analysis to understand the effects of the toxoflavin and tropolone produced by phytopathogenic <i>Burkholderia</i> on <i>Escherichia coli</i> . <i>Journal of Microbiology</i> , 2019, 57, 781-794.	2.8	8
760	Transcriptomic analyses of the acute ammonia stress response in the hepatopancreas of the kuruma shrimp (<i>Marsupenaeus japonicus</i>). <i>Aquaculture</i> , 2019, 513, 734328.	3.5	35
761	The Application of Convolutional Neural Network in Security Code Recognition. <i>Journal of Physics: Conference Series</i> , 2019, 1187, 042064.	0.4	1
762	Associated Bacteria Affect Sexual Reproduction by Altering Gene Expression and Metabolic Processes in a Biofilm Inhabiting Diatom. <i>Frontiers in Microbiology</i> , 2019, 10, 1790.	3.5	21
763	Whole Genome Sequencing of Extended-Spectrum Beta-Lactamase (ESBL)-Producing <i>Escherichia coli</i> Isolated From a Wastewater Treatment Plant in China. <i>Frontiers in Microbiology</i> , 2019, 10, 1797.	3.5	26
764	Antibiotic resistance and metabolic profiles as functional biomarkers that accurately predict the geographic origin of city metagenomics samples. <i>Biology Direct</i> , 2019, 14, 15.	4.6	17
765	Degradation profile of nixtamalized maize pericarp by the action of the microbial consortium PM-06. <i>AMB Express</i> , 2019, 9, 85.	3.0	7
766	Phylogenomic analysis of UDPâ€dependent glycosyltransferases provides insights into the evolutionary landscape of glycosylation in plant metabolism. <i>Plant Journal</i> , 2019, 100, 1273-1288.	5.7	75
767	Community structure and functional genes in radionuclide contaminated soils in Chernobyl and Fukushima. <i>FEMS Microbiology Letters</i> , 2019, 366, .	1.8	26
768	Genome Sequences of <i>Ambystoma Tigrinum</i> Virus Recovered during a Mass Die-off of Western Tiger Salamanders in Alberta, Canada. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	4
769	Nearly Complete Genome Sequence of a Sapelovirus A Strain Identified in Swine in Italy. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	3
770	Using metagenomics to reveal landscape scale patterns of denitrifiers in a montane forest ecosystem. <i>Soil Biology and Biochemistry</i> , 2019, 138, 107585.	8.8	16
771	Advances and Challenges in Metatranscriptomic Analysis. <i>Frontiers in Genetics</i> , 2019, 10, 904.	2.3	253
772	Transcriptome analysis to characterize the genes related to gonad growth and fatty acid metabolism in the sea urchin <i>Strongylocentrotus intermedius</i> . <i>Genes and Genomics</i> , 2019, 41, 1397-1415.	1.4	9

#	ARTICLE	IF	CITATIONS
773	Metagenomic Analysis of Virus Diversity and Relative Abundance in a Eutrophic Freshwater Harbour. <i>Viruses</i> , 2019, 11, 792.	3.3	24
774	The mycovirome of a fungal collection from the sea cucumber <i>Holothuria polii</i> . <i>Virus Research</i> , 2019, 273, 197737.	2.2	65
775	Dual RNA-Seq Analysis of the Pine- <i>Fusarium circinatum</i> Interaction in Resistant (<i>Pinus tecunumanii</i>) and Susceptible (<i>Pinus patula</i>) Hosts. <i>Microorganisms</i> , 2019, 7, 315.	3.6	18
776	Proteogenomics: From next-generation sequencing (NGS) and mass spectrometry-based proteomics to precision medicine. <i>Clinica Chimica Acta</i> , 2019, 498, 38-46.	1.1	38
777	Transcription and microbial profiling of body fluids using a massively parallel sequencing approach. <i>Forensic Science International: Genetics</i> , 2019, 43, 102149.	3.1	23
778	A reference genome for pea provides insight into legume genome evolution. <i>Nature Genetics</i> , 2019, 51, 1411-1422.	21.4	363
779	A library of human gut bacterial isolates paired with longitudinal multiomics data enables mechanistic microbiome research. <i>Nature Medicine</i> , 2019, 25, 1442-1452.	30.7	255
780	To assemble or not to resemble – A validated Comparative Metatranscriptomics Workflow (CoMW). <i>GigaScience</i> , 2019, 8, .	6.4	25
781	Stable distinct core eukaryotic viromes in different mosquito species from Guadeloupe, using single mosquito viral metagenomics. <i>Microbiome</i> , 2019, 7, 121.	11.1	109
782	Identification of discriminatory antibiotic resistance genes among environmental resistomes using extremely randomized tree algorithm. <i>Microbiome</i> , 2019, 7, 123.	11.1	35
783	Identification of a Novel Equine Papillomavirus in Semen from a Thoroughbred Stallion with a Penile Lesion. <i>Viruses</i> , 2019, 11, 713.	3.3	16
784	Different Pathways Mediate Amphotericin-Lactoferrin Drug Synergy in <i>Cryptococcus</i> and <i>Saccharomyces</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 2195.	3.5	5
785	Analysis of Microbial Community Dynamics during the Acclimatization Period of a Membrane Bioreactor Treating Table Olive Processing Wastewater. <i>Applied Sciences (Switzerland)</i> , 2019, 9, 3647.	2.5	4
786	De novo transcriptome profile of coccolithophorid alga <i>Emiliana huxleyi</i> CCMP371 at different calcium concentrations with proteome analysis. <i>PLoS ONE</i> , 2019, 14, e0221938.	2.5	11
787	Horizontally transmitted symbiont populations in deep-sea mussels are genetically isolated. <i>ISME Journal</i> , 2019, 13, 2954-2968.	9.8	42
788	Genomic analysis of the tribe Emesidini (Lepidoptera: Riodinidae). <i>Zootaxa</i> , 2019, 4668, zootaxa.4668.4.2.	0.5	10
789	Viral metagenomics updated the prevalence of human papillomavirus types in anogenital warts. <i>Emerging Microbes and Infections</i> , 2019, 8, 1291-1299.	6.5	9
790	Microbial Metabolism Modulates Antibiotic Susceptibility within the Murine Gut Microbiome. <i>Cell Metabolism</i> , 2019, 30, 800-823.e7.	16.2	70

#	ARTICLE	IF	CITATIONS
791	Unveiling resistome profiles in the sediments of an Antarctic volcanic island. <i>Environmental Pollution</i> , 2019, 255, 113240.	7.5	15
792	Metatranscriptomics reveals climate change effects on the rhizosphere microbiomes in European grassland. <i>Soil Biology and Biochemistry</i> , 2019, 138, 107604.	8.8	33
793	Aromatic compounds lead to increased abundance of antibiotic resistance genes in wastewater treatment bioreactors. <i>Water Research</i> , 2019, 166, 115073.	11.3	53
794	Distinct impact of antibiotics on the gut microbiome and resistome: a longitudinal multicenter cohort study. <i>BMC Biology</i> , 2019, 17, 76.	3.8	92
795	Characterization of an integrated, endogenous mouse mammary tumor virus-like (MMTV) betaretrovirus genome in a black Syrian hamster (<i>Mesocricetus auratus</i>). <i>Infection, Genetics and Evolution</i> , 2019, 75, 103995.	2.3	1
796	Metaviromics Reveals Unknown Viral Diversity in the Biting Midge <i>Culicoides impunctatus</i> . <i>Viruses</i> , 2019, 11, 865.	3.3	11
797	Adenovirus infection is associated with altered gut microbial communities in a non-human primate. <i>Scientific Reports</i> , 2019, 9, 13410.	3.3	32
798	Sex-dependent and -independent transcriptional changes during haploid phase gametogenesis in the sugar kelp <i>Saccharina latissima</i> . <i>PLoS ONE</i> , 2019, 14, e0219723.	2.5	15
799	Transcriptome of <i>Thalassicolla nucleata</i> Holobiont Reveals Details of a Radiolarian Symbiotic Relationship. <i>Frontiers in Marine Science</i> , 2019, 6, .	2.5	13
800	Identification of genomic loci associated with genotypic and phenotypic variation among <i>Pseudomonas aeruginosa</i> clinical isolates from pneumonia. <i>Microbial Pathogenesis</i> , 2019, 136, 103702.	2.9	2
801	Arsenic mobilization in a high arsenic groundwater revealed by metagenomic and Geochip analyses. <i>Scientific Reports</i> , 2019, 9, 12972.	3.3	23
802	Intraspecific Variation in Protists: Clues for Microevolution from <i>Potriospumella lacustris</i> (Chrysophyceae). <i>Genome Biology and Evolution</i> , 2019, 11, 2492-2504.	2.5	7
803	Comparison between transcriptomic responses to short-term stress exposures of a common Holarctic and endemic Lake Baikal amphipods. <i>BMC Genomics</i> , 2019, 20, 712.	2.8	17
804	Comparative analysis of amplicon and metagenomic sequencing methods reveals key features in the evolution of animal metaorganisms. <i>Microbiome</i> , 2019, 7, 133.	11.1	141
805	NCBI's Virus Discovery Hackathon: Engaging Research Communities to Identify Cloud Infrastructure Requirements. <i>Genes</i> , 2019, 10, 714.	2.4	13
806	HH-suite3 for fast remote homology detection and deep protein annotation. <i>BMC Bioinformatics</i> , 2019, 20, 473.	2.6	706
807	Comparative transcriptomic analysis of a wing-dimorphic stonefly reveals candidate wing loss genes. <i>EvoDevo</i> , 2019, 10, 21.	3.2	18
808	The whole-genome landscape of Burkitt lymphoma subtypes. <i>Blood</i> , 2019, 134, 1598-1607.	1.4	113

#	ARTICLE	IF	CITATIONS
809	The fecal resistome of dairy cattle is associated with diet during nursing. <i>Nature Communications</i> , 2019, 10, 4406.	12.8	100
810	Transcriptome analysis of hemocytes from the white shrimp <i>Litopenaeus vannamei</i> with the injection of dopamine. <i>Fish and Shellfish Immunology</i> , 2019, 94, 497-509.	3.6	21
811	Effects of Essential Oil Citral on the Growth, Mycotoxin Biosynthesis and Transcriptomic Profile of <i>Alternaria alternata</i> . <i>Toxins</i> , 2019, 11, 553.	3.4	45
812	Molecular Identification of a Novel Hantavirus in Malaysian Bronze Tube-Nosed Bats (<i>Murina aenea</i>). <i>Viruses</i> , 2019, 11, 887.	3.3	8
813	Sample Preservation and Storage Significantly Impact Taxonomic and Functional Profiles in Metaproteomics Studies of the Human Gut Microbiome. <i>Microorganisms</i> , 2019, 7, 367.	3.6	32
814	Characterisation of the <i>Carpinus betulus</i> L. Phyllosymbiont in Urban and Forest Areas. <i>Frontiers in Microbiology</i> , 2019, 10, 1110.	3.5	35
815	Comparative Genomic and Transcriptomic Analysis Suggests the Evolutionary Dynamic of GH3 Genes in Gramineae Crops. <i>Frontiers in Plant Science</i> , 2019, 10, 1297.	3.6	16
816	The EFI Web Resource for Genomic Enzymology Tools: Leveraging Protein, Genome, and Metagenome Databases to Discover Novel Enzymes and Metabolic Pathways. <i>Biochemistry</i> , 2019, 58, 4169-4182.	2.5	441
817	Application of metagenomic shotgun sequencing to detect vector-borne pathogens in clinical blood samples. <i>PLoS ONE</i> , 2019, 14, e0222915.	2.5	39
818	Transcriptome sequencing reveals phagocytosis as the main immune response in the pathogen-challenged sea urchin <i>Strongylocentrotus intermedius</i> . <i>Fish and Shellfish Immunology</i> , 2019, 94, 780-791.	3.6	14
819	Source identification of antibiotic resistance genes in a peri-urban river using novel crAssphage marker genes and metagenomic signatures. <i>Water Research</i> , 2019, 167, 115098.	11.3	54
820	Targeted metagenomic recovery of four divergent viruses reveals shared and distinctive characteristics of giant viruses of marine eukaryotes. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20190086.	4.0	22
821	Resistance Breeding of Common Bean Shapes the Physiology of the Rhizosphere Microbiome. <i>Frontiers in Microbiology</i> , 2019, 10, 2252.	3.5	41
822	Bioinformatics Identification of Anti-CRISPR Loci by Using Homology, Guilt-by-Association, and CRISPR Self-Targeting Spacer Approaches. <i>MSystems</i> , 2019, 4, .	3.8	38
823	Presence, Diversity, and Enrichment of Respiratory Reductive Dehalogenase and Non-respiratory Hydrolytic and Oxidative Dehalogenase Genes in Terrestrial Environments. <i>Frontiers in Microbiology</i> , 2019, 10, 1258.	3.5	20
824	Detecting viral sequences in NGS data. <i>Current Opinion in Virology</i> , 2019, 39, 41-48.	5.4	52
825	Taxonomic and Metabolic Incongruence in the Ancient Genus <i>Streptomyces</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 2170.	3.5	40
826	Occurrence of human pathogenic bacteria carrying antibiotic resistance genes revealed by metagenomic approach: A case study from an aquatic environment. <i>Journal of Environmental Sciences</i> , 2019, 80, 248-256.	6.1	31

#	ARTICLE	IF	CITATIONS
827	Effects of missing data and data type on phylotranscriptomic analysis of stony corals (Cnidaria: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 7	2.7	14
828	Metagenomic Characterization of the Viral Community of the South Scotia Ridge. <i>Viruses</i> , 2019, 11, 95.	3.3	22
829	Effects of activated carbon on anaerobic digestion “Methanogenic metabolism, mechanisms of antibiotics and antibiotic resistance genes removal. <i>Bioresource Technology Reports</i> , 2019, 5, 113-120.	2.7	41
830	A High-quality Draft Genome Assembly of <i>Sinella curviseta</i> : A Soil Model Organism (Collembola). <i>Genome Biology and Evolution</i> , 2019, 11, 521-530.	2.5	13
831	A single introduction of <i>Yersinia pestis</i> to Brazil during the 3rd plague pandemic. <i>PLoS ONE</i> , 2019, 14, e0209478.	2.5	5
832	The unique composition of Indian gut microbiome, gene catalogue, and associated fecal metabolome deciphered using multi-omics approaches. <i>GigaScience</i> , 2019, 8, .	6.4	143
833	Anaerobic Degradation of Sulfated Polysaccharides by Two Novel Kiritimatiellales Strains Isolated From Black Sea Sediment. <i>Frontiers in Microbiology</i> , 2019, 10, 253.	3.5	56
834	Marine biofilms constitute a bank of hidden microbial diversity and functional potential. <i>Nature Communications</i> , 2019, 10, 517.	12.8	100
835	Molecular characterization and expression patterns of <i>Phenacoccus solenopsis</i> (Hemiptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 Biochemistry and Physiology, 2019, 100, e21536.	1.5	1
836	The ketogenic diet influences taxonomic and functional composition of the gut microbiota in children with severe epilepsy. <i>Npj Biofilms and Microbiomes</i> , 2019, 5, 5.	6.4	179
837	Exploring the Fecal Microbial Composition and Metagenomic Functional Capacities Associated With Feed Efficiency in Commercial DLY Pigs. <i>Frontiers in Microbiology</i> , 2019, 10, 52.	3.5	77
838	Network-based microsynteny analysis identifies major differences and genomic outliers in mammalian and angiosperm genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 2165-2174.	7.1	89
839	The Genome of <i>Armadillidium vulgare</i> (Crustacea, Isopoda) Provides Insights into Sex Chromosome Evolution in the Context of Cytoplasmic Sex Determination. <i>Molecular Biology and Evolution</i> , 2019, 36, 727-741.	8.9	43
840	Genome Sequence of <i>Morganella morganii</i> DG56-16, Isolated from <i>Shinisaurus crocodilurus</i> . <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	1
841	Gut Virome Analysis of Cameroonians Reveals High Diversity of Enteric Viruses, Including Potential Interspecies Transmitted Viruses. <i>MSphere</i> , 2019, 4, .	2.9	57
842	The effect of ovine milk fermentation on the antithrombotic properties of polar lipids. <i>Journal of Functional Foods</i> , 2019, 54, 289-300.	3.4	28
843	mRNA and microRNA transcriptomics analyses in intermuscular bones of two carp species, rice flower carp (<i>Cyprinus carpio</i> var. <i>Quanzhounensis</i>) and Jian carp (<i>Cyprinus carpio</i> var. <i>Jian</i>). <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2019, 30, 71-80.	1.0	7
844	Complete Genome Sequence of the <i>Wolbachia</i> wAlbB Endosymbiont of <i>Aedes albopictus</i> . <i>Genome Biology and Evolution</i> , 2019, 11, 706-720.	2.5	44

#	ARTICLE	IF	CITATIONS
845	Whole-Genome Sequence Data Uncover Widespread Heterothallism in the Largest Group of Lichen-Forming Fungi. <i>Genome Biology and Evolution</i> , 2019, 11, 721-730.	2.5	15
846	Metagenome sequencing-based strain-level and functional characterization of supragingival microbiome associated with dental caries in children. <i>Journal of Oral Microbiology</i> , 2019, 11, 1557986.	2.7	43
847	Back to the Salt Mines: Genome and Transcriptome Comparisons of the Halophilic Fungus <i>Aspergillus salisburgensis</i> and Its Halotolerant Relative <i>Aspergillus sclerotialis</i> . <i>Genes</i> , 2019, 10, 381.	2.4	17
848	Annotated bacterial chromosomes from frame-shift-corrected long-read metagenomic data. <i>Microbiome</i> , 2019, 7, 61.	11.1	69
849	Arsenite Oxidation by a Newly Isolated Betaproteobacterium Possessing <i>ars</i> Genes and Diversity of the <i>ars</i> Gene Cluster in Bacterial Genomes. <i>Frontiers in Microbiology</i> , 2019, 10, 1210.	3.5	11
850	Proficiency Testing of Virus Diagnostics Based on Bioinformatics Analysis of Simulated <i>In Silico</i> High-Throughput Sequencing Data Sets. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	3.9	34
851	Genomic basis of antibiotic resistance in <i>Vibrio parahaemolyticus</i> strain JPA1. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2019, 114, e190053.	1.6	5
852	Fungi of Antarctica. , 2019, , .		49
853	NanoARG: a web service for detecting and contextualizing antimicrobial resistance genes from nanopore-derived metagenomes. <i>Microbiome</i> , 2019, 7, 88.	11.1	72
854	Genomic and Metagenomic Insights Into the Microbial Community in the Regenerating Intestine of the Sea Cucumber <i>Apostichopus japonicus</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 1165.	3.5	22
855	Overlooked Genetic Diversity of Ammonia Oxidizing Archaea Lineages in the Global Oceans. <i>Journal of Geophysical Research G: Biogeosciences</i> , 2019, 124, 1799-1811.	3.0	23
856	Sulfur metabolites that facilitate oceanic phytoplankton–bacteria carbon flux. <i>ISME Journal</i> , 2019, 13, 2536-2550.	9.8	70
857	Ancient duplications and grass-specific transposition influenced the evolution of LEAFY transcription factor genes. <i>Communications Biology</i> , 2019, 2, 237.	4.4	16
858	Description of strongly heat-inducible heat shock protein 70 transcripts from Baikal endemic amphipods. <i>Scientific Reports</i> , 2019, 9, 8907.	3.3	7
859	Genomics of Antarctic Fungi: A New Frontier. , 2019, , 319-338.		0
860	Deep learning enables high-quality and high-throughput prediction of enzyme commission numbers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 13996-14001.	7.1	151
861	Uncovering genome wide novel allelic variants for eating and cooking quality in a popular Indian rice cultivar, Samba Mahsuri. <i>Current Plant Biology</i> , 2019, 18, 100111.	4.7	2
862	Species-specific mechanisms of cytotoxicity toward immune cells determine the successful outcome of <i>Vibrio</i> infections. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 14238-14247.	7.1	62

#	ARTICLE	IF	CITATIONS
863	Sulfur-Oxidizing Symbionts without Canonical Genes for Autotrophic CO ₂ Fixation. MBio, 2019, 10, .	4.1	29
864	Horizontal transfer of a retrotransposon between parasitic nematodes and the common shrew. Mobile DNA, 2019, 10, 24.	3.6	18
865	Effect of Long-Term Farming Practices on Agricultural Soil Microbiome Members Represented by Metagenomically Assembled Genomes (MAGs) and Their Predicted Plant-Beneficial Genes. Genes, 2019, 10, 424.	2.4	61
866	Comparative genomics and genome biology of <i>Campylobacter showae</i> . Emerging Microbes and Infections, 2019, 8, 827-840.	6.5	8
867	What information can be obtained from the tears of a patient with primary open angle glaucoma?. Clinica Chimica Acta, 2019, 495, 529-537.	1.1	38
868	Total RNA Analysis of Bacterial Community Structural and Functional Shifts Throughout Vertebrate Decomposition. Journal of Forensic Sciences, 2019, 64, 1707-1719.	1.6	12
869	MiCoP: microbial community profiling method for detecting viral and fungal organisms in metagenomic samples. BMC Genomics, 2019, 20, 423.	2.8	22
870	Comparing the treatment effect of narrow spectrum antimicrobial, probiotic and fluid with amoxicillin in mink kits (<i>Neovison vison</i>) with pre-weaning diarrhea. Research in Veterinary Science, 2019, 125, 121-129.	1.9	2
871	Lignocellulose degradation in isopods: new insights into the adaptation to terrestrial life. BMC Genomics, 2019, 20, 462.	2.8	22
872	Whole Genome Sequencing and Comparative Genomic Analysis Reveal Allelic Variations Unique to a Purple Colored Rice Landrace (<i>Oryza sativa</i> ssp. <i>indica</i> cv. Purpleputtu). Frontiers in Plant Science, 2019, 10, 513.	3.6	21
873	Co-expression network analysis identifies gonad- and embryo-associated protein modules in the sentinel species <i>Gammarus fossarum</i> . Scientific Reports, 2019, 9, 7862.	3.3	13
874	High-throughput sequencing reveals no viral pathogens in eight cases of ocular adnexal extranodal marginal zone B-cell lymphoma. Experimental Eye Research, 2019, 185, 107677.	2.6	7
875	Uncovering the cellular and humoral immune responses of <i>Antheraea pernyi</i> hemolymph to <i>Antheraea pernyi</i> nucleopolyhedrovirus infection by transcriptome analysis. Journal of Invertebrate Pathology, 2019, 166, 107205.	3.2	9
876	Multi-omics of the gut microbial ecosystem in inflammatory bowel diseases. Nature, 2019, 569, 655-662.	27.8	1,638
877	An Alternative Bioassay for <i>Synchytrium endobioticum</i> Demonstrates the Expression of Potato Wart Resistance in Aboveground Plant Parts. Phytopathology, 2019, 109, 1043-1052.	2.2	4
878	HPV transcription in skin tumors. PLoS ONE, 2019, 14, e0217942.	2.5	10
879	Proteomic and Metabolomic Characteristics of Extremophilic Fungi Under Simulated Mars Conditions. Frontiers in Microbiology, 2019, 10, 1013.	3.5	36
880	Composite Metagenome-Assembled Genomes Reduce the Quality of Public Genome Repositories. MBio, 2019, 10, .	4.1	76

#	ARTICLE	IF	CITATIONS
881	Transcriptomic Analysis Identifies New Non-Target Site Glyphosate-Resistance Genes in <i>Conyza bonariensis</i> . <i>Plants</i> , 2019, 8, 157.	3.5	31
882	Comparison of de-novo assembly tools for plasmid metagenome analysis. <i>Genes and Genomics</i> , 2019, 41, 1077-1083.	1.4	6
883	Cyberinfrastructure to Improve Forest Health and Productivity: The Role of Tree Databases in Connecting Genomes, Phenomes, and the Environment. <i>Frontiers in Plant Science</i> , 2019, 10, 813.	3.6	24
884	Next-Generation Metagenomics: Methodological Challenges and Opportunities. <i>OMICS A Journal of Integrative Biology</i> , 2019, 23, 327-333.	2.0	47
885	Molecular cloning and characterisation of SaCLCa1, a novel protein of the chloride channel (CLC) family from the halophyte <i>Suaeda altissima</i> (L.) Pall. <i>Journal of Plant Physiology</i> , 2019, 240, 152995.	3.5	9
886	GRASP2: fast and memory-efficient gene-centric assembly and homolog search for metagenomic sequencing data. <i>BMC Bioinformatics</i> , 2019, 20, 276.	2.6	5
887	Geochemical-Compositional-Functional Changes in Arctic Soil Microbiomes Post Land Submergence Revealed by Metagenomics. <i>Microbes and Environments</i> , 2019, 34, 180-190.	1.6	6
888	Unprecedented reorganization of holocentric chromosomes provides insights into the enigma of lepidopteran chromosome evolution. <i>Science Advances</i> , 2019, 5, eaau3648.	10.3	66
889	Gut microbial beta-glucuronidase and glycerol/diol dehydratase activity contribute to dietary heterocyclic amine biotransformation. <i>BMC Microbiology</i> , 2019, 19, 99.	3.3	42
890	Network Integrative Genomic and Transcriptomic Analysis of Carbapenem-Resistant <i>Klebsiella pneumoniae</i> Strains Identifies Genes for Antibiotic Resistance and Virulence. <i>MSystems</i> , 2019, 4, .	3.8	15
891	Human contamination in bacterial genomes has created thousands of spurious proteins. <i>Genome Research</i> , 2019, 29, 954-960.	5.5	111
892	Comparative microbiome analysis of two different long-term pesticide contaminated soils revealed the anthropogenic influence on functional potential of microbial communities. <i>Science of the Total Environment</i> , 2019, 681, 413-423.	8.0	53
893	Development of a transcriptomic database for 14 species of scleractinian corals. <i>BMC Genomics</i> , 2019, 20, 387.	2.8	18
894	Expansion and Evolutionary Patterns of Glycosyltransferase Family 8 in Gramineae Crop Genomes and Their Expression under Salt and Cold Stresses in <i>Oryza sativa</i> ssp. <i>japonica</i> . <i>Biomolecules</i> , 2019, 9, 188.	4.0	30
895	Analysis of microbiome in raw chicken meat from butcher shops and packaged products in South Korea to detect the potential risk of foodborne illness. <i>Food Research International</i> , 2019, 122, 517-527.	6.2	24
896	Peptide-based functional annotation of carbohydrate-active enzymes by conserved unique peptide patterns (CUPP). <i>Biotechnology for Biofuels</i> , 2019, 12, 102.	6.2	55
897	Novel Circo-Like Virus Detected in a Croatian Bat Population. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	3
898	Development of a Blocking Primer to Inhibit the PCR Amplification of the 18S rDNA Sequences of <i>Litopenaeus vannamei</i> and Its Efficacy in <i>Crassostrea hongkongensis</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 830.	3.5	16

#	ARTICLE	IF	CITATIONS
899	A metagenomic analysis of the relationship between microorganisms and flavor development in Shaoxing mechanized huangjiu fermentation mashes. <i>International Journal of Food Microbiology</i> , 2019, 303, 9-18.	4.7	116
900	Integrated Analysis of Transcriptomic, miRNA and Proteomic Changes of a Novel Hybrid Yellow Catfish Uncovers Key Roles for miRNAs in Heterosis. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1437-1453.	3.8	30
901	Variation in pigmentation gene expression is associated with distinct aposematic color morphs in the poison frog <i>Dendrobates auratus</i> . <i>BMC Evolutionary Biology</i> , 2019, 19, 85.	3.2	25
902	Widespread gene duplication and adaptive evolution in the RNA interference pathways of the <i>Drosophila obscura</i> group. <i>BMC Evolutionary Biology</i> , 2019, 19, 99.	3.2	15
903	Bacterial Community Succession, Transmigration, and Differential Gene Transcription in a Controlled Vertebrate Decomposition Model. <i>Frontiers in Microbiology</i> , 2019, 10, 745.	3.5	25
904	Differences in resource use lead to coexistence of seed-transmitted microbial populations. <i>Scientific Reports</i> , 2019, 9, 6648.	3.3	17
905	Genome-wide characterization of drought stress responsive long non-coding RNAs in Tibetan wild barley. <i>Environmental and Experimental Botany</i> , 2019, 164, 124-134.	4.2	31
906	Prokaryotic and viral community of the sulfate-rich crust from Peñahueca ephemeral lake, an astrobiology analogue. <i>Environmental Microbiology</i> , 2019, 21, 3577-3600.	3.8	9
907	Transmission of a New Polerovirus Infecting Pepper by the Whitefly <i>Bemisia tabaci</i> . <i>Journal of Virology</i> , 2019, 93, .	3.4	54
908	Distribution and Phylogeny of Erythrocytic Necrosis Virus (ENV) in Salmon Suggests Marine Origin. <i>Viruses</i> , 2019, 11, 358.	3.3	11
909	Gene Prediction. <i>Methods in Molecular Biology</i> , 2019, , .	0.9	33
910	Leveraging Human Microbiome Features to Diagnose and Stratify Children with Irritable Bowel Syndrome. <i>Journal of Molecular Diagnostics</i> , 2019, 21, 449-461.	2.8	59
911	Marine DNA Viral Macro- and Microdiversity from Pole to Pole. <i>Cell</i> , 2019, 177, 1109-1123.e14.	28.9	541
912	Metabolic potential of uncultured bacteria and archaea associated with petroleum seepage in deep-sea sediments. <i>Nature Communications</i> , 2019, 10, 1816.	12.8	118
913	Mitovirus and Mitochondrial Coding Sequences from Basal Fungus <i>Entomophthora muscae</i> . <i>Viruses</i> , 2019, 11, 351.	3.3	21
914	Challenges and promise at the interface of metaproteomics and genomics: an overview of recent progress in metaproteogenomic data analysis. <i>Expert Review of Proteomics</i> , 2019, 16, 375-390.	3.0	86
915	Soil Organic Carbon Chemical Functional Groups under Different Revegetation Types Are Coupled with Changes in the Microbial Community Composition and the Functional Genes. <i>Forests</i> , 2019, 10, 240.	2.1	19
916	Taxonomic assignment of uncultivated prokaryotic virus genomes is enabled by gene-sharing networks. <i>Nature Biotechnology</i> , 2019, 37, 632-639.	17.5	569

#	ARTICLE	IF	CITATIONS
917	Estimate of the diversity of viral and bacterial assemblage in the coastal water of Lake Baikal. FEMS Microbiology Letters, 2019, 366, .	1.8	13
918	OrthoVenn2: a web server for whole-genome comparison and annotation of orthologous clusters across multiple species. Nucleic Acids Research, 2019, 47, W52-W58.	14.5	661
919	Metagenomics-Guided Survey, Isolation, and Characterization of Uranium Resistant Microbiota from the Savannah River Site, USA. Genes, 2019, 10, 325.	2.4	28
920	Red Sea SAR11 and <i>Prochlorococcus</i> Single-Cell Genomes Reflect Globally Distributed Pangenomes. Applied and Environmental Microbiology, 2019, 85, .	3.1	11
921	De Novo assembly and characterisation of the greentail prawn (<i>Metapenaeus bennettiae</i>) hepatopancreas transcriptome – identification of stress response and detoxification transcripts. Marine Genomics, 2019, 47, 100677.	1.1	13
922	Characterizing a Murine Model for Astrovirus Using Viral Isolates from Persistently Infected Immunocompromised Mice. Journal of Virology, 2019, 93, .	3.4	18
923	Genome-wide association study of resistance to stripe rust (<i>Puccinia striiformis</i> f. sp. <i>tritici</i>) in Sichuan wheat. BMC Plant Biology, 2019, 19, 147.	3.6	39
924	A long-term field experiment demonstrates the influence of tillage on the bacterial potential to produce soil structure-stabilizing agents such as exopolysaccharides and lipopolysaccharides. Environmental Microbiomes, 2019, 14, 1.	5.0	54
925	Choosing the Best Gene Predictions with GeneValidator. Methods in Molecular Biology, 2019, 1962, 257-267.	0.9	0
926	Structural and Functional Annotation of Eukaryotic Genomes with GenSAS. Methods in Molecular Biology, 2019, 1962, 29-51.	0.9	66
927	Ancient Polyploidy and Genome Evolution in Palms. Genome Biology and Evolution, 2019, 11, 1501-1511.	2.5	25
928	Broad-specificity GH131 β -glucanases are a hallmark of fungi and oomycetes that colonize plants. Environmental Microbiology, 2019, 21, 2724-2739.	3.8	18
929	Inadvertent Paralog Inclusion Drives Artifactual Topologies and Timetree Estimates in Phylogenomics. Molecular Biology and Evolution, 2019, 36, 1344-1356.	8.9	56
930	Metagenomic analysis of composition, function and cycling processes of microbial community in water, sediment and effluent of <i>Litopenaeus vannamei</i> farming environments under different culture modes. Aquaculture, 2019, 506, 280-293.	3.5	56
931	Carbon Fixation by Marine Ultrasmall Prokaryotes. Genome Biology and Evolution, 2019, 11, 1166-1177.	2.5	24
932	Sequencing-based methods and resources to study antimicrobial resistance. Nature Reviews Genetics, 2019, 20, 356-370.	16.3	263
933	Identification of Differentiating Metabolic Pathways between Infant Gut Microbiome Populations Reveals Depletion of Function-Level Adaptation to Human Milk in the Finnish Population. MSphere, 2019, 4, .	2.9	1
934	Virus Genomes from Deep Sea Sediments Expand the Ocean Megavirome and Support Independent Origins of Viral Gigantism. MBio, 2019, 10, .	4.1	85

#	ARTICLE	IF	CITATIONS
935	Shotgun Metagenomics of a Water Kefir Fermentation Ecosystem Reveals a Novel <i>Oenococcus</i> Species. <i>Frontiers in Microbiology</i> , 2019, 10, 479.	3.5	80
936	Microbial responses to anthropogenic dissolved organic carbon in the Arctic and Antarctic coastal seawaters. <i>Environmental Microbiology</i> , 2019, 21, 1466-1481.	3.8	28
937	Autometa: automated extraction of microbial genomes from individual shotgun metagenomes. <i>Nucleic Acids Research</i> , 2019, 47, e57-e57.	14.5	69
938	The complex geography of domestication of the African rice <i>Oryza glaberrima</i> . <i>PLoS Genetics</i> , 2019, 15, e1007414.	3.5	30
939	Infectious Complications Are Associated With Alterations in the Gut Microbiome in Pediatric Patients With Acute Lymphoblastic Leukemia. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 28.	3.9	48
940	CMY-1/MOX-family AmpC β -lactamases MOX-1, MOX-2 and MOX-9 were mobilized independently from three <i>Aeromonas</i> species. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 1202-1206.	3.0	17
941	Expanding anaerobic alkane metabolism in the domain of Archaea. <i>Nature Microbiology</i> , 2019, 4, 595-602.	13.3	133
942	Influence of salinity on the degradation of xenobiotic compounds in rhizospheric mangrove soil. <i>Environmental Pollution</i> , 2019, 249, 750-757.	7.5	15
943	De novo assembly and characterization of the transcriptome of the northern mauxia shrimp <i>Acetes chinensis</i> . <i>Marine Genomics</i> , 2019, 47, 100672.	1.1	4
944	Transmission of human-associated microbiota along family and social networks. <i>Nature Microbiology</i> , 2019, 4, 964-971.	13.3	149
945	Structural variation in the gut microbiome associates with host health. <i>Nature</i> , 2019, 568, 43-48.	27.8	244
946	Sunbeam: an extensible pipeline for analyzing metagenomic sequencing experiments. <i>Microbiome</i> , 2019, 7, 46.	11.1	134
947	Nine new RNA viruses associated with the fire ant <i>Solenopsis invicta</i> from its native range. <i>Virus Genes</i> , 2019, 55, 368-380.	1.6	22
948	Metagenomic analysis reveals distinct patterns of denitrification gene abundance across soil moisture, nitrate gradients. <i>Environmental Microbiology</i> , 2019, 21, 1255-1266.	3.8	49
949	From the Amazon: A comprehensive liver transcriptome dataset of the teleost fish tambaqui, <i>Colossoma macropomum</i> . <i>Data in Brief</i> , 2019, 23, 103751.	1.0	3
950	Characterization of the cecum microbiome from wild and captive rock ptarmigans indigenous to Arctic Norway. <i>PLoS ONE</i> , 2019, 14, e0213503.	2.5	18
951	Amino acid based <i>de Bruijn</i> graph algorithm for identifying complete coding genes from metagenomic and metatranscriptomic short reads. <i>Nucleic Acids Research</i> , 2019, 47, e30-e30.	14.5	7
952	A new genomic blueprint of the human gut microbiota. <i>Nature</i> , 2019, 568, 499-504.	27.8	901

#	ARTICLE	IF	CITATIONS
953	Alternative Transcription at Venom Genes and Its Role as a Complementary Mechanism for the Generation of Venom Complexity in the Common House Spider. <i>Frontiers in Ecology and Evolution</i> , 2019, 7, .	2.2	17
954	Bioinformatics applied to biotechnology: A review towards bioenergy research. <i>Biomass and Bioenergy</i> , 2019, 123, 195-224.	5.7	17
955	Sources of anammox granular sludge and their sustainability in treating low-strength wastewater. <i>Chemosphere</i> , 2019, 226, 229-237.	8.2	8
956	Identification of A Novel Picorna-Like Virus, Burpengary Virus, that is Negatively Associated with Chlamydial Disease in the Koala. <i>Viruses</i> , 2019, 11, 211.	3.3	6
957	Metagenomic analysis of microbe-mediated vitamin metabolism in the human gut microbiome. <i>BMC Genomics</i> , 2019, 20, 208.	2.8	81
958	Meta-Analysis of Salt Stress Transcriptome Responses in Different Rice Genotypes at the Seedling Stage. <i>Plants</i> , 2019, 8, 64.	3.5	41
959	Carbon fixation and energy metabolisms of a subseafloor olivine biofilm. <i>ISME Journal</i> , 2019, 13, 1737-1749.	9.8	39
960	Diversity and Evolution of Viral Pathogen Community in Cave Nectar Bats (<i>Eonycteris spelaea</i>). <i>Viruses</i> , 2019, 11, 250.	3.3	22
961	Microbial iron metabolism as revealed by gene expression profiles in contrasted Southern Ocean regimes. <i>Environmental Microbiology</i> , 2019, 21, 2360-2374.	3.8	27
962	Sequencing the Obligate Intracellular <i>Rhabdochlamydia helvetica</i> within Its Tick Host <i>Ixodes ricinus</i> to Investigate Their Symbiotic Relationship. <i>Genome Biology and Evolution</i> , 2019, 11, 1334-1344.	2.5	21
963	Improving Illumina assemblies with Hi-C and long reads: An example with the North African dromedary. <i>Molecular Ecology Resources</i> , 2019, 19, 1015-1026.	4.8	67
964	The NASA Twins Study: A multidimensional analysis of a year-long human spaceflight. <i>Science</i> , 2019, 364, .	12.6	576
965	Metagenomic analysis of the fecal microbiomes from <i>Escherichia coli</i> O157:H7-shedding and non-shedding cows on a single dairy farm. <i>Food Control</i> , 2019, 102, 76-80.	5.5	16
966	AnnoTree: visualization and exploration of a functionally annotated microbial tree of life. <i>Nucleic Acids Research</i> , 2019, 47, 4442-4448.	14.5	220
967	MGS-Fast: Metagenomic shotgun data fast annotation using microbial gene catalogs. <i>GigaScience</i> , 2019, 8, .	6.4	15
968	The Distribution of Tryptophan-Dependent Indole-3-Acetic Acid Synthesis Pathways in Bacteria Unraveled by Large-Scale Genomic Analysis. <i>Molecules</i> , 2019, 24, 1411.	3.8	76
969	Anti-inflammatory Gut Microbial Pathways Are Decreased During Crohn's Disease Exacerbations. <i>Journal of Crohn's and Colitis</i> , 2019, 13, 1439-1449.	1.3	39
970	Genomic adaptation to eutrophication of ammonia-oxidizing archaea in the Pearl River estuary. <i>Environmental Microbiology</i> , 2019, 21, 2320-2332.	3.8	23

#	ARTICLE	IF	CITATIONS
971	Transcriptome sequencing to unravel the molecular mechanisms underlying the cuticle liquefaction of <i>Antheraea pernyi</i> following <i>Antheraea pernyi</i> nucleopolyhedrovirus challenge. <i>Molecular Immunology</i> , 2019, 109, 108-115.	2.2	6
972	Microbial taxonomic, nitrogen cycling and phosphorus recycling community composition during long-term organic greenhouse farming. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	2.7	40
973	Prevalence, source and risk of antibiotic resistance genes in the sediments of Lake Tai (China) deciphered by metagenomic assembly: A comparison with other global lakes. <i>Environment International</i> , 2019, 127, 267-275.	10.0	84
974	Proposal of the reverse flow model for the origin of the eukaryotic cell based on comparative analyses of Asgard archaeal metabolism. <i>Nature Microbiology</i> , 2019, 4, 1138-1148.	13.3	143
975	Production Phase Affects the Bioaerosol Microbial Composition and Functional Potential in Swine Confinement Buildings. <i>Animals</i> , 2019, 9, 90.	2.3	27
976	Identification and reconstruction of novel antibiotic resistance genes from metagenomes. <i>Microbiome</i> , 2019, 7, 52.	11.1	84
977	Enrichment of periodontal pathogens from the biofilms of healthy adults. <i>Scientific Reports</i> , 2019, 9, 5491.	3.3	56
978	High-Quality Draft Genome Sequence of the Microcolonial Black Fungus <i>Aminium ludgeri</i> DSM 106916. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	6
979	Metagenomic insights into the abundance and composition of resistance genes in aquatic environments: Influence of stratification and geography. <i>Environment International</i> , 2019, 127, 371-380.	10.0	98
980	Comparative metagenomics study reveals pollution induced changes of microbial genes in mangrove sediments. <i>Scientific Reports</i> , 2019, 9, 5739.	3.3	32
981	Genomic and metatranscriptomic analyses of carbon remineralization in an Antarctic polynya. <i>Microbiome</i> , 2019, 7, 29.	11.1	13
982	Deep-Sea Biofilms, Historic Shipwreck Preservation and the Deepwater Horizon Spill. <i>Frontiers in Marine Science</i> , 2019, 6, .	2.5	27
983	Genome-centric metagenomics resolves microbial diversity and prevalent truncated denitrification pathways in a denitrifying PAO-enriched bioprocess. <i>Water Research</i> , 2019, 155, 275-287.	11.3	77
984	Identification of Eilat virus and prevalence of infection among <i>Culex pipiens</i> L. populations, Morocco, 2016. <i>Virology</i> , 2019, 530, 85-88.	2.4	7
985	DirtyGenes: testing for significant changes in gene or bacterial population compositions from a small number of samples. <i>Scientific Reports</i> , 2019, 9, 2373.	3.3	11
986	Origin and evolution of the octoploid strawberry genome. <i>Nature Genetics</i> , 2019, 51, 541-547.	21.4	469
987	Genome and transcriptome analysis of <i>Bacillus velezensis</i> BS37, an efficient surfactin producer from glycerol, in response to α -l-glutamine. <i>MicrobiologyOpen</i> , 2019, 8, e00794.	3.0	25
988	High diversity and rapid spatial turnover of integron gene cassettes in soil. <i>Environmental Microbiology</i> , 2019, 21, 1567-1574.	3.8	33

#	ARTICLE	IF	CITATIONS
989	Nitrification inhibitors effectively target N_2 -producing <i>Nitrosospora</i> spp. in tropical soil. <i>Environmental Microbiology</i> , 2019, 21, 1241-1254.	3.8	31
990	CAMISIM: simulating metagenomes and microbial communities. <i>Microbiome</i> , 2019, 7, 17.	11.1	117
991	First isolation of West Nile virus in Brazil. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2019, 114, e180332.	1.6	33
992	Challenges of next-generation sequencing targeting anaerobes. <i>Anaerobe</i> , 2019, 58, 47-52.	2.1	17
993	Potential of the <i>Burkholderia cepacia</i> Complex to Produce 4-Hydroxy-3-Methyl-2-Alkyquinolines. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 33.	3.9	23
994	Diatom genes originating from red and green algae: Implications for the secondary endosymbiosis models. <i>Marine Genomics</i> , 2019, 45, 72-78.	1.1	14
995	SqueezeMeta, A Highly Portable, Fully Automatic Metagenomic Analysis Pipeline. <i>Frontiers in Microbiology</i> , 2018, 9, 3349.	3.5	214
996	Evaluating Metagenomic Prediction of the Metaproteome in a 4.5-Year Study of a Patient with Crohn's Disease. <i>MSystems</i> , 2019, 4, .	3.8	40
997	Ruminal metagenomic analyses of goat data reveals potential functional microbiota by supplementation with essential oil-cobalt complexes. <i>BMC Microbiology</i> , 2019, 19, 30.	3.3	23
998	Marine DNA Viral Macro-and Micro-Diversity From Pole to Pole. <i>SSRN Electronic Journal</i> , 2019, , .	0.4	4
999	Metagenome Profiling Identifies Potential Biocontrol Agents for <i>Selaginella kraussiana</i> in New Zealand. <i>Genes</i> , 2019, 10, 106.	2.4	6
1000	Blubber transcriptome responses to repeated ACTH administration in a marine mammal. <i>Scientific Reports</i> , 2019, 9, 2718.	3.3	17
1001	Microdiversity and temporal dynamics of marine bacterial dimethylsulfoniopropionate genes. <i>Environmental Microbiology</i> , 2019, 21, 1687-1701.	3.8	38
1002	Orphan Genes Shared by Pathogenic Genomes Are More Associated with Bacterial Pathogenicity. <i>MSystems</i> , 2019, 4, .	3.8	15
1003	Metagenome-assembled genomes provide new insight into the microbial diversity of two thermal pools in Kamchatka, Russia. <i>Scientific Reports</i> , 2019, 9, 3059.	3.3	63
1004	Oral administration of antibiotics increased the potential mobility of bacterial resistance genes in the gut of the fish <i>Piaractus mesopotamicus</i> . <i>Microbiome</i> , 2019, 7, 24.	11.1	98
1005	Frequency of disturbance alters diversity, function, and underlying assembly mechanisms of complex bacterial communities. <i>Npj Biofilms and Microbiomes</i> , 2019, 5, 8.	6.4	70
1006	Dose-dependent impact of oxytetracycline on the veal calf microbiome and resistome. <i>BMC Genomics</i> , 2019, 20, 65.	2.8	17

#	ARTICLE	IF	CITATIONS
1007	R pyocin tail fiber structure reveals a receptor-binding domain with a lectin fold. PLoS ONE, 2019, 14, e0211432.	2.5	21
1008	Microbial residence time is a controlling parameter of the taxonomic composition and functional profile of microbial communities. ISME Journal, 2019, 13, 1589-1601.	9.8	24
1009	Sources and selection of snow-specific microbial communities in a Greenlandic sea ice snow cover. Scientific Reports, 2019, 9, 2290.	3.3	42
1010	Evolutionary Model of Cluster Divergence of the Emergent Marine Pathogen <i>Vibrio vulnificus</i> : From Genotype to Ecotype. MBio, 2019, 10, .	4.1	41
1011	Phylogenomic Analyses of Bradyrhizobium Reveal Uneven Distribution of the Lateral and Subpolar Flagellar Systems, Which Extends to Rhizobiales. Microorganisms, 2019, 7, 50.	3.6	16
1012	Gene expression and metabolite profiling analyses of developing pomegranate fruit peel reveal interactions between anthocyanin and punicalagin production. Tree Genetics and Genomes, 2019, 15, 1.	1.6	12
1013	Viral metagenomics revealed novel betatorquevirus species in pediatric inpatients with encephalitis/meningoencephalitis from Ghana. Scientific Reports, 2019, 9, 2360.	3.3	29
1014	Virome Diversity Correlates with Intestinal Microbiome Diversity in Adult Monozygotic Twins. Cell Host and Microbe, 2019, 25, 261-272.e5.	11.0	159
1015	Kingdom-wide comparison reveals the evolution of diurnal gene expression in Archaeplastida. Nature Communications, 2019, 10, 737.	12.8	52
1016	Unaligned Sequence Similarity Search Using Deep Learning. , 2019, , .		0
1017	GHOSTZ PW/GF: Distributed Parallel Homology Search System for Large-scale Metagenomic Analysis. , 2019, , .		0
1018	Trends of Microdiversity Reveal Depth-Dependent Evolutionary Strategies of Viruses in the Mediterranean. MSystems, 2019, 4, .	3.8	26
1019	Comprehensive Analysis Reveals the Evolution and Pathogenicity of <i>Aeromonas</i> , Viewed from Both Single Isolated Species and Microbial Communities. MSystems, 2019, 4, .	3.8	36
1020	Prokaryotic Population Dynamics and Viral Predation in a Marine Succession Experiment Using Metagenomics. Frontiers in Microbiology, 2019, 10, 2926.	3.5	17
1021	Reduced microbial potential for the degradation of phenolic compounds in the rhizosphere of apple plantlets grown in soils affected by replant disease. Environmental Microbiomes, 2019, 14, 8.	5.0	22
1022	Metagenome of Gut Microbiota of Children With Nonalcoholic Fatty Liver Disease. Frontiers in Pediatrics, 2019, 7, 518.	1.9	36
1023	Parallelized Pipeline for Whole Genome Shotgun Metagenomics with GHOSTZ-GPU and MEGAN. , 2019, , .		0
1024	Characterization of Core Microbiomes and Functional Profiles of Mesophilic Anaerobic Digesters Fed With Chlorella vulgaris Green Microalgae and Maize Silage. Frontiers in Energy Research, 2019, 7, .	2.3	19

#	ARTICLE	IF	CITATIONS
1025	In vitro Study of <i>Lactobacillus paracasei</i> CNCM I-1518 in Healthy and <i>Clostridioides difficile</i> Colonized Elderly Gut Microbiota. <i>Frontiers in Nutrition</i> , 2019, 6, 184.	3.7	12
1026	SeqScreen: a biocuration platform for robust taxonomic and biological process characterization of nucleic acid sequences of interest. , 2019, , .		7
1027	New insights into Sauropsid Papillomaviridae evolution and epizootiology: discovery of two novel papillomaviruses in native and invasive Island geckos. <i>Virus Evolution</i> , 2019, 5, vez051.	4.9	10
1028	Draft Genome Sequence of <i>Clostridium estertheticum</i> subsp. <i>laramiense</i> DSM 14864 ^T , Isolated from Spoiled Uncooked Beef. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	13
1029	SeqDeconv: A Sequence Deconvolution Tool for Genome Separation of Endosymbionts From Mixed Sequencing Samples. <i>Frontiers in Genetics</i> , 2019, 10, 853.	2.3	0
1030	Functional Traits Co-Occurring with Mobile Genetic Elements in the Microbiome of the Atacama Desert. <i>Diversity</i> , 2019, 11, 205.	1.7	5
1031	OrthoFinder: phylogenetic orthology inference for comparative genomics. <i>Genome Biology</i> , 2019, 20, 238.	8.8	3,367
1032	Genome-Scale Metabolic Networks Shed Light on the Carotenoid Biosynthesis Pathway in the Brown Algae <i>Saccharina japonica</i> and <i>Cladosiphon okamuranus</i> . <i>Antioxidants</i> , 2019, 8, 564.	5.1	19
1033	Meta-Transcriptomic Comparison of the RNA Viromes of the Mosquito Vectors <i>Culex pipiens</i> and <i>Culex torrentium</i> in Northern Europe. <i>Viruses</i> , 2019, 11, 1033.	3.3	64
1034	mPies: a novel metaproteomics tool for the creation of relevant protein databases and automatized protein annotation. <i>Biology Direct</i> , 2019, 14, 21.	4.6	13
1035	Transcriptomic analysis of α -synuclein knockdown after T3 spinal cord injury in rats. <i>BMC Genomics</i> , 2019, 20, 851.	2.8	6
1036	Candidate genes for grape white rot resistance based on SMRT and Illumina sequencing. <i>BMC Plant Biology</i> , 2019, 19, 501.	3.6	11
1037	Generation and Characterization of a Mouse-Adapted Makona Variant of Ebola Virus. <i>Viruses</i> , 2019, 11, 987.	3.3	13
1038	Comparative transcriptome analysis between floating and attached <i>Ulva prolifera</i> in studying green tides in the Yellow Sea. <i>Algal Research</i> , 2019, 44, 101712.	4.6	10
1039	Interaction of antibacterial silver nanoparticles and microbiota-dependent holobionts revealed by metatranscriptomic analysis. <i>Environmental Science: Nano</i> , 2019, 6, 3242-3255.	4.3	6
1040	Characteristics of Wetting-Induced Bacteriophage Blooms in Biological Soil Crust. <i>MBio</i> , 2019, 10, .	4.1	56
1041	Draft genome sequences of five <i>Calonectria</i> species from Eucalyptus plantations in China, <i>Celoporthes dispersa</i> , <i>Sporothrix phasma</i> and <i>Alectoria sarmentosa</i> . <i>IMA Fungus</i> , 2019, 10, 22.	3.8	17
1042	Sensitivity and specificity of metatranscriptomics as an arbovirus surveillance tool. <i>Scientific Reports</i> , 2019, 9, 19398.	3.3	28

#	ARTICLE	IF	CITATIONS
1043	Natural Infection of <i>Aedes aegypti</i> by Chikungunya and Dengue type 2 Virus in a Transition Area of North-Northeast Brazil. <i>Viruses</i> , 2019, 11, 1126.	3.3	12
1044	Viral Diversity of Microbats within the South West Botanical Province of Western Australia. <i>Viruses</i> , 2019, 11, 1157.	3.3	23
1045	Single-molecule real-time sequencing facilitates the analysis of transcripts and splice isoforms of anthers in Chinese cabbage (<i>Brassica rapa</i> L. ssp. <i>pekinensis</i>). <i>BMC Plant Biology</i> , 2019, 19, 517.	3.6	16
1046	<i>Schizosaccharomyces pombe</i> Can Reduce Acetic Acid Produced by Baijiu Spontaneous Fermentation Microbiota. <i>Microorganisms</i> , 2019, 7, 606.	3.6	20
1047	Evolution of BACON Domain Tandem Repeats in crAssphage and Novel Gut Bacteriophage Lineages. <i>Viruses</i> , 2019, 11, 1085.	3.3	20
1048	Genomic adaptations to chemosymbiosis in the deep-sea seep-dwelling tubeworm <i>Lamellibrachia luymesii</i> . <i>BMC Biology</i> , 2019, 17, 91.	3.8	33
1049	Review, Evaluation, and Directions for Gene-Targeted Assembly for Ecological Analyses of Metagenomes. <i>Frontiers in Genetics</i> , 2019, 10, 957.	2.3	8
1050	Transcriptome of Gonads From High Temperature Induced Sex Reversal During Sex Determination and Differentiation in Chinese Tongue Sole, <i>Cynoglossus semilaevis</i> . <i>Frontiers in Genetics</i> , 2019, 10, 1128.	2.3	38
1051	Relating Metatranscriptomic Profiles to the Micropollutant Biotransformation Potential of Complex Microbial Communities. <i>Environmental Science & Technology</i> , 2020, 54, 235-244.	10.0	29
1052	Differential Expression of Genes Related to the Formation of Giant Leaves in Triploid Poplar. <i>Forests</i> , 2019, 10, 920.	2.1	5
1053	Diversity and Evolution of Novel Invertebrate DNA Viruses Revealed by Meta-Transcriptomics. <i>Viruses</i> , 2019, 11, 1092.	3.3	16
1054	Obtaining Genome Sequences of Mutualistic Bacteria in Single <i>Microcystis</i> Colonies. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5047.	4.1	5
1055	Intestinal microbiota domination under extreme selective pressures characterized by metagenomic read cloud sequencing and assembly. <i>BMC Bioinformatics</i> , 2019, 20, 585.	2.6	7
1056	Gut-derived <i>Enterococcus faecium</i> from ulcerative colitis patients promotes colitis in a genetically susceptible mouse host. <i>Genome Biology</i> , 2019, 20, 252.	8.8	78
1057	The MG-RAST API explorer: an on-ramp for RESTful query composition. <i>BMC Bioinformatics</i> , 2019, 20, 561.	2.6	10
1058	Transcriptome responses to different herbivores reveal differences in defense strategies between populations of <i>Eruca sativa</i> . <i>BMC Genomics</i> , 2019, 20, 843.	2.8	6
1059	Modification of the genome topology network and its application to the comparison of group B <i>Streptococcus</i> genomes. <i>BMC Genomics</i> , 2019, 20, 886.	2.8	0
1060	Discovery of High Abundances of Aster-Like Nanoparticles in Pelagic Environments: Characterization and Dynamics. <i>Frontiers in Microbiology</i> , 2019, 10, 2376.	3.5	8

#	ARTICLE	IF	CITATIONS
1061	Do Organic Substrates Drive Microbial Community Interactions in Arctic Snow?. <i>Frontiers in Microbiology</i> , 2019, 10, 2492.	3.5	21
1062	Temperature Modulates Sex-Biased Gene Expression in the Gametophytes of the Kelp <i>Saccharina latissima</i> . <i>Frontiers in Marine Science</i> , 2019, 6, .	2.5	16
1063	Microbial Community Rearrangements in Power-to-Biomethane Reactors Employing Mesophilic Biogas Digestate. <i>Frontiers in Energy Research</i> , 2019, 7, .	2.3	19
1064	A Glyphosate Pulse to Brackish Long-Term Microcosms Has a Greater Impact on the Microbial Diversity and Abundance of Planktonic Than of Biofilm Assemblages. <i>Frontiers in Marine Science</i> , 2019, 6, .	2.5	8
1065	Metagenomic Insights into the Effects of Seasonal Temperature Variation on the Activities of Activated Sludge. <i>Microorganisms</i> , 2019, 7, 713.	3.6	14
1066	Nanangenines: drimane sesquiterpenoids as the dominant metabolite cohort of a novel Australian fungus, <i>Aspergillus nanangensis</i> . <i>Beilstein Journal of Organic Chemistry</i> , 2019, 15, 2631-2643.	2.2	22
1067	Complete genome sequences of <i>Streptomyces</i> spp. isolated from disease-suppressive soils. <i>BMC Genomics</i> , 2019, 20, 994.	2.8	16
1068	Different transcriptional response between susceptible and resistant common carp (<i>Cyprinus carpio</i>) fish hints on the mechanism of CyHV-3 disease resistance. <i>BMC Genomics</i> , 2019, 20, 1019.	2.8	21
1069	Evaluating global and local sequence alignment methods for comparing patient medical records. <i>BMC Medical Informatics and Decision Making</i> , 2019, 19, 263.	3.0	8
1070	Charting the diversity of uncultured viruses of Archaea and Bacteria. <i>BMC Biology</i> , 2019, 17, 109.	3.8	26
1071	Microbial genomes from non-human primate gut metagenomes expand the primate-associated bacterial tree of life with over 1000 novel species. <i>Genome Biology</i> , 2019, 20, 299.	8.8	58
1072	Draft genome of <i>Ompok bimaculatus</i> (Pabda fish). <i>BMC Research Notes</i> , 2019, 12, 825.	1.4	3
1073	Novel RNA viruses associated with <i>Plasmodium vivax</i> in human malaria and <i>Leucocytozoon</i> parasites in avian disease. <i>PLoS Pathogens</i> , 2019, 15, e1008216.	4.7	50
1074	Pingu virus: A new picornavirus in penguins from Antarctica. <i>Virus Evolution</i> , 2019, 5, vez047.	4.9	7
1075	Sucrose Promotes Strawberry Fruit Ripening and Affects Ripening-Related Processes. <i>International Journal of Genomics</i> , 2019, 2019, 1-14.	1.6	13
1076	Novel insights into molecular mechanisms of <i>Pseudourostyla cristata</i> encystment using comparative transcriptomics. <i>Scientific Reports</i> , 2019, 9, 19109.	3.3	10
1077	Massive gene amplification on a recently formed <i>Drosophila</i> Y chromosome. <i>Nature Ecology and Evolution</i> , 2019, 3, 1587-1597.	7.8	55
1078	Cooking shapes the structure and function of the gut microbiome. <i>Nature Microbiology</i> , 2019, 4, 2052-2063.	13.3	112

#	ARTICLE	IF	CITATIONS
1079	Whole Genome Analysis of Selected Human Group A Rotavirus Strains Revealed Evolution of DS-1-Like Single- and Double-Gene Reassortant Rotavirus Strains in Pakistan During 2015–2016. <i>Frontiers in Microbiology</i> , 2019, 10, 2641.	3.5	8
1080	Programmed Cell Death in <i>Neurospora crassa</i> Is Controlled by the Allorecognition Determinant <i>rcd-1</i> . <i>Genetics</i> , 2019, 213, 1387-1400.	2.9	32
1081	Distinct Metabolic Signals Underlie Clone by Environment Interplay in <i>Nebbiolo</i> Grapes Over Ripening. <i>Frontiers in Plant Science</i> , 2019, 10, 1575.	3.6	15
1082	Comparative Genomics Reveals Metabolic Specificity of <i>Endozoicomonas</i> Isolated from a Marine Sponge and the Genomic Repertoire for Host-Bacteria Symbioses. <i>Microorganisms</i> , 2019, 7, 635.	3.6	13
1083	Necrotizing enterocolitis is preceded by increased gut bacterial replication, <i>Klebsiella</i> , and fimbriae-encoding bacteria. <i>Science Advances</i> , 2019, 5, eaax5727.	10.3	120
1084	Assessing the performance of different approaches for functional and taxonomic annotation of metagenomes. <i>BMC Genomics</i> , 2019, 20, 960.	2.8	46
1085	In situ development of a methanotrophic microbiome in deep-sea sediments. <i>ISME Journal</i> , 2019, 13, 197-213.	9.8	61
1086	NCycDB: a curated integrative database for fast and accurate metagenomic profiling of nitrogen cycling genes. <i>Bioinformatics</i> , 2019, 35, 1040-1048.	4.1	134
1087	Comparative analysis of five <i>Mucor</i> species transcriptomes. <i>Genomics</i> , 2019, 111, 1306-1314.	2.9	14
1088	Metagenomic insights into the structure and function of intestinal microbiota of the farmed Pacific white shrimp (<i>Litopenaeus vannamei</i>). <i>Aquaculture</i> , 2019, 499, 109-118.	3.5	69
1089	Host-derived population genomics data provides insights into bacterial and diatom composition of the killer whale skin. <i>Molecular Ecology</i> , 2019, 28, 484-502.	3.9	42
1090	Cadmium accumulation capacity and resistance strategies of a cadmium-hypertolerant fern <i>Microsorium fortunei</i> . <i>Science of the Total Environment</i> , 2019, 649, 1209-1223.	8.0	10
1091	gcMeta: a Global Catalogue of Metagenomics platform to support the archiving, standardization and analysis of microbiome data. <i>Nucleic Acids Research</i> , 2019, 47, D637-D648.	14.5	70
1092	Biogeochemical Regimes in Shallow Aquifers Reflect the Metabolic Coupling of the Elements Nitrogen, Sulfur, and Carbon. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	47
1093	Enhanced bioinformatic profiling of VIDISCA libraries for virus detection and discovery. <i>Virus Research</i> , 2019, 263, 21-26.	2.2	18
1094	Transcriptome analysis and metabolic profiling reveal the key role of Δ^5 -linolenic acid in dormancy regulation of European pear. <i>Journal of Experimental Botany</i> , 2019, 70, 1017-1031.	4.8	27
1095	River Ganges water as reservoir of microbes with antibiotic and metal ion resistance genes: High throughput metagenomic approach. <i>Environmental Pollution</i> , 2019, 246, 443-451.	7.5	105
1096	Recovering microbial genomes from metagenomes in hypersaline environments: The Good, the Bad and the Ugly. <i>Systematic and Applied Microbiology</i> , 2019, 42, 30-40.	2.8	29

#	ARTICLE	IF	CITATIONS
1097	Phylogenetic barriers to horizontal transfer of antimicrobial peptide resistance genes in the human gut microbiota. <i>Nature Microbiology</i> , 2019, 4, 447-458.	13.3	68
1098	Genomic variation and strain-specific functional adaptation in the human gut microbiome during early life. <i>Nature Microbiology</i> , 2019, 4, 470-479.	13.3	164
1099	Shotgun metagenomics offers novel insights into taxonomic compositions, metabolic pathways and antibiotic resistance genes in fish gut microbiome. <i>Archives of Microbiology</i> , 2019, 201, 295-303.	2.2	56
1100	Comparative transcriptome analysis identifies genes associated with papilla development in the sea cucumber <i>Apostichopus japonicus</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2019, 29, 255-263.	1.0	4
1101	Massive Tandem Proliferation of ELIPs Supports Convergent Evolution of Desiccation Tolerance across Land Plants. <i>Plant Physiology</i> , 2019, 179, 1040-1049.	4.8	54
1102	RNA-Seq Reveals Flavonoid Biosynthesis-Related Genes in Pecan (<i>Carya illinoensis</i>) Kernels. <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 148-158.	5.2	33
1103	Gut microbiome-based secondary metabolite biosynthetic gene clusters detection in Parkinson's disease. <i>Neuroscience Letters</i> , 2019, 696, 93-98.	2.1	15
1104	Functional conserved non-coding elements among tunicates and chordates. <i>Developmental Biology</i> , 2019, 448, 101-110.	2.0	5
1105	Competition among Nasal Bacteria Suggests a Role for Siderophore-Mediated Interactions in Shaping the Human Nasal Microbiota. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	57
1106	Plastics in the marine environment are reservoirs for antibiotic and metal resistance genes. <i>Environment International</i> , 2019, 123, 79-86.	10.0	305
1107	Insights on the freshwater microbiomes metabolic changes associated with the world's largest mining disaster. <i>Science of the Total Environment</i> , 2019, 654, 1209-1217.	8.0	62
1108	Extensive Diversity of RNA Viruses in Australian Ticks. <i>Journal of Virology</i> , 2019, 93, .	3.4	116
1109	Considerations When Designing a Microbiome Study: Implications for Nursing Science. <i>Biological Research for Nursing</i> , 2019, 21, 125-141.	1.9	21
1110	An important resource for understanding bio-adhesion mechanisms: Cement gland transcriptomes of two goose barnacles, <i>Pollicipes pollicipes</i> and <i>Lepas anatifera</i> (Cirripedia, Thoracica). <i>Marine Genomics</i> , 2019, 45, 16-20.	1.1	11
1111	A metagenomic analysis framework for characterization of antibiotic resistomes in river environment: Application to an urban river in Beijing. <i>Environmental Pollution</i> , 2019, 245, 398-407.	7.5	68
1112	Transcriptional shifts during juvenile Coho salmon (<i>Oncorhynchus kisutch</i>) life stage changes in freshwater and early marine environments. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2019, 29, 32-42.	1.0	11
1113	Characterization of antibiotic resistance genes in the sediments of an urban river revealed by comparative metagenomics analysis. <i>Science of the Total Environment</i> , 2019, 653, 1513-1521.	8.0	45
1114	MAGpy: a reproducible pipeline for the downstream analysis of metagenome-assembled genomes (MAGs). <i>Bioinformatics</i> , 2019, 35, 2150-2152.	4.1	33

#	ARTICLE	IF	CITATIONS
1115	Antibiotic resistance genes in bacteriophages from diverse marine habitats. <i>Science of the Total Environment</i> , 2019, 654, 452-455.	8.0	39
1116	AFISsys - An autonomous instrument for the preservation of brackish water samples for microbial metatranscriptome analysis. <i>Water Research</i> , 2019, 149, 351-361.	11.3	4
1117	A novel genetic lineage of Tula orthohantavirus in Altai voles (<i>Microtus obscurus</i>) from Turkey. <i>Infection, Genetics and Evolution</i> , 2019, 67, 150-158.	2.3	12
1118	Virus discovery reveals frequent infection by diverse novel members of the Flaviviridae in wild lemurs. <i>Archives of Virology</i> , 2019, 164, 509-522.	2.1	11
1119	Comparative metagenomic and metatranscriptomic analyses reveal the breed effect on the rumen microbiome and its associations with feed efficiency in beef cattle. <i>Microbiome</i> , 2019, 7, 6.	11.1	150
1120	Extensive Unexplored Human Microbiome Diversity Revealed by Over 150,000 Genomes from Metagenomes Spanning Age, Geography, and Lifestyle. <i>Cell</i> , 2019, 176, 649-662.e20.	28.9	1,087
1121	Transcript profiling reveals an important role of cell wall remodeling and hormone signaling under salt stress in garlic. <i>Plant Physiology and Biochemistry</i> , 2019, 135, 87-98.	5.8	32
1122	Enhancing micro<scp>RNA</scp>167A expression in seed decreases the Î±â€‰linolenic acid content and increases seed size in <i>Camelina sativa</i>. <i>Plant Journal</i> , 2019, 98, 346-358.	5.7	36
1123	Transcriptomic analysis related to the flowering of the citrus hybrid <i>Microcitrangemonia</i> . <i>Current Plant Biology</i> , 2019, 18, 100097.	4.7	1
1124	Analysis of viral and bacterial communities in groundwater associated with contaminated land. <i>Science of the Total Environment</i> , 2019, 656, 1413-1426.	8.0	18
1125	Genomic Diversity, Virulence, and Antimicrobial Resistance of <i>Klebsiella pneumoniae</i> Strains from Cows and Humans. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	31
1126	Divergent methyl-coenzyme M reductase genes in a deep-subseafloor <i>Archaeoglobi</i> . <i>ISME Journal</i> , 2019, 13, 1269-1279.	9.8	76
1127	MMseqs2 desktop and local web server app for fast, interactive sequence searches. <i>Bioinformatics</i> , 2019, 35, 2856-2858.	4.1	321
1128	Resilience and Assemblage of Soil Microbiome in Response to Chemical Contamination Combined with Plant Growth. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	46
1129	Genome-wide analysis of the Hsf gene family in <i>Brassica oleracea</i> and a comparative analysis of the Hsf gene family in <i>B. oleracea</i> , <i>B. rapa</i> and <i>B. napus</i> . <i>Functional and Integrative Genomics</i> , 2019, 19, 515-531.	3.5	44
1130	High-throughput amplicon sequencing demonstrates extensive diversity of xylanase genes in the sediment of soda lake Dabusu. <i>Biotechnology Letters</i> , 2019, 41, 409-418.	2.2	2
1131	Fecal pollution can explain antibiotic resistance gene abundances in anthropogenically impacted environments. <i>Nature Communications</i> , 2019, 10, 80.	12.8	378
1132	Whole rumen metagenome sequencing allows classifying and predicting feed efficiency and intake levels in cattle. <i>Scientific Reports</i> , 2019, 9, 11.	3.3	108

#	ARTICLE	IF	CITATIONS
1133	Metagenomic Analysis of Samples from Three Bat Species Collected in the Amazon Rain Forest. Microbiology Resource Announcements, 2019, 8, .	0.6	5
1134	Complete Endogenous Retrovirus Genome Sequence from a Brazilian Vampire Bat (Desmodus Tj ETQq1 1 0.784314 rgBT /Oyerlock 10	0.6	2
1135	Exploring the unmapped DNA and RNA reads in a songbird genome. BMC Genomics, 2019, 20, 19.	2.8	21
1136	Transcriptome profiling reveals key roles of phagosome and NOD-like receptor pathway in spotting diseased Strongylocentrotus intermedius. Fish and Shellfish Immunology, 2019, 84, 521-531.	3.6	27
1137	Flexible design of multiple metagenomics classification pipelines with UGENE. Bioinformatics, 2019, 35, 1963-1965.	4.1	43
1138	Promises and pitfalls of using high-throughput sequencing for diet analysis. Molecular Ecology Resources, 2019, 19, 327-348.	4.8	138
1139	Elucidating functional microorganisms and metabolic mechanisms in a novel engineered ecosystem integrating C, N, P and S biotransformation by metagenomics. Water Research, 2019, 148, 219-230.	11.3	54
1140	Metagenomic Sequencing of HIV-1 in the Blood and Female Genital Tract Reveals Little Quasispecies Diversity during Acute Infection. Journal of Virology, 2019, 93, .	3.4	7
1141	PER extended-spectrum β -lactamases originate from Pararheinheimera spp. International Journal of Antimicrobial Agents, 2019, 53, 158-164.	2.5	12
1142	Novel <i>Caudovirales</i> associated with Marine Group I Thaumarchaeota assembled from metagenomes. Environmental Microbiology, 2019, 21, 1980-1988.	3.8	33
1143	Acid mine drainage affects the diversity and metal resistance gene profile of sediment bacterial community along a river. Chemosphere, 2019, 217, 790-799.	8.2	83
1144	A phylogenomic and ecological analysis of the globally abundant Marine Group II archaea (<i>Ca</i> .) Tj ETQq1 1 0.784314 rgBT /Oyerlock 10	9.8	158
1145	Gut microbiome structure and metabolic activity in inflammatory bowel disease. Nature Microbiology, 2019, 4, 293-305.	13.3	1,094
1146	The Impact of Bioinformatics Tools in the Development of Antimicrobial Drugs and Other Agents. , 2019, , 335-347.		2
1147	Microbiota and cancer immunotherapy: in search of microbial signals. Gut, 2019, 68, 385-388.	12.1	90
1148	Microbial Organic Matter Degradation Potential in Baltic Sea Sediments Is Influenced by Depositional Conditions and <i>In Situ</i> Geochemistry. Applied and Environmental Microbiology, 2019, 85, .	3.1	37
1149	Tolerance of Transplastomic Tobacco Plants Overexpressing a Theta Class Glutathione Transferase to Abiotic and Oxidative Stresses. Frontiers in Plant Science, 2018, 9, 1861.	3.6	13
1150	Phylogenomics of Endogonaceae and evolution of mycorrhizas within Mucoromycota. New Phytologist, 2019, 222, 511-525.	7.3	81

#	ARTICLE	IF	CITATIONS
1151	A full-ocean-depth rated modular lander and pressure-retaining sampler capable of collecting hadal-endemic microbes under in situ conditions. Deep-Sea Research Part I: Oceanographic Research Papers, 2019, 143, 50-57.	1.4	52
1152	Mangrove Sediment Microbiome: Adaptive Microbial Assemblages and Their Routed Biogeochemical Processes in Yunxiao Mangrove National Nature Reserve, China. Microbial Ecology, 2019, 78, 57-69.	2.8	66
1153	Opening the Black Box of Thermophilic Autotrophic Bacterial Diversity. , 2019, , 333-343.		2
1154	Comparative metagenomics of the gut microbiota in wild greylag geese (<i>Anser anser</i>) and ruddy shelducks (<i>Tadorna ferruginea</i>). MicrobiologyOpen, 2019, 8, e00725.	3.0	20
1155	<scp>BASTA</scp> â€“ Taxonomic classification of sequences and sequence bins using last common ancestor estimations. Methods in Ecology and Evolution, 2019, 10, 100-103.	5.2	83
1156	Bacterial contributions to delignification and lignocellulose degradation in forest soils with metagenomic and quantitative stable isotope probing. ISME Journal, 2019, 13, 413-429.	9.8	246
1157	Phenotypic and genotypic analyses of antimicrobial resistant bacteria in livestock in Uganda. Transboundary and Emerging Diseases, 2019, 66, 317-326.	3.0	28
1158	Emerging evolutionary paradigms in antibiotic discovery. Journal of Industrial Microbiology and Biotechnology, 2019, 46, 257-271.	3.0	76
1159	Metagenomic analysis of nitrogenâ€cycling genes in upper Mississippi river sediment with mussel assemblages. MicrobiologyOpen, 2019, 8, e00739.	3.0	10
1160	MG-RAST version 4â€”lessons learned from a decade of low-budget ultra-high-throughput metagenome analysis. Briefings in Bioinformatics, 2019, 20, 1151-1159.	6.5	98
1161	A review of methods and databases for metagenomic classification and assembly. Briefings in Bioinformatics, 2019, 20, 1125-1136.	6.5	368
1162	Federation in genomics pipelines: techniques and challenges. Briefings in Bioinformatics, 2019, 20, 235-244.	6.5	18
1163	Description and phylogeny of the mitochondrial genome of Sabethes chloropterus, Sabethes glaucodaemon and Sabethes belisarioi (Diptera: Culicidae). Genomics, 2019, 111, 607-611.	2.9	24
1164	Resources and tools for the high-throughput, multi-omic study of intestinal microbiota. Briefings in Bioinformatics, 2019, 20, 1032-1056.	6.5	10
1165	Reconstruction and in silico analysis of new Marinobacter adhaerens t76_800 with potential for long-chain hydrocarbon bioremediation associated with marine environmental lipases. Marine Genomics, 2020, 49, 100685.	1.1	5
1166	The â€“in vivo” lifestyleâ€™ of bile acid 7Î±-dehydroxylating bacteria: comparative genomics, metatranscriptomic, and bile acid metabolomics analysis of a defined microbial community in gnotobiotic mice. Gut Microbes, 2020, 11, 381-404.	9.8	80
1167	Ammonia stress reduces antibiotic efflux but enriches horizontal gene transfer of antibiotic resistance genes in anaerobic digestion. Bioresource Technology, 2020, 295, 122191.	9.6	59
1168	Comparative transcriptome analysis of Triplophysa yarkandensis in response to salinity and alkalinity stress. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2020, 33, 100629.	1.0	11

#	ARTICLE	IF	CITATIONS
1169	A metabolomic, transcriptomic profiling, and mineral nutrient metabolism study of the phytotoxicity mechanism of uranium. <i>Journal of Hazardous Materials</i> , 2020, 386, 121437.	12.4	54
1170	Microbial genomes retrieved from High Arctic lake sediments encode for adaptation to cold and oligotrophic environments. <i>Limnology and Oceanography</i> , 2020, 65, S233.	3.1	20
1171	Predominantly Antibiotic-resistant Intestinal Microbiome Persists in Patients With Pouchitis Who Respond to Antibiotic Therapy. <i>Gastroenterology</i> , 2020, 158, 610-624.e13.	1.3	53
1172	Biological Soil Crusts from Different Soil Substrates Harbor Distinct Bacterial Groups with the Potential to Produce Exopolysaccharides and Lipopolysaccharides. <i>Microbial Ecology</i> , 2020, 79, 326-341.	2.8	43
1173	Non-cyanobacterial diazotrophs dominate nitrogen-fixing communities in permafrost thaw ponds. <i>Limnology and Oceanography</i> , 2020, 65, S180.	3.1	19
1174	De novo genome assembly and comparative annotation reveals metabolic versatility in cellulolytic bacteria from cropland and forest soils. <i>Functional and Integrative Genomics</i> , 2020, 20, 89-101.	3.5	4
1175	Bacteriophage of the Skin Microbiome in Patients with Psoriasis and Healthy Family Controls. <i>Journal of Investigative Dermatology</i> , 2020, 140, 182-190.e5.	0.7	19
1176	Exploring the evolutionary dynamics of <i>Rhizobium</i> plasmids through bipartite network analysis. <i>Environmental Microbiology</i> , 2020, 22, 934-951.	3.8	7
1177	A Genome Resource for Several North American <i>Venturia inaequalis</i> Isolates with Multiple Fungicide Resistance Phenotypes. <i>Phytopathology</i> , 2020, 110, 544-546.	2.2	17
1178	MEGARes 2.0: a database for classification of antimicrobial drug, biocide and metal resistance determinants in metagenomic sequence data. <i>Nucleic Acids Research</i> , 2020, 48, D561-D569.	14.5	227
1179	Transcriptome-level effects of the model organic pollutant phenanthrene and its solvent acetone in three amphipod species. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2020, 33, 100630.	1.0	2
1180	Transcriptome analysis of <i>Aconitum carmichaelii</i> and exploration of the salsolinol biosynthetic pathway. <i>FASEB J</i> , 2020, 140, 104412.	2.2	7
1181	The utility of reptile blood transcriptomes in molecular ecology. <i>Molecular Ecology Resources</i> , 2020, 20, 308-317.	4.8	17
1182	Spatial and temporal axes impact ecology of the gut microbiome in juvenile European lobster (<i>Homarus gammarus</i>). <i>ISME Journal</i> , 2020, 14, 531-543.	9.8	35
1183	Viral and fungal pathogens associated with <i>Pneumolaelaps niutirani</i> (Acari: Laelapidae): a mite found in diseased nests of <i>Vespula</i> wasps. <i>Insectes Sociaux</i> , 2020, 67, 83-93.	1.2	9
1184	In silico analysis of metatranscriptomic data from the Antarctic vascular plant <i>Colobanthus quitensis</i> : Responses to a global warming scenario through changes in fungal gene expression levels. <i>Fungal Ecology</i> , 2020, 43, 100873.	1.6	13
1185	Long solids retention times and attached growth phase favor prevalence of comammox bacteria in nitrogen removal systems. <i>Water Research</i> , 2020, 169, 115268.	11.3	98
1186	Microaerobic conditions caused the overwhelming dominance of <i>Acinetobacter</i> spp. and the marginalization of <i>Rhodococcus</i> spp. in diesel fuel/crude oil mixture-amended enrichment cultures. <i>Archives of Microbiology</i> , 2020, 202, 329-342.	2.2	33

#	ARTICLE	IF	CITATIONS
1187	Effects of multiple climate change stressors on gene expression in blue rockfish (<i>Sebastes mystinus</i>). Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology, 2020, 239, 110580.	1.8	19
1188	Groundwater cable bacteria conserve energy by sulfur disproportionation. ISME Journal, 2020, 14, 623-634.	9.8	64
1189	<sc>EnTAP</sc>: Bringing faster and smarter functional annotation to non-model eukaryotic transcriptomes. Molecular Ecology Resources, 2020, 20, 591-604.	4.8	111
1190	Demographic and environmental drivers of metagenomic viral diversity in vampire bats. Molecular Ecology, 2020, 29, 26-39.	3.9	66
1191	Gene expression analysis of <i>Cyanophora paradoxa</i> reveals conserved abiotic stress responses between basal algae and flowering plants. New Phytologist, 2020, 225, 1562-1577.	7.3	10
1192	Structural equation models to disentangle the biological relationship between microbiota and complex traits: Methane production in dairy cattle as a case of study. Journal of Animal Breeding and Genetics, 2020, 137, 36-48.	2.0	30
1193	Enhancing DNA metabarcoding performance and applicability with bait capture enrichment and DNA from conservative ethanol. Molecular Ecology Resources, 2020, 20, 79-96.	4.8	15
1194	Discovery of hyperstable carbohydrate-active enzymes through metagenomics of extreme environments. FEBS Journal, 2020, 287, 1116-1137.	4.7	32
1195	Metagenomic analysis of sludge and early-stage biofilm communities of a submerged membrane bioreactor. Science of the Total Environment, 2020, 701, 134682.	8.0	43
1196	A Model of Hormonal Regulation of Stamen Abortion during Pre-Meiosis of <i>Litsea cubeba</i> . Genes, 2020, 11, 48.	2.4	12
1197	Meta-Transcriptome Profiling of Novel Invasive Pest <i>Spodoptera frugiperda</i> in Yunnan, China. Virologica Sinica, 2020, 35, 240-244.	3.0	0
1198	The transcriptome of <i>Pinus pinaster</i> under <i>Fusarium circinatum</i> challenge. BMC Genomics, 2020, 21, 28.	2.8	19
1199	Structure and function analysis of various brain subregions and pituitary in grass carp (<i>Ctenopharyngodon idellus</i>). Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2020, 33, 100653.	1.0	7
1200	UDSMProt: universal deep sequence models for protein classification. Bioinformatics, 2020, 36, 2401-2409.	4.1	117
1201	Metabolic analyses by metatranscriptomics highlight plasticity in phosphorus acquisition during monospecific and multispecies algal blooms. Hydrobiologia, 2020, 847, 1071-1085.	2.0	7
1202	Novel Viruses Found in Antricola Ticks Collected in Bat Caves in the Western Amazonia of Brazil. Viruses, 2020, 12, 48.	3.3	10
1203	Mobile resistome of human gut and pathogen drives anthropogenic bloom of antibiotic resistance. Microbiome, 2020, 8, 2.	11.1	80
1204	The metagenome-assembled genome of <i>Candidatus Oenococcus aquikefiri</i> from water kefir represents the species <i>Oenococcus sicerae</i> . Food Microbiology, 2020, 88, 103402.	4.2	24

#	ARTICLE	IF	CITATIONS
1205	Bacterial line of defense in <i>Dirinaria</i> lichen from two different ecosystems: First genomic insights of its mycobiont <i>Dirinaria</i> sp. GBRC AP01. <i>Microbiological Research</i> , 2020, 233, 126407.	5.3	3
1206	Microbial responses to perfluoroalkyl substances and perfluorooctanesulfonate (PFOS) desulfurization in the Antarctic marine environment. <i>Water Research</i> , 2020, 171, 115434.	11.3	39
1207	Tracking microbial evolution in the human gut using Hi-C reveals extensive horizontal gene transfer, persistence and adaptation. <i>Nature Microbiology</i> , 2020, 5, 343-353.	13.3	101
1208	Metabolic activity analyses demonstrate that <i>Lokiarchaeon</i> exhibits homoacetogenesis in sulfidic marine sediments. <i>Nature Microbiology</i> , 2020, 5, 248-255.	13.3	48
1209	A diverse uncultivated microbial community is responsible for organic matter degradation in the Black Sea sulphidic zone. <i>Environmental Microbiology</i> , 2021, 23, 2709-2728.	3.8	47
1210	A Bioinformatic Analysis of Integrative Mobile Genetic Elements Highlights Their Role in Bacterial Adaptation. <i>Cell Host and Microbe</i> , 2020, 27, 140-153.e9.	11.0	119
1211	Integrating high-throughput sequencing and metagenome analysis to reveal the characteristic and resistance mechanism of microbial community in metal contaminated sediments. <i>Science of the Total Environment</i> , 2020, 707, 136116.	8.0	83
1212	Ciliary force-responsive striated fibers promote basal body connections and cortical interactions. <i>Journal of Cell Biology</i> , 2020, 219, .	5.2	23
1213	Metagenomics reveals microbial community differences lead to differential nitrate production in anammox reactors with differing nitrogen loading rates. <i>Water Research</i> , 2020, 169, 115279.	11.3	62
1214	Genome-wide Transcriptional Analysis of <i>Tetrahymena thermophila</i> Response to Exogenous Cholesterol. <i>Journal of Eukaryotic Microbiology</i> , 2020, 67, 209-222.	1.7	4
1215	Microbial signatures of protected and impacted Northern Caribbean reefs: changes from Cuba to the Florida Keys. <i>Environmental Microbiology</i> , 2020, 22, 499-519.	3.8	25
1216	Transcriptomic signature of rapidly evolving immune genes in a highland fish. <i>Fish and Shellfish Immunology</i> , 2020, 97, 587-592.	3.6	5
1217	Characterization of a Y-specific duplication/insertion of the anti-Müllerian hormone type II receptor gene based on a chromosome-scale genome assembly of yellow perch, <i>Perca flavescens</i> . <i>Molecular Ecology Resources</i> , 2020, 20, 531-543.	4.8	76
1218	Long-term nutrient inputs shift soil microbial functional profiles of phosphorus cycling in diverse agroecosystems. <i>ISME Journal</i> , 2020, 14, 757-770.	9.8	280
1219	Raman-deuterium isotope probing to study metabolic activities of single bacterial cells in human intestinal microbiota. <i>Microbial Biotechnology</i> , 2020, 13, 572-583.	4.2	48
1220	PreDSLpmo: A neural network-based prediction tool for functional annotation of lytic polysaccharide monooxygenases. <i>Journal of Biotechnology</i> , 2020, 308, 148-155.	3.8	0
1221	Co-option of wing-patterning genes underlies the evolution of the treehopper helmet. <i>Nature Ecology and Evolution</i> , 2020, 4, 250-260.	7.8	38
1222	Ecogenomics of the SAR11 clade. <i>Environmental Microbiology</i> , 2020, 22, 1748-1763.	3.8	66

#	ARTICLE	IF	CITATIONS
1223	Metagenome sequencing of fingermillet-associated microbial consortia provides insights into structural and functional diversity of endophytes. 3 Biotech, 2020, 10, 15.	2.2	11
1224	Potential correlation between carbohydrate-active enzyme family 48 expressed by gut microbiota and the expression of intestinal epithelial AMP-activated protein kinase β . Journal of Food Biochemistry, 2020, 44, e13123.	2.9	2
1225	Rare rather than abundant microbial communities drive the effects of long-term greenhouse cultivation on ecosystem functions in subtropical agricultural soils. Science of the Total Environment, 2020, 706, 136004.	8.0	52
1226	TARGETED RESEQUENCING OF WETLAND SEDIMENT AS A TOOL FOR AVIAN INFLUENZA VIRUS SURVEILLANCE. Journal of Wildlife Diseases, 2020, 56, 397.	0.8	17
1227	Vibrio taketomensis sp. nov. by genome taxonomy. Systematic and Applied Microbiology, 2020, 43, 126048.	2.8	17
1228	Transcriptome Analysis of Apple Leaves Infected by the Rust Fungus <i>Gymnosporangium yamadae</i> at Two Sporulation Stages. Molecular Plant-Microbe Interactions, 2020, 33, 444-461.	2.6	17
1229	The Earth BioGenome project: opportunities and challenges for plant genomics and conservation. Plant Journal, 2020, 102, 222-229.	5.7	35
1230	eCAMI: simultaneous classification and motif identification for enzyme annotation. Bioinformatics, 2020, 36, 2068-2075.	4.1	27
1231	Taxonomic and functional diversity of the microbiome in a jet fuel contaminated site as revealed by combined application of in situ microcosms with metagenomic analysis. Science of the Total Environment, 2020, 708, 135152.	8.0	20
1232	Effective nitrogen removal in a granule-based partial-denitrification/anammox reactor treating low C/N sewage. Bioresource Technology, 2020, 297, 122467.	9.6	79
1233	Comparison of colonial volvocine algae based on phylotranscriptomic analysis of gene family evolution and natural selection. European Journal of Phycology, 2020, 55, 100-112.	2.0	10
1234	Transcriptomics of <i>Cherax quadricarinatus</i> hepatopancreas during infection with Decapod iridescent virus 1 (DIV1). Fish and Shellfish Immunology, 2020, 98, 832-842.	3.6	30
1235	The Genome of the Blind Soil-Dwelling and Ancestrally Wingless Dipluran Campodea augens: A Key Reference Hexapod for Studying the Emergence of Insect Innovations. Genome Biology and Evolution, 2020, 12, 3534-3549.	2.5	3
1236	Metabolic relationships of uncultured bacteria associated with the microalgae <i>Gambierdiscus</i> . Environmental Microbiology, 2020, 22, 1764-1783.	3.8	28
1237	From genotype to antibiotic susceptibility phenotype in the order Enterobacterales: a clinical perspective. Clinical Microbiology and Infection, 2020, 26, 643.e1-643.e7.	6.0	20
1238	Gut Microbiome Fermentation Determines the Efficacy of Exercise for Diabetes Prevention. Cell Metabolism, 2020, 31, 77-91.e5.	16.2	223
1239	Stable cellulase immobilized on graphene oxide@CMC-g-poly(AMPS-co-AAm) hydrogel for enhanced enzymatic hydrolysis of lignocellulosic biomass. Carbohydrate Polymers, 2020, 230, 115661.	10.2	55
1240	The unity and diversity of the ciliary central apparatus. Philosophical Transactions of the Royal Society B: Biological Sciences, 2020, 375, 20190164.	4.0	18

#	ARTICLE	IF	CITATIONS
1241	Gene Expression in the Salivary Gland of <i>Rhipicephalus (Boophilus) microplus</i> Fed on Tick-Susceptible and Tick-Resistant Hosts. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 477.	3.9	12
1242	Graph Theory-Based Sequence Descriptors as Remote Homology Predictors. <i>Biomolecules</i> , 2020, 10, 26.	4.0	13
1243	Metatranscriptomic Analysis of the Mouse Gut Microbiome Response to the Persistent Organic Pollutant 2,3,7,8-Tetrachlorodibenzofuran. <i>Metabolites</i> , 2020, 10, 1.	2.9	55
1244	Tomato RNA-seq Data Mining Reveals the Taxonomic and Functional Diversity of Root-Associated Microbiota. <i>Microorganisms</i> , 2020, 8, 38.	3.6	15
1245	Biotic and abiotic stress-responsive genes are stimulated to resist drought stress in purple wheat. <i>Journal of Integrative Agriculture</i> , 2020, 19, 33-50.	3.5	14
1246	Novel hepac- and pegi-like viruses in native Australian wildlife and non-human primates. <i>Virus Evolution</i> , 2020, 6, veaa064.	4.9	21
1247	Red fox viromes in urban and rural landscapes. <i>Virus Evolution</i> , 2020, 6, veaa065.	4.9	27
1248	Unravelling lactateâ€acetate and sugar conversion into butyrate by intestinal <i>Anaerobutyricum</i> and <i>Anaerostipes</i> species by comparative proteogenomics. <i>Environmental Microbiology</i> , 2020, 22, 4863-4875.	3.8	36
1249	First Steps in the Analysis of Prokaryotic Pan-Genomes. <i>Bioinformatics and Biology Insights</i> , 2020, 14, 117793222093806.	2.0	48
1250	Rational design of balanced dual-targeting antibiotics with limited resistance. <i>PLoS Biology</i> , 2020, 18, e3000819.	5.6	20
1251	Conserved Patterns in Developmental Processes and Phases, Rather than Genes, Unite the Highly Divergent Bilateria. <i>Life</i> , 2020, 10, 182.	2.4	2
1252	Deep sequencing detects human papillomavirus (HPV) in cervical cancers negative for HPV by PCR. <i>British Journal of Cancer</i> , 2020, 123, 1790-1795.	6.4	36
1253	Coral Bleaching Phenotypes Associated With Differential Abundances of Nucleocytoplasmic Large DNA Viruses. <i>Frontiers in Marine Science</i> , 2020, 7, .	2.5	16
1254	Molecular evolution pattern of Merkel cell polyomavirus identified by viral metagenomics in plasma of high-risk blood donors from the Brazilian Amazon. <i>Infection, Genetics and Evolution</i> , 2020, 85, 104563.	2.3	4
1255	IDseqâ€”An open source cloud-based pipeline and analysis service for metagenomic pathogen detection and monitoring. <i>GigaScience</i> , 2020, 9, .	6.4	170
1256	Ancestral gene duplications in mosses characterized by integrated phylogenomic analyses. <i>Journal of Systematics and Evolution</i> , 2022, 60, 144-159.	3.1	19
1257	ADEPT: a domain independent sequence alignment strategy for gpu architectures. <i>BMC Bioinformatics</i> , 2020, 21, 406.	2.6	19
1258	The Distribution of Genes Associated With Regulated Cell Death Is Decoupled From the Mitochondrial Phenotypes Within Unicellular Eukaryotic Hosts. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 536389.	3.7	1

#	ARTICLE	IF	CITATIONS
1259	Exogenous Melatonin Attenuates Post-Harvest Decay by Increasing Antioxidant Activity in Wax Apple (<i>Syzygium samarangense</i>). <i>Frontiers in Plant Science</i> , 2020, 11, 569779.	3.6	25
1260	Alternative Splicing Enhances the Transcriptome Complexity of <i>Liriodendron chinense</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 578100.	3.6	14
1261	Newly Explored <i>Faecalibacterium</i> Diversity Is Connected to Age, Lifestyle, Geography, and Disease. <i>Current Biology</i> , 2020, 30, 4932-4943.e4.	3.9	72
1262	Single Cell Genomics Reveals Viruses Consumed by Marine Protists. <i>Frontiers in Microbiology</i> , 2020, 11, 524828.	3.5	26
1263	The Gut Virome Database Reveals Age-Dependent Patterns of Virome Diversity in the Human Gut. <i>Cell Host and Microbe</i> , 2020, 28, 724-740.e8.	11.0	352
1264	New Lineage of Microbial Predators Adds Complexity to Reconstructing the Evolutionary Origin of Animals. <i>Current Biology</i> , 2020, 30, 4500-4509.e5.	3.9	24
1265	Clinical relevance of plasma virome dynamics in liver transplant recipients. <i>EBioMedicine</i> , 2020, 60, 103009.	6.1	21
1266	Comparative transcriptome analysis of eyestalk from the white shrimp <i>Litopenaeus vannamei</i> after the injection of dopamine. <i>Gene</i> , 2020, 763, 145115.	2.2	7
1267	Insect-specific viruses and arboviruses in adult male culicids from Midwestern Brazil. <i>Infection, Genetics and Evolution</i> , 2020, 85, 104561.	2.3	21
1268	Quantitative microbiome profiling links microbial community variation to the intestine regeneration rate of the sea cucumber <i>Apostichopus japonicus</i> . <i>Genomics</i> , 2020, 112, 5012-5020.	2.9	8
1269	Pre-meiotic, 24-nt reproductive phasiRNAs are abundant in anthers of wheat and barley but not rice and maize. <i>Plant Physiology</i> , 2020, 184, pp.00816.2020.	4.8	20
1270	The Class A Carbapenemases BKC-1 and GPC-1 Both Originate from the Bacterial Genus <i>Shinella</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	3.2	7
1271	Genome-Centric Metagenomic Insights into the Impact of Alkaline/Acid and Thermal Sludge Pretreatment on the Microbiome in Digestion Sludge. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	12
1272	Transcriptome characterization of BPG axis and expression profiles of ovarian steroidogenesis-related genes in the Japanese sardine. <i>BMC Genomics</i> , 2020, 21, 668.	2.8	11
1273	Purification, partial structural characterization and health benefits of exopolysaccharides from potential probiotic <i>Pediococcus acidilactici</i> NCDC 252. <i>Process Biochemistry</i> , 2020, 99, 79-86.	3.7	29
1274	Linear and branched α -D-Glucans degrading enzymes from versatile <i>Bacteroides uniformis</i> JCM 13288 ^T and their roles in cooperation with gut bacteria. <i>Gut Microbes</i> , 2020, 12, 1826761.	9.8	18
1275	obaDIA: one-step biological analysis pipeline for data-independent acquisition and other quantitative proteomics data. <i>Bioinformatics</i> , 2021, 37, 2066-2067.	4.1	3
1276	Anaerobic methane oxidation coupled to denitrification is an important potential methane sink in deep-sea cold seeps. <i>Science of the Total Environment</i> , 2020, 748, 142459.	8.0	32

#	ARTICLE	IF	CITATIONS
1277	Draft Genome Sequence of a <i>Tepidicella baoligensis</i> Strain Isolated from an Oil Reservoir. Microbiology Resource Announcements, 2020, 9, .	0.6	0
1278	Divergent genes in gerbils: prevalence, relation to GC-biased substitution, and phenotypic relevance. BMC Evolutionary Biology, 2020, 20, 134.	3.2	6
1279	IMA Genome - F13. IMA Fungus, 2020, 11, 19.	3.8	13
1280	Succession of Gut Microbial Structure in Twin Giant Pandas During the Dietary Change Stage and Its Role in Polysaccharide Metabolism. Frontiers in Microbiology, 2020, 11, 551038.	3.5	5
1281	A Need for Improved Cellulase Identification from Metagenomic Sequence Data. Applied and Environmental Microbiology, 2020, 87, .	3.1	2
1282	Labile Dissolved Organic Matter Compound Characteristics Select for Divergence in Marine Bacterial Activity and Transcription. Frontiers in Microbiology, 2020, 11, 588778.	3.5	26
1283	Metatranscriptomic Identification of Diverse and Divergent RNA Viruses in Green and Chlorarachniophyte Algae Cultures. Viruses, 2020, 12, 1180.	3.3	26
1284	Metagenomic analysis of the dust particles collected from the suction tube and the suction funnel of a dermatological laser smoke evacuator system. Lasers in Medical Science, 2021, 36, 1249-1260.	2.1	1
1285	Coronavirus discovery by metagenomic sequencing: a tool for pandemic preparedness. Journal of Clinical Virology, 2020, 131, 104594.	3.1	31
1286	Global analysis of repetitive DNA from unassembled sequence reads using RepeatExplorer2. Nature Protocols, 2020, 15, 3745-3776.	12.0	144
1287	MetaLAFFA: a flexible, end-to-end, distributed computing-compatible metagenomic functional annotation pipeline. BMC Bioinformatics, 2020, 21, 471.	2.6	12
1288	Transcriptomics of the Rooibos (<i>Aspalathus linearis</i>) Species Complex. BioTech, 2020, 9, 19.	2.6	4
1289	A Novel RNA Virus, <i>Macrobrachium rosenbergii</i> Golda Virus (MrGV), Linked to Mass Mortalities of the Larval Giant Freshwater Prawn in Bangladesh. Viruses, 2020, 12, 1120.	3.3	11
1290	Divergence of metabolites in three phylogenetically close <i>Monascus</i> species (<i>M. pilosus</i> , <i>M. ruber</i> , and) Tj ETQq1 1 0.784314 rgBT /Over 2.8 14	2.8	14
1291	Molecular characterization of the complete genome sequence of human Parechovirus 1 in Pakistan. Virus Research, 2020, 290, 198178.	2.2	1
1292	Transcriptome dataset for RNA-seq analysis of axolotl embryonic oropharyngeal endoderm explants. Data in Brief, 2020, 32, 106126.	1.0	1
1293	Temporal dynamics of bacterial communities during seed development and maturation. FEMS Microbiology Ecology, 2020, 96, .	2.7	43
1294	Metagenomic insights into the diversity of carbohydrate-degrading enzymes in the yak fecal microbial community. BMC Microbiology, 2020, 20, 302.	3.3	24

#	ARTICLE	IF	CITATIONS
1295	Integrative analysis of wood biomass and developing xylem transcriptome provide insights into mechanisms of lignin biosynthesis in wood formation of <i>Pinus massoniana</i> . <i>International Journal of Biological Macromolecules</i> , 2020, 163, 1926-1937.	7.5	15
1296	A Comprehensive Subcellular Atlas of the <i>Toxoplasma</i> Proteome via hyperLOPIT Provides Spatial Context for Protein Functions. <i>Cell Host and Microbe</i> , 2020, 28, 752-766.e9.	11.0	201
1297	Mitochondrial genome sequencing and phylogeny of <i>Haemagogus albomaculatus</i> , <i>Haemagogus leucocelaenus</i> , <i>Haemagogus spegazzinii</i> , and <i>Haemagogus tropicalis</i> (Diptera: Culicidae). <i>Scientific Reports</i> , 2020, 10, 16948.	3.3	12
1298	Meta-Transcriptomic Discovery of a Divergent Circovirus and a Chaphamaparvovirus in Captive Reptiles with Proliferative Respiratory Syndrome. <i>Viruses</i> , 2020, 12, 1073.	3.3	14
1299	Large-Scale Comparative Analyses of Tick Genomes Elucidate Their Genetic Diversity and Vector Capacities. <i>Cell</i> , 2020, 182, 1328-1340.e13.	28.9	145
1300	New insights into the immune regulation and tissue repair of <i>Litopenaeus vannamei</i> during temperature fluctuation using TMT-based proteomics. <i>Fish and Shellfish Immunology</i> , 2020, 106, 975-981.	3.6	8
1301	Metagenomic characterization of microbial communities on plasticized fabric materials exposed to harsh tropical environments. <i>International Biodeterioration and Biodegradation</i> , 2020, 154, 105061.	3.9	17
1302	Flocs are the main source of nitrous oxide in a high-rate anammox granular sludge reactor: insights from metagenomics and fed-batch experiments. <i>Water Research</i> , 2020, 186, 116321.	11.3	27
1303	Relatives of rubella virus in diverse mammals. <i>Nature</i> , 2020, 586, 424-428.	27.8	58
1304	metaFlye: scalable long-read metagenome assembly using repeat graphs. <i>Nature Methods</i> , 2020, 17, 1103-1110.	19.0	430
1305	A compromised developmental trajectory of the infant gut microbiome and metabolome in atopic eczema. <i>Gut Microbes</i> , 2020, 12, 1801964.	9.8	51
1306	TreeSAPP: the Tree-based Sensitive and Accurate Phylogenetic Profiler. <i>Bioinformatics</i> , 2020, 36, 4706-4713.	4.1	8
1307	Comparative analyses of saprotrophy in <i>Salisapilia sapeloensis</i> and diverse plant pathogenic oomycetes reveal lifestyle-specific gene expression. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	2.7	4
1308	The temporal RNA virome patterns of a lesser dawn bat (<i>Eonycteris spelaea</i>) colony revealed by deep sequencing. <i>Virus Evolution</i> , 2020, 6, veaa017.	4.9	10
1309	Genome Resource of a Hypervirulent Strain LN4 of <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> Causing Bacterial Blight of Rice. <i>Plant Disease</i> , 2020, 104, 2764-2767.	1.4	7
1310	Multicenter assessment of microbial community profiling using 16S rRNA gene sequencing and shotgun metagenomic sequencing. <i>Journal of Advanced Research</i> , 2020, 26, 111-121.	9.5	38
1311	Genome Sequence of the Euryhaline Javafish Medaka, <i>Oryzias javanicus</i> : A Small Aquarium Fish Model for Studies on Adaptation to Salinity. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 907-915.	1.8	22
1312	The gut microbiome stability is altered by probiotic ingestion and improved by the continuous supplementation of galactooligosaccharide. <i>Gut Microbes</i> , 2020, 12, 1785252.	9.8	39

#	ARTICLE	IF	CITATIONS
1313	ganon: precise metagenomics classification against large and up-to-date sets of reference sequences. Bioinformatics, 2020, 36, i12-i20.	4.1	39
1314	Is Phylotranscriptomics as Reliable as Phylogenomics?. Molecular Biology and Evolution, 2020, 37, 3672-3683.	8.9	52
1315	Sponge microbiome stability during environmental acquisition of highly specific photosymbionts. Environmental Microbiology, 2020, 22, 3593-3607.	3.8	20
1316	Metagenomic comparison of structure and function of microbial community between water, effluent and shrimp intestine of higher place <i>Litopenaeus vannamei</i> ponds. Journal of Applied Microbiology, 2020, 129, 243-255.	3.1	21
1317	Gut microbiome signatures of nursing home residents carrying Enterobacteria producing extended-spectrum β -lactamases. Antimicrobial Resistance and Infection Control, 2020, 9, 107.	4.1	12
1318	Diverse Microbial Composition of Sourdoughs From Different Origins. Frontiers in Microbiology, 2020, 11, 1212.	3.5	56
1319	Life at the Frozen Limit: Microbial Carbon Metabolism Across a Late Pleistocene Permafrost Chronosequence. Frontiers in Microbiology, 2020, 11, 1753.	3.5	16
1320	Additives affect the distribution of metabolic profile, microbial communities and antibiotic resistance genes in high-moisture sweet corn kernel silage. Bioresource Technology, 2020, 315, 123821.	9.6	33
1321	Comprehensive metagenomic insights into a unique mass gathering and bathing event reveals transient influence on a riverine ecosystem. Ecotoxicology and Environmental Safety, 2020, 202, 110938.	6.0	5
1322	Comprehensive and Functional Analysis of Horizontal Gene Transfer Events in Diatoms. Molecular Biology and Evolution, 2020, 37, 3243-3257.	8.9	28
1323	Assessment of ethanol tolerance of <i>Kluyveromyces marxianus</i> CCT 7735 selected by adaptive laboratory evolution. Applied Microbiology and Biotechnology, 2020, 104, 7483-7494.	3.6	25
1324	Transcriptomic analysis of flower opening response to relatively low temperatures in <i>Osmanthus fragrans</i> . BMC Plant Biology, 2020, 20, 337.	3.6	8
1325	Comparative genomics of rice false smut fungi <i>Ustilaginoidea virens</i> Uv-Gvt strain from India reveals genetic diversity and phylogenetic divergence. 3 Biotech, 2020, 10, 342.	2.2	10
1326	Data Processing for RNA/DNA Sequencing. , 2020, , 507-514.		0
1327	Exploiting the Biosynthetic Potency of Taxol from Fungal Endophytes of Conifers Plants; Genome Mining and Metabolic Manipulation. Molecules, 2020, 25, 3000.	3.8	33
1328	Anaerobic metabolism of Foraminifera thriving below the seafloor. ISME Journal, 2020, 14, 2580-2594.	9.8	31
1329	Soil as an extended composite phenotype of the microbial metagenome. Scientific Reports, 2020, 10, 10649.	3.3	41
1330	Isolation, identification, and whole genome sequence analysis of the alginate-degrading bacterium <i>Cobetia</i> sp. cqz5-12. Scientific Reports, 2020, 10, 10920.	3.3	5

#	ARTICLE	IF	CITATIONS
1331	De novo assembly and analysis of the transcriptome of the <i>Dermacentor marginatus</i> genes differentially expressed after blood-feeding and long-term starvation. <i>Parasites and Vectors</i> , 2020, 13, 563.	2.5	9
1332	Analysis of the vaginal microbiome of giant pandas using metagenomics sequencing. <i>MicrobiologyOpen</i> , 2020, 9, e1131.	3.0	8
1333	Tibetan Sheep Adapt to Plant Phenology in Alpine Meadows by Changing Rumen Microbial Community Structure and Function. <i>Frontiers in Microbiology</i> , 2020, 11, 587558.	3.5	21
1334	Comparative Genomics Reveals Novel Target Genes towards Specific Control of Plant-Parasitic Nematodes. <i>Genes</i> , 2020, 11, 1347.	2.4	29
1335	New viral biogeochemical roles revealed through metagenomic analysis of Lake Baikal. <i>Microbiome</i> , 2020, 8, 163.	11.1	43
1336	Do I have something in my teeth? The trouble with genetic analyses of diet from archaeological dental calculus. <i>Quaternary International</i> , 2023, 653-654, 33-46.	1.5	17
1337	Thermogenic hydrocarbon biodegradation by diverse depth-stratified microbial populations at a Scotian Basin cold seep. <i>Nature Communications</i> , 2020, 11, 5825.	12.8	72
1338	Duodenal Metatranscriptomics to Define Human and Microbial Functional Alterations Associated with Severe Obesity: A Pilot Study. <i>Microorganisms</i> , 2020, 8, 1811.	3.6	13
1339	De novo RNA-Seq analysis in sensitive rice cultivar and comparative transcript profiling in contrasting genotypes reveal genetic biomarkers for fluoride-stress response. <i>Environmental Pollution</i> , 2020, 267, 115378.	7.5	8
1340	Demonstrating an Integrated Antibiotic Resistance Gene Surveillance Approach in Puerto Rican Watersheds Post-Hurricane Maria. <i>Environmental Science & Technology</i> , 2020, 54, 15108-15119.	10.0	24
1341	Resource Partitioning Between Phytoplankton and Bacteria in the Coastal Baltic Sea. <i>Frontiers in Marine Science</i> , 2020, 7, .	2.5	6
1342	Serpentovirus (Nidovirus) and Orthoreovirus Coinfection in Captive Veiled Chameleons (<i>Chamaeleo</i>) Tj ETQq1 1 0.784314 rgBT /Overbo	3.3	13
1343	Gene duplication drives genome expansion in a major lineage of Thaumarchaeota. <i>Nature Communications</i> , 2020, 11, 5494.	12.8	55
1344	Coupled anaerobic methane oxidation and reductive arsenic mobilization in wetland soils. <i>Nature Geoscience</i> , 2020, 13, 799-805.	12.9	71
1345	Microbial Niche Diversification in the Galápagos Archipelago and Its Response to El Niño. <i>Frontiers in Microbiology</i> , 2020, 11, 575194.	3.5	7
1346	Multi-omics examination of Q fever fatigue syndrome identifies similarities with chronic fatigue syndrome. <i>Journal of Translational Medicine</i> , 2020, 18, 448.	4.4	21
1347	Gut Microbiota and Metabolic Specificity in Ulcerative Colitis and Crohn's Disease. <i>Frontiers in Medicine</i> , 2020, 7, 606298.	2.6	54
1348	Lower methane emissions were associated with higher abundance of ruminal <i>Prevotella</i> in a cohort of Colombian buffalos. <i>BMC Microbiology</i> , 2020, 20, 364.	3.3	22

#	ARTICLE	IF	CITATIONS
1349	Genome Survey Sequencing of In Vivo Mother Plant and In Vitro Plantlets of <i>Mikania cordata</i> . <i>Plants</i> , 2020, 9, 1665.	3.5	1
1350	The genome and transcriptome analysis of snake gourd provide insights into its evolution and fruit development and ripening. <i>Horticulture Research</i> , 2020, 7, 199.	6.3	22
1351	A Novel Anphevirus in <i>Aedes albopictus</i> Mosquitoes Is Distributed Worldwide and Interacts with the Host RNA Interference Pathway. <i>Viruses</i> , 2020, 12, 1264.	3.3	10
1352	Pervasive generation of non-canonical subgenomic RNAs by SARS-CoV-2. <i>Genome Medicine</i> , 2020, 12, 108.	8.2	54
1353	Zero-Valent Iron Sand Filtration Can Reduce Human and Plant Pathogenic Bacteria While Increasing Plant Growth Promoting Bacteria in Reclaimed Water. <i>Frontiers in Environmental Science</i> , 2020, 8, .	3.3	7
1354	Profiling Novel Alternative Splicing within Multiple Tissues Provides Useful Insights into Porcine Genome Annotation. <i>Genes</i> , 2020, 11, 1405.	2.4	3
1355	Microbial Processing of Jellyfish Detritus in the Ocean. <i>Frontiers in Microbiology</i> , 2020, 11, 590995.	3.5	19
1356	Mitochondrial Fostering: The Mitochondrial Genome May Play a Role in Plant Orphan Gene Evolution. <i>Frontiers in Plant Science</i> , 2020, 11, 600117.	3.6	15
1357	Novel NGS pipeline for virus discovery from a wide spectrum of hosts and sample types. <i>Virus Evolution</i> , 2020, 6, veaa091.	4.9	28
1358	Different amplitudes of temperature fluctuation induce distinct transcriptomic and metabolomic responses in the dung beetle <i>Phanaeus vindex</i> . <i>Journal of Experimental Biology</i> , 2020, 223, .	1.7	7
1359	Genomic analysis of <i>Helicobacter himalayensis</i> sp. nov. isolated from <i>Marmota himalayana</i> . <i>BMC Genomics</i> , 2020, 21, 826.	2.8	4
1360	Comparative Analysis of ROS Network Genes in Extremophile Eukaryotes. <i>International Journal of Molecular Sciences</i> , 2020, 21, 9131.	4.1	10
1361	Current Trends in Experimental and Computational Approaches to Combat Antimicrobial Resistance. <i>Frontiers in Genetics</i> , 2020, 11, 563975.	2.3	12
1362	High-Quality Genome-Scale Models From Error-Prone, Long-Read Assemblies. <i>Frontiers in Microbiology</i> , 2020, 11, 596626.	3.5	3
1363	Metagenomic Analysis of the Enteric RNA Virome of Infants from the Oukasie Clinic, North West Province, South Africa, Reveals Diverse Eukaryotic Viruses. <i>Viruses</i> , 2020, 12, 1260.	3.3	11
1364	Exploring the Influence of Signal Molecules on Marine Biofilms Development. <i>Frontiers in Microbiology</i> , 2020, 11, 571400.	3.5	16
1365	Adaptation mechanism of mango fruit (<i>Mangifera indica</i> L. cv. Chaunsa White) to heat suggest modulation in several metabolic pathways. <i>RSC Advances</i> , 2020, 10, 35531-35544.	3.6	9
1366	New Frontiers of Anaerobic Hydrocarbon Biodegradation in the Multi-Omics Era. <i>Frontiers in Microbiology</i> , 2020, 11, 590049.	3.5	33

#	ARTICLE	IF	CITATIONS
1367	In Silico Characterization and Phylogenetic Distribution of Extracellular Matrix Components in the Model Rhizobacteria <i>Pseudomonas fluorescens</i> F113 and Other <i>Pseudomonads</i> . <i>Microorganisms</i> , 2020, 8, 1740.	3.6	20
1368	Portiera Gets Wild: Genome Instability Provides Insights into the Evolution of Both Whiteflies and Their Endosymbionts. <i>Genome Biology and Evolution</i> , 2020, 12, 2107-2124.	2.5	14
1369	Electrolocation? The evidence for redox-mediated taxis in <i>Shewanella oneidensis</i> . <i>Molecular Microbiology</i> , 2020, 115, 1069-1079.	2.5	13
1370	Molecular signatures of the rediae, cercariae and adult stages in the complex life cycles of parasitic flatworms (Digenea: Psilostomatidae). <i>Parasites and Vectors</i> , 2020, 13, 559.	2.5	4
1371	Scion genotypes exert long distance control over rootstock transcriptome responses to low phosphate in grafted grapevine. <i>BMC Plant Biology</i> , 2020, 20, 367.	3.6	17
1372	Cytotoxic and genotoxic evaluation and the toxicological mechanism of uranium in <i>Vicia faba</i> root. <i>Environmental and Experimental Botany</i> , 2020, 179, 104227.	4.2	16
1373	The alteration of gut microbiome and metabolism in amyotrophic lateral sclerosis patients. <i>Scientific Reports</i> , 2020, 10, 12998.	3.3	69
1374	Synthetic DNA and biosecurity: Nuances of predicting pathogenicity and the impetus for novel computational approaches for screening oligonucleotides. <i>PLoS Pathogens</i> , 2020, 16, e1008649.	4.7	8
1375	Unraveling bacteria-mediated degradation of lignin-derived aromatic compounds in a freshwater environment. <i>Science of the Total Environment</i> , 2020, 749, 141236.	8.0	22
1376	Genomic and enzymatic evidence of acetogenesis by anaerobic methanotrophic archaea. <i>Nature Communications</i> , 2020, 11, 3941.	12.8	45
1377	Comparative Metagenomic Screening of Aromatic Hydrocarbon Degradation and Secondary Metabolite-Producing Genes in the Red Sea, the Suez Canal, and the Mediterranean Sea. <i>OMICS A Journal of Integrative Biology</i> , 2020, 24, 541-550.	2.0	4
1378	A guide to human microbiome research: study design, sample collection, and bioinformatics analysis. <i>Chinese Medical Journal</i> , 2020, 133, 1844-1855.	2.3	55
1379	Bactopia: a Flexible Pipeline for Complete Analysis of Bacterial Genomes. <i>MSystems</i> , 2020, 5, .	3.8	82
1380	Gut transcriptomic changes during hibernation in the greater horseshoe bat (<i>Rhinolophus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	2.0	4
1381	The Genome Sequence of Alpine <i>Megacarpaea delavayi</i> Identifies Species-Specific Whole-Genome Duplication. <i>Frontiers in Genetics</i> , 2020, 11, 812.	2.3	10
1382	Archives of human-dog relationships: Genetic and stable isotope analysis of Arctic fur clothing. <i>Journal of Anthropological Archaeology</i> , 2020, 59, 101200.	1.6	6
1383	Undinarchaeota illuminate DPANN phylogeny and the impact of gene transfer on archaeal evolution. <i>Nature Communications</i> , 2020, 11, 3939.	12.8	102
1384	Transcriptome analysis of the <i>Larimichthys polyactis</i> under heat and cold stress. <i>Cryobiology</i> , 2020, 96, 175-183.	0.7	15

#	ARTICLE	IF	CITATIONS
1385	Comprehensive chemotaxonomic and genomic profiling of a biosynthetically talented Australian fungus, <i>Aspergillus burnettii</i> sp. nov.. Fungal Genetics and Biology, 2020, 143, 103435.	2.1	19
1386	Microbial catabolism of lindane in distinct layers of acidic paddy soils combinedly affected by different water managements and bioremediation strategies. Science of the Total Environment, 2020, 746, 140992.	8.0	13
1387	GeneMark-EP+: eukaryotic gene prediction with self-training in the space of genes and proteins. NAR Genomics and Bioinformatics, 2020, 2, lqaa026.	3.2	256
1388	A new genomic taxonomy system for the <i>Synechococcus</i> collective. Environmental Microbiology, 2020, 22, 4557-4570.	3.8	32
1389	Producing polished prokaryotic pangenomes with the Panaroo pipeline. Genome Biology, 2020, 21, 180.	8.8	419
1390	Transcriptomic Profiling of <i>Cryptomeria fortunei</i> Hooibrenk Vascular Cambium Identifies Candidate Genes Involved in Phenylpropanoid Metabolism. Forests, 2020, 11, 766.	2.1	10
1391	Diverse variola virus (smallpox) strains were widespread in northern Europe in the Viking Age. Science, 2020, 369, .	12.6	108
1392	Reference Genome Assembly for Australian <i>Ascochyta rabiei</i> Isolate ArME14. G3: Genes, Genomes, Genetics, 2020, 10, 2131-2140.	1.8	15
1393	Reference Genome for the Highly Transformable <i>Setaria viridis</i> ME034V. G3: Genes, Genomes, Genetics, 2020, 10, 3467-3478.	1.8	36
1394	Alterations of Gut Microbiome in Tibetan Patients With Coronary Heart Disease. Frontiers in Cellular and Infection Microbiology, 2020, 10, 373.	3.9	32
1395	Low Abundance of Methanotrophs in Sediments of Shallow Boreal Coastal Zones With High Water Methane Concentrations. Frontiers in Microbiology, 2020, 11, 1536.	3.5	14
1396	Temporal Shotgun Metagenomics Revealed the Potential Metabolic Capabilities of Specific Microorganisms During Lambic Beer Production. Frontiers in Microbiology, 2020, 11, 1692.	3.5	21
1397	Comparative Genomics and Evolutionary Analysis of RNA-Binding Proteins of the CsrA Family in the Genus <i>Pseudomonas</i> . Frontiers in Molecular Biosciences, 2020, 7, 127.	3.5	27
1398	Improved Reference Genome for <i>Cyclotella cryptica</i> CCMP332, a Model for Cell Wall Morphogenesis, Salinity Adaptation, and Lipid Production in Diatoms (Bacillariophyta). G3: Genes, Genomes, Genetics, 2020, 10, 2965-2974.	1.8	14
1399	Transcriptomic comparison reveals modifications in gene expression, photosynthesis, and cell wall in woody plant as responses to external pH changes. Ecotoxicology and Environmental Safety, 2020, 203, 111007.	6.0	9
1400	RIGD: A Database for Intronless Genes in the Rosaceae. Frontiers in Genetics, 2020, 11, 868.	2.3	4
1401	Virus and Potential Host Microbes from Viral-Enriched Metagenomic Characterization in the High-Altitude Wetland, Salar de Huasco, Chile. Microorganisms, 2020, 8, 1077.	3.6	14
1402	Cultivar-specific transcriptome and pan-transcriptome reconstruction of tetraploid potato. Scientific Data, 2020, 7, 249.	5.3	27

#	ARTICLE	IF	CITATIONS
1403	Prevalence and Implications of Contamination in Public Genomic Resources: A Case Study of 43 Reference Arthropod Assemblies. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 721-730.	1.8	25
1404	Elucidation of metabolic responses in mud crab <i>Scylla paramamosain</i> challenged to WSSV infection by integration of metabolomics and transcriptomics. <i>Developmental and Comparative Immunology</i> , 2020, 113, 103799.	2.3	9
1405	Differential Expression of Fungal Genes Determines the Lifestyle of <i>Plectosphaerella</i> Strains During <i>Arabidopsis thaliana</i> Colonization. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 1299-1314.	2.6	9
1406	Microbiome and Metagenome Analyses of a Closed Habitat during Human Occupation. <i>MSystems</i> , 2020, 5, .	3.8	4
1407	Completion of draft bacterial genomes by long-read sequencing of synthetic genomic pools. <i>BMC Genomics</i> , 2020, 21, 519.	2.8	11
1408	Pan-Genome Scale Network Reconstruction: Harnessing Phylogenomics Increases the Quantity and Quality of Metabolic Models. <i>Biotechnology Journal</i> , 2020, 15, e1900519.	3.5	9
1409	Composition and functional characterization of the gut microbiome of freshwater pufferfish (<i>Tetraodon cutcutia</i>). <i>Archives of Microbiology</i> , 2020, 202, 2761-2770.	2.2	9
1410	Fast start-up of PN/A process in a single-stage packed bed and mechanism of nitrogen removal. <i>Environmental Science and Pollution Research</i> , 2020, 27, 40483-40494.	5.3	10
1411	Metagenomic analysis reveals the effects of cotton straw-derived biochar on soil nitrogen transformation in drip-irrigated cotton field. <i>Environmental Science and Pollution Research</i> , 2020, 27, 43929-43941.	5.3	13
1412	Kiwifruit Genome Database (KGD): a comprehensive resource for kiwifruit genomics. <i>Horticulture Research</i> , 2020, 7, 117.	6.3	47
1413	Microbial tropicalization driven by a strengthening western ocean boundary current. <i>Global Change Biology</i> , 2020, 26, 5613-5629.	9.5	16
1414	Genomic and transcriptomic evidence for descent from <i>Plasmodium</i> and loss of blood schizogony in <i>Hepatocystis</i> parasites from naturally infected red colobus monkeys. <i>PLoS Pathogens</i> , 2020, 16, e1008717.	4.7	18
1415	Circumpolar diversification of the <i>Ixodes uriae</i> tick virome. <i>PLoS Pathogens</i> , 2020, 16, e1008759.	4.7	27
1416	Complete genome sequence of <i>Sphingobium</i> sp. strain PAMC 28499 reveals a potential for degrading pectin with comparative genomics approach. <i>Genes and Genomics</i> , 2020, 42, 1087-1096.	1.4	5
1417	Illuminating the impact of diel vertical migration on visual gene expression in deep-sea shrimp. <i>Molecular Ecology</i> , 2020, 29, 3494-3510.	3.9	14
1418	Functional potential differences between <i>Firmicutes</i> and <i>Proteobacteria</i> in response to manure amendment in a reclaimed soil. <i>Canadian Journal of Microbiology</i> , 2020, 66, 689-697.	1.7	34
1419	Virome assembly and annotation in brain tissue based on next-generation sequencing. <i>Cancer Medicine</i> , 2020, 9, 6776-6790.	2.8	8
1420	Differential prevalence and host-association of antimicrobial resistance traits in disinfected and non-disinfected drinking water systems. <i>Science of the Total Environment</i> , 2020, 749, 141451.	8.0	22

#	ARTICLE	IF	CITATIONS
1421	Transcriptional Response of Osmolyte Synthetic Pathways and Membrane Transporters in a Euryhaline Diatom During Long-term Acclimation to a Salinity Gradient. <i>Journal of Phycology</i> , 2020, 56, 1712-1728.	2.3	16
1422	Consumption of a Western-Style Diet Modulates the Response of the Murine Gut Microbiome to Ciprofloxacin. <i>MSystems</i> , 2020, 5, .	3.8	23
1423	A carbohydrate-active enzyme (CAZy) profile links successful metabolic specialization of <i>Prevotella</i> to its abundance in gut microbiota. <i>Scientific Reports</i> , 2020, 10, 12411.	3.3	22
1424	Integrated analysis of mRNA and miRNA expression profiles reveals muscle growth differences between fast- and slow-growing king ratsnakes (<i>Elaphe carinata</i>). <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 2020, 248-249, 110482.	1.6	1
1425	Tracing animal genomic evolution with the chromosomal-level assembly of the freshwater sponge <i>Ephydatia muelleri</i> . <i>Nature Communications</i> , 2020, 11, 3676.	12.8	72
1426	SparkLeBLAST: Scalable Parallelization of BLAST Sequence Alignment Using Spark. , 2020, , .		1
1427	Composition and function of rhizosphere microbiome of <i>Panax notoginseng</i> with discrepant yields. <i>Chinese Medicine</i> , 2020, 15, 85.	4.0	18
1428	Comparative transcriptome analysis of high-growth and wild-type strains of <i>Pyropia yezoensis</i> . <i>Acta Botanica Croatica</i> , 2020, 79, 148-156.	0.7	5
1429	Characterization of an acid rock drainage microbiome and transcriptome at the Ely Copper Mine Superfund site. <i>PLoS ONE</i> , 2020, 15, e0237599.	2.5	7
1430	Complete genome sequences of two novel dicistroviruses detected in yellow crazy ants (<i>Anoplolepis</i>) Tj ETQq1 1 0.784314 rgBT /Ovelde	2.1	5
1431	Widespread protein lysine acetylation in gut microbiome and its alterations in patients with Crohn's disease. <i>Nature Communications</i> , 2020, 11, 4120.	12.8	32
1432	Transcriptome Profiling-Based Analysis of Carbohydrate-Active Enzymes in <i>Aspergillus terreus</i> Involved in Plant Biomass Degradation. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 564527.	4.1	12
1433	Atribacteria Reproducing over Millions of Years in the Atlantic Abyssal Subseafloor. <i>MBio</i> , 2020, 11, .	4.1	23
1434	Human pegivirus (HPgV, GBV-C) RNA in volunteer blood donors from a public hemotherapy service in Northern Brazil. <i>Virology Journal</i> , 2020, 17, 153.	3.4	10
1435	Testing the Two-Step Model of Plant Root Microbiome Acquisition Under Multiple Plant Species and Soil Sources. <i>Frontiers in Microbiology</i> , 2020, 11, 542742.	3.5	20
1436	Identification of Chitinolytic Enzymes in <i>Chitinolyticbacter meiyuanensis</i> and Mechanism of Efficiently Hydrolyzing Chitin to N-Acetyl Glucosamine. <i>Frontiers in Microbiology</i> , 2020, 11, 572053.	3.5	11
1437	Metagenomic analysis reveals linkages between cecal microbiota and feed efficiency in Xiayan chickens. <i>Poultry Science</i> , 2020, 99, 7066-7075.	3.4	14
1438	More than just a ticket canceller: the mitochondrial processing peptidase tailors complex precursor proteins at internal cleavage sites. <i>Molecular Biology of the Cell</i> , 2020, 31, 2657-2668.	2.1	10

#	ARTICLE	IF	CITATIONS
1439	Progress in quickly finding orthologs as reciprocal best hits: comparing blast, last, diamond and MMseqs2. BMC Genomics, 2020, 21, 741.	2.8	43
1440	De novo transcriptome assembly and mining of EST-SSR markers in <i>Gloriosa superba</i> . Journal of Genetics, 2020, 99, 1.	0.7	1
1441	Transcriptomic data on the transgenerational exposure of the keystone amphipod <i>Gammarus locusta</i> to simvastatin. Data in Brief, 2020, 32, 106248.	1.0	7
1442	Genomic profiling of bacterial and fungal communities and their predictive functionality during pulque fermentation by whole-genome shotgun sequencing. Scientific Reports, 2020, 10, 15115.	3.3	29
1443	Multifactorial Causes of Chronic Mortality in Juvenile Sturgeon (<i>Huso huso</i>). Animals, 2020, 10, 1866.	2.3	11
1444	Accurate reconstruction of bacterial pan- and core genomes with PEPPAN. Genome Research, 2020, 30, 1667-1679.	5.5	56
1445	Viral metagenomics reveals diverse anelloviruses in bone marrow specimens from hematologic patients. Journal of Clinical Virology, 2020, 132, 104643.	3.1	8
1446	Virome Sequencing of the Human Intestinal Mucosalâ€”Luminal Interface. Frontiers in Cellular and Infection Microbiology, 2020, 10, 582187.	3.9	14
1447	Deciphering the Microbial Taxonomy and Functionality of Two Diverse Mangrove Ecosystems and Their Potential Abilities To Produce Bioactive Compounds. MSystems, 2020, 5, .	3.8	23
1448	From Embryo to Adult: Low Temperatures Affect Phase Transitions of <i>Allium sativum</i> L. from Germination to Flowering. Agronomy, 2020, 10, 1651.	3.0	3
1449	Evolutionary Biologyâ€”A Transdisciplinary Approach. , 2020, , .		5
1450	Distinct Polysaccharide Utilization Determines Interspecies Competition between Intestinal <i>Prevotella</i> spp.. Cell Host and Microbe, 2020, 28, 838-852.e6.	11.0	86
1451	Uncovering the genomic potential of the Amazon River microbiome to degrade rainforest organic matter. Microbiome, 2020, 8, 151.	11.1	18
1452	Comparative genomic analysis reveals metabolic diversity of different <i>Paenibacillus</i> groups. Applied Microbiology and Biotechnology, 2020, 104, 10133-10143.	3.6	5
1453	Evolutionary analysis of the <i>Moringa oleifera</i> genome reveals a recent burst of plastid to nucleus gene duplications. Scientific Reports, 2020, 10, 17646.	3.3	12
1454	Insights into oleaginous phenotype of the yeast <i>Papiliotrema laurentii</i> . Fungal Genetics and Biology, 2020, 144, 103456.	2.1	5
1455	Reclassification of the Taxonomic Framework of Orders <i>Cellvibrionales</i> , <i>Oceanospirillales</i> , <i>Pseudomonadales</i> , and <i>Alteromonadales</i> in Class <i>Gammaproteobacteria</i> through Phylogenomic Tree Analysis. MSystems, 2020, 5, .	3.8	50
1456	Characterization of integrated prophages within diverse species of clinical nontuberculous mycobacteria. Virology Journal, 2020, 17, 124.	3.4	22

#	ARTICLE	IF	CITATIONS
1457	Insights into Ammonia Adaptation and Methanogenic Precursor Oxidation by Genome-Centric Analysis. Environmental Science & Technology, 2020, 54, 12568-12582.	10.0	57
1458	Seasonal dynamics and starvation impact on the gut microbiome of urochordate ascidian <i>Halocynthia roretzi</i> . Animal Microbiome, 2020, 2, 30.	3.8	16
1459	Genetic Adaptations of an Island Pit-Viper to a Unique Sedentary Life with Extreme Seasonal Food Availability. G3: Genes, Genomes, Genetics, 2020, 10, 1639-1646.	1.8	3
1460	The Virome of Acute Respiratory Diseases in Individuals at Risk of Zoonotic Infections. Viruses, 2020, 12, 960.	3.3	17
1461	Endosymbionts of Metazoans Dwelling in the PACManus Hydrothermal Vent: Diversity and Potential Adaptive Features Revealed by Genome Analysis. Applied and Environmental Microbiology, 2020, 86, .	3.1	6
1462	The Association between Insertion Sequences and Antibiotic Resistance Genes. MSphere, 2020, 5, .	2.9	60
1463	Transcriptome analysis reveals that the multiple metabolic pathways were related to gluten polymerization in different quality wheats (<i>Triticum aestivum</i> L.). Food Science and Nutrition, 2020, 8, 4573-4583.	3.4	4
1464	Nucleotide diversity of functionally different groups of immune response genes in Old World camels based on newly annotated and reference-guided assemblies. BMC Genomics, 2020, 21, 606.	2.8	15
1465	LSTrAP-Crowd: prediction of novel components of bacterial ribosomes with crowd-sourced analysis of RNA sequencing data. BMC Biology, 2020, 18, 114.	3.8	8
1466	Genome sequence of segmented filamentous bacteria present in the human intestine. Communications Biology, 2020, 3, 485.	4.4	27
1467	Metagenomic Insights into the Sewage RNA Virosphere of a Large City. Viruses, 2020, 12, 1050.	3.3	22
1468	Validating an Automated Nucleic Acid Extraction Device for Omics in Space Using Whole Cell Microbial Reference Standards. Frontiers in Microbiology, 2020, 11, 1909.	3.5	9
1469	Characterization of a Novel Chromosomal Class C β -Lactamase, YOC-1, and Comparative Genomics Analysis of a Multidrug Resistance Plasmid in <i>Yokenella regensburgei</i> W13. Frontiers in Microbiology, 2020, 11, 2021.	3.5	4
1470	Phylogenomic Analysis Supports Two Possible Origins for Latin American Strains of <i>Vibrio parahaemolyticus</i> Associated with Acute Hepatopancreatic Necrosis Disease (AHPND). Current Microbiology, 2020, 77, 3851-3860.	2.2	12
1471	The Molecular Machinery of Gametogenesis in <i>Geodia</i> Demosponges (Porifera): Evolutionary Origins of a Conserved Toolkit across Animals. Molecular Biology and Evolution, 2020, 37, 3485-3506.	8.9	19
1472	Diversity of Sea Star-Associated Densoviruses and Transcribed Endogenous Viral Elements of Densovirus Origin. Journal of Virology, 2020, 95, .	3.4	14
1473	Bacteria Contribute to Plant Secondary Compound Degradation in a Generalist Herbivore System. MBio, 2020, 11, .	4.1	30
1474	Investigating population-scale allelic differential expression in wild populations of <i>Oithona similis</i> (Cyclopoida, Claus, 1866). Ecology and Evolution, 2020, 10, 8894-8905.	1.9	9

#	ARTICLE	IF	CITATIONS
1475	Transcriptome Analysis of the Liver and Muscle Tissues of Black Carp (<i>Mylopharyngodon piceus</i>) of Different Growth Rates. <i>Marine Biotechnology</i> , 2020, 22, 706-716.	2.4	16
1476	N2 fixation dominates nitrogen cycling in a mangrove fiddler crab holobiont. <i>Scientific Reports</i> , 2020, 10, 13966.	3.3	25
1477	Bacterial Genome Wide Association Studies (bGWAS) and Transcriptomics Identifies Cryptic Antimicrobial Resistance Mechanisms in <i>Acinetobacter baumannii</i> . <i>Frontiers in Public Health</i> , 2020, 8, 451.	2.7	9
1478	Viral Metagenomic Profiling of Croatian Bat Population Reveals Sample and Habitat Dependent Diversity. <i>Viruses</i> , 2020, 12, 891.	3.3	20
1479	The <i>saccharibacterium</i> TM7x elicits differential responses across its host range. <i>ISME Journal</i> , 2020, 14, 3054-3067.	9.8	35
1480	Draft genome sequence of <i>scale drop disease virus</i> (SDDV) retrieved from metagenomic investigation of infected barramundi, <i>Lates calcarifer</i> (Bloch, 1790). <i>Journal of Fish Diseases</i> , 2020, 43, 1287-1298.	1.9	7
1481	Comparative Analysis of the Core Proteomes among the <i>Pseudomonas</i> Major Evolutionary Groups Reveals Species-Specific Adaptations for <i>Pseudomonas aeruginosa</i> and <i>Pseudomonas chlororaphis</i> . <i>Diversity</i> , 2020, 12, 289.	1.7	37
1482	Chikungunya virus Detection in <i>Aedes aegypti</i> and <i>Culex quinquefasciatus</i> during an Outbreak in the Amazon Region. <i>Viruses</i> , 2020, 12, 853.	3.3	8
1483	Costus stripe mosaic virus, a tentative new member of the genus Potyvirus. <i>Archives of Virology</i> , 2020, 165, 2541-2548.	2.1	3
1484	Mysterious syndrome causing high mortality in wild brown trout in Eastern Switzerland, pathology and search for a possible cause. <i>Journal of Fish Diseases</i> , 2020, 43, 1317-1324.	1.9	0
1485	Phylogeny and multiple independent whole-genome duplication events in the Brassicales. <i>American Journal of Botany</i> , 2020, 107, 1148-1164.	1.7	32
1486	Chromosome-Level Assembly of the Common Lizard (<i>Zootoca vivipara</i>) Genome. <i>Genome Biology and Evolution</i> , 2020, 12, 1953-1960.	2.5	13
1487	An outbreak of visceral white nodules disease caused by <i>Pseudomonas plecoglossicida</i> at a water temperature of 12°C in cultured large yellow croaker (<i>Larimichthys crocea</i>) in China. <i>Journal of Fish Diseases</i> , 2020, 43, 1353-1361.	1.9	52
1488	Complete Genome Sequence of an Alphacoronavirus from Common Vampire Bats in Peru. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	14
1489	Transcriptome Analysis of <i>Bursaphelenchus xylophilus</i> Uncovers the Impact of <i>Stenotrophomonas maltophilia</i> on Nematode and Pine Wilt Disease. <i>Forests</i> , 2020, 11, 908.	2.1	2
1490	A complete and flexible workflow for metaproteomics data analysis based on MetaProteomeAnalyzer and Prophane. <i>Nature Protocols</i> , 2020, 15, 3212-3239.	12.0	42
1491	The Gut Microbiome Is Associated with Clinical Response to Anti-PD-1/PD-L1 Immunotherapy in Gastrointestinal Cancer. <i>Cancer Immunology Research</i> , 2020, 8, 1251-1261.	3.4	155
1492	Analytical Performance Validation of Next-Generation Sequencing Based Clinical Microbiology Assays Using a K-mer Analysis Workflow. <i>Frontiers in Microbiology</i> , 2020, 11, 1883.	3.5	12

#	ARTICLE	IF	CITATIONS
1493	Integrated microbiota and metabolite profiles link Crohn's disease to sulfur metabolism. <i>Nature Communications</i> , 2020, 11, 4322.	12.8	79
1494	The complete chloroplast genomes of two Mexican plants of the annual herb <i>Datura stramonium</i> (Solanaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2823-2825.	0.4	6
1495	Analysis of the virome associated to grapevine downy mildew lesions reveals new mycovirus lineages. <i>Virus Evolution</i> , 2020, 6, veaa058.	4.9	104
1496	A Genome-Scale Insight into the Effect of Shear Stress During the Fed-Batch Production of Clavulanic Acid by <i>Streptomyces Clavuligerus</i> . <i>Microorganisms</i> , 2020, 8, 1255.	3.6	8
1497	Composition and Metabolic Functions of the Microbiome in Fermented Grain during Light-Flavor Baijiu Fermentation. <i>Microorganisms</i> , 2020, 8, 1281.	3.6	52
1498	Improved Reference Genome Uncovers Novel Sex-Linked Regions in the Guppy (<i>Poecilia reticulata</i>). <i>Genome Biology and Evolution</i> , 2020, 12, 1789-1805.	2.5	36
1499	Chlamydial contribution to anaerobic metabolism during eukaryotic evolution. <i>Science Advances</i> , 2020, 6, eabb7258.	10.3	18
1500	Resolving the Mortierellaceae phylogeny through synthesis of multi-gene phylogenetics and phylogenomics. <i>Fungal Diversity</i> , 2020, 104, 267-289.	12.3	57
1501	MAIRA- real-time taxonomic and functional analysis of long reads on a laptop. <i>BMC Bioinformatics</i> , 2020, 21, 390.	2.6	2
1502	Identification, Characterization, and Genomic Analysis of Novel <i>Serratia</i> Temperate Phages from a Gold Mine. <i>International Journal of Molecular Sciences</i> , 2020, 21, 6709.	4.1	11
1503	Microbiome and nitrate removal processes by microorganisms on the ancient Preah Vihear temple of Cambodia revealed by metagenomics and N-15 isotope analyses. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 9823-9837.	3.6	21
1504	Meta-transcriptomic identification of <i>Trypanosoma</i> spp. in native wildlife species from Australia. <i>Parasites and Vectors</i> , 2020, 13, 447.	2.5	14
1505	In-Depth In Silico Search for Cuttlefish (<i>Sepia officinalis</i>) Antimicrobial Peptides Following Bacterial Challenge of Haemocytes. <i>Marine Drugs</i> , 2020, 18, 439.	4.6	8
1506	Adaptation of <i>Coccomyxa</i> sp. to Extremely Low Light Conditions Causes Deep Chlorophyll and Oxygen Maxima in Acidic Pit Lakes. <i>Microorganisms</i> , 2020, 8, 1218.	3.6	16
1507	Impact of a Gastrointestinal Stable Probiotic Supplement <i>Bacillus coagulans</i> LBSC on Human Gut Microbiome Modulation. <i>Journal of Dietary Supplements</i> , 2021, 18, 577-596.	2.6	22
1508	Combined Proteome and Transcriptome Analysis of Heat-Primed <i>Azalea</i> Reveals New Insights Into Plant Heat Acclimation Memory. <i>Frontiers in Plant Science</i> , 2020, 11, 1278.	3.6	18
1509	Metagenomic and Metatranscriptomic Study of Microbial Metal Resistance in an Acidic Pit Lake. <i>Microorganisms</i> , 2020, 8, 1350.	3.6	15
1510	Spatial Metagenomics of Three Geothermal Sites in Pisciarelli Hot Spring Focusing on the Biochemical Resources of the Microbial Consortia. <i>Molecules</i> , 2020, 25, 4023.	3.8	11

#	ARTICLE	IF	CITATIONS
1511	Insights into the Evolutionary Origin of Mediterranean Sandfly Fever Viruses. <i>MSphere</i> , 2020, 5, .	2.9	17
1512	Nanoparticle treatment of maize analyzed through the metatranscriptome: compromised nitrogen cycling, possible phytopathogen selection, and plant hormesis. <i>Microbiome</i> , 2020, 8, 127.	11.1	26
1513	Metagenomic Analysis of the Virome of Mosquito Excreta. <i>MSphere</i> , 2020, 5, .	2.9	20
1514	Press Disturbance Alters Community Structure and Assembly Mechanisms of Bacterial Taxa and Functional Genes in Mesocosm-Scale Bioreactors. <i>MSystems</i> , 2020, 5, .	3.8	17
1515	Estimating the quality of eukaryotic genomes recovered from metagenomic analysis with EukCC. <i>Genome Biology</i> , 2020, 21, 244.	8.8	58
1516	Metalign: efficient alignment-based metagenomic profiling via containment min hash. <i>Genome Biology</i> , 2020, 21, 242.	8.8	29
1517	Abundant Taxa and Favorable Pathways in the Microbiome of Soda-Saline Lakes in Inner Mongolia. <i>Frontiers in Microbiology</i> , 2020, 11, 1740.	3.5	27
1518	Shotgun metagenomics of indigenous bacteria collected from the banks of the San Jacinto River for biodegradation of aromatic waste. <i>FEMS Microbiology Letters</i> , 2020, 367, .	1.8	1
1519	Non- <i>Ca</i> denitrifier nitrous oxide reductases dominate marine biomes. <i>Environmental Microbiology Reports</i> , 2020, 12, 681-692.	2.4	26
1520	Gammaproteobacteria mediating utilization of methyl-, sulfur- and petroleum organic compounds in deep ocean hydrothermal plumes. <i>ISME Journal</i> , 2020, 14, 3136-3148.	9.8	36
1521	Effects of Gut Microbiome and Short-Chain Fatty Acids (SCFAs) on Finishing Weight of Meat Rabbits. <i>Frontiers in Microbiology</i> , 2020, 11, 1835.	3.5	26
1522	Gut Microbiota-Associated Activation of TLR5 Induces Apolipoprotein A1 Production in the Liver. <i>Circulation Research</i> , 2020, 127, 1236-1252.	4.5	32
1523	Pan-genome analysis of <i>Paenibacillus polymyxa</i> strains reveals the mechanism of plant growth promotion and biocontrol. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1539-1558.	1.7	17
1524	Termite mounds contain soil-derived methanotroph communities kinetically adapted to elevated methane concentrations. <i>ISME Journal</i> , 2020, 14, 2715-2731.	9.8	21
1525	REINDEER: efficient indexing of <i>k</i> -mer presence and abundance in sequencing datasets. <i>Bioinformatics</i> , 2020, 36, i177-i185.	4.1	40
1526	Whole Genome Sequencing of SARS-CoV-2: Adapting Illumina Protocols for Quick and Accurate Outbreak Investigation during a Pandemic. <i>Genes</i> , 2020, 11, 949.	2.4	65
1527	Comparative Microbiome Study of Mummified Peach Fruits by Metagenomics and Metatranscriptomics. <i>Plants</i> , 2020, 9, 1052.	3.5	12
1528	Unveiling Viruses Associated with Gastroenteritis Using a Metagenomics Approach. <i>Viruses</i> , 2020, 12, 1432.	3.3	11

#	ARTICLE	IF	CITATIONS
1529	Complete and Circularized Genome Assemblies of the <i>Kroppenstedtia eburnea</i> Genus Type Strain and the <i>Kroppenstedtia pulmonis</i> Species Type Strain with MiSeq and MinION Sequence Data. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	0
1530	Viral rhodopsins 1 are a unique family of light-gated cation channels. <i>Nature Communications</i> , 2020, 11, 5707.	12.8	33
1531	Daily transcriptomes of the copepod <i>Calanus finmarchicus</i> during the summer solstice at high Arctic latitudes. <i>Scientific Data</i> , 2020, 7, 415.	5.3	6
1532	Diverse and abundant resistome in terrestrial and aquatic vertebrates revealed by transcriptional analysis. <i>Scientific Reports</i> , 2020, 10, 18870.	3.3	13
1533	Sustained organic loading disturbance favors nitrite accumulation in bioreactors with variable resistance, recovery and resilience of nitrification and nitrifiers. <i>Scientific Reports</i> , 2020, 10, 21388.	3.3	13
1534	The Neuromodulator-Encoding <i>sadA</i> Gene Is Widely Distributed in the Human Skin Microbiome. <i>Frontiers in Microbiology</i> , 2020, 11, 573679.	3.5	9
1535	Localized effect of treated wastewater effluent on the resistome of an urban watershed. <i>GigaScience</i> , 2020, 9, .	6.4	21
1536	Comparative genomics of <i>Klebsiella michiganensis</i> BD177 and related members of <i>Klebsiella</i> sp. reveal the symbiotic relationship with <i>Bactrocera dorsalis</i> . <i>BMC Genetics</i> , 2020, 21, 138.	2.7	5
1537	Comparative transcriptome analysis of scaled and scaleless skins in <i>Gymnocypris eckloni</i> provides insights into the molecular mechanism of scale degeneration. <i>BMC Genomics</i> , 2020, 21, 835.	2.8	1
1538	Diversity and Genomic Characterization of a Novel Parvarchaeota Family in Acid Mine Drainage Sediments. <i>Frontiers in Microbiology</i> , 2020, 11, 612257.	3.5	22
1539	Lateral Gene Transfer of Anion-Conducting Channelrhodopsins between Green Algae and Giant Viruses. <i>Current Biology</i> , 2020, 30, 4910-4920.e5.	3.9	42
1540	Dinoflagellate Host Chloroplasts and Mitochondria Remain Functional During <i>Amoebophrya</i> Infection. <i>Frontiers in Microbiology</i> , 2020, 11, 600823.	3.5	6
1541	First Draft Genome Assembly of the Malaysian Stingless Bee, <i>Heterotrigona itama</i> (Apidae, Meliponinae). <i>Data</i> , 2020, 5, 112.	2.3	0
1542	A Novel Family of <i>Acinetobacter</i> Mega-Plasmids Are Disseminating Multi-Drug Resistance Across the Globe While Acquiring Location-Specific Accessory Genes. <i>Frontiers in Microbiology</i> , 2020, 11, 605952.	3.5	18
1543	Genome-Resolved Metagenomics and Antibiotic Resistance Genes Analysis in Reclaimed Water Distribution Systems. <i>Water (Switzerland)</i> , 2020, 12, 3477.	2.7	7
1544	Predicting clinical resistance prevalence using sewage metagenomic data. <i>Communications Biology</i> , 2020, 3, 711.	4.4	37
1545	Benchmarking Orthogroup Inference Accuracy: Revisiting Orthobench. <i>Genome Biology and Evolution</i> , 2020, 12, 2258-2266.	2.5	23
1546	Shotgun metagenomic analysis reveals new insights into bacterial community profiles in tempeh. <i>BMC Research Notes</i> , 2020, 13, 562.	1.4	6

#	ARTICLE	IF	CITATIONS
1547	Comparative genomics of <i>Sporothrix</i> species and identification of putative pathogenic-gene determinants. <i>Future Microbiology</i> , 2020, 15, 1465-1481.	2.0	4
1548	Genome-Wide Identification of <i>Populus</i> Malectin/Malectin-Like Domain-Containing Proteins and Expression Analyses Reveal Novel Candidates for Signaling and Regulation of Wood Development. <i>Frontiers in Plant Science</i> , 2020, 11, 588846.	3.6	8
1549	Hydrogen-Oxidizing Bacteria Are Abundant in Desert Soils and Strongly Stimulated by Hydration. <i>MSystems</i> , 2020, 5, .	3.8	38
1550	Does the Microbiome Affect the Outcome of Renal Transplantation?. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 558644.	3.9	13
1551	Transcriptomic Responses to Darkness and the Survival Strategy of the Kelp <i>Saccharina latissima</i> in the Early Polar Night. <i>Frontiers in Marine Science</i> , 2020, 7, .	2.5	5
1552	Saccharibacteria as Organic Carbon Sinks in Hydrocarbon-Fueled Communities. <i>Frontiers in Microbiology</i> , 2020, 11, 587782.	3.5	22
1553	Integrated metagenomic and metatranscriptomic analyses of ultraviolet disinfection effects on antibiotic resistance genes and bacterial communities during wastewater treatment. <i>Ecotoxicology</i> , 2020, 30, 1610-1619.	2.4	5
1554	A collection of bacterial isolates from the pig intestine reveals functional and taxonomic diversity. <i>Nature Communications</i> , 2020, 11, 6389.	12.8	269
1555	Fungi.guru: Comparative genomic and transcriptomic resource for the fungi kingdom. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 3788-3795.	4.1	8
1556	Dysbiosis in marine aquaculture revealed through microbiome analysis: reverse ecology for environmental sustainability. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	2.7	10
1557	A Comparative Evaluation of Tools to Predict Metabolite Profiles From Microbiome Sequencing Data. <i>Frontiers in Microbiology</i> , 2020, 11, 595910.	3.5	21
1558	Metagenomic Analysis Reveals the Mechanism for the Observed Increase in Antibacterial Activity of Penicillin against Uncultured Bacteria <i>Candidatus Liberibacter asiaticus</i> Relative to Oxytetracycline in <i>Planta</i> . <i>Antibiotics</i> , 2020, 9, 874.	3.7	4
1559	Metabolic impact of persistent organic pollutants on gut microbiota. <i>Gut Microbes</i> , 2020, 12, 1848209.	9.8	22
1560	Coding-Complete Genome Sequence of Yada Yada Virus, a Novel Alphavirus Detected in Australian Mosquitoes. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	10
1561	Short De-Etiolation Increases the Rooting of VC801 Avocado Rootstock. <i>Plants</i> , 2020, 9, 1481.	3.5	7
1562	Meta-Transcriptomic Identification of Divergent Amnoonviridae in Fish. <i>Viruses</i> , 2020, 12, 1254.	3.3	16
1563	Proficiency Testing of Metagenomics-Based Detection of Food-Borne Pathogens Using a Complex Artificial Sequencing Dataset. <i>Frontiers in Microbiology</i> , 2020, 11, 575377.	3.5	7
1564	Transcriptome Sequencing of the Striped Cucumber Beetle, <i>Acalymma vittatum</i> (F.), Reveals Numerous Sex-Specific Transcripts and Xenobiotic Detoxification Genes. <i>BioTech</i> , 2020, 9, 21.	2.6	7

#	ARTICLE	IF	CITATIONS
1565	Metagenomic Approach with the NetoVIR Enrichment Protocol Reveals Virus Diversity within Ethiopian Honey Bees (<i>Apis mellifera simensis</i>). <i>Viruses</i> , 2020, 12, 1218.	3.3	16
1566	The CtrA Regulon of <i>Rhodobacter sphaeroides</i> Favors Adaptation to a Particular Lifestyle. <i>Journal of Bacteriology</i> , 2020, 202, .	2.2	8
1567	Draft Genome Sequence of an Adomavirus Associated with Raised Muroid Skin Lesions on Smallmouth Bass (<i>Micropterus dolomieu</i>). <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	5
1568	Novel genome sequences of cell-fusing agent virus allow comparison of virus phylogeny with the genetic structure of <i>Aedes aegypti</i> populations. <i>Virus Evolution</i> , 2020, 6, veaa018.	4.9	24
1569	Draft Genome Sequence of Psychrotolerant <i>Clostridium</i> sp. Strain M14, Isolated from Spoiled Uncooked Venison. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	3
1570	A Genomic Toolkit for the Mechanistic Dissection of Intractable Human Gut Bacteria. <i>Cell Host and Microbe</i> , 2020, 27, 1001-1013.e9.	11.0	39
1571	A multi-omics concentration-response framework uncovers novel understanding of triclosan effects in the chlorophyte <i>Scenedesmus vacuolatus</i> . <i>Journal of Hazardous Materials</i> , 2020, 397, 122727.	12.4	25
1572	Phylogenomic Analyses of Members of the Widespread Marine Heterotrophic Genus <i>Pseudovibrio</i> Suggest Distinct Evolutionary Trajectories and a Novel Genus, <i>Polycladibacter</i> gen. nov. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	6
1573	Basal-Level Effects of (p)ppGpp in the Absence of Branched-Chain Amino Acids in <i>Actinobacillus pleuropneumoniae</i> . <i>Journal of Bacteriology</i> , 2020, 202, .	2.2	4
1574	Metagenome Mining Reveals Hidden Genomic Diversity of Pelagimyophages in Aquatic Environments. <i>MSystems</i> , 2020, 5, .	3.8	23
1575	Draft Genome Sequence of <i>Desulfurobacterium thermolithotrophum</i> Strain HR11, a Novel Thermophilic Autotrophic Subspecies from a Deep-Sea Hydrothermal Vent. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	1
1576	Hurricanes Accelerate Dissolved Organic Carbon Cycling in Coastal Ecosystems. <i>Frontiers in Marine Science</i> , 2020, 7, .	2.5	23
1577	Selective carbon sources influence the end products of microbial nitrate respiration. <i>ISME Journal</i> , 2020, 14, 2034-2045.	9.8	61
1578	Identification and molecular characterization of the first complete genome sequence of Human Parechovirus type 15. <i>Scientific Reports</i> , 2020, 10, 6759.	3.3	5
1579	Chromosomal-level genome assembly of the scimitar-horned oryx: Insights into diversity and demography of a species extinct in the wild. <i>Molecular Ecology Resources</i> , 2020, 20, 1668-1681.	4.8	26
1580	The Effect of Spring Water Geochemistry on Copper Proteins in Tengchong Hot Springs, China. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	4
1581	Genome diversification in globally distributed novel marine Proteobacteria is linked to environmental adaptation. <i>ISME Journal</i> , 2020, 14, 2060-2077.	9.8	106
1582	pepFunk: a tool for peptide-centric functional analysis of metaproteomic human gut microbiome studies. <i>Bioinformatics</i> , 2020, 36, 4171-4179.	4.1	7

#	ARTICLE	IF	CITATIONS
1583	Sorghum Growth Promotion by Paraburkholderia tropica and Herbaspirillum frisingense: Putative Mechanisms Revealed by Genomics and Metagenomics. Microorganisms, 2020, 8, 725.	3.6	34
1584	Under-the-Radar Dengue Virus Infections in Natural Populations of Aedes aegypti Mosquitoes. MSphere, 2020, 5, .	2.9	19
1585	Virome of a Feline Outbreak of Diarrhea and Vomiting Includes Bocaviruses and a Novel Chapparovirus. Viruses, 2020, 12, 506.	3.3	42
1586	Precise phylogenetic analysis of microbial isolates and genomes from metagenomes using PhyloPhlAn 3.0. Nature Communications, 2020, 11, 2500.	12.8	368
1587	MetaSanity: an integrated microbial genome evaluation and annotation pipeline. Bioinformatics, 2020, 36, 4341-4344.	4.1	20
1588	Metatranscriptomic Analysis of Oil-Exposed Seawater Bacterial Communities Archived by an Environmental Sample Processor (ESP). Microorganisms, 2020, 8, 744.	3.6	10
1589	Diversity, Transmission, and Cophylogeny of Ledanteviruses (Rhabdoviridae: Ledantevirus) and Nycteribiid Bat Flies Parasitizing Angolan Soft-Furred Fruit Bats in Bundibugyo District, Uganda. Microorganisms, 2020, 8, 750.	3.6	21
1590	Transcriptome analysis reveals metabolic regulation mechanism of microalga Chlorella pyrenoidosa in response to the mixed culture with yeast Yarrowia lipolytica. Journal of Applied Phycology, 2020, 32, 2841-2849.	2.8	5
1591	Progression of regeneration in demosponge Cinachyrella cf cavernosa based on wound location. Hydrobiologia, 2020, 847, 2555-2571.	2.0	1
1592	The First Draft Genome of the Plasterer Bee Colletes gigas (Hymenoptera: Colletidae: Colletes). Genome Biology and Evolution, 2020, 12, 860-866.	2.5	12
1593	Perturbations of the Gut Microbiome and Metabolome in Children with Calcium Oxalate Kidney Stone Disease. Journal of the American Society of Nephrology: JASN, 2020, 31, 1358-1369.	6.1	43
1594	Co-occurrence of antibiotic, biocide, and heavy metal resistance genes in bacteria from metal and radionuclide contaminated soils at the Savannah River Site. Microbial Biotechnology, 2020, 13, 1179-1200.	4.2	89
1595	A systematic machine learning and data type comparison yields metagenomic predictors of infant age, sex, breastfeeding, antibiotic usage, country of origin, and delivery type. PLoS Computational Biology, 2020, 16, e1007895.	3.2	21
1596	Chromosome-scale assembly of the Kandelia obovata genome. Horticulture Research, 2020, 7, 75.	6.3	38
1597	Heat-evolved microalgal symbionts increase coral bleaching tolerance. Science Advances, 2020, 6, eaba2498.	10.3	129
1598	Multi-omics reveals that the rumen microbiome and its metabolome together with the host metabolome contribute to individualized dairy cow performance. Microbiome, 2020, 8, 64.	11.1	165
1599	Genome reconstruction of the non-culturable spinach downy mildew Peronospora effusa by metagenome filtering. PLoS ONE, 2020, 15, e0225808.	2.5	14
1600	Online searching platform for the antibiotic resistome in bacterial tree of life and global habitats. FEMS Microbiology Ecology, 2020, 96, .	2.7	19

#	ARTICLE	IF	CITATIONS
1601	Testing the advantages and disadvantages of short- and long- read eukaryotic metagenomics using simulated reads. BMC Bioinformatics, 2020, 21, 220.	2.6	57
1602	Isolation and characterization of a marine bacterium <i>Vibrio diabolicus</i> strain L2-2 capable of biotransforming sulfonamides. Environmental Research, 2020, 188, 109718.	7.5	13
1603	Cultivation-independent and cultivation-dependent metagenomes reveal genetic and enzymatic potential of microbial community involved in the degradation of a complex microbial polymer. Microbiome, 2020, 8, 76.	11.1	59
1604	Depth-dependent mycoplankton glycoside hydrolase gene activity in the open ocean—evidence from the Tara Oceans eukaryote metatranscriptomes. ISME Journal, 2020, 14, 2361-2365.	9.8	20
1605	Comprehensive database and evolutionary dynamics of U12-type introns. Nucleic Acids Research, 2020, 48, 7066-7078.	14.5	35
1606	Small RNA and Transcriptome Sequencing Reveals miRNA Regulation of Floral Thermogenesis in <i>Nelumbo nucifera</i> . International Journal of Molecular Sciences, 2020, 21, 3324.	4.1	9
1607	Comparative Genomic and Proteomic Analyses of Three Widespread Phytophthora Species: <i>Phytophthora chlamydospora</i> , <i>Phytophthora gonapodyides</i> and <i>Phytophthora pseudosyringae</i> . Microorganisms, 2020, 8, 653.	3.6	36
1608	High-Throughput Sequencing Reveals a Potentially Novel <i>Sulfurovum</i> Species Dominating the Microbial Communities of the Seawater—Sediment Interface of a Deep-Sea Cold Seep in South China Sea. Microorganisms, 2020, 8, 687.	3.6	27
1609	AcrFinder: genome mining anti-CRISPR operons in prokaryotes and their viruses. Nucleic Acids Research, 2020, 48, W358-W365.	14.5	40
1610	Complete genome sequence and antimicrobial activity of <i>Bacillus velezensis</i> JT3-1, a microbial germicide isolated from yak feces. 3 Biotech, 2020, 10, 231.	2.2	16
1611	PhyloMCL: Accurate clustering of hierarchical orthogroups guided by phylogenetic relationship and inference of polyploidy events. Methods in Ecology and Evolution, 2020, 11, 943-954.	5.2	9
1612	Whole Genome Sequencing and Comparative Genomic Analyses of <i>Lysinibacillus pakistanensis</i> LZH-9, a Halotolerant Strain with Excellent COD Removal Capability. Microorganisms, 2020, 8, 716.	3.6	3
1613	Microbial sulfate reduction facilitates seasonal variation of arsenic concentration in groundwater of Jiangnan Plain, Central China. Science of the Total Environment, 2020, 735, 139327.	8.0	32
1614	Combining whole-genome shotgun sequencing and rRNA gene amplicon analyses to improve detection of microbe—microbe interaction networks in plant leaves. ISME Journal, 2020, 14, 2116-2130.	9.8	56
1615	An information and statistical analysis pipeline for microbial metagenomic sequencing data. Handbook of Statistics, 2020, 43, 67-80.	0.6	0
1616	A catalog of microbial genes from the bovine rumen unveils a specialized and diverse biomass-degrading environment. GigaScience, 2020, 9, .	6.4	35
1617	Dental Calculus as a Tool to Study the Evolution of the Mammalian Oral Microbiome. Molecular Biology and Evolution, 2020, 37, 3003-3022.	8.9	28
1618	Genomes of the dinoflagellate <i>Polarella glacialis</i> encode tandemly repeated single-exon genes with adaptive functions. BMC Biology, 2020, 18, 56.	3.8	64

#	ARTICLE	IF	CITATIONS
1619	Phylogenomic synteny network analyses reveal ancestral transpositions of auxin response factor genes in plants. <i>Plant Methods</i> , 2020, 16, 70.	4.3	8
1620	Genome mining of the citrus pathogen <i>Elsinoë fawcettii</i> ; prediction and prioritisation of candidate effectors, cell wall degrading enzymes and secondary metabolite gene clusters. <i>PLoS ONE</i> , 2020, 15, e0227396.	2.5	9
1621	Comparing Gut Microbiome in Mothers' Own Breast Milk- and Formula-Fed Moderate-Late Preterm Infants. <i>Frontiers in Microbiology</i> , 2020, 11, 891.	3.5	29
1622	Characterization of Nitrate-Dependent As(III)-Oxidizing Communities in Arsenic-Contaminated Soil and Investigation of Their Metabolic Potentials by the Combination of DNA-Stable Isotope Probing and Metagenomics. <i>Environmental Science & Technology</i> , 2020, 54, 7366-7377.	10.0	82
1623	Draft Genome of the Macadamia Husk Spot Pathogen, <i>Pseudocercospora macadamiae</i> . <i>Phytopathology</i> , 2020, 110, 1503-1506.	2.2	2
1624	<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.	3.3	20
1625	Gut microbial species and metabolic pathways associated with response to treatment with immune checkpoint inhibitors in metastatic melanoma. <i>Melanoma Research</i> , 2020, 30, 235-246.	1.2	42
1626	Adverse effects of electronic cigarettes on the disease-naïve oral microbiome. <i>Science Advances</i> , 2020, 6, eaaz0108.	10.3	43
1627	Tax4Fun2: prediction of habitat-specific functional profiles and functional redundancy based on 16S rRNA gene sequences. <i>Environmental Microbiomes</i> , 2020, 15, 11.	5.0	323
1628	Genetics of colour variation in wild versus cultured queen loach, <i>Botia dario</i> (Hamilton, 1822). <i>Genomics</i> , 2020, 112, 3256-3267.	2.9	9
1629	Determining the Genetic Characteristics of Resistance and Virulence of the "Epidermidis Cluster Group" Through Pan-Genome Analysis. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 274.	3.9	16
1630	Can We Use Functional Genetics to Predict the Fate of Nitrogen in Estuaries?. <i>Frontiers in Microbiology</i> , 2020, 11, 1261.	3.5	19
1631	Application of acidic conditions and inert-gas sparging to achieve high-efficiency nitrous oxide recovery during nitrite denitrification. <i>Water Research</i> , 2020, 182, 116001.	11.3	20
1632	Directed remodeling of the mouse gut microbiome inhibits the development of atherosclerosis. <i>Nature Biotechnology</i> , 2020, 38, 1288-1297.	17.5	70
1633	<i>Alteromonas</i> Myovirus V22 Represents a New Genus of Marine Bacteriophages Requiring a Tail Fiber Chaperone for Host Recognition. <i>MSystems</i> , 2020, 5, .	3.8	15
1634	Description of <i>Paenibacillus yunnanensis</i> sp. nov., Isolated from a Tepid Spring. <i>Current Microbiology</i> , 2020, 77, 3174-3178.	2.2	5
1635	Metabolic mechanisms of <i>Coilia nasus</i> in the natural food intake state during migration. <i>Genomics</i> , 2020, 112, 3294-3305.	2.9	9
1636	Genome-wide identification and comparative analysis of the ADH gene family in Chinese white pear (<i>Pyrus bretschneideri</i>) and other Rosaceae species. <i>Genomics</i> , 2020, 112, 3484-3496.	2.9	20

#	ARTICLE	IF	CITATIONS
1637	Amending microbiota by targeting intestinal inflammation with TNF blockade attenuates development of colorectal cancer. <i>Nature Cancer</i> , 2020, 1, 723-734.	13.2	50
1638	A Novel Microbialite-Associated Phototrophic Chloroflexi Lineage Exhibiting a Quasi-Clonal Pattern along Depth. <i>Genome Biology and Evolution</i> , 2020, 12, 1207-1216.	2.5	11
1639	Importance of <i>Defluviitalea raffenordii</i> for Hydrolytic Biomass Degradation in Co-Culture with <i>Hungateiclostridium thermocellum</i> . <i>Microorganisms</i> , 2020, 8, 915.	3.6	13
1640	<i>Pontiella desulfatans</i> gen. nov., sp. nov., and <i>Pontiella sulfatireligans</i> sp. nov., Two Marine Anaerobes of the Pontellaceae fam. nov. Producing Sulfated Glycosaminoglycan-like Exopolymers. <i>Microorganisms</i> , 2020, 8, 920.	3.6	31
1641	Identification of Conserved Gene-Regulatory Networks that Integrate Environmental Sensing and Growth in the Root Cambium. <i>Current Biology</i> , 2020, 30, 2887-2900.e7.	3.9	22
1642	Low-coverage genomic data resolve the population divergence and gene flow history of an Australian rain forest fig wasp. <i>Molecular Ecology</i> , 2020, 29, 3649-3666.	3.9	4
1643	Novel partiti-like viruses are conditional mutualistic symbionts in their normal lepidopteran host, African armyworm, but parasitic in a novel host, Fall armyworm. <i>PLoS Pathogens</i> , 2020, 16, e1008467.	4.7	34
1644	Isolation of <i>Clostridium</i> from Yunnan-Tibet hot springs and description of <i>Clostridium thermarum</i> sp. nov. with lignocellulosic ethanol production. <i>Systematic and Applied Microbiology</i> , 2020, 43, 126104.	2.8	23
1645	Impact of DNA Extraction Method on Variation in Human and Built Environment Microbial Community and Functional Profiles Assessed by Shotgun Metagenomics Sequencing. <i>Frontiers in Microbiology</i> , 2020, 11, 953.	3.5	40
1646	Prediction of Antimicrobial Resistance in Gram-Negative Bacteria From Whole-Genome Sequencing Data. <i>Frontiers in Microbiology</i> , 2020, 11, 1013.	3.5	40
1647	Transcriptome Analysis Identifies Candidate Target Genes Involved in Glyphosate-Resistance Mechanism in <i>Lolium multiflorum</i> . <i>Plants</i> , 2020, 9, 685.	3.5	13
1648	Unexpected Genetic Diversity of Two Novel Swine MRVs in Italy. <i>Viruses</i> , 2020, 12, 574.	3.3	3
1649	Complete, high-quality genomes from long-read metagenomic sequencing of two wolf lichen thalli reveals enigmatic genome architecture. <i>Genomics</i> , 2020, 112, 3150-3156.	2.9	16
1650	The gene-rich genome of the scallop <i>Pecten maximus</i> . <i>GigaScience</i> , 2020, 9, .	6.4	53
1651	Microbial Nitrogen Metabolism in Chloraminated Drinking Water Reservoirs. <i>MSphere</i> , 2020, 5, .	2.9	28
1652	Genomic insights into a plant growth-promoting <i>Pseudomonas koreensis</i> strain with cyclic lipopeptide-mediated antifungal activity. <i>MicrobiologyOpen</i> , 2020, 9, e1092.	3.0	26
1653	GTDB: an integrated resource for glycosyltransferase sequences and annotations. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	3.0	9
1654	Alterations in the Ocular Surface Microbiome in Traumatic Corneal Ulcer Patients. , 2020, 61, 35.		21

#	ARTICLE	IF	CITATIONS
1655	Comparative Genomic Analysis Reveals the Metabolism and Evolution of the Thermophilic Archaeal Genus Metallosphaera. <i>Frontiers in Microbiology</i> , 2020, 11, 1192.	3.5	8
1656	Mosquito-Borne Viral Diseases: Control and Prevention in the Genomics Era. , 2020, , .		1
1657	Metagenomic analysis of the lung microbiome in pulmonary tuberculosis - a pilot study. <i>Emerging Microbes and Infections</i> , 2020, 9, 1444-1452.	6.5	19
1658	Winter warming in Alaska accelerates lignin decomposition contributed by Proteobacteria. <i>Microbiome</i> , 2020, 8, 84.	11.1	47
1659	Genome and sequence determinants governing the expression of horizontally acquired DNA in bacteria. <i>ISME Journal</i> , 2020, 14, 2347-2357.	9.8	16
1660	Oral Capsulized Fecal Microbiota Transplantation for Eradication of Carbapenemase-producing Enterobacteriaceae Colonization With a Metagenomic Perspective. <i>Clinical Infectious Diseases</i> , 2021, 73, e166-e175.	5.8	33
1661	Metagenome Assembly and Metagenome-Assembled Genome Sequences from a Historical Oil Field Located in Wietze, Germany. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	13
1662	Evolution of Salmonella enterica serotype Typhimurium driven by anthropogenic selection and niche adaptation. <i>PLoS Genetics</i> , 2020, 16, e1008850.	3.5	48
1663	A case study of salivary microbiome in smokers and non-smokers in Hungary: analysis by shotgun metagenome sequencing. <i>Journal of Oral Microbiology</i> , 2020, 12, 1773067.	2.7	18
1664	A Modular Metagenomics Pipeline Allowing for the Inclusion of Prior Knowledge Using the Example of Anaerobic Digestion. <i>Microorganisms</i> , 2020, 8, 669.	3.6	1
1665	Comparative Genomics of the Rhodococcus Genus Shows Wide Distribution of Biodegradation Traits. <i>Microorganisms</i> , 2020, 8, 774.	3.6	25
1666	A Novel Retrovirus (Gunnisonâ€™s Prairie Dog Retrovirus) Associated With Thymic Lymphoma in Gunnisonâ€™s Prairie Dogs in Colorado, USA. <i>Viruses</i> , 2020, 12, 606.	3.3	6
1667	Genomic consequences of dietary diversification and parallel evolution due to nectarivory in leaf-nosed bats. <i>GigaScience</i> , 2020, 9, .	6.4	18
1668	Gray whale transcriptome reveals longevity adaptations associated with DNA repair and ubiquitination. <i>Aging Cell</i> , 2020, 19, e13158.	6.7	27
1669	Reprogramming of the Developmental Program of Rhus javanica During Initial Stage of Gall Induction by Schlechtendalia chinensis. <i>Frontiers in Plant Science</i> , 2020, 11, 471.	3.6	25
1670	Transcriptome Analysis of Jojoba (Simmondsia chinensis) during Seed Development and Liquid Wax Ester Biosynthesis. <i>Plants</i> , 2020, 9, 588.	3.5	15
1671	A Divergent Articulavirus in an Australian Gecko Identified Using Meta-Transcriptomics and Protein Structure Comparisons. <i>Viruses</i> , 2020, 12, 613.	3.3	19
1672	Characterization and Analysis of the Full-Length Transcriptomes of Multiple Organs in Pseudotaxus chienii (W.C.Cheng) W.C.Cheng. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4305.	4.1	4

#	ARTICLE	IF	CITATIONS
1673	Draft genomic sequence of <i>Armillaria gallica</i> 012m: insights into its symbiotic relationship with <i>Gastrodia elata</i> . <i>Brazilian Journal of Microbiology</i> , 2020, 51, 1539-1552.	2.0	21
1674	New bacterial and archaeal lineages discovered in organic rich sediments of a large tropical Bay. <i>Marine Genomics</i> , 2020, 54, 100789.	1.1	22
1675	Metagenomic analysis reveals antibiotic resistance genes in the bovine rumen. <i>Microbial Pathogenesis</i> , 2020, 149, 104350.	2.9	13
1676	A high-quality genome sequence of alkaligrass provides insights into halophyte stress tolerance. <i>Science China Life Sciences</i> , 2020, 63, 1269-1282.	4.9	19
1677	Metatranscriptomic Insights Into the Response of River Biofilm Communities to Ionic and Nano-Zinc Oxide Exposures. <i>Frontiers in Microbiology</i> , 2020, 11, 267.	3.5	8
1678	From pine to pasture: land use history has long-term impacts on soil bacterial community composition and functional potential. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	2.7	9
1679	Characterization of antibiotic resistance and host-microbiome interactions in the human upper respiratory tract during influenza infection. <i>Microbiome</i> , 2020, 8, 39.	11.1	41
1680	First transcriptome of the Neotropical pest <i>Euschistus heros</i> (Hemiptera: Pentatomidae) with dissection of its siRNA machinery. <i>Scientific Reports</i> , 2020, 10, 4856.	3.3	20
1681	Genome reconstruction reveals distinct assemblages of Gallionellaceae in surface and subsurface redox transition zones. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	2.7	26
1682	Comparative transcriptomic analysis of deep- and shallow-water barnacle species (<i>Cirripedia</i>), Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tj ETQq1 1 0.784314 rgBT /Overlock 10 2020, 21, 240.	2.8	18
1683	A Novel, Integron-Regulated, Class C β -Lactamase. <i>Antibiotics</i> , 2020, 9, 123.	3.7	11
1684	Identification and Characterization of the First Virulent Phages, Including a Novel Jumbo Virus, Infecting <i>Ochrobactrum</i> spp.. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2096.	4.1	3
1685	Evolutionary genetics of canine respiratory coronavirus and recent introduction into Swedish dogs. <i>Infection, Genetics and Evolution</i> , 2020, 82, 104290.	2.3	8
1686	Estimating relative biomasses of organisms in microbiota using α -phylopeptidomics. <i>Microbiome</i> , 2020, 8, 30.	11.1	34
1687	Impact of process temperature and organic loading rate on cellulolytic / hydrolytic biofilm microbiomes during biomethanation of ryegrass silage revealed by genome-centered metagenomics and metatranscriptomics. <i>Environmental Microbiomes</i> , 2020, 15, 7.	5.0	13
1689	Uncovering diversity and metabolic spectrum of animals in dead zone sediments. <i>Communications Biology</i> , 2020, 3, 106.	4.4	16
1690	Predictable modulation of cancer treatment outcomes by the gut microbiota. <i>Microbiome</i> , 2020, 8, 28.	11.1	102
1691	Exosomes Transmit Viral Genetic Information and Immune Signals may cause Immunosuppression and Immune Tolerance in ALV-J Infected HD11 cells. <i>International Journal of Biological Sciences</i> , 2020, 16, 904-920.	6.4	7

#	ARTICLE	IF	CITATIONS
1692	Changes in Bacterial Populations and Their Metabolism over 90 Sequential Cultures on Wheat-Based Thin Stillage. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 4717-4729.	5.2	7
1693	Performance of Metagenomic Next-Generation Sequencing for the Diagnosis of Viral Meningoencephalitis in a Resource-Limited Setting. <i>Open Forum Infectious Diseases</i> , 2020, 7, ofaa046.	0.9	26
1694	Isopod holobionts as promising models for lignocellulose degradation. <i>Biotechnology for Biofuels</i> , 2020, 13, 49.	6.2	23
1695	The Changes in the Frog Gut Microbiome and Its Putative Oxygen-Related Phenotypes Accompanying the Development of Gastrointestinal Complexity and Dietary Shift. <i>Frontiers in Microbiology</i> , 2020, 11, 162.	3.5	24
1696	First draft genome for the sand-hopper <i>Trinorchestia longiramus</i> . <i>Scientific Data</i> , 2020, 7, 85.	5.3	8
1697	Discovery of a novel integron-borne aminoglycoside resistance gene present in clinical pathogens by screening environmental bacterial communities. <i>Microbiome</i> , 2020, 8, 41.	11.1	38
1698	The association between microbial community and ileal gene expression on intestinal wall thickness alterations in chickens. <i>Poultry Science</i> , 2020, 99, 1847-1861.	3.4	13
1699	Novel phosphate-solubilizing bacteria enhance soil phosphorus cycling following ecological restoration of land degraded by mining. <i>ISME Journal</i> , 2020, 14, 1600-1613.	9.8	194
1700	Gut Microbiomes of Endangered Przewalski's Horse Populations in Short- and Long-Term Captivity: Implication for Species Reintroduction Based on the Soft-Release Strategy. <i>Frontiers in Microbiology</i> , 2020, 11, 363.	3.5	13
1701	Association of colitis with gut-microbiota dysbiosis in clathrin adapter AP-1B knockout mice. <i>PLoS ONE</i> , 2020, 15, e0228358.	2.5	17
1702	Inferring Tunicate Relationships and the Evolution of the Tunicate Hox Cluster with the Genome of <i>Corella inflata</i> . <i>Genome Biology and Evolution</i> , 2020, 12, 948-964.	2.5	12
1703	Linking regional shifts in microbial genome adaptation with surface ocean biogeochemistry. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190254.	4.0	33
1704	Rewiring of Microbiota Networks in Erosive Inflammation of the Stomach and Small Bowel. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 299.	4.1	7
1705	Genome sequence of the fungus <i>Pycnoporus sanguineus</i> , which produces cinnabaric acid and pH- and thermo- stable laccases. <i>Gene</i> , 2020, 742, 144586.	2.2	8
1706	Seasonal reproductive state determines gene expression in the hypothalamus of a latitudinal migratory songbird during the spring and autumn migration. <i>Molecular and Cellular Endocrinology</i> , 2020, 508, 110794.	3.2	10
1707	Metagenomics Unravels Differential Microbiome Composition and Metabolic Potential in Rapid Sand Filters Purifying Surface Water Versus Groundwater. <i>Environmental Science & Technology</i> , 2020, 54, 5197-5206.	10.0	51
1708	A Giant Genome for a Giant Crayfish (<i>Cherax quadricarinatus</i>) With Insights Into cox1 Pseudogenes in Decapod Genomes. <i>Frontiers in Genetics</i> , 2020, 11, 201.	2.3	23
1709	Time-Course RNAseq Reveals <i>Exserohilum turcicum</i> Effectors and Pathogenicity Determinants. <i>Frontiers in Microbiology</i> , 2020, 11, 360.	3.5	23

#	ARTICLE	IF	CITATIONS
1710	Metabolic response of prokaryotic microbes to sporadic hypoxia in a eutrophic subtropical estuary. <i>Marine Pollution Bulletin</i> , 2020, 154, 111064.	5.0	6
1711	Transcriptome Analysis of the Cytokinin Response in <i>Medicago truncatula</i> . <i>Journal of Plant Biology</i> , 2020, 63, 189-202.	2.1	2
1712	An improved de novo genome assembly of the common marmoset genome yields improved contiguity and increased mapping rates of sequence data. <i>BMC Genomics</i> , 2020, 21, 243.	2.8	9
1713	New Viral Sequences Identified in the Flavescence Dorée Phytoplasma Vector <i>Scaphoideus titanus</i> . <i>Viruses</i> , 2020, 12, 287.	3.3	14
1714	Horizontal transfer and evolution of transposable elements in vertebrates. <i>Nature Communications</i> , 2020, 11, 1362.	12.8	58
1715	Metagenomic analysis of bacterial species in tongue microbiome of current and never smokers. <i>Npj Biofilms and Microbiomes</i> , 2020, 6, 11.	6.4	32
1716	What Is in <i>Umbilicaria pustulata</i> ? A Metagenomic Approach to Reconstruct the Holo-Genome of a Lichen. <i>Genome Biology and Evolution</i> , 2020, 12, 309-324.	2.5	37
1717	Runaway GC Evolution in Gerbil Genomes. <i>Molecular Biology and Evolution</i> , 2020, 37, 2197-2210.	8.9	14
1718	Morpho-Physiological and Genomic Evaluation of <i>Juglans</i> Species Reveals Regional Maladaptation to Cold Stress. <i>Frontiers in Plant Science</i> , 2020, 11, 229.	3.6	6
1719	Metagenomic analysis reveals the microbiome and resistome in migratory birds. <i>Microbiome</i> , 2020, 8, 26.	11.1	109
1720	The Computational Diet: A Review of Computational Methods Across Diet, Microbiome, and Health. <i>Frontiers in Microbiology</i> , 2020, 11, 393.	3.5	32
1721	Molecular Mechanisms Underpinning Aggregation in <i>Acidiphilium</i> sp. C61 Isolated from Iron-Rich Pelagic Aggregates. <i>Microorganisms</i> , 2020, 8, 314.	3.6	5
1722	High resolution metagenomic characterization of complex infectomes in paediatric acute respiratory infection. <i>Scientific Reports</i> , 2020, 10, 3963.	3.3	26
1723	Comparative and population genomics approaches reveal the basis of adaptation to deserts in a small rodent. <i>Molecular Ecology</i> , 2020, 29, 1300-1314.	3.9	39
1724	A genomic perspective on the taxonomy of the subtribe Carcharodina (Lepidoptera: Hesperidae). <i>Journal of Overlooked Lepidoptera</i> , 2020, 10, 50.	0.5	10
1725	BarleyNet: A Network-Based Functional Omics Analysis Server for Cultivated Barley, <i>Hordeum vulgare</i> L.. <i>Frontiers in Plant Science</i> , 2020, 11, 98.	3.6	17
1726	Systematic and Comparative Evaluation of Software Programs for Template-Based Modeling of Protein Structures. <i>Biotechnology Journal</i> , 2020, 15, e1900343.	3.5	5
1727	An Integrated Metagenome Catalog Reveals New Insights into the Murine Gut Microbiome. <i>Cell Reports</i> , 2020, 30, 2909-2922.e6.	6.4	85

#	ARTICLE	IF	CITATIONS
1728	Marine Sediments Illuminate Chlamydiae Diversity and Evolution. <i>Current Biology</i> , 2020, 30, 1032-1048.e7.	3.9	52
1729	Denitrification performance and microbial community under salinity and MIT stresses for reverse osmosis concentrate treatment. <i>Separation and Purification Technology</i> , 2020, 242, 116799.	7.9	17
1730	The First Draft Genome Assembly of Snow Sheep (<i>Ovis nivicola</i>). <i>Genome Biology and Evolution</i> , 2020, 12, 1330-1336.	2.5	14
1731	Isolation and characterization of a novel cripavirus, the first Dicistroviridae family member infecting the cotton mealybug <i>Phenacoccus solenopsis</i> . <i>Archives of Virology</i> , 2020, 165, 1987-1994.	2.1	6
1732	Genomic and Phenotypic Characterization of a Lytic Bacteriophage CF1 Infecting the Multi-drug Resistant Bacterium <i>Citrobacter freundii</i> . <i>Biotechnology and Bioprocess Engineering</i> , 2020, 25, 384-393.	2.6	1
1733	Yaravirus: A novel 80-nm virus infecting <i>Acanthamoeba castellanii</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 16579-16586.	7.1	41
1734	Transcriptome and cell wall degrading enzyme-related gene analysis of <i>Pestalotiopsis neglecta</i> in response to sodium phenophorbide a. <i>Pesticide Biochemistry and Physiology</i> , 2020, 169, 104639.	3.6	5
1735	Interactive Gene Expression Patterns of Susceptible and Resistant <i>Lens ervoides</i> Recombinant Inbred Lines and the Necrotroph <i>Ascochyta lentis</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 1259.	3.5	1
1736	Hybrid de novo genome assembly of red gromwell (<i>Lithospermum erythrorhizon</i>) reveals evolutionary insight into shikonin biosynthesis. <i>Horticulture Research</i> , 2020, 7, 82.	6.3	31
1737	Characterization of the phenotypic and genotypic tolerance to abiotic stresses of natural populations of <i>Heterorhabditis bacteriophora</i> . <i>Scientific Reports</i> , 2020, 10, 10500.	3.3	16
1738	An efficient single-cell transcriptomics workflow for microbial eukaryotes benchmarked on <i>Giardia intestinalis</i> cells. <i>BMC Genomics</i> , 2020, 21, 448.	2.8	8
1739	Measuring Genome Sizes Using Read-Depth, k-mers, and Flow Cytometry: Methodological Comparisons in Beetles (Coleoptera). <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3047-3060.	1.8	78
1740	Distinctive Growth and Transcriptional Changes of the Diatom <i>Seminavis robusta</i> in Response to Quorum Sensing Related Compounds. <i>Frontiers in Microbiology</i> , 2020, 11, 1240.	3.5	21
1741	Adaptation of Carbon Source Utilization Patterns of <i>Geobacter metallireducens</i> During Sessile Growth. <i>Frontiers in Microbiology</i> , 2020, 11, 1271.	3.5	3
1742	Effect of a Flaxseed Lignan Intervention on Circulating Bile Acids in a Placebo-Controlled Randomized, Crossover Trial. <i>Nutrients</i> , 2020, 12, 1837.	4.1	11
1743	Secondary Metabolism in the Gill Microbiota of Shipworms (Teredinidae) as Revealed by Comparison of Metagenomes and Nearly Complete Symbiont Genomes. <i>MSystems</i> , 2020, 5, .	3.8	15
1744	<i>Deinococcus detaillensis</i> sp. nov., isolated from humus soil in Antarctica. <i>Archives of Microbiology</i> , 2020, 202, 2493-2498.	2.2	8
1745	Comparison of microsatellite distribution patterns in twenty-nine beetle genomes. <i>Gene</i> , 2020, 757, 144919.	2.2	10

#	ARTICLE	IF	CITATIONS
1746	A network-based integrated framework for predicting virus-prokaryote interactions. NAR Genomics and Bioinformatics, 2020, 2, lqaa044.	3.2	69
1747	The Rhizosphere Microbiome of Mikania micrantha Provides Insight Into Adaptation and Invasion. Frontiers in Microbiology, 2020, 11, 1462.	3.5	21
1748	Broccoli: Combining Phylogenetic and Network Analyses for Orthology Assignment. Molecular Biology and Evolution, 2020, 37, 3389-3396.	8.9	65
1749	BlobToolKit – Interactive Quality Assessment of Genome Assemblies. G3: Genes, Genomes, Genetics, 2020, 10, 1361-1374.	1.8	883
1750	Phenylalanine increases chrysanthemum flower immunity against <i>Botrytis cinerea</i> attack. Plant Journal, 2020, 104, 226-240.	5.7	30
1751	Bacteroides thetaiotaomicron-Infecting Bacteriophage Isolates Inform Sequence-Based Host Range Predictions. Cell Host and Microbe, 2020, 28, 371-379.e5.	11.0	54
1752	Shotgun metagenomics of dust microbiome from flight deck and cabin in civil aviation aircraft. Indoor Air, 2020, 30, 1199-1212.	4.3	19
1753	The genome, transcriptome, and proteome of the fish parasite Pomphorhynchus laevis (Acanthocephala). PLoS ONE, 2020, 15, e0232973.	2.5	19
1754	RNA-Seq analysis and development of SSR and KASP markers in lentil (<i>Lens culinaris</i> Medikus subsp.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	8.2	15
1755	Mulching practices alter soil microbial functional diversity and benefit to soil quality in orchards on the Loess Plateau. Journal of Environmental Management, 2020, 271, 110985.	7.8	34
1756	Metagenomic analysis reveals significant differences in microbiome and metabolic profiles in the rumen of sheep fed low N diet with increased urea supplementation. FEMS Microbiology Ecology, 2020, 96, .	2.7	10
1757	Metatranscriptomic Analysis of Virus Diversity in Urban Wild Birds with Parectic Disease. Journal of Virology, 2020, 94, .	3.4	21
1758	Advantages and Limits of Metagenomic Assembly and Binning of a Giant Virus. MSystems, 2020, 5, .	3.8	14
1759	Widespread conservation and lineage-specific diversification of genome-wide DNA methylation patterns across arthropods. PLoS Genetics, 2020, 16, e1008864.	3.5	56
1760	CCPRD: A Novel Analytical Framework for the Comprehensive Proteomic Reference Database Construction of NonModel Organisms. ACS Omega, 2020, 5, 15370-15384.	3.5	7
1761	Alterations of gut microbiota contribute to the progression of unruptured intracranial aneurysms. Nature Communications, 2020, 11, 3218.	12.8	56
1762	ZEAMAP, a Comprehensive Database Adapted to the Maize Multi-Omics Era. IScience, 2020, 23, 101241.	4.1	63
1763	Evaluation of experimental protocols for shotgun whole-genome metagenomic discovery of antibiotic resistance genes. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, PP, 1-1.	3.0	2

#	ARTICLE	IF	CITATIONS
1764	Cooperation between passive and active silicon transporters clarifies the ecophysiology and evolution of biosilicification in sponges. <i>Science Advances</i> , 2020, 6, eaba9322.	10.3	22
1765	Complete Genome Sequencing and Transcriptome Analysis of Nitrogen Metabolism of <i>Succinivibrio dextrinosolvens</i> Strain Z6 Isolated From Dairy Cow Rumen. <i>Frontiers in Microbiology</i> , 2020, 11, 1826.	3.5	22
1766	Genome-based analysis to understanding rapid resuscitation of cryopreserved anammox consortia via sequential supernatant addition. <i>Science of the Total Environment</i> , 2020, 744, 140785.	8.0	16
1767	<i>Bacillus tepidophilus</i> sp. nov., isolated from tepid spring. <i>Archives of Microbiology</i> , 2020, 202, 2367-2371.	2.2	8
1768	Dominant denitrifying bacteria are important hosts of antibiotic resistance genes in pig farm anoxic-oxic wastewater treatment processes. <i>Environment International</i> , 2020, 143, 105897.	10.0	44
1769	Effects of forced taxonomic transitions on metabolic composition and function in microbial microcosms. <i>Environmental Microbiology Reports</i> , 2020, 12, 514-524.	2.4	10
1770	A comparative study of microbial community and functions of type 2 diabetes mellitus patients with obesity and healthy people. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 7143-7153.	3.6	31
1771	The <i>Seminavis robusta</i> genome provides insights into the evolutionary adaptations of benthic diatoms. <i>Nature Communications</i> , 2020, 11, 3320.	12.8	55
1772	Effect of ammonia on anaerobic digestion of municipal solid waste: Inhibitory performance, bioaugmentation and microbiome functional reconstruction. <i>Chemical Engineering Journal</i> , 2020, 401, 126159.	12.7	76
1773	Metagenomics approach the intestinal microbiome structure and function in the anti-H1N1 of a traditional chinese medicine acid polysaccharide. <i>Microbial Pathogenesis</i> , 2020, 147, 104351.	2.9	9
1774	Phylogenomics reveals convergent evolution of red-violet coloration in land plants and the origins of the anthocyanin biosynthetic pathway. <i>Molecular Phylogenetics and Evolution</i> , 2020, 151, 106904.	2.7	35
1775	Metagenome-wide association analysis identifies microbial determinants of post-antibiotic ecological recovery in the gut. <i>Nature Ecology and Evolution</i> , 2020, 4, 1256-1267.	7.8	98
1776	Signatures of adaptation to a monocot host in the plant-parasitic cyst nematode <i>Heterodera sacchari</i> . <i>Plant Journal</i> , 2020, 103, 1263-1274.	5.7	9
1777	Comparative Analysis of Whole-Genome and Methylome Profiles of a Smooth and a Rough <i>Mycobacterium abscessus</i> Clinical Strain. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 13-22.	1.8	10
1778	sraX: A Novel Comprehensive Resistome Analysis Tool. <i>Frontiers in Microbiology</i> , 2020, 11, 52.	3.5	15
1779	Characterization and source identification of antibiotic resistance genes in the sediments of an interconnected river-lake system. <i>Environment International</i> , 2020, 137, 105538.	10.0	80
1780	Investigation on the influence of isolated environment on human psychological and physiological health. <i>Science of the Total Environment</i> , 2020, 716, 136972.	8.0	19
1781	A single unidirectional piRNA cluster similar to the <i>flamenco</i> locus is the major source of EVE-derived transcription and small RNAs in <i>Aedes aegypti</i> mosquitoes. <i>Rna</i> , 2020, 26, 581-594.	3.5	26

#	ARTICLE	IF	CITATIONS
1782	Metagenomic Characterization of Intestinal Regions in Pigs With Contrasting Feed Efficiency. <i>Frontiers in Microbiology</i> , 2020, 11, 32.	3.5	54
1783	Iron metabolic pathways in the processes of sponge plasticity. <i>PLoS ONE</i> , 2020, 15, e0228722.	2.5	11
1784	Characterization of Growth Morphology and Pathology, and Draft Genome Sequencing of <i>Botrytis fabae</i> , the Causal Organism of Chocolate Spot of Faba Bean (<i>Vicia faba</i> L.). <i>Frontiers in Microbiology</i> , 2020, 11, 217.	3.5	9
1785	Streamlining universal single-copy orthologue and ultraconserved element design: A case study in <i>Collembola</i> . <i>Molecular Ecology Resources</i> , 2020, 20, 706-717.	4.8	10
1786	Southern Chinese populations harbour non-nucleatum <i>Fusobacteria</i> possessing homologues of the colorectal cancer-associated FadA virulence factor. <i>Gut</i> , 2020, 69, 1998-2007.	12.1	42
1787	High-resolution structural insights into the heliorhodopsin family. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 4131-4141.	7.1	58
1788	Pre- and post-sequencing recommendations for functional annotation of human fecal metagenomes. <i>BMC Bioinformatics</i> , 2020, 21, 74.	2.6	13
1789	Carnelian uncovers hidden functional patterns across diverse study populations from whole metagenome sequencing reads. <i>Genome Biology</i> , 2020, 21, 47.	8.8	14
1790	Comparative genomic analysis of <i>Proteus</i> spp. isolated from tree shrews indicated unexpectedly high genetic diversity. <i>PLoS ONE</i> , 2020, 15, e0229125.	2.5	10
1791	Metagenomic Insights Into the Cycling of Dimethylsulfoniopropionate and Related Molecules in the Eastern China Marginal Seas. <i>Frontiers in Microbiology</i> , 2020, 11, 157.	3.5	22
1792	Transcriptomic characterisation of neuropeptides and their putative cognate G protein-coupled receptors during late embryo and stage-1 juvenile development of the Aotearoa-New Zealand crayfish, <i>Paraneophrops zealandicus</i> . <i>General and Comparative Endocrinology</i> , 2020, 292, 113443.	1.8	7
1793	Genomic Characterization of Newly Completed Genomes of <i>Botulinum Neurotoxin</i> -Producing Species from Argentina, Australia, and Africa. <i>Genome Biology and Evolution</i> , 2020, 12, 229-242.	2.5	8
1794	Microbiome of the deep Lake Baikal, a unique oxic bathypelagic habitat. <i>Limnology and Oceanography</i> , 2020, 65, 1471-1488.	3.1	60
1795	Hybridization and introgression drive genome evolution of Dutch elm disease pathogens. <i>Nature Ecology and Evolution</i> , 2020, 4, 626-638.	7.8	44
1796	Genome-wide annotation, comparison and functional genomics of carbohydrate-active enzymes in legumes infecting <i>Fusarium oxysporum</i> formae speciales. <i>Mycology</i> , 2020, 11, 56-70.	4.4	12
1797	PSORTm: a bacterial and archaeal protein subcellular localization prediction tool for metagenomics data. <i>Bioinformatics</i> , 2020, 36, 3043-3048.	4.1	10
1798	Ab Initio Construction and Evolutionary Analysis of Protein-Coding Gene Families with Partially Homologous Relationships: Closely Related <i>Drosophila</i> Genomes as a Case Study. <i>Genome Biology and Evolution</i> , 2020, 12, 185-202.	2.5	2
1799	Does Quorum Sensing play a role in microbial shifts along spontaneous fermentation of cocoa beans? An in silico perspective. <i>Food Research International</i> , 2020, 131, 109034.	6.2	33

#	ARTICLE	IF	CITATIONS
1800	First Report of <i>Kosakonia radicincitans</i> Bacteraemia from Europe (Austria) - Identification and Whole-Genome Sequencing of Strain DSM 107547. <i>Scientific Reports</i> , 2020, 10, 1948.	3.3	10
1801	ARGminer: a web platform for the crowdsourcing-based curation of antibiotic resistance genes. <i>Bioinformatics</i> , 2020, 36, 2966-2973.	4.1	37
1802	Genome Analysis of <i>Lactobacillus plantarum</i> Isolated From Some Indian Fermented Foods for Bacteriocin Production and Probiotic Marker Genes. <i>Frontiers in Microbiology</i> , 2020, 11, 40.	3.5	66
1803	High Genomic Variability in Equine Infectious Anemia Virus Obtained from Naturally Infected Horses in Pantanal, Brazil: An Endemic Region Case. <i>Viruses</i> , 2020, 12, 207.	3.3	7
1804	Crosstalk in the darkness: bulb vernalization activates meristem transition via circadian rhythm and photoperiodic pathway. <i>BMC Plant Biology</i> , 2020, 20, 77.	3.6	14
1805	Current Trends in Diagnostics of Viral Infections of Unknown Etiology. <i>Viruses</i> , 2020, 12, 211.	3.3	49
1806	Anaerobic reactor applied to laundry wastewater treatment: Unveiling the microbial community by gene and genome-centric approaches. <i>International Biodeterioration and Biodegradation</i> , 2020, 149, 104916.	3.9	15
1807	Extended Snake Venomics by Top-Down In-Source Decay: Investigating the Newly Discovered Anatolian Meadow Viper Subspecies, <i>Vipera anatolica senliki</i> . <i>Journal of Proteome Research</i> , 2020, 19, 1731-1749.	3.7	15
1808	Transcriptional reprogramming strategies and miRNA-mediated regulation networks of <i>Taxus media</i> induced into callus cells from tissues. <i>BMC Genomics</i> , 2020, 21, 168.	2.8	8
1809	Transcriptome-based target enrichment baits for stony corals (Cnidaria: Anthozoa: Scleractinia). <i>Molecular Ecology Resources</i> , 2020, 20, 807-818.	4.8	26
1810	Symbiotic lifestyle triggers drastic changes in the gene expression of the algal endosymbiont <i>Breviolum minutum</i> (Symbiodiniaceae). <i>Ecology and Evolution</i> , 2020, 10, 451-466.	1.9	33
1811	Transcriptome analysis of phototransduction-related genes in tentacles of the sea cucumber <i>Apostichopus japonicus</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2020, 34, 100675.	1.0	5
1812	Temporal shotgun metagenomics of an Ecuadorian coffee fermentation process highlights the predominance of lactic acid bacteria. <i>Current Research in Biotechnology</i> , 2020, 2, 1-15.	3.7	42
1813	Viromics and infectivity analysis reveal the release of infective plant viruses from wastewater into the environment. <i>Water Research</i> , 2020, 177, 115628.	11.3	49
1814	Protein design under competing conditions for the availability of amino acids. <i>Scientific Reports</i> , 2020, 10, 2684.	3.3	4
1815	Shifts in reclamation management strategies shape the role of exopolysaccharide and lipopolysaccharide-producing bacteria during soil formation. <i>Microbial Biotechnology</i> , 2020, 13, 584-598.	4.2	31
1816	In-Depth Understanding of <i>Camellia oleifera</i> Self-Incompatibility by Comparative Transcriptome, Proteome and Metabolome. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1600.	4.1	24
1817	The Genome of <i>Caenorhabditis bovis</i> . <i>Current Biology</i> , 2020, 30, 1023-1031.e4.	3.9	35

#	ARTICLE	IF	CITATIONS
1818	Interactions of thallium with marine phytoplankton. <i>Geochimica Et Cosmochimica Acta</i> , 2020, 276, 1-13.	3.9	30
1819	A clinically important, plasmid-borne antibiotic resistance gene (β -lactamase TEM-116) present in desert soils. <i>Science of the Total Environment</i> , 2020, 719, 137497.	8.0	14
1820	Combining genomics and epidemiology to track mumps virus transmission in the United States. <i>PLoS Biology</i> , 2020, 18, e3000611.	5.6	37
1821	Bacteriophages Isolated from Stunted Children Can Regulate Gut Bacterial Communities in an Age-Specific Manner. <i>Cell Host and Microbe</i> , 2020, 27, 199-212.e5.	11.0	85
1822	Clades of huge phages from across Earth's ecosystems. <i>Nature</i> , 2020, 578, 425-431.	27.8	331
1823	Comparative genomics applied to <i>Mucor</i> species with different lifestyles. <i>BMC Genomics</i> , 2020, 21, 135.	2.8	23
1824	A 19-isolate reference-quality global pangenome for the fungal wheat pathogen <i>Zymoseptoria tritici</i> . <i>BMC Biology</i> , 2020, 18, 12.	3.8	95
1825	Machine learning-aided analyses of thousands of draft genomes reveal specific features of activated sludge processes. <i>Microbiome</i> , 2020, 8, 16.	11.1	42
1826	Uncovering a hidden diversity: optimized protocols for the extraction of dsDNA bacteriophages from soil. <i>Microbiome</i> , 2020, 8, 17.	11.1	52
1827	The number of k-mer matches between two DNA sequences as a function of k and applications to estimate phylogenetic distances. <i>PLoS ONE</i> , 2020, 15, e0228070.	2.5	30
1828	Assembly of hundreds of novel bacterial genomes from the chicken caecum. <i>Genome Biology</i> , 2020, 21, 34.	8.8	112
1829	Gut Microbiota Plasticity Influences the Adaptability of Wild and Domestic Animals in Co-inhabited Areas. <i>Frontiers in Microbiology</i> , 2020, 11, 125.	3.5	23
1830	Giant virus diversity and host interactions through global metagenomics. <i>Nature</i> , 2020, 578, 432-436.	27.8	207
1831	A comparative genomic analysis between methicillin-resistant <i>Staphylococcus aureus</i> strains of hospital acquired and community infections in Yunnan province of China. <i>BMC Infectious Diseases</i> , 2020, 20, 137.	2.9	12
1832	A time-resolved dual transcriptome analysis reveals the molecular regulating network underlying the compatible/incompatible interactions between cabbage (<i>Brassica oleracea</i>) and <i>Fusarium oxysporum</i> f. sp. <i>conglutinans</i> . <i>Plant and Soil</i> , 2020, 448, 455-478.	3.7	7
1833	Characterizing the microbiomes of Antarctic sponges: a functional metagenomic approach. <i>Scientific Reports</i> , 2020, 10, 645.	3.3	50
1834	Ecogenomics of the Marine Benthic Filamentous Cyanobacterium <i>Adonis</i> . <i>Microbial Ecology</i> , 2020, 80, 249-265.	2.8	4
1835	Metagenomic insights into the profile of antibiotic resistomes in a large drinking water reservoir. <i>Environment International</i> , 2020, 136, 105449.	10.0	65

#	ARTICLE	IF	CITATIONS
1836	VAMPr: VARIant Mapping and Prediction of antibiotic resistance via explainable features and machine learning. PLoS Computational Biology, 2020, 16, e1007511.	3.2	50
1837	Identifying viruses from metagenomic data using deep learning. Quantitative Biology, 2020, 8, 64-77.	0.5	302
1838	A new lineage of segmented RNA viruses infecting animals. Virus Evolution, 2020, 6, vez061.	4.9	37
1839	Soil microbial diversity drops with land-use change in a high mountain temperate forest: a metagenomics survey. Environmental Microbiology Reports, 2020, 12, 185-194.	2.4	23
1840	Aquatic and terrestrial cyanobacteria produce methane. Science Advances, 2020, 6, eaax5343.	10.3	178
1841	Genome-resolved metagenomics analysis provides insights into the ecological role of Thaumarchaeota in the Amazon River and its plume. BMC Microbiology, 2020, 20, 13.	3.3	15
1842	Precision Medicine Informatics: Principles, Prospects, and Challenges. IEEE Access, 2020, 8, 13593-13612.	4.2	26
1843	Expression Atlas of <i>Selaginella moellendorffii</i> Provides Insights into the Evolution of Vasculature, Secondary Metabolism, and Roots. Plant Cell, 2020, 32, 853-870.	6.6	39
1844	Genomic analyses of a "living fossil": The endangered dove tree. Molecular Ecology Resources, 2020, 20, 756-769.	4.8	26
1845	Functional dynamics of bacterial species in the mouse gut microbiome revealed by metagenomic and metatranscriptomic analyses. PLoS ONE, 2020, 15, e0227886.	2.5	65
1846	A sense of place: transcriptomics identifies environmental signatures in Cabernet Sauvignon berry skins in the late stages of ripening. BMC Plant Biology, 2020, 20, 41.	3.6	20
1847	Piphillin predicts metagenomic composition and dynamics from DADA2-corrected 16S rDNA sequences. BMC Genomics, 2020, 21, 56.	2.8	54
1848	Are viruses associated with disc herniation? A clinical case series. BMC Musculoskeletal Disorders, 2020, 21, 27.	1.9	5
1849	Whole genome sequence of an edible and medicinal mushroom, <i>Herichium erinaceus</i> (Basidiomycota,) Tj ETQq1 1 0,784314 rgBT /Overlo	2.9	41
1850	Metagenomics as a Public Health Risk Assessment Tool in a Study of Natural Creek Sediments Influenced by Agricultural and Livestock Runoff: Potential and Limitations. Applied and Environmental Microbiology, 2020, 86, .	3.1	27
1851	Enrichment of novel Actinomycetales and the detection of monooxygenases during aerobic 1,4-dioxane biodegradation with uncontaminated and contaminated inocula. Applied Microbiology and Biotechnology, 2020, 104, 2255-2269.	3.6	12
1852	Soil quality shapes the composition of microbial community stress response and core cell metabolism functional genes. Applied Soil Ecology, 2020, 148, 103483.	4.3	11
1853	Effects of spaceflight on the composition and function of the human gut microbiota. Gut Microbes, 2020, 11, 807-819.	9.8	32

#	ARTICLE	IF	CITATIONS
1854	Integrating Computational Methods to Investigate the Macroecology of Microbiomes. <i>Frontiers in Genetics</i> , 2019, 10, 1344.	2.3	7
1855	Comparative genomic analysis of selenium utilization traits in different marine environments. <i>Journal of Microbiology</i> , 2020, 58, 113-122.	2.8	3
1856	Comparative genomics of <i>Lactobacillus fermentum</i> suggests a free-living lifestyle of this lactic acid bacterial species. <i>Food Microbiology</i> , 2020, 89, 103448.	4.2	34
1857	Functional profiles of phycospheric microorganisms during a marine dinoflagellate bloom. <i>Water Research</i> , 2020, 173, 115554.	11.3	26
1858	Zwiesel bat banyangvirus, a potentially zoonotic Huaiyangshan banyangvirus (Formerly known as) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	3.3	24
1859	Metagenomics methods for the study of plant-associated microbial communities: A review. <i>Journal of Microbiological Methods</i> , 2020, 170, 105860.	1.6	91
1860	The diversity of microbial community and function varied in response to different agricultural residues composting. <i>Science of the Total Environment</i> , 2020, 715, 136983.	8.0	86
1861	Microbial diversity, ecological networks and functional traits associated to materials used in drinking water distribution systems. <i>Water Research</i> , 2020, 173, 115586.	11.3	45
1862	Diversity and Host Interactions among Virulent and Temperate Baltic Sea <i>Flavobacterium</i> Phages. <i>Viruses</i> , 2020, 12, 158.	3.3	11
1863	Honey-bee-associated prokaryotic viral communities reveal wide viral diversity and a profound metabolic coding potential. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 10511-10519.	7.1	36
1864	To Petabytes and beyond: recent advances in probabilistic and signal processing algorithms and their application to metagenomics. <i>Nucleic Acids Research</i> , 2020, 48, 5217-5234.	14.5	16
1865	Transcriptome reconstruction and functional analysis of eukaryotic marine plankton communities via high-throughput metagenomics and metatranscriptomics. <i>Genome Research</i> , 2020, 30, 647-659.	5.5	50
1866	Metagenomic analysis of microbial community and function reveals the response of soil respiration to the conversion of cropland to plantations in the Loess Plateau of China. <i>Global Ecology and Conservation</i> , 2020, 23, e01067.	2.1	9
1867	Influenza infection elicits an expansion of gut population of endogenous <i>Bifidobacterium animalis</i> which protects mice against infection. <i>Genome Biology</i> , 2020, 21, 99.	8.8	73
1868	The influence of upflow velocity and hydraulic retention time changes on taxonomic and functional characterization in Fluidized Bed Reactor treating commercial laundry wastewater in co-digestion with domestic sewage. <i>Biodegradation</i> , 2020, 31, 73-89.	3.0	12
1869	A self-sustaining synergetic microalgal-bacterial granular sludge process towards energy-efficient and environmentally sustainable municipal wastewater treatment. <i>Water Research</i> , 2020, 179, 115884.	11.3	160
1870	CCMetagen: comprehensive and accurate identification of eukaryotes and prokaryotes in metagenomic data. <i>Genome Biology</i> , 2020, 21, 103.	8.8	91
1871	Molecular Response to High Hydrostatic Pressure: Time-Series Transcriptomic Analysis of Shallow-Water Sea Cucumber <i>Apostichopus japonicus</i> . <i>Frontiers in Genetics</i> , 2020, 11, 355.	2.3	2

#	ARTICLE	IF	CITATIONS
1872	Rocket Science: The Effect of Spaceflight on Germination Physiology, Ageing, and Transcriptome of <i>Eruca sativa</i> Seeds. <i>Life</i> , 2020, 10, 49.	2.4	19
1873	The First Genome Survey of the Antarctic Krill (<i>Euphausia superba</i>) Provides a Valuable Genetic Resource for Polar Biomedical Research. <i>Marine Drugs</i> , 2020, 18, 185.	4.6	9
1874	Multiple Metabolic Innovations and Losses Are Associated with Major Transitions in Land Plant Evolution. <i>Current Biology</i> , 2020, 30, 1783-1800.e11.	3.9	42
1875	NGS-based characterization of microbial diversity and functional profiling of solid tannery waste metagenomes. <i>Genomics</i> , 2020, 112, 2903-2913.	2.9	31
1876	Genome- and Community-Level Interaction Insights into Carbon Utilization and Element Cycling Functions of <i>Hydrothermarchaeota</i> in Hydrothermal Sediment. <i>MSystems</i> , 2020, 5, .	3.8	75
1877	A Continuum of Evolving De Novo Genes Drives Protein-Coding Novelty in <i>Drosophila</i> . <i>Journal of Molecular Evolution</i> , 2020, 88, 382-398.	1.8	60
1878	Plasmodesmata play a critical role in promoting the germination of floral buds in <i>Ilex verticillata</i> . <i>Plant Growth Regulation</i> , 2020, 91, 349-357.	3.4	3
1879	Bioactive compounds induced in <i>Physalis angulata</i> L. by methyl-jasmonate: an investigation of compound accumulation patterns and biosynthesis-related candidate genes. <i>Plant Molecular Biology</i> , 2020, 103, 341-354.	3.9	15
1880	Pan-genomics of virus and its applications. , 2020, , 237-250.		0
1881	Transcriptome analyses suggest a molecular mechanism for the SIPC response of <i>Amphibalanus amphitrite</i> . <i>Biochemical and Biophysical Research Communications</i> , 2020, 525, 823-829.	2.1	2
1882	Parallel Evolution in the Integration of a Co-obligate Aphid Symbiosis. <i>Current Biology</i> , 2020, 30, 1949-1957.e6.	3.9	54
1883	Distribution survey, phytochemical and transcriptome analysis to identify candidate genes involved in biosynthesis of functional components in <i>Zanthoxylum nitidum</i> . <i>Industrial Crops and Products</i> , 2020, 150, 112345.	5.2	8
1884	Tracking resistomes, virulence genes, and bacterial pathogens in long-term manure-amended greenhouse soils. <i>Journal of Hazardous Materials</i> , 2020, 396, 122618.	12.4	55
1885	Overexpression of LITPS2 from a cultivar of lily (<i>Lilium</i> "Siberia"™) enhances the monoterpenoids content in tobacco flowers. <i>Plant Physiology and Biochemistry</i> , 2020, 151, 391-399.	5.8	24
1886	Microbiome structure and function in rhizosphere of Jerusalem artichoke grown in saline land. <i>Science of the Total Environment</i> , 2020, 724, 138259.	8.0	44
1887	Bacteriophage-mediated extracellular DNA release is important for the structural stability of aerobic granular sludge. <i>Science of the Total Environment</i> , 2020, 726, 138392.	8.0	5
1888	Phylogenomics of <i>Rhodocyclales</i> and its distribution in wastewater treatment systems. <i>Scientific Reports</i> , 2020, 10, 3883.	3.3	22
1889	Application of Viral Metagenomics for Study of Emerging and Reemerging Tick-Borne Viruses. <i>Vector-Borne and Zoonotic Diseases</i> , 2020, 20, 557-565.	1.5	8

#	ARTICLE	IF	CITATIONS
1890	Portable nanopore analytics: are we there yet?. <i>Bioinformatics</i> , 2020, 36, 4399-4405.	4.1	22
1891	Distinct Life Histories Impact Dikaryotic Genome Evolution in the Rust Fungus <i>Puccinia striiformis</i> Causing Stripe Rust in Wheat. <i>Genome Biology and Evolution</i> , 2020, 12, 597-617.	2.5	34
1892	Draft Genome Sequences of Novel <i>Campylobacter</i> Species Isolated from Nonhuman Primates. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	0
1893	Metagenomic Sequences of Three Drinking Water and Two Shower Hose Biofilm Samples Treated with or without Copper-Silver Ionization. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	1
1894	Genomic Sequence of a New <i>Alphavirus</i> Detected in Comber (<i>Serranus cabrilla</i>). <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	0
1895	Dairy Products and Dairy-Processing Environments as a Reservoir of Antibiotic Resistance and Quorum-Quenching Determinants as Revealed through Functional Metagenomics. <i>MSystems</i> , 2020, 5, .	3.8	18
1896	Insights into the Synthesis, Secretion and Curing of Barnacle Cyprid Adhesive via Transcriptomic and Proteomic Analyses of the Cement Gland. <i>Marine Drugs</i> , 2020, 18, 186.	4.6	10
1897	The Treasure Vault Can be Opened: Large-Scale Genome Skimming Works Well Using Herbarium and Silica Gel Dried Material. <i>Plants</i> , 2020, 9, 432.	3.5	59
1898	No More Tears: Mining Sequencing Data for Novel Bt Cry Toxins with CryProcessor. <i>Toxins</i> , 2020, 12, 204.	3.4	19
1899	Fermentation Ability of Gut Microbiota of Wild Japanese Macaques in the Highland and Lowland Yakushima: In Vitro Fermentation Assay and Genetic Analyses. <i>Microbial Ecology</i> , 2020, 80, 459-474.	2.8	10
1900	Heat stress response in the closest algal relatives of land plants reveals conserved stress signaling circuits. <i>Plant Journal</i> , 2020, 103, 1025-1048.	5.7	65
1901	Chinese Liquor Fermentation: Identification of Key Flavor-Producing <i>Lactobacillus</i> spp. by Quantitative Profiling with Indigenous Internal Standards. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	41
1902	Reference Human Rotavirus A Genome Sequence from a Previously Vaccinated Child with Diarrhea in Nigeria. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	0
1903	Altered gut microbial profile is associated with abnormal metabolism activity of Autism Spectrum Disorder. <i>Gut Microbes</i> , 2020, 11, 1246-1267.	9.8	166
1904	Site-Specific Conditions Change the Response of Bacterial Producers of Soil Structure-Stabilizing Agents Such as Exopolysaccharides and Lipopolysaccharides to Tillage Intensity. <i>Frontiers in Microbiology</i> , 2020, 11, 568.	3.5	18
1905	Metagenomic Next-Generation Sequencing in Clinical Microbiology. <i>Clinical Microbiology Newsletter</i> , 2020, 42, 53-59.	0.7	8
1906	Tolerance to arsenic contaminant among multidrug-resistant and copper-tolerant <i>Salmonella</i> successful clones is associated with diverse <i>ars</i> operons and genetic contexts. <i>Environmental Microbiology</i> , 2020, 22, 2829-2842.	3.8	17
1907	Being red, blue and green: the genetic basis of coloration differences in the strawberry poison frog (<i>Oophaga pumilio</i>). <i>BMC Genomics</i> , 2020, 21, 301.	2.8	20

#	ARTICLE	IF	CITATIONS
1908	The effect of antibiotic cocktails on host immune status is dynamic and does not always correspond to changes in gut microbiota. Applied Microbiology and Biotechnology, 2020, 104, 4995-5009.	3.6	17
1909	Abundance and diversity of microbial arsenic biotransformation genes in the sludge of full-scale anaerobic digesters from a municipal wastewater treatment plant. Environment International, 2020, 138, 105535.	10.0	33
1910	Deep DNA metagenomic sequencing reveals oral microbiome divergence between monozygotic twins discordant for multiple sclerosis severity. Journal of Neuroimmunology, 2020, 343, 577237.	2.3	4
1911	Host-microbiota interaction helps to explain the bottom-up effects of climate change on a small rodent species. ISME Journal, 2020, 14, 1795-1808.	9.8	29
1912	Insights into response to food intake in anadromous <i>Coilia nasus</i> through stomach transcriptome analysis. Aquaculture Research, 2020, 51, 2799-2812.	1.8	7
1913	Linking extracellular enzymes to phylogeny indicates a predominantly particle-associated lifestyle of deep-sea prokaryotes. Science Advances, 2020, 6, eaaz4354.	10.3	63
1914	Annotated Genome Sequence of <i>Aspergillus tanneri</i> NIH1004. Microbiology Resource Announcements, 2020, 9, .	0.6	2
1915	Complementary Metagenomic Approaches Improve Reconstruction of Microbial Diversity in a Forest Soil. MSystems, 2020, 5, .	3.8	45
1916	Transcriptomic analysis of sea cucumber (<i>Holothuria leucospilota</i>) coelomocytes revealed the echinoderm cytokine response during immune challenge. BMC Genomics, 2020, 21, 306.	2.8	10
1917	Impact of intestinal parasites on microbiota and cobalamin gene sequences: a pilot study. Parasites and Vectors, 2020, 13, 200.	2.5	33
1918	Immune Suppressive Extracellular Vesicle Proteins of <i>Leptopilina heterotoma</i> Are Encoded in the Wasp Genome. G3: Genes, Genomes, Genetics, 2020, 10, 1-12.	1.8	12
1919	<i>De Novo</i> Genome Assembly of <i>Populus simonii</i> Further Supports That <i>Populus simonii</i> and <i>Populus trichocarpa</i> Belong to Different Sections. G3: Genes, Genomes, Genetics, 2020, 10, 455-466.	1.8	21
1920	Comprehensive metagenomic analysis of blastic plasmacytoid dendritic cell neoplasm. Blood Advances, 2020, 4, 1006-1011.	5.2	10
1921	Small and mighty: adaptation of superphylum Patescibacteria to groundwater environment drives their genome simplicity. Microbiome, 2020, 8, 51.	11.1	205
1922	Structure and function of the Arctic and Antarctic marine microbiota as revealed by metagenomics. Microbiome, 2020, 8, 47.	11.1	61
1923	Postnatal Gut Immunity and Microbiota Development Is Minimally Affected by Prenatal Inflammation in Preterm Pigs. Frontiers in Immunology, 2020, 11, 420.	4.8	11
1924	De novo Sequencing and Analysis of <i>Salvia hispanica</i> Tissue-Specific Transcriptome and Identification of Genes Involved in Terpenoid Biosynthesis. Plants, 2020, 9, 405.	3.5	11
1925	Molecular Drivers of Lymphocyte Organization in Vertebrate Mucosal Surfaces: Revisiting the TNF Superfamily Hypothesis. Journal of Immunology, 2020, 204, 2697-2711.	0.8	11

#	ARTICLE	IF	CITATIONS
1926	Sustained RNA virome diversity in Antarctic penguins and their ticks. ISME Journal, 2020, 14, 1768-1782.	9.8	56
1927	Microbial Diversity and Metabolic Potential in the Stratified Sansha Yongle Blue Hole in the South China Sea. Scientific Reports, 2020, 10, 5949.	3.3	27
1928	Diversity and potential biogeochemical impacts of viruses in bulk and rhizosphere soils. Environmental Microbiology, 2021, 23, 588-599.	3.8	62
1929	Taxonomic and functional analysis of soil microbial communities in a mining site across a metal(loid) contamination gradient. European Journal of Soil Science, 2021, 72, 1190-1205.	3.9	13
1930	High throughput BLAST algorithm using spark and cassandra. Journal of Supercomputing, 2021, 77, 1879-1896.	3.6	4
1931	Next Generation Sequencing Methods: Pushing the Boundaries. , 2021, , 19-46.		0
1932	Extraordinary diversity of viruses in deep-sea sediments as revealed by metagenomics without prior virion separation. Environmental Microbiology, 2021, 23, 728-743.	3.8	27
1933	Post-glacial establishment of locally adapted fish populations over a steep salinity gradient. Journal of Evolutionary Biology, 2021, 34, 138-156.	1.7	28
1934	Toward a high-quality pan-genome landscape of <i>Bacillus subtilis</i> by removal of confounding strains. Briefings in Bioinformatics, 2021, 22, 1951-1971.	6.5	46
1935	Advanced nitrogen removal in a fixed-bed anaerobic ammonia oxidation reactor following an anoxic/oxic reactor: Nitrogen removal contributions and mechanisms. Bioresource Technology, 2021, 320, 124297.	9.6	8
1936	ALeS: adaptive-length spaced-seed design. Bioinformatics, 2021, 37, 1206-1210.	4.1	2
1937	Genomic Architecture of Rapid Parallel Adaptation to Fresh Water in a Wild Fish. Molecular Biology and Evolution, 2021, 38, 1317-1329.	8.9	17
1938	Sequence analysis of 43-year old samples of <i>Plantago lanceolata</i> show that <i>Plantain virus X</i> is synonymous with <i>Actinidia virus X</i> and is widely distributed. Plant Pathology, 2021, 70, 249-258.	2.4	24
1939	Side effects of free nitrous acid on the sewer resistome and mobilome. Chemical Engineering Journal, 2021, 405, 126657.	12.7	3
1940	Exploring transcriptional switches from pairwise, temporal and population RNA-Seq data using deepTS. Briefings in Bioinformatics, 2021, 22, .	6.5	5
1941	High-yield strain of fusidic acid obtained by atmospheric and room temperature plasma mutagenesis and the transcriptional changes involved in improving its production in fungus <i>Fusidium coccineum</i> . Journal of Applied Microbiology, 2021, 130, 405-415.	3.1	10
1942	Complete Genome Sequencing Provides Novel Insight Into the Virulence Repertoires and Phylogenetic Position of Dry Beans Pathogen <i>Curtobacterium flaccumfaciens</i> pv. <i>flaccumfaciens</i> . Phytopathology, 2021, 111, 268-280.	2.2	26
1943	A unified catalog of 204,938 reference genomes from the human gut microbiome. Nature Biotechnology, 2021, 39, 105-114.	17.5	628

#	ARTICLE	IF	CITATIONS
1944	Community Organization and Metagenomics of Bacterial Assemblages Across Local Scale pH Gradients in Northern Forest Soils. <i>Microbial Ecology</i> , 2021, 81, 758-769.	2.8	10
1945	Chromosome-Scale Genome Assemblies of Aphids Reveal Extensively Rearranged Autosomes and Long-Term Conservation of the X Chromosome. <i>Molecular Biology and Evolution</i> , 2021, 38, 856-875.	8.9	54
1946	High-quality chromosome-level genomes of two tilapia species reveal their evolution of repeat sequences and sex chromosomes. <i>Molecular Ecology Resources</i> , 2021, 21, 543-560.	4.8	40
1947	Analysis of heavy metal-related indices in the Eboling permafrost on the Tibetan Plateau. <i>Catena</i> , 2021, 196, 104907.	5.0	8
1948	Genomic Features of Parthenogenetic Animals. <i>Journal of Heredity</i> , 2021, 112, 19-33.	2.4	55
1949	Benchmarking orthology methods using phylogenetic patterns defined at the base of Eukaryotes. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	24
1950	A chromosome-level genome assembly of the woolly apple aphid, <i>Eriosoma lanigerum</i> Hausmann (Hemiptera: Aphididae). <i>Molecular Ecology Resources</i> , 2021, 21, 316-326.	4.8	28
1951	Acidobacteria are active and abundant members of diverse atmospheric H ₂ -oxidizing communities detected in temperate soils. <i>ISME Journal</i> , 2021, 15, 363-376.	9.8	23
1952	A chromosome-scale assembly of allotetraploid <i>Brassica juncea</i> (AABB) elucidates comparative architecture of the A and B genomes. <i>Plant Biotechnology Journal</i> , 2021, 19, 602-614.	8.3	62
1953	Ecogenomics and metabolic potential of the South Atlantic Ocean microbiome. <i>Science of the Total Environment</i> , 2021, 765, 142758.	8.0	16
1954	Draft genomes of <i>Perkinsus olsenii</i> and <i>Perkinsus chesapeaki</i> reveal polyploidy and regional differences in heterozygosity. <i>Genomics</i> , 2021, 113, 677-688.	2.9	11
1955	Interpreting lacustrine bulk sediment $\delta^{15}\text{N}$ values using metagenomics in a tropical hypersaline lake system. <i>Journal of Paleolimnology</i> , 2021, 65, 151-168.	1.6	4
1956	Functional metagenomic landscape of polluted river reveals potential genes involved in degradation of xenobiotic pollutants. <i>Environmental Research</i> , 2021, 192, 110332.	7.5	24
1957	Polystyrene nanoplastic induces oxidative stress, immune defense, and glycometabolism change in <i>Daphnia pulex</i> : Application of transcriptome profiling in risk assessment of nanoplastics. <i>Journal of Hazardous Materials</i> , 2021, 402, 123778.	12.4	99
1958	Antagonistic action of <i>Streptomyces pratensis</i> S10 on <i>Fusarium graminearum</i> and its complete genome sequence. <i>Environmental Microbiology</i> , 2021, 23, 1925-1940.	3.8	18
1959	Application of the immobilized enzyme on magnetic graphene oxide nano-carrier as a versatile bi-functional tool for efficient removal of dye from water. <i>Bioresource Technology</i> , 2021, 319, 124228.	9.6	73
1960	Metagenomic exploration of antibiotic resistome in treated wastewater effluents and their receiving water. <i>Science of the Total Environment</i> , 2021, 765, 142755.	8.0	33
1961	New insight into microbial degradation of mycotoxins during anaerobic digestion. <i>Waste Management</i> , 2021, 119, 215-225.	7.4	12

#	ARTICLE	IF	CITATIONS
1962	Precision targeting of bacterial pathogen via bi-functional nanozyme activated by biofilm microenvironment. <i>Biomaterials</i> , 2021, 268, 120581.	11.4	54
1963	The communities and functional profiles of viroplankton along a salinity gradient in a subtropical estuary. <i>Science of the Total Environment</i> , 2021, 759, 143499.	8.0	16
1964	Marine <i>Dadabacteria</i> exhibit genome streamlining and phototrophy-driven niche partitioning. <i>ISME Journal</i> , 2021, 15, 1248-1256.	9.8	39
1965	Expression profiles of neotropical termites reveal microbiota-associated, caste-biased genes and biotechnological targets. <i>Insect Molecular Biology</i> , 2021, 30, 152-164.	2.0	1
1966	Assessing the Diversity of Benthic Sulfate-Reducing Microorganisms in Northwestern Gulf of Mexico by Illumina Sequencing of <i>dsrB</i> Gene. <i>Microbial Ecology</i> , 2021, 81, 908-921.	2.8	6
1967	Behavioral and molecular response of the insect parasitic nematode <i>Steinernema carpocapsae</i> to cues emitted by a host, the red palm weevil, <i>Rhynchophorus ferrugineus</i> . <i>Molecular and Biochemical Parasitology</i> , 2021, 241, 111345.	1.1	4
1968	Metagenomic assessment of the global diversity and distribution of bacteria and fungi. <i>Environmental Microbiology</i> , 2021, 23, 316-326.	3.8	42
1969	Profiling prokaryotic community in pit mud of Chinese strong-aroma type liquor by using oligotrophic culturing. <i>International Journal of Food Microbiology</i> , 2021, 337, 108951.	4.7	13
1970	Geographic pattern of antibiotic resistance genes in the metagenomes of the giant panda. <i>Microbial Biotechnology</i> , 2021, 14, 186-197.	4.2	28
1971	The composition of antibiotic resistance genes is not affected by grazing but is determined by microorganisms in grassland soils. <i>Science of the Total Environment</i> , 2021, 761, 143205.	8.0	19
1972	A metagenomic assessment of microbial communities in anaerobic bioreactors and sediments: Taxonomic and functional relationships. <i>Anaerobe</i> , 2021, 68, 102296.	2.1	4
1973	State-of-the-art genome inference in the human MHC. <i>International Journal of Biochemistry and Cell Biology</i> , 2021, 131, 105882.	2.8	22
1974	Virome characterization of <i>Cryptosporidium parvum</i> isolates from Azerbaijan unveiled a new myovirus and a putative new RNA virus unrelated to described viral sequences. <i>Virology</i> , 2021, 553, 51-61.	2.4	24
1975	Dynamics of microbial stress responses driven by abiotic changes along a temporal gradient in Deception Island, Maritime Antarctica. <i>Science of the Total Environment</i> , 2021, 758, 143671.	8.0	9
1976	Probing periodontal microbial dark matter using metataxonomics and metagenomics. <i>Periodontology</i> 2000, 2021, 85, 12-27.	13.4	16
1977	GreenPhylDB v5: a comparative pangenomic database for plant genomes. <i>Nucleic Acids Research</i> , 2021, 49, D1464-D1471.	14.5	22
1978	Physiological and Proteomic Signatures Reveal Mechanisms of Superior Drought Resilience in Pearl Millet Compared to Wheat. <i>Frontiers in Plant Science</i> , 2020, 11, 600278.	3.6	44
1979	The deletion of <i>Schizosaccharomyces pombe</i> decreased the production of flavor-related metabolites during traditional Baijiu fermentation. <i>Food Research International</i> , 2021, 140, 109872.	6.2	10

#	ARTICLE	IF	CITATIONS
1980	Plant resistome profiling in evolutionary old bog vegetation provides new clues to understand emergence of multi-resistance. <i>ISME Journal</i> , 2021, 15, 921-937.	9.8	33
1981	Elevated CO ₂ and nitrate levels increase wheat root-associated bacterial abundance and impact rhizosphere microbial community composition and function. <i>ISME Journal</i> , 2021, 15, 1073-1084.	9.8	30
1982	Identification of Natural CRISPR Systems and Targets in the Human Microbiome. <i>Cell Host and Microbe</i> , 2021, 29, 94-106.e4.	11.0	20
1983	Anaerobic bacterial degradation of protein and lipid macromolecules in subarctic marine sediment. <i>ISME Journal</i> , 2021, 15, 833-847.	9.8	38
1984	Microbial Key Players Involved in P Turnover Differ in Artificial Soil Mixtures Depending on Clay Mineral Composition. <i>Microbial Ecology</i> , 2021, 81, 897-907.	2.8	14
1985	Responses of the sugarcane rhizosphere microbiota to different levels of water stress. <i>Applied Soil Ecology</i> , 2021, 159, 103817.	4.3	12
1986	Automated Prediction and Annotation of Small Open Reading Frames in Microbial Genomes. <i>Cell Host and Microbe</i> , 2021, 29, 121-131.e4.	11.0	22
1987	Comparative genomics of <i>Clostridium</i> species associated with vacuum-packed meat spoilage. <i>Food Microbiology</i> , 2021, 95, 103687.	4.2	25
1988	Cyanobacterial blooms in wastewater treatment facilities: Significance and emerging monitoring strategies. <i>Journal of Microbiological Methods</i> , 2021, 180, 106123.	1.6	11
1989	Responses of functional miRNA-mRNA regulatory modules to a high-fat diet in the liver of hybrid yellow catfish (<i>Pelteobagrus fulvidraco</i> × <i>P. vachelli</i>). <i>Genomics</i> , 2021, 113, 1207-1220.	2.9	7
1990	The Developmental and Genetic Architecture of the Sexually Selected Male Ornament of Swordtails. <i>Current Biology</i> , 2021, 31, 911-922.e4.	3.9	24
1991	Metagenomic insights into Chinese northeast suancai: Predominance and diversity of genes associated with nitrogen metabolism in traditional household suancai fermentation. <i>Food Research International</i> , 2021, 139, 109924.	6.2	21
1992	Heavy metal could drive co-selection of antibiotic resistance in terrestrial subsurface soils. <i>Journal of Hazardous Materials</i> , 2021, 411, 124848.	12.4	81
1993	Microbial ecology of the newly discovered serpentinite-hosted Old City hydrothermal field (southwest Indian ridge). <i>ISME Journal</i> , 2021, 15, 818-832.	9.8	29
1994	Transcriptional landscape of rice roots at the single-cell resolution. <i>Molecular Plant</i> , 2021, 14, 384-394.	8.3	131
1995	Linked by Ancestral Bonds: Multiple Whole-Genome Duplications and Reticulate Evolution in a Brassicaceae Tribe. <i>Molecular Biology and Evolution</i> , 2021, 38, 1695-1714.	8.9	21
1996	Genomic Insights of “ <i>Candidatus Nitrosocaldaceae</i> ”-Based on Nine New Metagenome-Assembled Genomes, Including “ <i>Candidatus Nitrosothermus</i> ”-Gen Nov. and Two New Species of “ <i>Candidatus Nitrosocaldus</i> ”. <i>Frontiers in Microbiology</i> , 2020, 11, 608832.	3.5	13
1997	CheckV assesses the quality and completeness of metagenome-assembled viral genomes. <i>Nature Biotechnology</i> , 2021, 39, 578-585.	17.5	569

#	ARTICLE	IF	CITATIONS
1998	Isolation, identification and artificial inoculation of <i>Ustilago esculenta</i> on <i>Zizania latifolia</i> . Horticultural Plant Journal, 2021, 7, 347-358.	5.0	11
1999	<i>Thermogemmata fonticola</i> gen. nov., sp. nov., the first thermophilic planctomycete of the order Gemmatales from a Kamchatka hot spring. Systematic and Applied Microbiology, 2021, 44, 126157.	2.8	22
2000	Reducing the cell lysis to enhance yield of acid-stable alpha amylase by deletion of multiple peptidoglycan hydrolase-related genes in <i>Bacillus amyloliquefaciens</i> . International Journal of Biological Macromolecules, 2021, 167, 777-786.	7.5	12
2001	High-accuracy long-read amplicon sequences using unique molecular identifiers with Nanopore or PacBio sequencing. Nature Methods, 2021, 18, 165-169.	19.0	198
2002	High-throughput Metagenomics for Identification of Pathogens in the Clinical Settings. Small Methods, 2021, 5, 2000792.	8.6	96
2003	Mini-metagenome analysis of psychrophilic electroactive biofilms based on single cell sorting. Science of the Total Environment, 2021, 762, 144328.	8.0	9
2004	SCycDB: A curated functional gene database for metagenomic profiling of sulphur cycling pathways. Molecular Ecology Resources, 2021, 21, 924-940.	4.8	52
2005	Effects of nitrogen deficiency on the transcriptome of the oleaginous alga <i>Parachlorella kessleri</i> TY. European Journal of Phycology, 2021, 56, 203-215.	2.0	1
2006	TOA: A software package for automated functional annotation in non-model plant species. Molecular Ecology Resources, 2021, 21, 621-636.	4.8	10
2007	Identification of biogenic amine-producing microbes during fermentation of ganjang, a Korean traditional soy sauce, through metagenomic and metatranscriptomic analyses. Food Control, 2021, 121, 107681.	5.5	19
2008	Desert truffle genomes reveal their reproductive modes and new insights into plant-fungal interaction and ectendomycorrhizal lifestyle. New Phytologist, 2021, 229, 2917-2932.	7.3	19
2009	The Function and Evolution of Motile DNA Replication Systems in Ciliates. Current Biology, 2021, 31, 66-76.e6.	3.9	76
2010	Virome of Bat Guano from Nine Northern California Roosts. Journal of Virology, 2021, 95, .	3.4	24
2011	Genome analysis reveals probiotic propensities of <i>Paenibacillus polymyxa</i> HK4. Genomics, 2021, 113, 861-873.	2.9	27
2012	Investigating the effector suite profile of Australian <i>Fusarium oxysporum</i> isolates from agricultural and natural ecosystems. Plant Pathology, 2021, 70, 387-396.	2.4	3
2013	A new insight on the effects of iron oxides and dissimilated metal-reducing bacteria on CH ₄ emissions in constructed wetland matrix systems. Bioresource Technology, 2021, 320, 124296.	9.6	20
2014	Timing the origin of eukaryotic cellular complexity with ancient duplications. Nature Ecology and Evolution, 2021, 5, 92-100.	7.8	61
2015	<i>Bacillus alkalicellulosilyticus</i> sp. nov., isolated from extremely alkaline bauxite residue (red mud) site. Archives of Microbiology, 2021, 203, 719-723.	2.2	12

#	ARTICLE	IF	CITATIONS
2016	Phylogenomic inference of the interrelationships of Lake Baikal sponges. <i>Systematics and Biodiversity</i> , 2021, 19, 209-217.	1.2	4
2017	Performance and microbial communities of a novel integrated industrial-scale pulp and paper wastewater treatment plant. <i>Journal of Cleaner Production</i> , 2021, 278, 123896.	9.3	40
2018	The dual interplay of RAV5 in activating nitrate reductases and repressing catalase activity to improve disease resistance in cassava. <i>Plant Biotechnology Journal</i> , 2021, 19, 785-800.	8.3	25
2019	Linking microbial <i>Sphagnum</i> degradation and acetate mineralization in acidic peat bogs: from global insights to a genome-centric case study. <i>ISME Journal</i> , 2021, 15, 293-303.	9.8	14
2020	Wolbachia affects reproduction in the spider mite <i>Tetranychus truncatus</i> (Acari: Tetranychidae) by regulating chorion protein S38 like and Rop. <i>Insect Molecular Biology</i> , 2021, 30, 18-29.	2.0	5
2021	Digging metagenomic data of pangolins revealed SARS-CoV-2 related viruses and other significant viruses. <i>Journal of Medical Virology</i> , 2021, 93, 1786-1791.	5.0	15
2022	Biofilm matrix disrupts nematode motility and predatory behavior. <i>ISME Journal</i> , 2021, 15, 260-269.	9.8	28
2023	Characterization of putative circular plasmids in sponge-associated bacterial communities using a selective multiply-primed rolling circle amplification. <i>Molecular Ecology Resources</i> , 2021, 21, 110-121.	4.8	6
2024	Comparative transcriptomics of ice-crawlers demonstrates cold specialization constrains niche evolution in a relict lineage. <i>Evolutionary Applications</i> , 2021, 14, 360-382.	3.1	5
2025	Environmental stability impacts the differential sensitivity of marine microbiomes to increases in temperature and acidity. <i>ISME Journal</i> , 2021, 15, 19-28.	9.8	35
2026	Discovery and surveillance of viruses from salmon in British Columbia using viral immune-response biomarkers, metatranscriptomics, and high-throughput RT-PCR. <i>Virus Evolution</i> , 2021, 7, veaa069.	4.9	13
2027	A metagenomic-based method to study hospital air dust resistome. <i>Chemical Engineering Journal</i> , 2021, 406, 126854.	12.7	29
2028	First transcriptome assembly of a newly discovered vent mussel, <i>Gigantidas vrijenhoeki</i> , at Onnuri Vent Field on the northern Central Indian Ridge. <i>Marine Genomics</i> , 2021, 57, 100819.	1.1	6
2029	Challenges in gene-oriented approaches for pangenome content discovery. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	8
2030	Gene expression during bacterivorous growth of a widespread marine heterotrophic flagellate. <i>ISME Journal</i> , 2021, 15, 154-167.	9.8	13
2031	Bridging the membrane lipid divide: bacteria of the FCB group superphylum have the potential to synthesize archaeal ether lipids. <i>ISME Journal</i> , 2021, 15, 168-182.	9.8	62
2032	Comparative genomics reveals insights into cyanobacterial evolution and habitat adaptation. <i>ISME Journal</i> , 2021, 15, 211-227.	9.8	118
2033	Genotyping-by-sequencing to determine the genetic structure of a Tibetan medicinal plant <i>Swertia musotii</i> Franch.. <i>Genetic Resources and Crop Evolution</i> , 2021, 68, 469-484.	1.6	3

#	ARTICLE	IF	CITATIONS
2034	Chromosome-level de novo genome assembly of <i>Sarcophaga peregrina</i> provides insights into the evolutionary adaptation of flesh flies. <i>Molecular Ecology Resources</i> , 2021, 21, 251-262.	4.8	16
2035	Effects of the prebiotic inulin-type fructans on post-antibiotic reconstitution of the gut microbiome. <i>Journal of Applied Microbiology</i> , 2021, 130, 634-649.	3.1	4
2036	Metagenomic insights into seasonal variations in the soil microbial community and function in a <i>Larix gmelinii</i> forest of Mohe, China. <i>Journal of Forestry Research</i> , 2021, 32, 371-383.	3.6	7
2037	Current challenges and best-practice protocols for microbiome analysis. <i>Briefings in Bioinformatics</i> , 2021, 22, 178-193.	6.5	268
2038	Predicting drug-metagenome interactions: Variation in the microbial β -glucuronidase level in the human gut metagenomes. <i>PLoS ONE</i> , 2021, 16, e0244876.	2.5	15
2039	Metagenomic Assembly: Reconstructing Genomes from Metagenomes. <i>Methods in Molecular Biology</i> , 2021, 2242, 139-152.	0.9	1
2040	Metatranscriptomics in Microbiome Study: A Comprehensive Approach. , 2021, , 1-36.		3
2041	Host population diversity as a driver of viral infection cycle in wild populations of green sulfur bacteria with long standing virus-host interactions. <i>ISME Journal</i> , 2021, 15, 1569-1584.	9.8	16
2042	Metagenomics analysis of the gut microbiome in healthy and bacterial pneumonia forest musk deer. <i>Genes and Genomics</i> , 2021, 43, 43-53.	1.4	13
2045	Viral evolution sustains a dengue outbreak of enhanced severity. <i>Emerging Microbes and Infections</i> , 2021, 10, 536-544.	6.5	6
2047	Metagenomic analysis of the cow, sheep, reindeer and red deer rumen. <i>Scientific Reports</i> , 2021, 11, 1990.	3.3	32
2048	Advances in Biotechnological Tools and Techniques for Metatranscriptomics. , 2021, , 567-579.		0
2049	Advances and Challenges in Metatranscriptomic Analysis. , 2021, , 453-469.		2
2050	Whole-Genome Comparisons of Ergot Fungi Reveals the Divergence and Evolution of Species within the Genus <i>Claviceps</i> Are the Result of Varying Mechanisms Driving Genome Evolution and Host Range Expansion. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	17
2051	The complete genomic sequence of the novel myovirus RP13 infecting <i>Ralstonia solanacearum</i> , the causative agent of bacterial wilt. <i>Archives of Virology</i> , 2021, 166, 651-654.	2.1	2
2052	Interannual dynamics, diversity and evolution of the virome in <i>Sclerotinia sclerotiorum</i> from a single crop field. <i>Virus Evolution</i> , 2021, 7, veab032.	4.9	56
2053	Nerve growth factor interacts with CHRM4 and promotes neuroendocrine differentiation of prostate cancer and castration resistance. <i>Communications Biology</i> , 2021, 4, 22.	4.4	25
2054	Virulence factor-related gut microbiota genes and immunoglobulin A levels as novel markers for machine learning-based classification of autism spectrum disorder. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 545-554.	4.1	19

#	ARTICLE	IF	CITATIONS
2055	Interpopulation differences of retroduplication variations (RDVs) in rice retrogenes and their phenotypic correlations. Computational and Structural Biotechnology Journal, 2021, 19, 600-611.	4.1	1
2056	The Gut Microbiome Is Altered in Postmenopausal Women With Osteoporosis and Osteopenia. JBMR Plus, 2021, 5, e10452.	2.7	48
2057	Transcriptome Profiles in the Spleen of the Chinese Giant Salamander (<i>Andrias davidianus</i>) Challenged with <i>Citrobacter freundii</i> . Russian Journal of Bioorganic Chemistry, 2021, 47, 252-260.	1.0	1
2058	Comparative genomics reveals new functional insights in uncultured MAST species. ISME Journal, 2021, 15, 1767-1781.	9.8	18
2059	Competitive Exclusion and Metabolic Dependency among Microorganisms Structure the Cellulose Economy of an Agricultural Soil. MBio, 2021, 12, .	4.1	23
2060	Oxford nanopore sequencing in clinical microbiology and infection diagnostics. Briefings in Bioinformatics, 2021, 22, .	6.5	28
2061	Integrated mRNA and miRNA expression profile analysis of female and male gonads in <i>Hyriopsis cumingii</i> . Scientific Reports, 2021, 11, 665.	3.3	11
2062	Prediction and analysis of metagenomic operons via MetaRon: a pipeline for prediction of Metagenome and whole-genome operons. BMC Genomics, 2021, 22, 60.	2.8	2
2064	Harnessing CRISPR-Cas system diversity for gene editing technologies. Journal of Biomedical Research, 2021, 35, 91.	1.6	1
2065	A draft transcriptome of a parasite <i>Neocamacolaimus parasiticus</i> (Camacolaimidae, Plectida). Journal of Nematology, 2021, 53, 1-4.	0.9	4
2066	Diversity analysis of thermophilic hydrogenogenic carboxydrotrophs by carbon monoxide dehydrogenase amplicon sequencing using new primers. Extremophiles, 2021, 25, 61-76.	2.3	4
2068	Integrated mRNA and Small RNA Sequencing for Analyzing Leaf Spot Pathogen <i>Didymella segeticola</i> and Its Host, Tea (<i>Camellia sinensis</i>), During Infection. Molecular Plant-Microbe Interactions, 2021, 34, 127-130.	2.6	11
2071	Genomic signatures of the evolution of defence against its natural enemies in the poisonous and medicinal plant <i>Datura stramonium</i> (Solanaceae). Scientific Reports, 2021, 11, 882.	3.3	17
2072	Expansion and persistence of antibiotic-specific resistance genes following antibiotic treatment. Gut Microbes, 2021, 13, 1-19.	9.8	24
2073	Whole-Genome Sequencing for Bacterial Virulence Assessment. , 2021, , 45-68.		0
2074	Metagenomic Applications for Infectious Disease Testing in Clinical Laboratories. , 2021, , 111-131.		0
2075	Whole-metagenome shotgun sequencing of pig faecal microbiome. Italian Journal of Animal Science, 2021, 20, 1147-1155.	1.9	5
2076	Computational Genomics. , 2021, , 213-241.		0

#	ARTICLE	IF	CITATIONS
2077	Metagenomic sequencing reveals a lack of virus exchange between native and invasive freshwater fish across the Murrayâ€“Darling Basin, Australia. <i>Virus Evolution</i> , 2021, 7, veab034.	4.9	27
2078	Diversification of mammalian deltaviruses by host shifting. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	41
2079	Horseshoe crab genomes reveal the evolution of genes and microRNAs after three rounds of whole genome duplication. <i>Communications Biology</i> , 2021, 4, 83.	4.4	31
2080	Newly discovered Asgard archaea Hermodarchaeota potentially degrade alkanes and aromatics via alkyl/benzyl-succinate synthase and benzoyl-CoA pathway. <i>ISME Journal</i> , 2021, 15, 1826-1843.	9.8	40
2081	Comparative Analysis of Core and Accessory Genes in Coexpression Network. <i>Methods in Molecular Biology</i> , 2021, 2242, 45-58.	0.9	2
2083	Combined genomic, transcriptomic, and metabolomic analyses provide insights into chayote (<i>Sechium</i>) Tj ETQq1 1,0,784314,rgBT /Ove	6.3	39
2084	A Multi-Omics Characterization of the Natural Product Potential of Tropical Filamentous Marine Cyanobacteria. <i>Marine Drugs</i> , 2021, 19, 20.	4.6	19
2085	Polinton-like viruses are abundant in aquatic ecosystems. <i>Microbiome</i> , 2021, 9, 13.	11.1	32
2086	Associations of the gut microbiome with hepatic adiposity in the Multiethnic Cohort Adiposity Phenotype Study. <i>Gut Microbes</i> , 2021, 13, 1965463.	9.8	16
2087	Full-Length Transcriptome Analysis of Four Different Tissues of <i>Cephalotaxus oliveri</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 787.	4.1	16
2088	An unusual overrepresentation of genetic factors related to iron homeostasis in the genome of the fluorescent <i>Pseudomonas</i> sp. ABC1. <i>Microbial Biotechnology</i> , 2021, 14, 1060-1072.	4.2	1
2090	Metagenomic Insights Into the Microbial Assemblage Capable of Quorum Sensing and Quorum Quenching in Particulate Organic Matter in the Yellow Sea. <i>Frontiers in Microbiology</i> , 2020, 11, 602010.	3.5	7
2093	The gut virome in Irritable Bowel Syndrome differs from that of controls. <i>Gut Microbes</i> , 2021, 13, 1-15.	9.8	36
2094	Bioinformatics resources for SARS-CoV-2 discovery and surveillance. <i>Briefings in Bioinformatics</i> , 2021, 22, 631-641.	6.5	38
2095	Positive selection analysis reveals the deep-sea adaptation of a hadal sea cucumber (<i>Paelopatides</i> sp.) to the Mariana Trench. <i>Journal of Oceanology and Limnology</i> , 2021, 39, 266-281.	1.3	9
2096	Metagenomic Approaches to Analyze Antimicrobial Resistance: An Overview. <i>Frontiers in Genetics</i> , 2020, 11, 575592.	2.3	41
2097	<i>S. pseudintermedius</i> and <i>S. aureus</i> lineages with transmission ability circulate as causative agents of infections in pets for years. <i>BMC Veterinary Research</i> , 2021, 17, 42.	1.9	31
2098	Decrease in acetyl-CoA pathway utilizing butyrate-producing bacteria is a key pathogenic feature of alcohol-induced functional gut microbial dysbiosis and development of liver disease in mice. <i>Gut Microbes</i> , 2021, 13, 1946367.	9.8	34

#	ARTICLE	IF	CITATIONS
2099	The Isolate <i>Caproiciproducens</i> sp. 7D4C2 Produces n-Caproate at Mildly Acidic Conditions From Hexoses: Genome and rBOX Comparison With Related Strains and Chain-Elongating Bacteria. <i>Frontiers in Microbiology</i> , 2020, 11, 594524.	3.5	33
2100	The discovery, distribution, and diversity of DNA viruses associated with <i>Drosophila melanogaster</i> in Europe. <i>Virus Evolution</i> , 2021, 7, veab031.	4.9	25
2101	Detection of <i>Trypanosoma cruzi</i> in the saliva of diverse neotropical bats. <i>Zoonoses and Public Health</i> , 2021, 68, 271-276.	2.2	15
2102	A Fast Word Embedding Based Classifier to Profile Target Gene Databases in Metagenomic Samples. <i>Lecture Notes in Computer Science</i> , 2021, , 116-126.	1.3	0
2103	Relationship Between Peat Type and Microbial Ecology in Sphagnum-Containing Peatlands of the Adirondack Mountains, NY, USA. <i>Microbial Ecology</i> , 2021, 82, 429-441.	2.8	4
2104	Upregulation of the PPAR signaling pathway and accumulation of lipids are related to the morphological and structural transformation of the dragon-eye goldfish eye. <i>Science China Life Sciences</i> , 2021, 64, 1031-1049.	4.9	27
2105	A Draft Genome Assembly of <i>Culex pipiens pallens</i> (Diptera: Culicidae) Using PacBio Sequencing. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	9
2106	MicrobeAnnotator: a user-friendly, comprehensive functional annotation pipeline for microbial genomes. <i>BMC Bioinformatics</i> , 2021, 22, 11.	2.6	61
2107	Can Cyanobacterial Diversity in the Source Predict the Diversity in Sludge and the Risk of Toxin Release in a Drinking Water Treatment Plant?. <i>Toxins</i> , 2021, 13, 25.	3.4	18
2108	Role of human Pegivirus infections in whole <i>Plasmodium falciparum</i> sporozoite vaccination and controlled human malaria infection in African volunteers. <i>Virology Journal</i> , 2021, 18, 28.	3.4	3
2109	A Comprehensive Guide to Potato Transcriptome. <i>Methods in Molecular Biology</i> , 2021, 2354, 155-192.	0.9	0
2111	The Impact of Migration on the Gut Metagenome of South Asian Canadians. <i>Gut Microbes</i> , 2021, 13, 1-29.	9.8	14
2112	Heterochronic Fecal Microbiota Transfer Reverses Hallmarks of the Aging Murine Gut, Eye and Brain. <i>SSRN Electronic Journal</i> , 0, , .	0.4	3
2113	Genome Recovery, Functional Profiling, and Taxonomic Classification from Metagenomes. <i>Methods in Molecular Biology</i> , 2021, 2242, 153-172.	0.9	2
2114	Simple, Reliable, and Time-Efficient Manual Annotation of Bacterial Genomes with MAISEN. <i>Methods in Molecular Biology</i> , 2021, 2242, 221-229.	0.9	3
2115	Comparative Genomics, from the Annotated Genome to Valuable Biological Information: A Case Study. <i>Methods in Molecular Biology</i> , 2021, 2242, 91-112.	0.9	0
2116	The repertoire of ABC proteins in <i>Clostridioides difficile</i> . <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 2905-2920.	4.1	5
2118	metaXplor: an interactive viral and microbial metagenomic data manager. <i>GigaScience</i> , 2021, 10, .	6.4	4

#	ARTICLE	IF	CITATIONS
2120	Wastewater Treatment for Bioenergy Purposes Using a Metaproteomic Approach. , 2021, , 253-278.		1
2121	Virome composition in marine fish revealed by meta-transcriptomics. Virus Evolution, 2021, 7, veab005.	4.9	58
2122	Viromics of extant insect orders unveil the evolution of the flavi-like superfamily. Virus Evolution, 2021, 7, veab030.	4.9	35
2123	Plasma proteomics of green turtles (<i>Chelonia mydas</i>) reveals pathway shifts and potential biomarker candidates associated with health and disease. , 2021, 9, coab018.		4
2125	Phytoplankton consortia as a blueprint for mutually beneficial eukaryote-bacteria ecosystems based on the biocoenosis of Botryococcus consortia. Scientific Reports, 2021, 11, 1726.	3.3	12
2126	Re-purposing software for functional characterization of the microbiome. Microbiome, 2021, 9, 4.	11.1	7
2127	The draft genome sequence of the grove snail <i>Cepaea nemoralis</i> . G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	15
2128	Genomic and transcriptomic resources for candidate gene discovery in the Ranunculids. Applications in Plant Sciences, 2021, 9, e11407.	2.1	4
2129	Function Analysis of P450 and GST Genes to Imidacloprid in Aphis craccivora (Koch). Frontiers in Physiology, 2020, 11, 624287.	2.8	21
2130	Comparative genomics reveals high rates of horizontal transfer and strong purifying selection on rhizobial symbiosis genes. Proceedings of the Royal Society B: Biological Sciences, 2021, 288, 20201804.	2.6	13
2131	Longitudinal dynamics of gut bacteriome, mycobiome and virome after fecal microbiota transplantation in graft-versus-host disease. Nature Communications, 2021, 12, 65.	12.8	51
2133	First Genome of Labyrinthula sp., an Opportunistic Seagrass Pathogen, Reveals Novel Insight into Marine Protist Phylogeny, Ecology and CAZyme Cell-Wall Degradation. Microbial Ecology, 2021, 82, 498-511.	2.8	3
2134	EUKulele: Taxonomic annotation of the unsung eukaryotic microbes. Journal of Open Source Software, 2021, 6, 2817.	4.6	19
2135	Metatranscriptomics: A Promising Tool to Depict Dynamics of Microbial Community Structure and Function. , 2021, , 471-491.		3
2136	Isolation and genotyping of novel T4 cyanophages associated with diverse coral reef invertebrates. Coral Reefs, 2021, 40, 485-504.	2.2	1
2137	Fine Mapping of the "Black Peel Color in Pomegranate (<i>Punica granatum</i> L.) Strongly Suggests That a Mutation in the Anthocyanidin Reductase (ANR) Gene Is Responsible for the Trait. Frontiers in Plant Science, 2021, 12, 642019.	3.6	17
2139	A potential new recombinant echovirus 18 strain detected in a 4-year-old child with encephalitis in China in 2019. Archives of Virology, 2021, 166, 1231-1236.	2.1	3
2140	Systematic errors in orthology inference and their effects on evolutionary analyses. IScience, 2021, 24, 102110.	4.1	27

#	ARTICLE	IF	CITATIONS
2142	Genome Sequence of a <i>Minacovirus</i> Strain from a Farmed Mink in The Netherlands. Microbiology Resource Announcements, 2021, 10, .	0.6	4
2143	De novo assembly of the <i>Mytilus taylorii</i> transcriptome and identification of sesquiterpene synthases. Archives of Biochemistry and Biophysics, 2021, 698, 108742.	3.0	2
2144	Critical evaluation of short, long, and hybrid assembly for contextual analysis of antibiotic resistance genes in complex environmental metagenomes. Scientific Reports, 2021, 11, 3753.	3.3	53
2145	Application of computational approaches to analyze metagenomic data. Journal of Microbiology, 2021, 59, 233-241.	2.8	9
2146	The <i>Mastigamoeba balamuthi</i> Genome and the Nature of the Free-Living Ancestor of <i>Entamoeba</i> . Molecular Biology and Evolution, 2021, 38, 2240-2259.	8.9	14
2147	Virus Prospecting in Crickets—Discovery and Strain Divergence of a Novel Iflavirus in Wild and Cultivated <i>Acheta domesticus</i> . Viruses, 2021, 13, 364.	3.3	14
2149	Detecting high-scoring local alignments in pangenome graphs. Bioinformatics, 2021, 37, 2266-2274.	4.1	6
2151	Evolutionary dynamics of transposable elements in bdelloid rotifers. ELife, 2021, 10, .	6.0	26
2152	Mitochondrial Coevolution, but not Nuclear Compensation, Drives Evolution of OXPHOS Complexes in Bivalves. Molecular Biology and Evolution, 2021, 38, 2597-2614.	8.9	21
2153	Diatom fucan polysaccharide precipitates carbon during algal blooms. Nature Communications, 2021, 12, 1150.	12.8	58
2154	Expanded catalog of microbial genes and metagenome-assembled genomes from the pig gut microbiome. Nature Communications, 2021, 12, 1106.	12.8	116
2155	Analysis of the difference between aged and degenerated pit mud microbiome in fermentation cellars for Chinese <i>Luzhou</i> flavor baijiu by metatranscriptomics. Journal of the Science of Food and Agriculture, 2021, 101, 4621-4631.	3.5	14
2156	An Expanded Gene Catalog of Mouse Gut Metagenomes. MSphere, 2021, 6, .	2.9	13
2157	Plant Co-expression Annotation Resource: a web server for identifying targets for genetically modified crop breeding pipelines. BMC Bioinformatics, 2021, 22, 46.	2.6	0
2160	Comprehensive Metatranscriptome Analysis of the Reef-Building Holobiont <i>Millepora complanata</i> . Frontiers in Marine Science, 2021, 8, .	2.5	2
2161	Overexpression of A Biotic Stress-Inducible <i>Pvgsu</i> Gene Activates Early Protective Responses in Tobacco under Combined Heat and Drought. International Journal of Molecular Sciences, 2021, 22, 2352.	4.1	10
2162	Comparison of the Microsatellite Distribution Patterns in the Genomes of Euarchontoglires at the Taxonomic Level. Frontiers in Genetics, 2021, 12, 622724.	2.3	11
2165	The First Whole Genome Sequence and Characterisation of Avian Nephritis Virus Genotype 3. Viruses, 2021, 13, 235.	3.3	7

#	ARTICLE	IF	CITATIONS
2166	Temperature Stress Induces Shift From Co-Existence to Competition for Organic Carbon in Microalgae-Bacterial Photobioreactor Community “Enabling Continuous Production of Microalgal Biomass. <i>Frontiers in Microbiology</i> , 2021, 12, 607601.	3.5	10
2168	High Resolution Metatranscriptomic Characterization of the Pulmonary RNA Virome After Lung Transplantation. <i>Transplantation</i> , 2021, Publish Ahead of Print, 2546-2553.	1.0	5
2169	Comparative genomics reveals broad genetic diversity, extensive recombination and nascent ecological adaptation in <i>Micrococcus luteus</i> . <i>BMC Genomics</i> , 2021, 22, 124.	2.8	15
2170	Breast milk urea as a nitrogen source for urease positive <i>Bifidobacterium infantis</i> . <i>FEMS Microbiology Ecology</i> , 2021, 97, .	2.7	10
2172	Functional capacities of microbial communities to carry out large scale geochemical processes are maintained during ex situ anaerobic incubation. <i>PLoS ONE</i> , 2021, 16, e0245857.	2.5	11
2174	A Highly Contiguous Genome Assembly of a Polyphagous Predatory Mite <i>Stratiolaelaps scimitus</i> (Womersley) (Acari: Laelapidae). <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	2
2176	Sugarcane/peanut intercropping system improves physicochemical properties by changing N and P cycling and organic matter turnover in root zone soil. <i>PeerJ</i> , 2021, 9, e10880.	2.0	22
2177	Distribution of Mixotrophy and Desiccation Survival Mechanisms across Microbial Genomes in an Arid Biological Soil Crust Community. <i>MSystems</i> , 2021, 6, .	3.8	29
2178	The Distribution of Several Genomic Virulence Determinants Does Not Corroborate the Established Serotyping Classification of <i>Bacillus thuringiensis</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 2244.	4.1	6
2179	Hybrid Genome Assembly and Gene Repertoire of the Root Endophyte <i>Clitopilus hobsonii</i> QYL-10 (Entolomataceae, Agaricales, Basidiomycetes). <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 711-714.	2.6	7
2180	Genome-scale phylogenetic analyses confirm <i>Olpidium</i> as the closest living zoosporic fungus to the non-flagellated, terrestrial fungi. <i>Scientific Reports</i> , 2021, 11, 3217.	3.3	24
2181	A comprehensive and high-quality collection of <i>Escherichia coli</i> genomes and their genes. <i>Microbial Genomics</i> , 2021, 7, .	2.0	38
2182	Characterizing and Evaluating the Zoonotic Potential of Novel Viruses Discovered in Vampire Bats. <i>Viruses</i> , 2021, 13, 252.	3.3	35
2183	Multimomics analysis reveals the presence of a microbiome in the gut of fetal lambs. <i>Gut</i> , 2021, 70, 853-864.	12.1	52
2184	Metagenomic Analysis Reveals Microbial Community Structure and Metabolic Potential for Nitrogen Acquisition in the Oligotrophic Surface Water of the Indian Ocean. <i>Frontiers in Microbiology</i> , 2021, 12, 518865.	3.5	17
2185	Taxonomic and functional analyses of intact microbial communities thriving in extreme, astrobiology-relevant, anoxic sites. <i>Microbiome</i> , 2021, 9, 50.	11.1	14
2186	The gut microbiome modulates the protective association between a Mediterranean diet and cardiometabolic disease risk. <i>Nature Medicine</i> , 2021, 27, 333-343.	30.7	179
2187	Comparative Fungal Community Analyses Using Metatranscriptomics and Internal Transcribed Spacer Amplicon Sequencing from Norway Spruce. <i>MSystems</i> , 2021, 6, .	3.8	16

#	ARTICLE	IF	CITATIONS
2188	Protein-Based Vaccine Protect Against <i>Piscirickettsia salmonis</i> in Atlantic Salmon (<i>Salmo salar</i>). <i>Frontiers in Immunology</i> , 2021, 12, 602689.	4.8	7
2189	The <i>Ulva prolifera</i> genome reveals the mechanism of green tides. <i>Journal of Oceanology and Limnology</i> , 2021, 39, 1458-1470.	1.3	10
2190	Insights into long non-coding RNA regulation of anthocyanin carrot root pigmentation. <i>Scientific Reports</i> , 2021, 11, 4093.	3.3	9
2191	RNA sequencing-based exploration of the effects of far-red light on lncRNAs involved in the shade-avoidance response of <i>D. officinale</i> . <i>PeerJ</i> , 2021, 9, e10769.	2.0	10
2194	Soil Organic Matter, Soil Structure, and Bacterial Community Structure in a Post-Agricultural Landscape. <i>Frontiers in Earth Science</i> , 2021, 9, .	1.8	9
2195	The phylogenetic and global distribution of bacterial polyhydroxyalkanoate bioplastic-degrading genes. <i>Environmental Microbiology</i> , 2021, 23, 1717-1731.	3.8	25
2197	Microbiome-based environmental monitoring of a dairy processing facility highlights the challenges associated with low microbial-load samples. <i>Npj Science of Food</i> , 2021, 5, 4.	5.5	18
2198	Limited effects of long-term daily cranberry consumption on the gut microbiome in a placebo-controlled study of women with recurrent urinary tract infections. <i>BMC Microbiology</i> , 2021, 21, 53.	3.3	21
2199	Differences in microbial community response to nitrogen fertilization result in unique enzyme shifts between arbuscular and ectomycorrhizal-dominated soils. <i>Global Change Biology</i> , 2021, 27, 2049-2060.	9.5	24
2200	Are silver nanoparticles better than triclosan as a daily antimicrobial? Answers from the perspectives of gut microbiome disruption and pathogenicity. <i>Science of the Total Environment</i> , 2021, 756, 143983.	8.0	9
2201	Characterization of the human skin resistome and identification of two microbiota cutotypes. <i>Microbiome</i> , 2021, 9, 47.	11.1	42
2202	<i>Oceanomicrobium pacificus</i> gen. nov., sp. nov., a member of the family Rhodobacteraceae isolated from seawater of tropical western Pacific. <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 303-311.	1.7	2
2203	A new <i>Cannabis</i> genome assembly associates elevated cannabidiol (CBD) with hemp introgressed into marijuana. <i>New Phytologist</i> , 2021, 230, 1665-1679.	7.3	87
2204	Contribution of horizontal gene transfer to the functionality of microbial biofilm on a macroalgae. <i>ISME Journal</i> , 2021, 15, 807-817.	9.8	28
2205	A Combined Metagenomics and Metatranscriptomics Approach to Unravel Costa Rican Cocoa Box Fermentation Processes Reveals Yet Unreported Microbial Species and Functionalities. <i>Frontiers in Microbiology</i> , 2021, 12, 641185.	3.5	28
2206	Genome annotation of disease-causing microorganisms. <i>Briefings in Bioinformatics</i> , 2021, 22, 845-854.	6.5	13
2207	Responses of Coastal Marine Microbiomes Exposed to Anthropogenic Dissolved Organic Carbon. <i>Environmental Science & Technology</i> , 2021, 55, 9609-9621.	10.0	16
2209	Is Metagenomic Analysis an Effective Way to Analyze Fish Feeding Habits? A Case of the Yellowfin Sea Bream <i>Acanthopagrus latus</i> (Houttuyn) in Daya Bay. <i>Frontiers in Marine Science</i> , 2021, 8, .	2.5	6

#	ARTICLE	IF	CITATIONS
2210	Freshwater sponge hosts and their green algae symbionts: a tractable model to understand intracellular symbiosis. <i>PeerJ</i> , 2021, 9, e10654.	2.0	11
2211	De Novo Transcriptome Assembly of Two <i>Microsorium</i> Fern Species Identifies Enzymes Required for Two Upstream Pathways of Phytoecdysteroids. <i>International Journal of Molecular Sciences</i> , 2021, 22, 2085.	4.1	4
2212	Characterization of the development dynamics within the linear growth bamboo leaf. <i>Physiologia Plantarum</i> , 2021, 172, 1518-1534.	5.2	5
2213	Multi-omics analysis reveals structure and function of biofilm microbial communities in a pre-denitrification biofilter. <i>Science of the Total Environment</i> , 2021, 757, 143908.	8.0	47
2215	Genome sequencing and annotation and phylogenomic analysis of the medicinal mushroom <i>Amauroderma rugosum</i> , a traditional medicinal species in the family Ganodermataceae. <i>Mycologia</i> , 2021, 113, 268-277.	1.9	7
2217	Sulfur Metabolites Play Key System-Level Roles in Modulating Denitrification. <i>MSystems</i> , 2021, 6, .	3.8	10
2218	Benefits of Iterative Searches of Large Databases to Interpret Large Human Gut Metaproteomic Data Sets. <i>Journal of Proteome Research</i> , 2021, 20, 1522-1534.	3.7	15
2219	Large-scale genome sequencing reveals the driving forces of viruses in microalgal evolution. <i>Cell Host and Microbe</i> , 2021, 29, 250-266.e8.	11.0	48
2220	Functional characterization of thermotolerant microbial consortium for lignocellulolytic enzymes with central role of Firmicutes in rice straw depolymerization. <i>Scientific Reports</i> , 2021, 11, 3032.	3.3	49
2221	De Novo Transcriptomic Analyses Revealed Some Detoxification Genes and Related Pathways Responsive to Noposion Yihaogong® 5% EC (Lambda-Cyhalothrin 5%) Exposure in <i>Spodoptera frugiperda</i> Third-Instar Larvae. <i>Insects</i> , 2021, 12, 132.	2.2	16
2222	A large genome with chromosome-scale assembly sheds light on the evolutionary success of a true toad (<i>Bufo gargarizans</i>). <i>Molecular Ecology Resources</i> , 2021, 21, 1256-1273.	4.8	32
2223	Ammonium Removal in Aquaponics Indicates Participation of <i>Comammox Nitrospira</i> . <i>Current Microbiology</i> , 2021, 78, 894-903.	2.2	12
2225	Evidence for reduced immune gene diversity and activity during the evolution of termites. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2021, 288, 20203168.	2.6	9
2226	Overview of bioinformatic methods for analysis of antibiotic resistome from genome and metagenome data. <i>Journal of Microbiology</i> , 2021, 59, 270-280.	2.8	16
2227	ASaiM-MT: a validated and optimized ASaiM workflow for metatranscriptomics analysis within Galaxy framework. <i>F1000Research</i> , 2021, 10, 103.	1.6	1
2229	Taxonomic, functional and expression analysis of viral communities associated with marine sponges. <i>PeerJ</i> , 2021, 9, e10715.	2.0	10
2230	<i>Salmonella enterica</i> Serovars Dublin and Enteritidis Comparative Proteomics Reveals Differential Expression of Proteins Involved in Stress Resistance, Virulence, and Anaerobic Metabolism. <i>Infection and Immunity</i> , 2021, 89, .	2.2	6
2231	Detection of Tioman Virus in <i>Pteropus vampyrus</i> Near Flores, Indonesia. <i>Viruses</i> , 2021, 13, 563.	3.3	3

#	ARTICLE	IF	CITATIONS
2232	Antifungal Activity and Possible Mode of Action of Ningnanmycin Against Tea Gray Blight Disease Pathogen <i>Pseudopezalotiopsis camelliae-sinensis</i> . <i>Phytopathology</i> , 2021, 111, 1735-1742.	2.2	10
2233	Detection of horizontal gene transfer in the genome of the choanoflagellate <i>Salpingoeca rosetta</i> . <i>Scientific Reports</i> , 2021, 11, 5993.	3.3	14
2234	Removing auto-activators from yeast-two-hybrid assays by conditional negative selection. <i>Scientific Reports</i> , 2021, 11, 5477.	3.3	6
2235	Whole-Genome Sequencing and Comparative Genomics of Three <i>Helicobacter pylori</i> Strains Isolated from the Stomach of a Patient with Adenocarcinoma. <i>Pathogens</i> , 2021, 10, 331.	2.8	5
2236	Marine sediments harbor diverse archaea and bacteria with the potential for anaerobic hydrocarbon degradation via fumarate addition. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	2.7	13
2237	Two Archaeal Metagenome-Assembled Genomes from El Tatio Provide New Insights into the Crenarchaeota Phylum. <i>Genes</i> , 2021, 12, 391.	2.4	5
2238	Changing expression patterns of TonB-dependent transporters suggest shifts in polysaccharide consumption over the course of a spring phytoplankton bloom. <i>ISME Journal</i> , 2021, 15, 2336-2350.	9.8	42
2239	Insights into the cyanosphere: capturing the respective metabolisms of cyanobacteria and chemotrophic bacteria in natural conditions?. <i>Environmental Microbiology Reports</i> , 2021, 13, 364-374.	2.4	11
2240	The Genome of the Margined White Butterfly (<i>Pieris macdunnoughii</i>): Sex Chromosome Insights and the Power of Polishing with PoolSeq Data. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	7
2241	Integrating Metagenomic and Bayesian Analyses to Evaluate the Performance and Confidence of CrAssphage as an Indicator for Tracking Human Sewage Contamination in China. <i>Environmental Science & Technology</i> , 2021, 55, 4992-5000.	10.0	13
2242	A De Novo Transcriptome Assembly of <i>Ceratopteris richardii</i> Provides Insights into the Evolutionary Dynamics of Complex Gene Families in Land Plants. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	34
2243	<i>Raoultella terrigena</i> : Current state of knowledge, after two recently identified clinical cases in Eastern Europe. <i>Clinical Case Reports (discontinued)</i> , 2021, 9, e04089.	0.5	2
2244	The microbiome of the Black Sea water column analyzed by shotgun and genome centric metagenomics. <i>Environmental Microbiomes</i> , 2021, 16, 5.	5.0	35
2245	Selective enrichment and metagenomic analysis of three novel comammox <i>Nitrospira</i> in a urine-fed membrane bioreactor. <i>ISME Communications</i> , 2021, 1, .	4.2	27
2246	A Persistent Giant Algal Virus, with a Unique Morphology, Encodes an Unprecedented Number of Genes Involved in Energy Metabolism. <i>Journal of Virology</i> , 2021, 95, .	3.4	31
2247	OMAmer: tree-driven and alignment-free protein assignment to subfamilies outperforms closest sequence approaches. <i>Bioinformatics</i> , 2021, 37, 2866-2873.	4.1	5
2248	Impacts of <i>Microcystis</i> on the Dissemination of the Antibiotic Resistome in Cyanobacterial Blooms. <i>ACS ES&T Water</i> , 2021, 1, 1263-1273.	4.6	5
2251	Genomic characterization of 99 viruses from the bunyavirus families Nairoviridae, Peribunyaviridae, and Phenuiviridae, including 35 previously unsequenced viruses. <i>PLoS Pathogens</i> , 2021, 17, e1009315.	4.7	23

#	ARTICLE	IF	CITATIONS
2252	Comparative Metagenomics Reveals Microbial Signatures of Sugarcane Phyllosphere in Organic Management. <i>Frontiers in Microbiology</i> , 2021, 12, 623799.	3.5	17
2253	Transcriptional activity differentiates families of Marine Group II <i>Euryarchaeota</i> in the coastal ocean. <i>ISME Communications</i> , 2021, 1, .	4.2	2
2255	In silico determination of nitrogen metabolism in microbes from extreme conditions using metagenomics. <i>Archives of Microbiology</i> , 2021, 203, 2521-2540.	2.2	4
2256	Molecular mechanisms of local adaptation for salt tolerance in a treefrog. <i>Molecular Ecology</i> , 2021, 30, 2065-2086.	3.9	18
2257	Genomic Insights Into the Pathogenicity of a Novel Biofilm-Forming <i>Enterococcus</i> sp. Bacteria (<i>Enterococcus lacertideformus</i>) Identified in Reptiles. <i>Frontiers in Microbiology</i> , 2021, 12, 635208.	3.5	6
2259	ViroMatch: A Computational Pipeline for the Detection of Viral Sequences from Complex Metagenomic Data. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	11
2260	Monitoring Microbial Populations and Antibiotic Resistance Gene Enrichment Associated with Arctic Waste Stabilization Ponds. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	3.1	5
2261	A chromosome-level genome of the spider <i>Trichonephila antipodiana</i> reveals the genetic basis of its polyphagy and evidence of an ancient whole-genome duplication event. <i>GigaScience</i> , 2021, 10, .	6.4	187
2262	Specific Microbial Taxa and Functional Capacity Contribute to Chicken Abdominal Fat Deposition. <i>Frontiers in Microbiology</i> , 2021, 12, 643025.	3.5	28
2263	Coupled microbiome analyses highlights relative functional roles of bacteria in a bivalve hatchery. <i>Environmental Microbiomes</i> , 2021, 16, 7.	5.0	7
2265	The effects of ALA-PDT on microbiota in pilosebaceous units of patients with severe acne: A metagenomic study. <i>Photodiagnosis and Photodynamic Therapy</i> , 2021, 33, 102050.	2.6	9
2266	A chromosome-level genome assembly for the Pacific oyster <i>Crassostrea gigas</i> . <i>GigaScience</i> , 2021, 10, .	6.4	88
2267	<i>Agromyces laixinhei</i> sp. nov. isolated from bat feces in China. <i>Journal of Microbiology</i> , 2021, 59, 467-475.	2.8	4
2270	The Crown Pearl: a draft genome assembly of the European freshwater pearl mussel <i>Margaritifera margaritifera</i> (Linnaeus, 1758). <i>DNA Research</i> , 2021, 28, .	3.4	15
2271	Taxonomic analysis of metagenomic data with kASA. <i>Nucleic Acids Research</i> , 2021, 49, e68-e68.	14.5	2
2272	Diversity and functional landscapes in the microbiota of animals in the wild. <i>Science</i> , 2021, 372, .	12.6	96
2273	Longitudinal study of the scalp microbiome suggests coconut oil to enrich healthy scalp commensals. <i>Scientific Reports</i> , 2021, 11, 7220.	3.3	13
2274	A Novel Rubi-Like Virus in the Pacific Electric Ray (<i>Tetronarce californica</i>) Reveals the Complex Evolutionary History of the Matonaviridae. <i>Viruses</i> , 2021, 13, 585.	3.3	12

#	ARTICLE	IF	CITATIONS
2275	A Hybrid Genome Assembly Resource for <i>Podosphaera xanthii</i> , the Main Causal Agent of Powdery Mildew Disease in Cucurbits. <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 319-324.	2.6	14
2276	Gene Duplications Trace Mitochondria to the Onset of Eukaryote Complexity. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	24
2277	Fine-scale metabolic discontinuity in a stratified prokaryote microbiome of a Red Sea deep halocline. <i>ISME Journal</i> , 2021, 15, 2351-2365.	9.8	11
2278	Bacterial cyclic diguanylate signaling networks sense temperature. <i>Nature Communications</i> , 2021, 12, 1986.	12.8	35
2279	Tutorial: assessing metagenomics software with the CAMI benchmarking toolkit. <i>Nature Protocols</i> , 2021, 16, 1785-1801.	12.0	36
2280	Expression analysis of genes related to cold tolerance in <i>Dendroctonus valens</i> . <i>PeerJ</i> , 2021, 9, e10864.	2.0	9
2281	Inflammation in children with cystic fibrosis: contribution of bacterial production of long-chain fatty acids. <i>Pediatric Research</i> , 2021, 90, 99-108.	2.3	13
2282	Identification of a unique endoplasmic retention motif in the <i>Xenopus</i> GIRK5 channel and its contribution to oocyte maturation. <i>FEBS Open Bio</i> , 2021, 11, 1093-1108.	2.3	4
2283	Microbial predation accelerates granulation and modulates microbial community composition. <i>BMC Microbiology</i> , 2021, 21, 91.	3.3	9
2284	Soil Microbiome Structure and Function in Ecopiles Used to Remediate Petroleum-Contaminated Soil. <i>Frontiers in Environmental Science</i> , 2021, 9, .	3.3	11
2286	Shifts in morphology, gene expression, and selection underlie web loss in Hawaiian Tetragnatha spiders. <i>Bmc Ecology and Evolution</i> , 2021, 21, 48.	1.6	6
2287	A Degeneration Gradient of Poplar Trees Contributes to the Taxonomic, Functional, and Resistome Diversity of Bacterial Communities in Rhizosphere Soils. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3438.	4.1	10
2288	Impact of manipulation of glycerol/diol dehydratase activity on intestinal microbiota ecology and metabolism. <i>Environmental Microbiology</i> , 2021, 23, 1765-1779.	3.8	10
2290	Rice Plantâ€“Soil Microbiome Interactions Driven by Root and Shoot Biomass. <i>Diversity</i> , 2021, 13, 125.	1.7	4
2291	Microbial responses to herbivory-induced vegetation changes in a high-Arctic peatland. <i>Polar Biology</i> , 2021, 44, 899-911.	1.2	3
2293	Striking parallels between dorsoventral patterning in <i>Drosophila</i> and <i>Gryllus</i> reveal a complex evolutionary history behind a model gene regulatory network. <i>ELife</i> , 2021, 10, .	6.0	20
2295	Accurate and sensitive detection of microbial eukaryotes from whole metagenome shotgun sequencing. <i>Microbiome</i> , 2021, 9, 58.	11.1	60
2297	Non-responder phenotype reveals apparent microbiome-wide antibiotic tolerance in the murine gut. <i>Communications Biology</i> , 2021, 4, 316.	4.4	2

#	ARTICLE	IF	CITATIONS
2298	Comparative Transcriptome and Expression Profiling of Resistant and Susceptible Banana Cultivars during Infection by <i>Fusarium oxysporum</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 3002.	4.1	19
2299	Comparative genome analyses suggest a hemibiotrophic lifestyle and virulence differences for the beech bark disease fungal pathogens <i>Neonectria faginata</i> and <i>Neonectria coccinea</i> . <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	2
2300	The Molecular Basis of Kale Domestication: Transcriptional Profiling of Developing Leaves Provides New Insights Into the Evolution of a <i>Brassica oleracea</i> Vegetative Morphotype. <i>Frontiers in Plant Science</i> , 2021, 12, 637115.	3.6	12
2303	Recovery of complete genomes and non-chromosomal replicons from activated sludge enrichment microbial communities with long read metagenome sequencing. <i>Npj Biofilms and Microbiomes</i> , 2021, 7, 23.	6.4	29
2304	AgroSeek: a system for computational analysis of environmental metagenomic data and associated metadata. <i>BMC Bioinformatics</i> , 2021, 22, 117.	2.6	5
2305	The complete chloroplast genome of <i>Abutilon theophrasti</i> medic (Malvaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 912-913.	0.4	1
2306	Ultrafast functional profiling of RNA-seq data for nonmodel organisms. <i>Genome Research</i> , 2021, 31, 713-720.	5.5	15
2307	Metagenomic analysis of microbiota and antibiotic resistome in household activated carbon drinking water purifiers. <i>Environment International</i> , 2021, 148, 106394.	10.0	25
2308	Diversity and N ₂ O Production Potential of Fungi in an Oceanic Oxygen Minimum Zone. <i>Journal of Fungi</i> (Basel, Switzerland), 2021, 7, 218.	3.5	17
2309	Role of dietary fiber in the recovery of the human gut microbiome and its metabolome. <i>Cell Host and Microbe</i> , 2021, 29, 394-407.e5.	11.0	137
2310	TALE: Transformer-based protein function Annotation with joint sequenceâ€Label Embedding. <i>Bioinformatics</i> , 2021, 37, 2825-2833.	4.1	52
2311	Metagenomic Data Assembly â€The Way of Decoding Unknown Microorganisms. <i>Frontiers in Microbiology</i> , 2021, 12, 613791.	3.5	67
2314	MetaPrism: A versatile toolkit for joint taxa/gene analysis of metagenomic sequencing data. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	1
2316	PhotoModPlus: A web server for photosynthetic protein prediction from genome neighborhood features. <i>PLoS ONE</i> , 2021, 16, e0248682.	2.5	0
2317	Nutrient-driven genome evolution revealed by comparative genomics of chrysomonad flagellates. <i>Communications Biology</i> , 2021, 4, 328.	4.4	7
2318	Prediction of Selected Biosynthetic Pathways for the Lipopolysaccharide Components in <i>Porphyromonas gingivalis</i> . <i>Pathogens</i> , 2021, 10, 374.	2.8	1
2319	Soil Metagenome Sequences from a Geothermal Site at Mount Melbourne in Antarctica. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	0
2320	DIAMOND+MEGAN: Fast and Easy Taxonomic and Functional Analysis of Short and Long Microbiome Sequences. <i>Current Protocols</i> , 2021, 1, e59.	2.9	55

#	ARTICLE	IF	CITATIONS
2321	Effect of immobilized anthraquinone-2-sulfonate on antibiotic resistance genes and microbial community in biofilms of anaerobic reactors. <i>Journal of Environmental Management</i> , 2021, 282, 111967.	7.8	3
2322	A protocol combining breath testing and ex vivo fermentations to study the human gut microbiome. <i>STAR Protocols</i> , 2021, 2, 100227.	1.2	0
2323	Predicted Input of Uncultured Fungal Symbionts to a Lichen Symbiosis from Metagenome-Assembled Genomes. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	19
2326	Transcriptome analyses and weighted gene coexpression network analysis reveal key pathways and genes involved in the rapid cold resistance of the Chinese white wax scale insect. <i>Archives of Insect Biochemistry and Physiology</i> , 2021, 107, e21781.	1.5	11
2328	The gut microbiome in subclinical atherosclerosis: a population-based multiphenotype analysis. <i>Rheumatology</i> , 2021, 61, 258-269.	1.9	13
2329	Fast and sensitive taxonomic assignment to metagenomic contigs. <i>Bioinformatics</i> , 2021, 37, 3029-3031.	4.1	110
2330	Microbial Community Field Surveys Reveal Abundant <i>Pseudomonas</i> Population in Sorghum Rhizosphere Composed of Many Closely Related Phylotypes. <i>Frontiers in Microbiology</i> , 2021, 12, 598180.	3.5	20
2331	Revealing taxon-specific heavy metal-resistance mechanisms in denitrifying phosphorus removal sludge using genome-centric metaproteomics. <i>Microbiome</i> , 2021, 9, 67.	11.1	34
2332	Microbial Diversity and Mercury Methylation Activity in Periphytic Biofilms at a Run-of-River Hydroelectric Dam and Constructed Wetlands. <i>MSphere</i> , 2021, 6, .	2.9	7
2333	Microbial genetic and transcriptional contributions to oxalate degradation by the gut microbiota in health and disease. <i>ELife</i> , 2021, 10, .	6.0	30
2334	Connecting structure to function with the recovery of over 1000 high-quality metagenome-assembled genomes from activated sludge using long-read sequencing. <i>Nature Communications</i> , 2021, 12, 2009.	12.8	177
2335	Subâ€œthic photosynthesis in hot desert habitats. <i>Environmental Microbiology</i> , 2021, 23, 3867-3880.	3.8	10
2337	First Description of the Composition and the Functional Capabilities of the Skin Microbial Community Accompanying Severe Scabies Infestation in Humans. <i>Microorganisms</i> , 2021, 9, 907.	3.6	2
2338	Whole-genome sequence-based analysis of the <i>Paenibacillus aquistagni</i> strain DK1, a polyethylene-degrading bacterium isolated from landfill. <i>World Journal of Microbiology and Biotechnology</i> , 2021, 37, 80.	3.6	5
2340	Unraveling the Metabolic Potential of Asgardarchaeota in a Sediment from the Mediterranean Hydrocarbon-Contaminated Water Basin Mar Piccolo (Taranto, Italy). <i>Microorganisms</i> , 2021, 9, 859.	3.6	5
2342	Antarctic <i>Rahnella inusitata</i> : A Producer of Cold-Stable Î²-Galactosidase Enzymes. <i>International Journal of Molecular Sciences</i> , 2021, 22, 4144.	4.1	8
2343	<i>Affinibrenneria salicis</i> gen. nov. sp. nov. isolated from <i>Salix matsudana</i> bark canker. <i>Archives of Microbiology</i> , 2021, 203, 3473-3481.	2.2	2
2344	The chromosomeâ€œscale reference genome of safflower (<i>Carthamus tinctorius</i>) provides insights into linoleic acid and flavonoid biosynthesis. <i>Plant Biotechnology Journal</i> , 2021, 19, 1725-1742.	8.3	60

#	ARTICLE	IF	CITATIONS
2345	Reductive evolution and unique predatory mode in the CPR bacterium <i>Vampirococcus lugosii</i> . <i>Nature Communications</i> , 2021, 12, 2454.	12.8	64
2346	Discovery of a New, Recurrent Enzyme in Bacterial Phosphonate Degradation: (<i>R</i>)-1-Hydroxy-2-aminoethylphosphonate Ammonia-lyase. <i>Biochemistry</i> , 2021, 60, 1214-1225.	2.5	19
2347	Metagenomic shotgun sequencing reveals host species as an important driver of virome composition in mosquitoes. <i>Scientific Reports</i> , 2021, 11, 8448.	3.3	26
2349	The Asgard Archaeal-Unique Contribution to Protein Families of the Eukaryotic Common Ancestor Was 0.3%. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	6
2351	Genome-Wide Analysis of the Late Embryogenesis Abundant (LEA) and Abscissic Acid-, Stress-, and Ripening-Induced (ASR) Gene Superfamily from <i>Canavalia rosea</i> and Their Roles in Salinity/Alkaline and Drought Tolerance. <i>International Journal of Molecular Sciences</i> , 2021, 22, 4554.	4.1	19
2353	Differential expressions of anthocyanin synthesis genes underlie flower color divergence in a sympatric <i>Rhododendron sanguineum</i> complex. <i>BMC Plant Biology</i> , 2021, 21, 204.	3.6	15
2354	The virome of German bats: comparing virus discovery approaches. <i>Scientific Reports</i> , 2021, 11, 7430.	3.3	21
2355	Elevated rates of horizontal gene transfer in the industrialized human microbiome. <i>Cell</i> , 2021, 184, 2053-2067.e18.	28.9	167
2356	Evaluation of the Microba Community Profiler for Taxonomic Profiling of Metagenomic Datasets From the Human Gut Microbiome. <i>Frontiers in Microbiology</i> , 2021, 12, 643682.	3.5	25
2357	Exploring the Diversity of Fungal DyPs in Mangrove Soils to Produce and Characterize Novel Biocatalysts. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 321.	3.5	5
2358	A critical assessment of gene catalogs for metagenomic analysis. <i>Bioinformatics</i> , 2021, 37, 2848-2857.	4.1	15
2359	Sequencing, assembly and annotation of the whole-insect genome of <i>Lymantria dispar dispar</i>, the European gypsy moth. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	5
2360	Grassland fairy rings of <i>Leucocalocybe mongolica</i> represent the center of a rich soil microbial community. <i>Brazilian Journal of Microbiology</i> , 2021, 52, 1357-1369.	2.0	8
2361	Characteristics and variation of fecal bacterial communities and functions in isolated systolic and diastolic hypertensive patients. <i>BMC Microbiology</i> , 2021, 21, 128.	3.3	9
2362	Adherent-invasive <i>E.Âcoli</i> metabolism of propanediol in Crohnâ€™s disease regulates phagocytes to drive intestinal inflammation. <i>Cell Host and Microbe</i> , 2021, 29, 607-619.e8.	11.0	60
2363	Simultaneous nitrate and sulfate dependent anaerobic oxidation of methane linking carbon, nitrogen and sulfur cycles. <i>Water Research</i> , 2021, 194, 116928.	11.3	43
2365	Ecophysiological Features Shape the Distribution of Prophages and CRISPR in Sulfate Reducing Prokaryotes. <i>Microorganisms</i> , 2021, 9, 931.	3.6	3
2369	First detection of a novel â€˜unknown hostâ€™ flavivirus in a Malaysian rodent. <i>Access Microbiology</i> , 2021, 3, 000223.	0.5	1

#	ARTICLE	IF	CITATIONS
2370	Comparative genomics of the coconut crab and other decapod crustaceans: exploring the molecular basis of terrestrial adaptation. BMC Genomics, 2021, 22, 313.	2.8	11
2371	Prediction, enrichment and isolation identify a responsive, competitive community of cellulolytic microorganisms from a municipal landfill. FEMS Microbiology Ecology, 2021, 97, .	2.7	3
2373	Cross-comparison of methods for quantifying antibiotic resistance in agricultural soils amended with dairy manure and compost. Science of the Total Environment, 2021, 766, 144321.	8.0	16
2374	Dysbiosis in Metabolic Genes of the Gut Microbiomes of Patients with an Ileo-anal Pouch Resembles That Observed in Crohn's Disease. MSys, 2021, 6, .	3.8	19
2375	HAG1 and SWI3A/B control of male germ line development in <i>P. patens</i> suggests conservation of epigenetic reproductive control across land plants. Plant Reproduction, 2021, 34, 149-173.	2.2	9
2376	ASaiM-MT: a validated and optimized ASaiM workflow for metatranscriptomics analysis within Galaxy framework. F1000Research, 2021, 10, 103.	1.6	8
2377	Complete genome sequence of Photobacterium ganghwense C2.2: A new polyhydroxyalkanoate production candidate. MicrobiologyOpen, 2021, 10, e1182.	3.0	4
2378	The pivotal protein profile between the conjoined twins and normal mosquitofish <i>Gambusia affinis</i> based on iTRAQ proteomic analysis. Fish Physiology and Biochemistry, 2021, 47, 939-950.	2.3	0
2379	Metabolic pathways inferred from a bacterial marker gene illuminate ecological changes across South Pacific frontal boundaries. Nature Communications, 2021, 12, 2213.	12.8	25
2380	Draft Genome of the Sea Cucumber <i>Holothuria glaberrima</i> , a Model for the Study of Regeneration. Frontiers in Marine Science, 2021, 8, .	2.5	14
2381	The gill transcriptome reveals unique antimicrobial features that protect <i>Nibea albiflora</i> from <i>Cryptocaryon irritans</i> infection. Journal of Fish Diseases, 2021, 44, 1215-1227.	1.9	6
2382	Effect of probiotics on diversity and function of gut microbiota in <i>Moschus berezovskii</i> . Archives of Microbiology, 2021, 203, 3305-3315.	2.2	6
2385	Interspecies Genomic Variation and Transcriptional Activeness of Secondary Metabolism-Related Genes in <i>Aspergillus Section Fumigati</i> . Frontiers in Fungal Biology, 2021, 2, .	2.0	5
2386	Characterizing rumen microbiota and CAZyme profile of Indian dromedary camel (<i>Camelus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tj 5	8.3	25
2387	Metagenomic and bioanalytical insights into quorum sensing of methanogens in anaerobic digestion systems with or without the addition of conductive filter. Science of the Total Environment, 2021, 763, 144509.	8.0	37
2388	Large-Scale Annotation and Evolution Analysis of MiRNA in Insects. Genome Biology and Evolution, 2021, 13, .	2.5	15
2389	Dynamics of rumen gene expression, microbiome colonization, and their interplay in goats. BMC Genomics, 2021, 22, 288.	2.8	18
2390	Effects of different rotational legume crops and residue management regimes on soil microbial properties and functions in a sugarcane farming system. Journal of Plant Nutrition and Soil Science, 2021, 184, 398-408.	1.9	2

#	ARTICLE	IF	CITATIONS
2391	Revisiting the <i>Schistosoma japonicum</i> life cycle transcriptome for new insights into lung schistosomula development. <i>Experimental Parasitology</i> , 2021, 223, 108080.	1.2	7
2393	Identification of the Potential Role of the Rumen Microbiome in Milk Protein and Fat Synthesis in Dairy Cows Using Metagenomic Sequencing. <i>Animals</i> , 2021, 11, 1247.	2.3	16
2395	Integrated Analysis of the Transcriptome and Metabolome Revealed Candidate Genes Involved in GA3-Induced Dormancy Release in <i>Leymus chinensis</i> Seeds. <i>International Journal of Molecular Sciences</i> , 2021, 22, 4161.	4.1	10
2397	Insights on the Evolutionary Genomics of the <i>Blautia</i> Genus: Potential New Species and Genetic Content Among Lineages. <i>Frontiers in Microbiology</i> , 2021, 12, 660920.	3.5	33
2398	Algae Biofilm Reduces Microbe-Derived Dissolved Organic Nitrogen Discharges: Performance and Mechanisms. <i>Environmental Science & Technology</i> , 2021, 55, 6227-6238.	10.0	42
2400	Unraveling microbiomes associated with decomposition of needles of two <i>Pinus</i> species with contrasting fire-adaptive strategies. <i>Biology and Fertility of Soils</i> , 2021, 57, 715-729.	4.3	2
2401	<i>In Vivo</i> Competitions between <i>Fibrobacter succinogenes</i> , <i>Ruminococcus flavefaciens</i> , and <i>Ruminococcus albus</i> in a Gnotobiotic Sheep Model Revealed by Multi-Omic Analyses. <i>MBio</i> , 2021, 12, .	4.1	26
2402	Characterisation of the Viral Community Associated with the Alfalfa Weevil (<i>Hypera postica</i>) and Its Host Plant, Alfalfa (<i>Medicago sativa</i>). <i>Viruses</i> , 2021, 13, 791.	3.3	10
2403	Bacteria Make a Living Breathing the Nitroheterocyclic Insensitive Munitions Compound 3-Nitro-1,2,4-triazol-5-one (NTO). <i>Environmental Science & Technology</i> , 2021, 55, 5806-5814.	10.0	12
2404	The genome of <i>Geosiphon pyriformis</i> reveals ancestral traits linked to the emergence of the arbuscular mycorrhizal symbiosis. <i>Current Biology</i> , 2021, 31, 1570-1577.e4.	3.9	30
2405	Calf Diarrhea Caused by Prolonged Expansion of Autochthonous Gut Enterobacteriaceae and Their Lytic Bacteriophages. <i>MSystems</i> , 2021, 6, .	3.8	15
2406	An Introduction to Next Generation Sequencing Bioinformatic Analysis in Gut Microbiome Studies. <i>Biomolecules</i> , 2021, 11, 530.	4.0	62
2408	Sensitive protein alignments at tree-of-life scale using DIAMOND. <i>Nature Methods</i> , 2021, 18, 366-368.	19.0	1,195
2409	Proteomic Identification and Meta-Analysis in <i>Salvia hispanica</i> RNA-Seq de novo Assemblies. <i>Plants</i> , 2021, 10, 765.	3.5	2
2410	Sex-Biased Gene Expression and Evolution in the Cerebrum and Syrinx of Chinese Hwamei (<i>Garrulax</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	2.4	1
2411	Draft genome of a biparental beetle species, <i>Lethrus apterus</i> . <i>BMC Genomics</i> , 2021, 22, 301.	2.8	0
2413	Identification of a Novel Papillomavirus Type (MfoiPV1) Associated with Acrochordon in a Stone Marten (<i>Martes foina</i>). <i>Pathogens</i> , 2021, 10, 539.	2.8	1
2414	Terpenoid Biosynthesis Dominates among Secondary Metabolite Clusters in <i>Mucoromycotina</i> Genomes. <i>Journal of Fungi</i> (Basel, Switzerland), 2021, 7, 285.	3.5	14

#	ARTICLE	IF	CITATIONS
2415	Hidden Resistome: Enrichment Reveals the Presence of Clinically Relevant Antibiotic Resistance Determinants in Treated Wastewater-Irrigated Soils. <i>Environmental Science & Technology</i> , 2021, 55, 6814-6827.	10.0	31
2416	Metabolic capabilities mute positive response to direct and indirect impacts of warming throughout the soil profile. <i>Nature Communications</i> , 2021, 12, 2089.	12.8	36
2417	Cellular fate of intersex differentiation. <i>Cell Death and Disease</i> , 2021, 12, 388.	6.3	8
2419	GeneMark-HM: improving gene prediction in DNA sequences of human microbiome. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab047.	3.2	4
2420	A Primer on the Analysis of High-Throughput Sequencing Data for Detection of Plant Viruses. <i>Microorganisms</i> , 2021, 9, 841.	3.6	36
2422	Global analysis of the apple fruit microbiome: are all apples the same?. <i>Environmental Microbiology</i> , 2021, 23, 6038-6055.	3.8	64
2423	Balancing selection maintains hyper-divergent haplotypes in <i>Caenorhabditis elegans</i> . <i>Nature Ecology and Evolution</i> , 2021, 5, 794-807.	7.8	89
2424	Categorization of Orthologous Gene Clusters in 92 Ascomycota Genomes Reveals Functions Important for Phytopathogenicity. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 337.	3.5	3
2425	NGScloud2: optimized bioinformatic analysis using Amazon Web Services. <i>PeerJ</i> , 2021, 9, e11237.	2.0	4
2426	Potential role of indolelactate and butyrate in multiple sclerosis revealed by integrated microbiome-metabolome analysis. <i>Cell Reports Medicine</i> , 2021, 2, 100246.	6.5	37
2427	Genome sequence, transcriptome, and annotation of rodent malaria parasite <i>Plasmodium yoelii</i> nigeriensis N67. <i>BMC Genomics</i> , 2021, 22, 303.	2.8	7
2428	Tissue-specific transcriptome analysis of drought stress and rehydration in <i>Trachycarpus fortunei</i> at seedling. <i>PeerJ</i> , 2021, 9, e10933.	2.0	4
2429	iBLAST: Incremental BLAST of new sequences via automated e-value correction. <i>PLoS ONE</i> , 2021, 16, e0249410.	2.5	3
2432	Differential expression of starch and sucrose metabolic genes linked to varying biomass yield in <i>Miscanthus</i> hybrids. <i>Biotechnology for Biofuels</i> , 2021, 14, 98.	6.2	8
2434	Extended Evaluation of Viral Diversity in Lake Baikal through Metagenomics. <i>Microorganisms</i> , 2021, 9, 760.	3.6	15
2438	Casting Light on the Adaptation Mechanisms and Evolutionary History of the Widespread <i>Sumerlaeota</i> . <i>MBio</i> , 2021, 12, .	4.1	12
2439	Virome Diversity among Mosquito Populations in a Sub-Urban Region of Marseille, France. <i>Viruses</i> , 2021, 13, 768.	3.3	19
2440	MolluscDB: a genome and transcriptome database for molluscs. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2021, 376, 20200157.	4.0	17

#	ARTICLE	IF	CITATIONS
2441	Genome-Based Targeted Sequencing as a Reproducible Microbial Community Profiling Assay. <i>MSphere</i> , 2021, 6, .	2.9	4
2442	Comparative Gene Expression Analysis Reveals Mechanism of <i>Pinus contorta</i> Response to the Fungal Pathogen <i>Dothistroma septosporum</i> . <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 397-409.	2.6	10
2443	Reply to Evidence that microbes identified as tick-borne pathogens are nutritional endosymbionts. <i>Cell</i> , 2021, 184, 2261-2262.	28.9	0
2444	De novo assembly of a new <i>Olea europaea</i> genome accession using nanopore sequencing. <i>Horticulture Research</i> , 2021, 8, 64.	6.3	41
2445	Extensive microbial diversity within the chicken gut microbiome revealed by metagenomics and culture. <i>PeerJ</i> , 2021, 9, e10941.	2.0	79
2446	Establishment of <i>Culex modestus</i> in Belgium and a Glance into the Virome of Belgian Mosquito Species. <i>MSphere</i> , 2021, 6, .	2.9	19
2447	Analysis of Different Size Fractions Provides a More Complete Perspective of Viral Diversity in a Freshwater Embayment. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	3.1	9
2448	Prophage Genomics and Ecology in the Family Rhodobacteraceae. <i>Microorganisms</i> , 2021, 9, 1115.	3.6	22
2450	A high-quality carabid genome assembly provides insights into beetle genome evolution and cold adaptation. <i>Molecular Ecology Resources</i> , 2021, 21, 2145-2165.	4.8	13
2451	The Presence of Ancient Core Genes Reveals Endogenization from Diverse Viral Ancestors in Parasitoid Wasps. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	14
2452	Challenges in benchmarking metagenomic profilers. <i>Nature Methods</i> , 2021, 18, 618-626.	19.0	63
2453	Bacteriophage-Host Association in the Phytoplasma Insect Vector <i>Euscelidius variegatus</i> . <i>Pathogens</i> , 2021, 10, 612.	2.8	9
2454	The Significance of Genotypic Diversity in Coral Competitive Interaction: A Transcriptomic Perspective. <i>Frontiers in Ecology and Evolution</i> , 2021, 9, .	2.2	1
2455	Transcriptomic Analysis for the Identification of Metabolic Pathway Genes Related to Toluene Response in <i>Ardisia pusilla</i> . <i>Plants</i> , 2021, 10, 1011.	3.5	4
2456	Characterization and complexity of transcriptome in <i>Gymnocypris przewalskii</i> using single-molecule long-read sequencing and RNA-seq. <i>DNA Research</i> , 2021, 28, .	3.4	3
2457	DNA adenine methylation is involved in persister formation in <i>E. coli</i> . <i>Microbiological Research</i> , 2021, 246, 126709.	5.3	16
2458	Type II Photosynthetic Reaction Center Genes of Avocado (<i>Persea americana</i> Mill.) Bark Microbial Communities are Dominated by Aerobic Anoxygenic Alphaproteobacteria. <i>Current Microbiology</i> , 2021, 78, 2623-2630.	2.2	2
2459	Metatranscriptome Library Preparation Influences Analyses of Viral Community Activity During a Brown Tide Bloom. <i>Frontiers in Microbiology</i> , 2021, 12, 664189.	3.5	12

#	ARTICLE	IF	CITATIONS
2460	Population transcriptomic sequencing reveals allopatric divergence and local adaptation in <i>Pseudotaxus chienii</i> (Taxaceae). <i>BMC Genomics</i> , 2021, 22, 388.	2.8	11
2461	Dynamic transcriptome and histomorphology analysis of developmental traits of hindlimb thigh muscle from <i>Odorrana tormota</i> and its adaptability to different life history stages. <i>BMC Genomics</i> , 2021, 22, 369.	2.8	1
2462	pLannotate: engineered plasmid annotation. <i>Nucleic Acids Research</i> , 2021, 49, W516-W522.	14.5	20
2463	Diversity and distribution of viruses inhabiting the deepest ocean on Earth. <i>ISME Journal</i> , 2021, 15, 3094-3110.	9.8	55
2464	Transcription of human papillomaviruses in <scp>nonmelanoma</scp> skin cancers of the immunosuppressed. <i>International Journal of Cancer</i> , 2021, 149, 1341-1347.	5.1	7
2465	Resilience in Greenland intertidal <i>Mytilus</i> : The hidden stress defense. <i>Science of the Total Environment</i> , 2021, 767, 144366.	8.0	25
2466	Draft genome sequence of the pulse crop blackgram [<i>Vigna mungo</i> (L.) Hepper] reveals potential R-genes. <i>Scientific Reports</i> , 2021, 11, 11247.	3.3	20
2468	Unbiased Characterization of the Microbiome and Virome of Questing Ticks. <i>Frontiers in Microbiology</i> , 2021, 12, 627327.	3.5	11
2469	Gut microbiota of frugo-folivorous sifakas across environments. <i>Animal Microbiome</i> , 2021, 3, 39.	3.8	12
2470	<i>Bremerella alba</i> sp. nov., a novel planctomycete isolated from the surface of the macroalga <i>Fucus spiralis</i> . <i>Systematic and Applied Microbiology</i> , 2021, 44, 126189.	2.8	14
2472	Microbial Hotspots in Lithic Microhabitats Inferred from DNA Fractionation and Metagenomics in the Atacama Desert. <i>Microorganisms</i> , 2021, 9, 1038.	3.6	19
2473	High-quality reference genome for <i>Clonorchis sinensis</i> . <i>Genomics</i> , 2021, 113, 1605-1615.	2.9	19
2474	Integrated mRNA and Small RNA Sequencing for Analyzing Tea Leaf Spot Pathogen <i>Lasiodiplodia theobromae</i>, Under In Vitro Conditions and the Course of Infection. <i>Phytopathology</i> , 2021, 111, 882-885.	2.2	3
2475	Metagenomes, Metatranscriptomes, and Metagenome-Assembled Genomes from Chesapeake and Delaware Bay (USA) Water Samples. <i>Microbiology Resource Announcements</i> , 2021, 10, e0026221.	0.6	6
2476	DeepGOWeb: fast and accurate protein function prediction on the (Semantic) Web. <i>Nucleic Acids Research</i> , 2021, 49, W140-W146.	14.5	15
2477	Molecular detection of cosaviruses in a patient with acute flaccid paralysis and in sewage samples in Germany. <i>Virus Research</i> , 2021, 297, 198285.	2.2	1
2478	Exogenous putrescine activates the arginine-polyamine pathway and inhibits the decomposition of endogenous polyamine in <i>Anthurium andraeanum</i> under chilling stress. <i>Scientia Horticulturae</i> , 2021, 282, 110047.	3.6	8
2479	Beyond taxonomy: Validating functional inference approaches in the context of fishâ€™farm impact assessments. <i>Molecular Ecology Resources</i> , 2021, 21, 2264-2277.	4.8	8

#	ARTICLE	IF	CITATIONS
2480	Evaluation of Metagenomic-Enabled Antibiotic Resistance Surveillance at a Conventional Wastewater Treatment Plant. <i>Frontiers in Microbiology</i> , 2021, 12, 657954.	3.5	46
2481	Pathogenic potential assessment of the Shiga toxin-producing <i>Escherichia coli</i> by a source attribution—considered machine learning model. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	8
2483	Chromosome-Level Assembly of the Atlantic Silverside Genome Reveals Extreme Levels of Sequence Diversity and Structural Genetic Variation. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	20
2484	A rooted phylogeny resolves early bacterial evolution. <i>Science</i> , 2021, 372, .	12.6	128
2485	Haplotype-resolved genome assembly enables gene discovery in the red palm weevil <i>Rhynchophorus ferrugineus</i> . <i>Scientific Reports</i> , 2021, 11, 9987.	3.3	20
2486	Diversity of nitrogen cycling genes at a Midwest long-term ecological research site with different management practices. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 4309-4327.	3.6	5
2487	Re-examination of two diatom reference genomes using long-read sequencing. <i>BMC Genomics</i> , 2021, 22, 379.	2.8	22
2488	Metagenomics Analysis Reveals the Microbial Communities, Antimicrobial Resistance Gene Diversity and Potential Pathogen Transmission Risk of Two Different Landfills in China. <i>Diversity</i> , 2021, 13, 230.	1.7	9
2489	Membrane Bound Aminopeptidase B of a Potential Probiotic <i>Pediococcus acidilactici</i> NCDC 252: Purification, Physicochemical and Kinetic Characterization. <i>International Journal of Peptide Research and Therapeutics</i> , 2021, 27, 1641-1655.	1.9	2
2491	Host-Parasite Interaction of Atlantic salmon (<i>Salmo salar</i>) and the Ectoparasite <i>Neoparamoeba perurans</i> in Amoebic Gill Disease. <i>Frontiers in Immunology</i> , 2021, 12, 672700.	4.8	22
2492	Comparative phylogenetics of repetitive elements in a diverse order of flowering plants (Brassicales). <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	15
2494	Dual RNA-Sequencing Analysis of Resistant (<i>Pinus pinea</i>) and Susceptible (<i>Pinus radiata</i>) Hosts during <i>Fusarium circinatum</i> Challenge. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5231.	4.1	14
2495	Gene-level metagenomic architectures across diseases yield high-resolution microbiome diagnostic indicators. <i>Nature Communications</i> , 2021, 12, 2907.	12.8	33
2498	Transcriptome analysis reveals significant difference in gene expression and pathways between two peanut cultivars under Al stress. <i>Gene</i> , 2021, 781, 145535.	2.2	19
2499	Mobile genetic elements mediate the mixotrophic evolution of novel <i>Alicyclobacillus</i> species for acid mine drainage adaptation. <i>Environmental Microbiology</i> , 2021, 23, 3896-3912.	3.8	12
2500	Two high-quality <i>de novo</i> genomes from single ethanol-preserved specimens of tiny metazoans (<i>Collembola</i>). <i>GigaScience</i> , 2021, 10, .	6.4	17
2501	Multiple lineages of <i>Streptomyces</i> produce antimicrobials within passalid beetle galleries across eastern North America. <i>ELife</i> , 2021, 10, .	6.0	11
2502	Facultative symbiosis with a saprotrophic soil fungus promotes potassium uptake in American sweetgum trees. <i>Plant, Cell and Environment</i> , 2021, 44, 2793-2809.	5.7	23

#	ARTICLE	IF	CITATIONS
2503	Ketogenic diet-mediated steroid metabolism reprogramming improves the immune microenvironment and myelin growth in spinal cord injury rats according to gene and co-expression network analyses. <i>Aging</i> , 2021, 13, 12973-12995.	3.1	7
2504	Discovery and Characterization of Actively Replicating DNA and Retro-Transcribing Viruses in Lower Vertebrate Hosts Based on RNA Sequencing. <i>Viruses</i> , 2021, 13, 1042.	3.3	8
2505	The effects of combined environmental factors on the intestinal flora of mice based on ground simulation experiments. <i>Scientific Reports</i> , 2021, 11, 11373.	3.3	1
2506	Propionate Fermentative Genes of the Gut Microbiome Decrease in Inflammatory Bowel Disease. <i>Journal of Clinical Medicine</i> , 2021, 10, 2176.	2.4	7
2508	Virus Diversity and Loads in Crickets Reared for Feed: Implications for Husbandry. <i>Frontiers in Veterinary Science</i> , 2021, 8, 642085.	2.2	11
2509	Gene Expression Profile of the Human Colorectal Carcinoma LoVo Cells Treated With Sporamin and Thapsigargin. <i>Frontiers in Oncology</i> , 2021, 11, 621462.	2.8	3
2510	Genome analysis of <i>Spiroplasma citri</i> strains from different host plants and its leafhopper vectors. <i>BMC Genomics</i> , 2021, 22, 373.	2.8	8
2511	Comparative transcriptome analyses for metribuzin tolerance provide insights into key genes and mechanisms restoring photosynthetic efficiency in bread wheat (<i>Triticum aestivum</i> L.). <i>Genomics</i> , 2021, 113, 910-918.	2.9	12
2512	Microbial Ecological Mechanism for Long-Term Production of High Concentrations of ϵ -Caproate via Lactate-Driven Chain Elongation. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	3.1	20
2513	Deep ocean metagenomes provide insight into the metabolic architecture of bathypelagic microbial communities. <i>Communications Biology</i> , 2021, 4, 604.	4.4	107
2514	Metabolic flexibility allows bacterial habitat generalists to become dominant in a frequently disturbed ecosystem. <i>ISME Journal</i> , 2021, 15, 2986-3004.	9.8	89
2515	Covariation of the Fecal Microbiome with Diet in Nonpasserine Birds. <i>MSphere</i> , 2021, 6, .	2.9	22
2516	Species and population specific gene expression in blood transcriptomes of marine turtles. <i>BMC Genomics</i> , 2021, 22, 346.	2.8	9
2517	Probiotic consumption relieved human stress and anxiety symptoms possibly via modulating the neuroactive potential of the gut microbiota. <i>Neurobiology of Stress</i> , 2021, 14, 100294.	4.0	70
2518	A stony coral cell atlas illuminates the molecular and cellular basis of coral symbiosis, calcification, and immunity. <i>Cell</i> , 2021, 184, 2973-2987.e18.	28.9	111
2519	The genome of the venomous snail <i>Lautoconus ventricosus</i> sheds light on the origin of conotoxin diversity. <i>GigaScience</i> , 2021, 10, .	6.4	29
2521	Patients With Common Variable Immunodeficiency (CVID) Show Higher Gut Bacterial Diversity and Levels of Low-Abundance Genes Than the Healthy Housemates. <i>Frontiers in Immunology</i> , 2021, 12, 671239.	4.8	13
2522	antiSMASH 6.0: improving cluster detection and comparison capabilities. <i>Nucleic Acids Research</i> , 2021, 49, W29-W35.	14.5	1,520

#	ARTICLE	IF	CITATIONS
2523	Bisphenol A biodegradation differs between mudflat and mangrove forest sediments. <i>Chemosphere</i> , 2021, 270, 128664.	8.2	14
2524	Whole-Genome Analysis of <i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> IS900 Insertions Reveals Strain Type-Specific Modalities. <i>Frontiers in Microbiology</i> , 2021, 12, 660002.	3.5	7
2525	Transcriptome Analysis Identifies a Gene Cluster for the Biosynthesis of Biruloquinone, a Rare Phenanthraquinone, in a Lichen-Forming Fungus <i>Cladonia macilenta</i> . <i>Journal of Fungi</i> (Basel, Switzerland), 2021, 7, 1041.	0.0	0
2526	Metagenomic analysis of urban wastewater resistome and mobilome: A support for antimicrobial resistance surveillance in an endemic country. <i>Environmental Pollution</i> , 2021, 276, 116736.	7.5	30
2527	The microbiota of healthy dogs demonstrates individualized responses to synbiotic supplementation in a randomized controlled trial. <i>Animal Microbiome</i> , 2021, 3, 36.	3.8	8
2528	Indicator species drive the key ecological functions of microbiota in a river impacted by acid mine drainage generated by rare earth elements mining in South China. <i>Environmental Microbiology</i> , 2022, 24, 919-937.	3.8	18
2529	Evaluation of morphological traits, hormonal metabolism, and transcriptional abundance in bitter melon (<i>Momordica charantia</i> L.) plants in response to ethephon inducement. <i>Scientia Horticulturae</i> , 2021, 282, 110033.	3.6	3
2530	Distinct composition and metabolic functions of human gut microbiota are associated with cachexia in lung cancer patients. <i>ISME Journal</i> , 2021, 15, 3207-3220.	9.8	51
2531	Identification of tick-borne pathogens by metagenomic next-generation sequencing in <i>Dermacentor nuttalli</i> and <i>Ixodes persulcatus</i> in Inner Mongolia, China. <i>Parasites and Vectors</i> , 2021, 14, 287.	2.5	32
2532	A Chromosome-Level Assembly of Blunt Snout Bream (<i>Megalobrama amblycephala</i>) Genome Reveals an Expansion of Olfactory Receptor Genes in Freshwater Fish. <i>Molecular Biology and Evolution</i> , 2021, 38, 4238-4251.	8.9	32
2533	Molecular mechanisms of mutualistic and antagonistic interactions in a plant-pollinator association. <i>Nature Ecology and Evolution</i> , 2021, 5, 974-986.	7.8	30
2534	A molecular survey of canine respiratory viruses in New Zealand. <i>New Zealand Veterinary Journal</i> , 2021, 69, 224-233.	0.9	6
2538	Genomics-Enabled Novel Insight Into the Pathovar-Specific Population Structure of the Bacterial Leaf Streak Pathogen <i>Xanthomonas translucens</i> in Small Grain Cereals. <i>Frontiers in Microbiology</i> , 2021, 12, 674952.	3.5	31
2540	Long-read metagenomics retrieves complete single-contig bacterial genomes from canine feces. <i>BMC Genomics</i> , 2021, 22, 330.	2.8	41
2541	Enlightening the taxonomy darkness of human gut microbiomes with a cultured biobank. <i>Microbiome</i> , 2021, 9, 119.	11.1	479
2542	Selective DNA and Protein Isolation From Marine Macrophyte Surfaces. <i>Frontiers in Microbiology</i> , 2021, 12, 665999.	3.5	3
2543	Potential and expression of carbohydrate utilization by marine fungi in the global ocean. <i>Microbiome</i> , 2021, 9, 106.	11.1	28
2544	Gut microbiome contributions to altered metabolism in a pig model of undernutrition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	18

#	ARTICLE	IF	CITATIONS
2545	A dynamic intron retention program regulates the expression of several hundred genes during pollen meiosis. <i>Plant Reproduction</i> , 2021, 34, 225-242.	2.2	17
2546	Early-Life Immune System Maturation in Chickens Using a Synthetic Community of Cultured Gut Bacteria. <i>MSystems</i> , 2021, 6, .	3.8	68
2547	Pests, diseases, and aridity have shaped the genome of <i>Corymbia citriodora</i> . <i>Communications Biology</i> , 2021, 4, 537.	4.4	21
2548	Transcriptional profile of oil palm pathogen, <i>Ganoderma boninense</i> , reveals activation of lignin degradation machinery and possible evasion of host immune response. <i>BMC Genomics</i> , 2021, 22, 326.	2.8	12
2549	Responses of cyanobacterial aggregate microbial communities to algal blooms. <i>Water Research</i> , 2021, 196, 117014.	11.3	31
2551	Novel functional sequences uncovered through a bovine multiassembly graph. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	42
2552	The diversity of opsins in Lake Baikal amphipods (Amphipoda: Gammaridae). <i>Bmc Ecology and Evolution</i> , 2021, 21, 81.	1.6	9
2553	Variation of Metagenome From Feedstock to Digestate in Full-Scale Biogas Plants. <i>Frontiers in Microbiology</i> , 2021, 12, 660225.	3.5	7
2554	Rhizomal Reclassification of Living Organisms. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5643.	4.1	16
2555	Comparison of nodule endophyte composition, diversity, and gene content between <i>Medicago truncatula</i> genotypes. <i>Phytobiomes Journal</i> , 0, , .	2.7	1
2556	Four novel picornaviruses detected in Magellanic Penguins (<i>Spheniscus magellanicus</i>) in Chile. <i>Virology</i> , 2021, 560, 116-123.	2.4	5
2558	The gutSMASH web server: Automated identification of primary metabolic gene clusters from the gut microbiota. <i>Nucleic Acids Research</i> , 2021, 49, W263-W270.	14.5	26
2559	Recommendations for the introduction of metagenomic next-generation sequencing in clinical virology, part II: bioinformatic analysis and reporting. <i>Journal of Clinical Virology</i> , 2021, 138, 104812.	3.1	39
2560	Gut microbiota in healthy and unhealthy long-living people. <i>Gene</i> , 2021, 779, 145510.	2.2	17
2561	A Chromosome-Level Genome Assembly of <i>Ephesia elutella</i> (Hübner, 1796) (Lepidoptera: Tortricidae). <i>Genome Biology and Evolution</i> , 2021, 13, 1-10.	2.5	4
2562	Not just shades of grey: life is full of colour for the ocellate river stingray (<i>Potamotrygon motoro</i>). <i>Journal of Experimental Biology</i> , 2021, 224, .	1.7	8
2563	Chemosynthetic and photosynthetic bacteria contribute differentially to primary production across a steep desert aridity gradient. <i>ISME Journal</i> , 2021, 15, 3339-3356.	9.8	48
2564	Genomic and proteomic profiles of biofilms on microplastics are decoupled from artificial surface properties. <i>Environmental Microbiology</i> , 2021, 23, 3099-3115.	3.8	43

#	ARTICLE	IF	CITATIONS
2565	Integrating taxonomic, functional, and strain-level profiling of diverse microbial communities with bioBakery 3. <i>ELife</i> , 2021, 10, .	6.0	808
2566	Changes in rhizosphere soil microbial communities across plant developmental stages of high and low methane emitting rice genotypes. <i>Soil Biology and Biochemistry</i> , 2021, 156, 108233.	8.8	14
2570	Comparative genomics analysis of two banana Fusarium wilt biocontrol endophytes <i>Bacillus subtilis</i> R31 and TR21 provides insights into their differences on phytobeneficial trait. <i>Genomics</i> , 2021, 113, 900-909.	2.9	14
2571	RT-qPCR assay for detection of mink astrovirus in outbreaks of diarrhea on Danish mink farms. <i>PLoS ONE</i> , 2021, 16, e0252022.	2.5	0
2572	Land-use change from cropland to plantations affects the abundance of nitrogen cycle-related microorganisms and genes in the Loess Plateau of China. <i>Applied Soil Ecology</i> , 2021, 161, 103873.	4.3	12
2573	Cotton transcriptome analysis reveals novel biological pathways that eliminate reactive oxygen species (ROS) under sodium bicarbonate (NaHCO ₃) alkaline stress. <i>Genomics</i> , 2021, 113, 1157-1169.	2.9	27
2574	Metagenome and analysis of metabolic potential of the microbial community in pit mud used for Chinese strong-flavor liquor production. <i>Food Research International</i> , 2021, 143, 110294.	6.2	33
2575	Microbial sulfate reduction by <i>Desulfovibrio</i> is an important source of hydrogen sulfide from a large swine finishing facility. <i>Scientific Reports</i> , 2021, 11, 10720.	3.3	18
2576	The <i>Rhododendron</i> Plant Genome Database (RPGD): a comprehensive online omics database for <i>Rhododendron</i> . <i>BMC Genomics</i> , 2021, 22, 376.	2.8	16
2578	Slippery when wet: cross-species transmission of divergent coronaviruses in bony and jawless fish and the evolutionary history of the <i>Coronaviridae</i> . <i>Virus Evolution</i> , 2021, 7, veab050.	4.9	23
2579	High-Quality Reference Genome Sequence for the Oomycete Vegetable Pathogen <i>Phytophthora capsici</i> Strain LT1534. <i>Microbiology Resource Announcements</i> , 2021, 10, e0029521.	0.6	4
2580	HIV-1 Infection Alters the Viral Composition of Plasma in Men Who Have Sex with Men. <i>MSphere</i> , 2021, 6, .	2.9	16
2581	Database-independent de novo metaproteomics of complex microbial communities. <i>Cell Systems</i> , 2021, 12, 375-383.e5.	6.2	35
2582	Efficient Nitrification and Low-Level N ₂ O Emission in a Weakly Acidic Bioreactor at Low Dissolved-Oxygen Levels Are Due to Comammox. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	3.1	19
2583	Studying the Genetic Diversity of Yam Bean Using a New Draft Genome Assembly. <i>Agronomy</i> , 2021, 11, 953.	3.0	7
2584	Particulate Metabolites and Transcripts Reflect Diel Oscillations of Microbial Activity in the Surface Ocean. <i>MSystems</i> , 2021, 6, .	3.8	29
2585	Fish farm effluents as a source of antibiotic resistance gene dissemination on Jeju Island, South Korea. <i>Environmental Pollution</i> , 2021, 276, 116764.	7.5	31
2586	Insight into the function and evolution of the Wood–Ljungdahl pathway in <i>Actinobacteria</i> . <i>ISME Journal</i> , 2021, 15, 3005-3018.	9.8	55

#	ARTICLE	IF	CITATIONS
2587	Analysis of accumulation and phytotoxicity mechanism of uranium and cadmium in two sweet potato cultivars. <i>Journal of Hazardous Materials</i> , 2021, 409, 124997.	12.4	44
2589	Novel Mycoviruses Discovered in the Mycovirome of a Necrotrophic Fungus. <i>MBio</i> , 2021, 12, .	4.1	66
2590	Diversity and infectivity of the RNA virome among different cryptic species of an agriculturally important insect vector: whitefly <i>Bemisia tabaci</i> . <i>Npj Biofilms and Microbiomes</i> , 2021, 7, 43.	6.4	21
2592	PHROG: families of prokaryotic virus proteins clustered using remote homology. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab067.	3.2	134
2593	Degradation of ester linkages in rice straw components by <i>Sphingobium</i> species recovered from the sea bottom using a non- α -secretory tannase family β -glucuronidase. <i>Environmental Microbiology</i> , 2021, 23, 4151-4167.	3.8	0
2595	Integrated Multi-omics Investigations Reveal the Key Role of Synergistic Microbial Networks in Removing Plasticizer Di-(2-Ethylhexyl) Phthalate from Estuarine Sediments. <i>MSystems</i> , 2021, 6, e0035821.	3.8	18
2596	De novo genome sequencing of mycoparasite <i>Mycogone perniciosus</i> strain MgR1 sheds new light on its biological complexity. <i>Brazilian Journal of Microbiology</i> , 2021, 52, 1545-1556.	2.0	2
2597	Wheat Rhizosphere Metagenome Reveals Newfound Potential Soil Zn-Mobilizing Bacteria Contributing to Cultivars' Variation in Grain Zn Concentration. <i>Frontiers in Microbiology</i> , 2021, 12, 689855.	3.5	4
2599	The Genomic Impact of Mycoheterotrophy in Orchids. <i>Frontiers in Plant Science</i> , 2021, 12, 632033.	3.6	9
2601	Development of a Multiplex PCR Assay for Genotyping the Fish Pathogen <i>Piscirickettsia salmonis</i> Through Comparative Genomics. <i>Frontiers in Microbiology</i> , 2021, 12, 673216.	3.5	6
2604	The tracheal virome of broiler chickens with respiratory disease complex in Iran: the metagenomics study. <i>Iranian Journal of Microbiology</i> , 2021, 13, 337-344.	0.8	1
2606	Rooting the Animal Tree of Life. <i>Molecular Biology and Evolution</i> , 2021, 38, 4322-4333.	8.9	93
2607	Metagenomic compendium of 189,680 DNA viruses from the human gut microbiome. <i>Nature Microbiology</i> , 2021, 6, 960-970.	13.3	248
2608	The occurrence of antibiotic resistance genes in the microbiota of yak, beef and dairy cattle characterized by a metagenomic approach. <i>Journal of Antibiotics</i> , 2021, 74, 508-518.	2.0	11
2609	The Usefulness of a Duplex RT-qPCR during the Recent Yellow Fever Brazilian Epidemic: Surveillance of Vaccine Adverse Events, Epizootics and Vectors. <i>Pathogens</i> , 2021, 10, 693.	2.8	5
2610	Evaluating microbiome-directed fibre snacks in gnotobiotic mice and humans. <i>Nature</i> , 2021, 595, 91-95.	27.8	70
2611	Linking genomic and physiological characteristics of psychrophilic <i>Arthrobacter</i> to metagenomic data to explain global environmental distribution. <i>Microbiome</i> , 2021, 9, 136.	11.1	9
2612	Gene Expression Profile and Co-Expression Network of Pearl Gentian Grouper under Cold Stress by Integrating Illumina and PacBio Sequences. <i>Animals</i> , 2021, 11, 1745.	2.3	12

#	ARTICLE	IF	CITATIONS
2613	Identical sequences found in distant genomes reveal frequent horizontal transfer across the bacterial domain. <i>ELife</i> , 2021, 10, .	6.0	23
2614	Whole Transcriptome Analysis Reveals a Potential Regulatory Mechanism of LncRNA-FNIP2/miR-24-3p/FNIP2 Axis in Chicken Adipogenesis. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 653798.	3.7	14
2616	Microbial Biofilm Diversity and Prevalence of Antibiotic Resistance Genes in Drinking Water Distribution System of Peshawar, Pakistan. <i>Water (Switzerland)</i> , 2021, 13, 1788.	2.7	1
2617	Simulation study and comparative evaluation of viral contiguous sequence identification tools. <i>BMC Bioinformatics</i> , 2021, 22, 329.	2.6	18
2618	Whole genome data from <i>Curtobacterium flaccumfaciens</i> pv. <i>flaccumfaciens</i> strains associated with tan spot of mungbean and soybean reveal diverse plasmid profiles. <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 1216-1222.	2.6	7
2619	Morphometric and population genomic evidence for species divergence in the <i>Chimarrichthys</i> fish complex of the Tibetan Plateau. <i>Molecular Phylogenetics and Evolution</i> , 2021, 159, 107117.	2.7	5
2620	Metagenomics of mine tailing rhizospheric communities and its selection for plant establishment towards bioremediation. <i>Microbiological Research</i> , 2021, 247, 126732.	5.3	15
2621	A de novo transcriptional atlas in <i>Danaus plexippus</i> reveals variability in dosage compensation across tissues. <i>Communications Biology</i> , 2021, 4, 791.	4.4	9
2622	Viromes in marine ecosystems reveal remarkable invertebrate RNA virus diversity. <i>Science China Life Sciences</i> , 2022, 65, 426-437.	4.9	22
2623	Freshwater <i>Chlorobia</i> Exhibit Metabolic Specialization among Cosmopolitan and Endemic Populations. <i>MSystems</i> , 2021, 6, .	3.8	8
2625	Bacterioplankton respond with similar transcriptional activity to allochthonous dissolved organic matter in coastal and offshore Lake Michigan. <i>Limnology and Oceanography</i> , 2021, 66, 3162-3175.	3.1	2
2626	Arabinogalactan-proteins from non-coniferous gymnosperms have unusual structural features. <i>Carbohydrate Polymers</i> , 2021, 261, 117831.	10.2	11
2627	Genome-Wide Identification, Structure Characterization, Expression Pattern Profiling, and Substrate Specificity of the Metal Tolerance Protein Family in <i>Canavalia rosea</i> (Sw.) DC. <i>Plants</i> , 2021, 10, 1340.	3.5	4
2629	Challenges, Strategies, and Perspectives for Reference-Independent Longitudinal Multi-Omic Microbiome Studies. <i>Frontiers in Genetics</i> , 2021, 12, 666244.	2.3	8
2630	Microbial species performance responses to environmental changes: genomic traits and nutrient availability. <i>Ecology</i> , 2021, 102, e03382.	3.2	3
2631	<i>In situ</i> microcosms deployed at the coast of British Columbia (Canada) to study dilbit weathering and associated microbial communities under marine conditions. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	2.7	7
2632	The elusive parasite: comparing macroscopic, immunological, and genomic approaches to identifying malaria in human skeletal remains from Sayala, Egypt (third to sixth centuries AD). <i>Archaeological and Anthropological Sciences</i> , 2021, 13, 115.	1.8	11
2633	Interplay of Biologically Active Carbon Filtration and Chlorine-Based Disinfection in Mitigating the Dissemination of Antibiotic Resistance Genes in Water Reuse Distribution Systems. <i>Environmental Science & Technology</i> , 2021, 55, 8329-8340.	10.0	17

#	ARTICLE	IF	CITATIONS
2634	The Diversity of Viral Community in Invasive Fruit Flies (<i>Bactrocera</i> and <i>Zeugodacus</i>) Revealed by Meta-transcriptomics. <i>Microbial Ecology</i> , 2022, 83, 739-752.	2.8	14
2635	Implementing metatranscriptomics to unveil the mechanism of bioaugmentation adopted in a continuous anaerobic process treating cow manure. <i>Bioresource Technology</i> , 2021, 330, 124962.	9.6	21
2636	Co-expression network analysis identifies novel molecular pathways associated with cadmium and pyriproxyfen testicular toxicity in <i>Gammarus fossarum</i> . <i>Aquatic Toxicology</i> , 2021, 235, 105816.	4.0	9
2638	A spinach genome assembly with remarkable completeness, and its use for rapid identification of candidate genes for agronomic traits. <i>DNA Research</i> , 2021, 28, .	3.4	11
2639	The Genome Assembly and Annotation of the Apollo Butterfly <i>Parnassius apollo</i> , a Flagship Species for Conservation Biology. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	19
2640	Covariance of Phytoplankton, Bacteria, and Zooplankton Communities Within Microcystis Blooms in San Francisco Estuary. <i>Frontiers in Microbiology</i> , 2021, 12, 632264.	3.5	7
2641	Combined analysis of metagenomic data revealed consistent changes of gut microbiome structure and function in inflammatory bowel disease. <i>Journal of Applied Microbiology</i> , 2021, 131, 3018-3031.	3.1	14
2642	Bioinformatics Accelerates the Major Tetrad: A Real Boost for the Pharmaceutical Industry. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6184.	4.1	16
2644	Characterization of nucleic acids from extracellular vesicle-enriched human sweat. <i>BMC Genomics</i> , 2021, 22, 425.	2.8	21
2645	Decreased Abundance of <i>Akkermansia muciniphila</i> Leads to the Impairment of Insulin Secretion and Glucose Homeostasis in Lean Type 2 Diabetes. <i>Advanced Science</i> , 2021, 8, e2100536.	11.2	68
2646	Evidence of Transcriptional Shutoff by Pathogenic Viral Haemorrhagic Septicaemia Virus in Rainbow Trout. <i>Viruses</i> , 2021, 13, 1129.	3.3	4
2647	Global mRNA and miRNA Analysis Reveal Key Processes in the Initial Response to Infection with WSSV in the Pacific Whiteleg Shrimp. <i>Viruses</i> , 2021, 13, 1140.	3.3	11
2648	Mitogenomics and Evolutionary History of Rodent Whipworms (<i>Trichuris</i> spp.) Originating from Three Biogeographic Regions. <i>Life</i> , 2021, 11, 540.	2.4	2
2649	Comparative Genomic Insights Into the Taxonomic Classification, Diversity, and Secondary Metabolic Potentials of <i>Kitasatospora</i> , a Genus Closely Related to <i>Streptomyces</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 683814.	3.5	11
2650	A Comparative Analysis on the Structure and Function of the <i>Panax notoginseng</i> Rhizosphere Microbiome. <i>Frontiers in Microbiology</i> , 2021, 12, 673512.	3.5	16
2652	Development of a kinetic model to evaluate thiosulfate-driven denitrification and anammox (TDDA) process. <i>Water Research</i> , 2021, 198, 117155.	11.3	21
2653	Genomic insights into the sessile life and biofouling of barnacles (Crustacea: Cirripedia). <i>Heliyon</i> , 2021, 7, e07291.	3.2	7
2654	Evaluation of a Next-Generation Sequencing Metagenomics Assay to Detect and Quantify DNA Viruses in Plasma from Transplant Recipients. <i>Journal of Molecular Diagnostics</i> , 2021, 23, 719-731.	2.8	11

#	ARTICLE	IF	CITATIONS
2655	Precise Species Identification for <i>Acinetobacter</i> : a Genome-Based Study with Description of Two Novel <i>Acinetobacter</i> Species. <i>MSystems</i> , 2021, 6, e0023721.	3.8	13
2656	A synbiotic intervention modulates meta-omics signatures of gut redox potential and acidity in elective caesarean born infants. <i>BMC Microbiology</i> , 2021, 21, 191.	3.3	13
2658	ORFograph: search for novel insecticidal protein genes in genomic and metagenomic assembly graphs. <i>Microbiome</i> , 2021, 9, 149.	11.1	3
2660	Diversity and metagenome analysis of a hydrocarbon-degrading bacterial consortium from asphalt lakes located in Wietze, Germany. <i>AMB Express</i> , 2021, 11, 89.	3.0	22
2661	Genome Assembly of the Cold-Tolerant Leaf Beetle <i>Gonioctena quinquepunctata</i> , an Important Resource for Studying Its Evolution and Reproductive Barriers between Species. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	2
2662	Genomic analyses provide comprehensive insights into the domestication of bast fiber crop ramie (<i>Boehmeria nivea</i>). <i>Plant Journal</i> , 2021, 107, 787-800.	5.7	18
2663	A global metagenomic map of urban microbiomes and antimicrobial resistance. <i>Cell</i> , 2021, 184, 3376-3393.e17.	28.9	164
2664	Development and application of the Faba_bean_130K targeted next-generation sequencing SNP genotyping platform based on transcriptome sequencing. <i>Theoretical and Applied Genetics</i> , 2021, 134, 3195-3207.	3.6	13
2665	Microbiomes attached to fresh perennial ryegrass are temporally resilient and adapt to changing ecological niches. <i>Microbiome</i> , 2021, 9, 143.	11.1	9
2666	An integrated gene catalog and over 10,000 metagenome-assembled genomes from the gastrointestinal microbiome of ruminants. <i>Microbiome</i> , 2021, 9, 137.	11.1	110
2667	Role of organic matter and microbial communities in mercury retention and methylation in sediments near run-of-river hydroelectric dams. <i>Science of the Total Environment</i> , 2021, 774, 145686.	8.0	17
2668	Caloric restriction disrupts the microbiota and colonization resistance. <i>Nature</i> , 2021, 595, 272-277.	27.8	109
2669	The Evolution of Interdependence in a Four-Way Mealybug Symbiosis. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	9
2670	Ecology of inorganic sulfur auxiliary metabolism in widespread bacteriophages. <i>Nature Communications</i> , 2021, 12, 3503.	12.8	97
2673	Triple RNA-Seq characterizes aphid gene expression in response to infection with unequally virulent strains of the endosymbiont <i>Hamiltonella defensa</i> . <i>BMC Genomics</i> , 2021, 22, 449.	2.8	10
2674	Characterization of the Blood and Cerebrospinal Fluid Microbiome in Children with Bacterial Meningitis and Its Potential Correlation with Inflammation. <i>MSystems</i> , 2021, 6, e0004921.	3.8	10
2675	Homeotic transformation from stamen to petal in <i>Lilium</i> is associated with MADS-box genes and hormone signal transduction. <i>Plant Growth Regulation</i> , 2021, 95, 49-64.	3.4	8
2676	A few dominant bacteria and their genomic basis in mediating distinct ecosystem functions. <i>Environmental Microbiology</i> , 2021, 23, 4478-4488.	3.8	2

#	ARTICLE	IF	CITATIONS
2679	Reshaping of bacterial molecular hydrogen metabolism contributes to the outgrowth of commensal <i>E. coli</i> during gut inflammation. <i>ELife</i> , 2021, 10, .	6.0	9
2680	Dietary fiber intake, the gut microbiome, and chronic systemic inflammation in a cohort of adult men. <i>Genome Medicine</i> , 2021, 13, 102.	8.2	62
2681	A microbial eukaryote with a unique combination of purple bacteria and green algae as endosymbionts. <i>Science Advances</i> , 2021, 7, .	10.3	21
2684	A chromosomal assembly of the soybean cyst nematode genome. <i>Molecular Ecology Resources</i> , 2021, 21, 2407-2422.	4.8	10
2685	Complete genome sequence of <i>Arthrobacter</i> sp. PAMC25564 and its comparative genome analysis for elucidating the role of CAZymes in cold adaptation. <i>BMC Genomics</i> , 2021, 22, 403.	2.8	11
2686	ARG-SHINE: improve antibiotic resistance class prediction by integrating sequence homology, functional information and deep convolutional neural network. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab066.	3.2	6
2687	Transcriptome analysis provides insights into copper toxicology in piebald naked carp (<i>Gymnocypris</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf .	2.8	3
2688	Comparative Study of Metagenomics and Metatranscriptomics to Reveal Microbiomes in Overwintering Pepper Fruits. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6202.	4.1	6
2692	Genome analysis to decipher syntrophy in the bacterial consortium â€˜SCPâ€™™ for azo dye degradation. <i>BMC Microbiology</i> , 2021, 21, 177.	3.3	12
2693	Comparative transcriptome analysis reveals genes and pathways associated with anthocyanins in strawberry. <i>Journal of Berry Research</i> , 2021, 11, 317-332.	1.4	7
2695	Physiological and Transcriptomic Variability Indicative of Differences in Key Functions Within a Single Coral Colony. <i>Frontiers in Marine Science</i> , 2021, 8, .	2.5	10
2697	Comparative anatomical and transcriptomic analyses of the color variation of leaves in <i>Aquilaria sinensis</i> . <i>PeerJ</i> , 2021, 9, e11586.	2.0	1
2698	Codon usage bias and dinucleotide preference in 29 <i>Drosophila</i> species. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	5
2699	Whole-genome microsynteny-based phylogeny of angiosperms. <i>Nature Communications</i> , 2021, 12, 3498.	12.8	53
2700	Going to extremes â€“ a metagenomic journey into the dark matter of life. <i>FEMS Microbiology Letters</i> , 2021, 368, .	1.8	16
2701	Virome comparison of deferred blood donations obtained from different geographic regions in the Sao Paulo State, Brazil. <i>Transfusion and Apheresis Science</i> , 2021, 60, 103106.	1.0	1
2703	Helarchaeota and co-occurring sulfate-reducing bacteria in subseafloor sediments from the Costa Rica Margin. <i>ISME Communications</i> , 2021, 1, .	4.2	16
2704	Gut Microbiota Dysbiosis Accelerates Prostate Cancer Progression Through Increased LPCAT1 Expression and Enhanced DNA Repair Pathways. <i>Frontiers in Oncology</i> , 2021, 11, 679712.	2.8	18

#	ARTICLE	IF	CITATIONS
2705	VB ₁₂ Path for Accurate Metagenomic Profiling of Microbially Driven Cobalamin Synthesis Pathways. <i>MSystems</i> , 2021, 6, e0049721.	3.8	5
2706	Indoor bacterial, fungal and viral species and functional genes in urban and rural schools in Shanxi Province, China—association with asthma, rhinitis and rhinoconjunctivitis in high school students. <i>Microbiome</i> , 2021, 9, 138.	11.1	34
2707	efam: an <i>e</i>xpanded, metaproteome-supported HMM profile database of viral protein <i>fam</i>ilies. <i>Bioinformatics</i> , 2021, 37, 4202-4208.	4.1	15
2708	Mantis: flexible and consensus-driven genome annotation. <i>GigaScience</i> , 2021, 10, .	6.4	22
2709	Insights into Autotrophic Activities and Carbon Flow in Iron-Rich Pelagic Aggregates (Iron Snow). <i>Microorganisms</i> , 2021, 9, 1368.	3.6	2
2710	Comparative genomics of the <i>Pseudomonas corrugata</i> subgroup reveals high species diversity and allows the description of <i>Pseudomonas ogarae</i> sp. nov.. <i>Microbial Genomics</i> , 2021, 7, .	2.0	19
2711	Diverse Viruses Carrying Genes for Microbial Extremotolerance in the Atacama Desert Hyperarid Soil. <i>MSystems</i> , 2021, 6, .	3.8	27
2712	Rapid ecosystem-scale consequences of acute deoxygenation on a Caribbean coral reef. <i>Nature Communications</i> , 2021, 12, 4522.	12.8	42
2714	Rampant prophage movement among transient competitors drives rapid adaptation during infection. <i>Science Advances</i> , 2021, 7, .	10.3	14
2715	Chromosome-Level Genome Sequence of the Black Koji Fungus <i>Aspergillus luchuensis</i> RIB2601. <i>Microbiology Resource Announcements</i> , 2021, 10, e0038421.	0.6	4
2716	Towards omics-based predictions of planktonic functional composition from environmental data. <i>Nature Communications</i> , 2021, 12, 4361.	12.8	16
2717	Optimizing experimental design for genome sequencing and assembly with Oxford Nanopore Technologies. <i>GigaByte</i> , 0, 2021, 1-26.	0.0	10
2719	Identification of Three Clf-Sdr Subfamily Proteins in <i>Staphylococcus warneri</i> , and Comparative Genomics Analysis of a Locus Encoding CWA Proteins in <i>Staphylococcus</i> Species. <i>Frontiers in Microbiology</i> , 2021, 12, 691087.	3.5	0
2720	Genome sequence of the cardiopulmonary canid nematode <i>Angiostrongylus vasorum</i> reveals species-specific genes with potential involvement in coagulopathy. <i>Genomics</i> , 2021, 113, 2695-2701.	2.9	2
2721	Transcriptome landscapes of multiple tissues highlight the genes involved in the flavor metabolic pathway in Chinese chive (<i>Allium tuberosum</i>). <i>Genomics</i> , 2021, 113, 2145-2157.	2.9	13
2722	RaFAH: Host prediction for viruses of Bacteria and Archaea based on protein content. <i>Patterns</i> , 2021, 2, 100274.	5.9	53
2723	Linking meta-omics to the kinetics of denitrification intermediates reveals pH-dependent causes of N ₂ O emissions and nitrite accumulation in soil. <i>ISME Journal</i> , 2022, 16, 26-37.	9.8	40
2724	Genomic Analysis of <i>Sarcomyxa edulis</i> Reveals the Basis of Its Medicinal Properties and Evolutionary Relationships. <i>Frontiers in Microbiology</i> , 2021, 12, 652324.	3.5	6

#	ARTICLE	IF	CITATIONS
2725	Comparative transcriptome analysis reveals regulatory network and regulators associated with proanthocyanidin accumulation in persimmon. BMC Plant Biology, 2021, 21, 356.	3.6	13
2727	Two Reference-Quality Sea Snake Genomes Reveal Their Divergent Evolution of Adaptive Traits and Venom Systems. Molecular Biology and Evolution, 2021, 38, 4867-4883.	8.9	20
2728	Quantifying the effects of hydrogen on carbon assimilation in a seafloor microbial community associated with ultramafic rocks. ISME Journal, 2022, 16, 257-271.	9.8	12
2729	Biosynthetic potential of uncultured Antarctic soil bacteria revealed through long-read metagenomic sequencing. ISME Journal, 2022, 16, 101-111.	9.8	40
2730	A novel thylakoid-less isolate fills a billion-year gap in the evolution of Cyanobacteria. Current Biology, 2021, 31, 2857-2867.e4.	3.9	30
2731	Paraliobacillus salinarum sp. nov., isolated from saline soil in Yingkou, China. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	1.7	4
2732	A microbial consortium-based product promotes potato yield by recruiting rhizosphere bacteria involved in nitrogen and carbon metabolisms. Microbial Biotechnology, 2021, 14, 1961-1975.	4.2	8
2733	Functional diversity of microbial communities in inactive seafloor sulfide deposits. FEMS Microbiology Ecology, 2021, 97, .	2.7	16
2734	Bacteriophage classification for assembled contigs using graph convolutional network. Bioinformatics, 2021, 37, i25-i33.	4.1	50
2735	Pathogenic and Indigenous Denitrifying Bacteria are Transcriptionally Active and Key Multi-Antibiotic-Resistant Players in Wastewater Treatment Plants. Environmental Science & Technology, 2021, 55, 10862-10874.	10.0	60
2736	Characterization of Spacesuit Associated Microbial Communities and Their Implications for NASA Missions. Frontiers in Microbiology, 2021, 12, 608478.	3.5	5
2737	Root Endophytes and Ginkgo biloba Are Likely to Share and Compensate Secondary Metabolic Processes, and Potentially Exchange Genetic Information by LTR-RTs. Frontiers in Plant Science, 2021, 12, 704985.	3.6	12
2738	PZLAST: an ultra-fast amino acid sequence similarity search server against public metagenomes. Bioinformatics, 2021, 37, 3944-3946.	4.1	5
2740	Chironomus ramosus Larval Microbiome Composition Provides Evidence for the Presence of Detoxifying Enzymes. Microorganisms, 2021, 9, 1571.	3.6	10
2742	Next-Generation Sequencing Analysis of the Tineola bisselliella Larval Gut Transcriptome Reveals Candidate Enzymes for Keratin Digestion. Genes, 2021, 12, 1113.	2.4	3
2743	Exploration of the <i>Ixodes ricinus</i> virosphere unveils an extensive virus diversity including novel coltiviruses and other reoviruses. Virus Evolution, 2021, 7, veab066.	4.9	8
2744	Evolutionary transition to XY sex chromosomes associated with Y-linked duplication of a male hormone gene in a terrestrial isopod. Heredity, 2021, 127, 266-277.	2.6	5
2746	Identification and characteristics of a novel aminoglycoside phosphotransferase, APH(3-III), from an MDR clinical isolate of <i>Brucella intermedia</i> . Journal of Antimicrobial Chemotherapy, 2021, 76, 2787-2794.	3.0	5

#	ARTICLE	IF	CITATIONS
2747	Ancient saltern metagenomics: tracking changes in microbes and their viruses from the underground to the surface. <i>Environmental Microbiology</i> , 2021, 23, 3477-3498.	3.8	6
2748	Monitoring of hospital sewage shows both promise and limitations as an early-warning system for carbapenemase-producing <i>Enterobacterales</i> in a low-prevalence setting. <i>Water Research</i> , 2021, 200, 117261.	11.3	24
2749	Impact of water quality variations on the microbial metagenome across coastal waters in Shenzhen, south China. <i>Ocean and Coastal Management</i> , 2021, 208, 105612.	4.4	4
2750	Metatranscriptomics for the Human Microbiome and Microbial Community Functional Profiling. <i>Annual Review of Biomedical Data Science</i> , 2021, 4, 279-311.	6.5	36
2752	Genome-wide identification and expression analysis of aquaporin family in <i>Canavalia rosea</i> and their roles in the adaptation to saline-alkaline soils and drought stress. <i>BMC Plant Biology</i> , 2021, 21, 333.	3.6	13
2753	Seasonal Variation in Transcriptomic Profiling of <i>Tetrastigma hemsleyanum</i> Fully Developed Tuberous Roots Enriches Candidate Genes in Essential Metabolic Pathways and Phytohormone Signaling. <i>Frontiers in Plant Science</i> , 2021, 12, 659645.	3.6	12
2754	Diversity and function of culturable actinobacteria in the root-associated of <i>Salvia miltiorrhiza</i> Bunge. <i>PeerJ</i> , 2021, 9, e11749.	2.0	3
2756	Metagenome-Assembled Genomes Contribute to Unraveling of the Microbiome of Cocoa Fermentation. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0058421.	3.1	11
2757	Holocene life and microbiome profiling in ancient tropical Lake Chalco, Mexico. <i>Scientific Reports</i> , 2021, 11, 13848.	3.3	8
2758	Sulfate differentially stimulates but is not respired by diverse anaerobic methanotrophic archaea. <i>ISME Journal</i> , 2022, 16, 168-177.	9.8	21
2760	PON-Sol2: Prediction of Effects of Variants on Protein Solubility. <i>International Journal of Molecular Sciences</i> , 2021, 22, 8027.	4.1	10
2761	Glacier ice archives nearly 15,000-year-old microbes and phages. <i>Microbiome</i> , 2021, 9, 160.	11.1	59
2763	Genome mapping coupled with CRISPR gene editing reveals a P450 gene confers avermectin resistance in the beet armyworm. <i>PLoS Genetics</i> , 2021, 17, e1009680.	3.5	44
2764	Molecular Mechanisms of Coral Persistence Within Highly Urbanized Locations in the Port of Miami, Florida. <i>Frontiers in Marine Science</i> , 2021, 8, .	2.5	14
2766	orthofisher: a broadly applicable tool for automated gene identification and retrieval. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	12
2767	Whole genome analysis of Aichivirus A, isolated from a child, suffering from gastroenteritis, in Pakistan. <i>Virus Research</i> , 2021, 299, 198437.	2.2	2
2768	Draft genome of <i>Puya raimondii</i> (Bromeliaceae), the Queen of the Andes. <i>Genomics</i> , 2021, 113, 2537-2546.	2.9	4
2769	Metagenomics: a path to understanding the gut microbiome. <i>Mammalian Genome</i> , 2021, 32, 282-296.	2.2	27

#	ARTICLE	IF	CITATIONS
2770	Effects of graphene on morphology, microstructure and transcriptomic profiling of <i>Pinus tabuliformis</i> Carr. roots. <i>PLoS ONE</i> , 2021, 16, e0253812.	2.5	13
2771	<i>Rhodococcus</i> comparative genomics reveals a phylogenomic-dependent non-ribosomal peptide synthetase distribution: insights into biosynthetic gene cluster connection to an orphan metabolite. <i>Microbial Genomics</i> , 2021, 7, .	2.0	10
2772	Transcriptome sequencing and drought resistance gene annotation in <i>Quercus liaotungensis</i> leaves. <i>Acta Physiologiae Plantarum</i> , 2021, 43, 1.	2.1	1
2773	SAUTE: sequence assembly using target enrichment. <i>BMC Bioinformatics</i> , 2021, 22, 375.	2.6	9
2776	Mating-Type Locus Organization and Mating-Type Chromosome Differentiation in the Bipolar Edible Button Mushroom <i>Agaricus bisporus</i> . <i>Genes</i> , 2021, 12, 1079.	2.4	17
2777	Male Differentiation in the Marine Copepod <i>Oithona nana</i> Reveals the Development of a New Nervous Ganglion and Lin12-Notch-Repeat Protein-Associated Proteolysis. <i>Biology</i> , 2021, 10, 657.	2.8	1
2778	Disproportionate microbial responses to decadal drainage on a Siberian floodplain. <i>Global Change Biology</i> , 2021, 27, 5124-5140.	9.5	8
2780	Dynamics of Baltic Sea phages driven by environmental changes. <i>Environmental Microbiology</i> , 2021, 23, 4576-4594.	3.8	5
2781	Termite gas emissions select for hydrogenotrophic microbial communities in termite mounds. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	15
2782	Multicomponent nature underlies the extraordinary mechanical properties of spider dragline silk. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	51
2785	Fishing for the Virome of Tropical Tuna. <i>Viruses</i> , 2021, 13, 1291.	3.3	8
2786	Four chromosome scale genomes and a pan-genome annotation to accelerate pecan tree breeding. <i>Nature Communications</i> , 2021, 12, 4125.	12.8	49
2787	Linking plasmid-based beta-lactamases to their bacterial hosts using single-cell fusion PCR. <i>ELife</i> , 2021, 10, .	6.0	18
2788	Complexity and Local Specificity of the Virome Associated with Tospovirus-Transmitting Thrips Species. <i>Journal of Virology</i> , 2021, 95, e0059721.	3.4	25
2789	Genome sequences and in silico effector mining of <i>Corynespora cassicola</i> CC_29 and <i>Corynespora olivacea</i> CBS 114450. <i>Archives of Microbiology</i> , 2021, 203, 5257-5265.	2.2	6
2791	Transcriptomic response of <i>Daphnia magna</i> to nitrogen- or phosphorus-limited diet. <i>Ecology and Evolution</i> , 2021, 11, 11009-11019.	1.9	3
2792	Deep Ancestral Introgression Shapes Evolutionary History of Dragonflies and Damselflies. <i>Systematic Biology</i> , 2022, 71, 526-546.	5.6	32
2793	In-situ expressions of comammox <i>Nitrospira</i> along the Yangtze River. <i>Water Research</i> , 2021, 200, 117241.	11.3	18

#	ARTICLE	IF	CITATIONS
2794	DeepGraphGO: graph neural network for large-scale, multispecies protein function prediction. <i>Bioinformatics</i> , 2021, 37, i262-i271.	4.1	50
2795	Chromosome-level genome assembly and population genetic analysis of a critically endangered rhododendron provide insights into its conservation. <i>Plant Journal</i> , 2021, 107, 1533-1545.	5.7	35
2796	Transcriptome Characterization and Identification of Molecular Markers (SNP, SSR, and Indels) in the Medicinal Plant <i>Sarcandra glabra</i> spp.. <i>BioMed Research International</i> , 2021, 2021, 1-11.	1.9	6
2799	Tracking the transition to agriculture in Southern Europe through ancient DNA analysis of dental calculus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	29
2800	<i>Exiguobacterium algae</i> sp. nov. and <i>Exiguobacterium qingdaonense</i> sp. nov., two novel moderately halotolerant bacteria isolated from the coastal algae. <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 1399-1406.	1.7	12
2801	Airborne and indigenous microbiomes co-drive the rebound of antibiotic resistome during compost storage. <i>Environmental Microbiology</i> , 2021, 23, 7483-7496.	3.8	10
2802	Comparative Genomics Revealing Insights into Niche Separation of the Genus <i>Methylophilus</i> . <i>Microorganisms</i> , 2021, 9, 1577.	3.6	0
2805	The integrin-mediated adhesive complex in the ancestor of animals, fungi, and amoebae. <i>Current Biology</i> , 2021, 31, 3073-3085.e3.	3.9	6
2806	Trehalose-Induced Remodelling of the Human Microbiota Affects <i>Clostridioides difficile</i> Infection Outcome in an In Vitro Colonic Model: A Pilot Study. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 670935.	3.9	18
2807	Inheritance of DNA methylation differences in the mangrove <i>Rhizophora mangle</i> . <i>Evolution & Development</i> , 2021, 23, 351-374.	2.0	13
2808	Dispersal strategies shape persistence and evolution of human gut bacteria. <i>Cell Host and Microbe</i> , 2021, 29, 1167-1176.e9.	11.0	66
2809	TRAPID 2.0: a web application for taxonomic and functional analysis of <i>de novo</i> transcriptomes. <i>Nucleic Acids Research</i> , 2021, 49, e101-e101.	14.5	21
2810	Characterizations of heavy metal contamination, microbial community, and resistance genes in a tailing of the largest copper mine in China. <i>Environmental Pollution</i> , 2021, 280, 116947.	7.5	80
2811	Improved draft reference genome for the Glassy-winged Sharpshooter (<i>Homalodisca</i>) Tj ETQq1 1 0.784314 rgBT1/Overlock 10 Tf 502	1.8	9
2812	Landfill microbiome harbour plastic degrading genes: A metagenomic study of solid waste dumping site of Gujarat, India. <i>Science of the Total Environment</i> , 2021, 779, 146184.	8.0	41
2813	Large-scale protein level comparison of Deltaproteobacteria reveals cohesive metabolic groups. <i>ISME Journal</i> , 2022, 16, 307-320.	9.8	71
2816	Draft Genome Sequences of Two <i>Cadophora</i> Strains Isolated from Water and a Nonalcoholic Beverage Ingredient. <i>Microbiology Resource Announcements</i> , 2021, 10, e0036821.	0.6	0
2817	Genomic Diversity of CRESS DNA Viruses in the Eukaryotic Virome of Swine Feces. <i>Microorganisms</i> , 2021, 9, 1426.	3.6	8

#	ARTICLE	IF	CITATIONS
2818	Dual species dynamic transcripts reveal the interaction mechanisms between <i>Chrysanthemum morifolium</i> and <i>Alternaria alternata</i> . <i>BMC Genomics</i> , 2021, 22, 523.	2.8	8
2819	Defensive hypervariable regions confer superinfection exclusion in microviruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	13
2820	Invasion history shapes host transcriptomic response to a body-snatching parasite. <i>Molecular Ecology</i> , 2021, 30, 4321-4337.	3.9	2
2821	Single worm transcriptomics identifies a developmental core network of oscillating genes with deep conservation across nematodes. <i>Genome Research</i> , 2021, 31, 1590-1601.	5.5	18
2822	An Exploratory Study for the Association of Gut Microbiome with Efficacy of Immune Checkpoint Inhibitor in Patients with Hepatocellular Carcinoma. <i>Journal of Hepatocellular Carcinoma</i> , 2021, Volume 8, 809-822.	3.7	17
2823	Comparative genome and transcriptome analyses reveal innate differences in response to host plants by two color forms of the two-spotted spider mite <i>Tetranychus urticae</i> . <i>BMC Genomics</i> , 2021, 22, 569.	2.8	4
2824	Metagenomic insights into soil microbial communities involved in carbon cycling along an elevation climosequences. <i>Environmental Microbiology</i> , 2021, 23, 4631-4645.	3.8	48
2825	Subcellular Distribution of Dietary Methyl-Mercury in <i>Gammarus fossarum</i> and Its Impact on the Amphipod Proteome. <i>Environmental Science & Technology</i> , 2021, 55, 10514-10523.	10.0	4
2826	Lytic archaeal viruses infect abundant primary producers in Earth's crust. <i>Nature Communications</i> , 2021, 12, 4642.	12.8	28
2827	Structural and Functional Genomics of the Resistance of Cacao to <i>Phytophthora palmivora</i> . <i>Pathogens</i> , 2021, 10, 961.	2.8	9
2828	Exploring the Prevalence and Distribution Patterns of Antibiotic Resistance Genes in Bovine Gut Microbiota Using a Metagenomic Approach. <i>Microbial Drug Resistance</i> , 2021, 27, 980-990.	2.0	6
2830	Genomic diversity and ecology of human-associated <i>Akkermansia</i> species in the gut microbiome revealed by extensive metagenomic assembly. <i>Genome Biology</i> , 2021, 22, 209.	8.8	65
2831	Transcriptome analysis identifies putative genes involved in triterpenoid biosynthesis in <i>Platycodon grandiflorus</i> . <i>Planta</i> , 2021, 254, 34.	3.2	18
2832	<i>Pelorhabdus rhamnosifermentans</i> gen. nov., sp. nov., a strictly anaerobic rhamnose degrader from freshwater lake sediment. <i>Systematic and Applied Microbiology</i> , 2021, 44, 126225.	2.8	8
2833	The USDA-ARS Ag100Pest Initiative: High-Quality Genome Assemblies for Agricultural Pest Arthropod Research. <i>Insects</i> , 2021, 12, 626.	2.2	31
2834	Benchmark of thirteen bioinformatic pipelines for metagenomic virus diagnostics using datasets from clinical samples. <i>Journal of Clinical Virology</i> , 2021, 141, 104908.	3.1	28
2835	De novo transcriptome assembly of the Southern Ocean copepod <i>Rhincalanus gigas</i> sheds light on developmental changes in gene expression. <i>Marine Genomics</i> , 2021, 58, 100835.	1.1	8
2836	Sex-Biased Gene Expression of <i>Mesobuthus martensii</i> Collected from Gansu Province, China, Reveals Their Different Therapeutic Potentials. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-15.	1.2	3

#	ARTICLE	IF	CITATIONS
2837	Genetic and phenotypic analysis of the pathogenic potential of two novel <i>Chlamydia gallinacea</i> strains compared to <i>Chlamydia psittaci</i> . <i>Scientific Reports</i> , 2021, 11, 16516.	3.3	9
2838	Ecogenomics and Adaptation Strategies of Southern Ocean Viral Communities. <i>MSystems</i> , 2021, 6, e0039621.	3.8	11
2839	Comprehensive Strain-Level Analysis of the Gut Microbe <i>Faecalibacterium prausnitzii</i> in Patients with Liver Cirrhosis. <i>MSystems</i> , 2021, 6, e0077521.	3.8	6
2840	Complete genome sequencing and comparative genome analysis of the extremely halophilic archaea, <i>Haloterrigena daqingensis</i> . <i>Biotechnology and Applied Biochemistry</i> , 2022, 69, 1482-1488.	3.1	3
2842	Genomic characterization of three marine fungi, including <i>Emericellopsis atlantica</i> sp. nov. with signatures of a generalist lifestyle and marine biomass degradation. <i>IMA Fungus</i> , 2021, 12, 21.	3.8	23
2843	Technology dictates algorithms: recent developments in read alignment. <i>Genome Biology</i> , 2021, 22, 249.	8.8	51
2844	The microbial population structure and function of peanut peanut and their effects on aflatoxin contamination. <i>LWT - Food Science and Technology</i> , 2021, 148, 111285.	5.2	4
2846	Metatranscriptomic analysis identifies different viral-like sequences in two neotropical <i>Mansoniini</i> mosquito species. <i>Virus Research</i> , 2021, 301, 198455.	2.2	4
2847	Host Colonization as a Major Evolutionary Force Favoring the Diversity and the Emergence of the Worldwide Multidrug-Resistant <i>Escherichia coli</i> ST131. <i>MBio</i> , 2021, 12, e0145121.	4.1	13
2848	The Sisal Virome: Uncovering the Viral Diversity of Agave Varieties Reveals New and Organ-Specific Viruses. <i>Microorganisms</i> , 2021, 9, 1704.	3.6	5
2849	Expanding Asgard members in the domain of Archaea sheds new light on the origin of eukaryotes. <i>Science China Life Sciences</i> , 2022, 65, 818-829.	4.9	18
2850	De Novo Transcriptome Assembly, Functional Annotation and SSR Marker Discovery of Qinling Takin (<i>Budorcas taxicolor bedfordi</i>). <i>Animals</i> , 2021, 11, 2366.	2.3	2
2851	Seasonality affects function and complexity but not diversity of the rhizosphere microbiome in European temperate grassland. <i>Science of the Total Environment</i> , 2021, 784, 147036.	8.0	12
2852	Comparative study of gut microbiota from captive and confiscated-rescued wild pangolins. <i>Journal of Genetics and Genomics</i> , 2021, 48, 825-835.	3.9	20
2853	Biogeochemical Gradients in a Serpentinization-Influenced Aquifer: Implications for Gas Exchange Between the Subsurface and Atmosphere. <i>Journal of Geophysical Research G: Biogeosciences</i> , 2021, 126, e2020JG006209.	3.0	10
2854	Exploring the evolutionary process of alkannin/shikonin O-acetyltransferases by a reliable <i>Lithospermum erythrorhizon</i> genome. <i>DNA Research</i> , 2021, 28, .	3.4	5
2855	Conservation of Resistance-Nodulation-Cell Division Efflux Pump-Mediated Antibiotic Resistance in <i>Burkholderia cepacia</i> Complex and <i>Burkholderia pseudomallei</i> Complex Species. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, e0092021.	3.2	6
2856	Computational Structural Genomics Unravels Common Folds and Novel Families in the Secretome of Fungal Phytopathogen <i>Magnaporthe oryzae</i> . <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 1267-1280.	2.6	49

#	ARTICLE	IF	CITATIONS
2859	Metagenomic Analysis of Fecal Archaea, Bacteria, Eukaryota, and Virus in Przewalski's Horses Following Anthelmintic Treatment. <i>Frontiers in Veterinary Science</i> , 2021, 8, 708512.	2.2	6
2860	The role of oxygen in stimulating methane production in wetlands. <i>Global Change Biology</i> , 2021, 27, 5831-5847.	9.5	23
2862	Diversity and functions of bacterial communities in water and sediment from the watershed of the Tama River flowing a highly urbanized area. <i>Fisheries Science</i> , 2021, 87, 697-715.	1.6	5
2863	Genome-Resolved Meta-Analysis of the Microbiome in Oil Reservoirs Worldwide. <i>Microorganisms</i> , 2021, 9, 1812.	3.6	10
2864	GNNfam. , 2021, , .		0
2865	Phylum barrier and <i>Escherichia coli</i> intra-species phylogeny drive the acquisition of antibiotic-resistance genes. <i>Microbial Genomics</i> , 2021, 7, .	2.0	9
2866	Identification and Characterization of a Novel Aminoglycoside 3''-Nucleotidyltransferase, ANT(3'')-IId, From <i>Acinetobacter lwoffii</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 728216.	3.5	0
2867	The Resistome and Mobilome of Multidrug-Resistant <i>Staphylococcus sciuri</i> C2865 Unveil a Transferable Trimethoprim Resistance Gene, Designated <i>dmrE</i> , Spread Unnoticed. <i>MSystems</i> , 2021, 6, e0051121.	3.8	7
2869	A Draft Genome of the Ginger Species <i>Alpinia nigra</i> and New Insights into the Genetic Basis of Flexistylus. <i>Genes</i> , 2021, 12, 1297.	2.4	6
2870	Metabolic Differentiation of Co-occurring <i>Accumulibacter</i> Clades Revealed through Genome-Resolved Metatranscriptomics. <i>MSystems</i> , 2021, 6, e0047421.	3.8	15
2871	Metagenomic Insights Into Ecosystem Function in the Microbial Mats of a Large Hypersaline Coastal Lagoon System. <i>Frontiers in Marine Science</i> , 2021, 8, .	2.5	2
2872	Genomic comparison of non-photosynthetic plants from the family Balanophoraceae with their photosynthetic relatives. <i>PeerJ</i> , 2021, 9, e12106.	2.0	7
2873	Audit of laboratory sensitivity of human papillomavirus and cytology testing in a cervical screening program. <i>International Journal of Cancer</i> , 2021, 149, 2083-2090.	5.1	4
2874	Altered synthesis of genes associated with short-chain fatty acids in the gut of patients with atrial fibrillation. <i>BMC Genomics</i> , 2021, 22, 634.	2.8	23
2875	Utilization of Transcriptome, Small RNA, and Degradome Sequencing to Provide Insights Into Drought Stress and Rewatering Treatment in <i>Medicago ruthenica</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 675903.	3.6	9
2876	Human reference gut microbiome catalog including newly assembled genomes from under-represented Asian metagenomes. <i>Genome Medicine</i> , 2021, 13, 134.	8.2	47
2877	Metagenomic insights into the effects of submerged plants on functional potential of microbial communities in wetland sediments. <i>Marine Life Science and Technology</i> , 2021, 3, 405-415.	4.6	19
2878	Methane-derived carbon flows into host-virus networks at different trophic levels in soil. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	38

#	ARTICLE	IF	CITATIONS
2879	Elucidation of the speciation history of three sister species of crown-of-thorns starfish (<i>Acanthaster</i> spp.) based on genomic analysis. DNA Research, 2021, 28, .	3.4	6
2880	Premature neonatal gut microbial community patterns supporting an epithelial TLR-mediated pathway for necrotizing enterocolitis. BMC Microbiology, 2021, 21, 225.	3.3	11
2882	Comparative transcriptomics provides a strategy for phylogenetic analysis and SSR marker development in Chaenomeles. Scientific Reports, 2021, 11, 16441.	3.3	2
2883	Safety Assessment of <i>Lactiplantibacillus</i> (formerly <i>Lactobacillus</i>) plantarum Q180. Journal of Microbiology and Biotechnology, 2021, 31, 1420-1429.	2.1	7
2885	Genome erosion and evidence for an intracellular niche “exploring the biology of mycoplasmas in Atlantic salmon. Aquaculture, 2021, 541, 736772.	3.5	27
2887	Post-weaning shifts in microbiome composition and metabolism revealed by over 25€000 pig gut metagenome-assembled genomes. Microbial Genomics, 2021, 7, .	2.0	9
2888	The Transcriptional Response of Soil Bacteria to Long-Term Warming and Short-Term Seasonal Fluctuations in a Terrestrial Forest. Frontiers in Microbiology, 2021, 12, 666558.	3.5	8
2889	A high-quality draft genome for Melaleuca alternifolia (tea tree): a new platform for evolutionary genomics of myrtaceous terpene-rich species. GigaByte, 0, 2021, 1-15.	0.0	11
2890	High-quality genome assembly of the soybean fungal pathogen <i>Cercospora kikuchii</i>. G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	5
2891	Homeostasis drives intense microbial trace metal processing on marine particles. Limnology and Oceanography, 2021, 66, 3842-3855.	3.1	8
2893	Coordinated Diel Gene Expression of Cyanobacteria and Their Microbiome. Microorganisms, 2021, 9, 1670.	3.6	7
2894	Enhanced Recovery of Microbial Genes and Genomes From a Marine Water Column Using Long-Read Metagenomics. Frontiers in Microbiology, 2021, 12, 708782.	3.5	17
2895	Genome- and community-level interaction insights into the ecological role of archaea in rare earth element mine drainage in South China. Water Research, 2021, 201, 117331.	11.3	18
2896	Metagenomic analysis of a mega-city river network reveals microbial compositional heterogeneity among urban and peri-urban river stretch. Science of the Total Environment, 2021, 783, 146960.	8.0	12
2897	Metagenomics-Based Analysis of the Age-Related Cumulative Effect of Antibiotic Resistance Genes in Gut Microbiota. Antibiotics, 2021, 10, 1006.	3.7	12
2898	Heuristic algorithms for best match graph editing. Algorithms for Molecular Biology, 2021, 16, 19.	1.2	2
2899	Revealing the community and metabolic potential of active methanotrophs by targeted metagenomics in the Zoige wetland of the Tibetan Plateau. Environmental Microbiology, 2021, 23, 6520-6535.	3.8	8
2900	Microbial signatures in the lower airways of mechanically ventilated COVID-19 patients associated with poor clinical outcome. Nature Microbiology, 2021, 6, 1245-1258.	13.3	101

#	ARTICLE	IF	CITATIONS
2902	K fertilizer alleviates N ₂ O emissions by regulating the abundance of nitrifying and denitrifying microbial communities in the soil-plant system. <i>Journal of Environmental Management</i> , 2021, 291, 112579.	7.8	15
2903	Proteorhodopsin Phototrophy in Antarctic Coastal Waters. <i>MSphere</i> , 2021, 6, e0052521.	2.9	2
2905	Draft genome assemblies for tree pathogens <i>Phytophthora pseudosyringae</i> and <i>Phytophthora boehmeriae</i> . <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	4
2906	Newly identified proviruses in <i>Thermotogota</i> suggest that viruses are the vehicles on the highways of interphylum gene sharing. <i>Environmental Microbiology</i> , 2021, 23, 7105-7120.	3.8	4
2907	North Sea spring bloom-associated Gammaproteobacteria fill diverse heterotrophic niches. <i>Environmental Microbiomes</i> , 2021, 16, 15.	5.0	32
2908	Using Reduced Amino-Acid Alphabets and Simulated Annealing to Identify Antimicrobial Peptides. <i>Lecture Notes in Networks and Systems</i> , 2022, , 11-21.	0.7	0
2909	Long-term effects of acetylene on denitrifying N ₂ O production: Biomass performance and microbial community. <i>Journal of Water Process Engineering</i> , 2021, 42, 102137.	5.6	9
2910	The gut microbiome buffers dietary adaptation in Bronze Age domesticated dogs. <i>IScience</i> , 2021, 24, 102816.	4.1	7
2911	Elucidation of an anaerobic pathway for metabolism of L-carnitine-derived ¹³ C-butyrobetaine to trimethylamine in human gut bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	30
2912	Metagenomic approaches reveal differences in genetic diversity and relative abundance of nitrifying bacteria and archaea in contrasting soils. <i>Scientific Reports</i> , 2021, 11, 15905.	3.3	28
2913	Bog ecosystems as a playground for plant-microbe coevolution: bryophytes and vascular plants harbour functionally adapted bacteria. <i>Microbiome</i> , 2021, 9, 170.	11.1	28
2914	Genome Sequence of <i>Rhizoctonia solani</i> Anastomosis Group 4 Strain Rhs4ca, a Widespread Pathomycete in Field Crops. <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 826-829.	2.6	12
2915	Longitudinal study on the effects of growth-promoting and therapeutic antibiotics on the dynamics of chicken cloacal and litter microbiomes and resistomes. <i>Microbiome</i> , 2021, 9, 178.	11.1	30
2920	Deciphering Symbiotic Interactions of <i>Candidatus Aenigmarchaeota</i> with Inferred Horizontal Gene Transfers and Co-occurrence Networks. <i>MSystems</i> , 2021, 6, e0060621.	3.8	11
2921	Revealing RNA virus diversity and evolution in unicellular algae transcriptomes. <i>Virus Evolution</i> , 2021, 7, .	4.9	28
2922	Coral microbiome manipulation elicits metabolic and genetic restructuring to mitigate heat stress and evade mortality. <i>Science Advances</i> , 2021, 7, .	10.3	114
2923	Conditional stomatal closure in a fern shares molecular features with flowering plant active stomatal responses. <i>Current Biology</i> , 2021, 31, 4560-4570.e5.	3.9	12
2924	Transcriptome-wide SNPs for <i>Botrychium lunaria</i> ferns enable fine-grained analysis of ploidy and population structure. <i>Molecular Ecology Resources</i> , 2022, 22, 254-271.	4.8	3

#	ARTICLE	IF	CITATIONS
2925	Expansion of Internal Hyphal Growth in <i>Fusarium</i> Head Blightâ€“Infected Grains Contributes to the Elevated Mycotoxin Production During the Malting Process. <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 793-802.	2.6	9
2926	Functional meta-omics provide critical insights into long- and short-read assemblies. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	6
2930	Genetic and physiological traits conferring tolerance to ocean acidification in mesophotic corals. <i>Global Change Biology</i> , 2021, 27, 5276-5294.	9.5	13
2931	Phage Diversity in the Human Gut Microbiome: a Taxonomistâ€™s Perspective. <i>MSystems</i> , 2021, 6, e0079921.	3.8	15
2932	Comparative Genomics Provides Insights into the Genetic Diversity and Evolution of the DPANN Superphylum. <i>MSystems</i> , 2021, 6, e0060221.	3.8	9
2933	PhyloFisher: A phylogenomic package for resolving eukaryotic relationships. <i>PLoS Biology</i> , 2021, 19, e3001365.	5.6	51
2934	Sequencing and de Novo Assembly of Abaca (<i>Musa textilis</i> NÃ©e) var. Abuab Genome. <i>Genes</i> , 2021, 12, 1202.	2.4	9
2936	Increase in carbohydrate content and variation in microbiome are related to the drought tolerance of <i>Codonopsis pilosula</i> . <i>Plant Physiology and Biochemistry</i> , 2021, 165, 19-35.	5.8	12
2937	The worm affair: fidelity and environmental adaptation in symbiont species that coâ€“occur in vestimentiferan tubeworms. <i>Environmental Microbiology Reports</i> , 2021, 13, 744-752.	2.4	3
2938	Removal of geosmin and 2-methylisoborneol from aquaculture water by novel, alginate-based carriers: Performance and metagenomic analysis. <i>Journal of Water Process Engineering</i> , 2021, 42, 102125.	5.6	6
2939	Orthology Clusters from Gene Trees with <i>Possvm</i> . <i>Molecular Biology and Evolution</i> , 2021, 38, 5204-5208.	8.9	12
2940	Effect of dietary <i>Bacillus licheniformis</i> on growth, intestinal health, and resistance to nitrite stress in Pacific white shrimp <i>Litopenaeus vannamei</i> . <i>Aquaculture International</i> , 2021, 29, 2555-2573.	2.2	3
2941	Spatial and Temporal Dynamics of Prokaryotic and Viral Community Assemblages in a Lotic System (Manatee Springs, Florida). <i>Applied and Environmental Microbiology</i> , 2021, 87, e0064621.	3.1	10
2942	Sulfidogenic Microbial Communities of the Uzen High-Temperature Oil Field in Kazakhstan. <i>Microorganisms</i> , 2021, 9, 1818.	3.6	13
2943	Gut-microbiota-targeted diets modulate human immune status. <i>Cell</i> , 2021, 184, 4137-4153.e14.	28.9	482
2944	Revealing the role of Plant Growth Promoting Rhizobacteria in suppressive soils against <i>Fusarium oxysporum</i> f.sp. <i>cubense</i> based on metagenomic analysis. <i>Heliyon</i> , 2021, 7, e07636.	3.2	14
2945	Studying the virome in psychiatric disease. <i>Schizophrenia Research</i> , 2021, 234, 78-86.	2.0	3
2946	Comparative Genomics Reveals Thermal Adaptation and a High Metabolic Diversity in <i>Candidatus</i> <i>Bathyarchaeia</i> . <i>MSystems</i> , 2021, 6, e0025221.	3.8	20

#	ARTICLE	IF	CITATIONS
2947	Alterations in bile acid metabolizing gut microbiota and specific bile acid genes as a precision medicine to subclassify NAFLD. <i>Physiological Genomics</i> , 2021, 53, 336-348.	2.3	17
2948	Temporal and nutritional effects on the weaner pig ileal microbiota. <i>Animal Microbiome</i> , 2021, 3, 58.	3.8	2
2949	Diversity and abundance of the functional genes and bacteria associated with RDX degradation at a contaminated site pre- and post-biostimulation. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 6463-6475.	3.6	3
2951	Conservative and Atypical Ferritins of Sponges. <i>International Journal of Molecular Sciences</i> , 2021, 22, 8635.	4.1	7
2952	Population Genomics Reveals Gene Flow and Adaptive Signature in Invasive Weed <i>Mikania micrantha</i> . <i>Genes</i> , 2021, 12, 1279.	2.4	2
2953	Isolation of a Virulent <i>Aeromonas salmonicida</i> subsp. <i>masoucida</i> Bacteriophage and Its Application in Phage Therapy in Turbot (<i>Scophthalmus maximus</i>). <i>Applied and Environmental Microbiology</i> , 2021, 87, e0146821.	3.1	17
2954	Transcriptome analysis of two <i>Pogostemon cablin</i> chemotypes reveals genes related to patchouli alcohol biosynthesis. <i>PeerJ</i> , 2021, 9, e12025.	2.0	11
2955	A chromosome-scale genome assembly and karyotype of the ctenophore <i>Hormiphora californensis</i> . <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	18
2956	Tumor microbiome contributes to an aggressive phenotype in the basal-like subtype of pancreatic cancer. <i>Communications Biology</i> , 2021, 4, 1019.	4.4	57
2957	Pan-transcriptome identifying master genes and regulation network in response to drought and salt stresses in Alfalfa (<i>Medicago sativa</i> L.). <i>Scientific Reports</i> , 2021, 11, 17203.	3.3	16
2958	Ancient viral integrations in marsupials: a potential antiviral defence. <i>Virus Evolution</i> , 2021, 7, veab076.	4.9	7
2959	Unveiling the Gut Microbiota and Resistome of Wild Cotton Mice, <i>Peromyscus gossypinus</i> , from Heavy Metal- and Radionuclide-Contaminated Sites in the Southeastern United States. <i>Microbiology Spectrum</i> , 2021, 9, e0009721.	3.0	4
2960	Living to the High Extreme: Unraveling the Composition, Structure, and Functional Insights of Bacterial Communities Thriving in the Arsenic-Rich Salar de Huasco Altiplanic Ecosystem. <i>Microbiology Spectrum</i> , 2021, 9, e0044421.	3.0	16
2962	Magnetotactic bacteria from the human gut microbiome associated with orientation and navigation regions of the brain. <i>Journal of Oceanology and Limnology</i> , 0, , 1.	1.3	5
2963	Microbial Plankton Community Structure and Function Responses to Vitamin B ₁₂ and B ₁ Amendments in an Upwelling System. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0152521.	3.1	15
2964	Dynamics of the fecal microbiome and antimicrobial resistome in commercial piglets during the weaning period. <i>Scientific Reports</i> , 2021, 11, 18091.	3.3	5
2965	Subacute Exposure to an Environmentally Relevant Dose of Di-(2-ethylhexyl) Phthalate during Gestation Alters the Cecal Microbiome, but Not Pregnancy Outcomes in Mice. <i>Toxics</i> , 2021, 9, 215.	3.7	5
2966	Microbiome degrading linear alkylbenzene sulfonate in activated sludge. <i>Journal of Hazardous Materials</i> , 2021, 418, 126365.	12.4	9

#	ARTICLE	IF	CITATIONS
2967	Underrepresented high diversity of class 1 integrons in the environment uncovered by PacBio sequencing using a new primer. <i>Science of the Total Environment</i> , 2021, 787, 147611.	8.0	11
2968	Acesulfame aerobic biodegradation by enriched consortia and <i>Chelatococcus</i> spp.: Kinetics, transformation products, and genomic characterization. <i>Water Research</i> , 2021, 202, 117454.	11.3	21
2969	A Taxon-Wise Insight Into Rock Weathering and Nitrogen Fixation Functional Profiles of Proglacial Systems. <i>Frontiers in Microbiology</i> , 2021, 12, 627437.	3.5	7
2970	Transcriptome and Resequencing Analyses Provide Insight into Differences in Organic Acid Accumulation in Two Pear Varieties. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9622.	4.1	5
2971	Examining Signatures of Natural Selection in Antifungal Resistance Genes Across <i>Aspergillus</i> Fungi. <i>Frontiers in Fungal Biology</i> , 2021, 2, .	2.0	2
2973	Trycycler: consensus long-read assemblies for bacterial genomes. <i>Genome Biology</i> , 2021, 22, 266.	8.8	175
2974	A Synergistic Consortium Involved in <i>rac</i> -Dichlorprop Degradation as Revealed by DNA Stable Isotope Probing and Metagenomic Analysis. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0156221.	3.1	6
2975	Deep Investigating the Changes of Gut Microbiome and Its Correlation With the Shifts of Host Serum Metabolome Around Parturition in Sows. <i>Frontiers in Microbiology</i> , 2021, 12, 729039.	3.5	7
2976	Submerged macrophytes recruit unique microbial communities and drive functional zonation in an aquatic system. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 7517-7528.	3.6	9
2977	FunOrder: A robust and semi-automated method for the identification of essential biosynthetic genes through computational molecular co-evolution. <i>PLoS Computational Biology</i> , 2021, 17, e1009372.	3.2	9
2978	Chronic liver disease enables gut <i>Enterococcus faecalis</i> colonization to promote liver carcinogenesis. <i>Nature Cancer</i> , 2021, 2, 1039-1054.	13.2	26
2979	The Response of Airborne Mycobiome to Dust Storms in the Eastern Mediterranean. <i>Journal of Fungi</i> (Basel, Switzerland), 2021, 7, 802.	3.5	6
2980	Selective butanol production from carbon monoxide by an enriched anaerobic culture. <i>Science of the Total Environment</i> , 2022, 806, 150579.	8.0	13
2981	Performance of Multiple Metagenomics Pipelines in Understanding Microbial Diversity of a Low-Biomass Spacecraft Assembly Facility. <i>Frontiers in Microbiology</i> , 2021, 12, 685254.	3.5	9
2982	Host-symbiont transcriptomic changes during natural bleaching and recovery in the leaf coral <i>Pavona decussata</i> . <i>Science of the Total Environment</i> , 2022, 806, 150656.	8.0	10
2983	2-Arachidonoylglycerol as an Endogenous Cue Negatively Regulates Attachment of the Mussel <i>Perna viridis</i> . <i>Frontiers in Marine Science</i> , 2021, 8, .	2.5	2
2985	Genome-Wide Transcription Factor DNA Binding Sites and Gene Regulatory Networks in <i>Clostridium thermocellum</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 695517.	3.5	3
2986	Effects of a long-term anoxic warming scenario on microbial community structure and functional potential of permafrost-affected soil. <i>Permafrost and Periglacial Processes</i> , 2021, 32, 641-656.	3.4	11

#	ARTICLE	IF	CITATIONS
2987	Structure-aware proteinâ€“protein interaction site prediction using deep graph convolutional network. <i>Bioinformatics</i> , 2021, 38, 125-132.	4.1	64
2988	Comparative analysis of long nonâ€“coding RNAâ€“expression profiles induced by resveratrol and metformin treatment for hepatic insulin resistance. <i>International Journal of Molecular Medicine</i> , 2021, 48, .	4.0	7
2989	Over 50,000 Metagenomically Assembled Draft Genomes for the Human Oral Microbiome Reveal New Taxa. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 246-259.	6.9	38
2990	Comparative genomic analysis reveals metabolic flexibility of <i>Woesearchaeota</i> . <i>Nature Communications</i> , 2021, 12, 5281.	12.8	25
2992	Chromosome-Level Genome Sequence of <i>Aspergillus chevalieri</i> M1, Isolated from Katsuobushi. <i>Microbiology Resource Announcements</i> , 2021, 10, e0038521.	0.6	1
2993	Tracing Eukaryotic Ribosome Biogenesis Factors Into the Archaeal Domain Sheds Light on the Evolution of Functional Complexity. <i>Frontiers in Microbiology</i> , 2021, 12, 739000.	3.5	11
2994	Comparative Genomics Provides Insight into the Function of Broad-Host Range Sponge Symbionts. <i>MBio</i> , 2021, 12, e0157721.	4.1	5
2995	Chromosome-Level Genome Assembly and Annotation of the Fiber Flax (<i>Linum usitatissimum</i>) Genome. <i>Frontiers in Genetics</i> , 2021, 12, 735690.	2.3	15
2996	Identification of tick-borne pathogens using metagenomic analyses in <i>H. longicornis</i> feeding on humans in downtown Beijing. <i>Animal Diseases</i> , 2021, 1, .	1.4	1
2997	Genomic Stability and Genetic Defense Systems in <i>Dolosigranulum pigrum</i> , a Candidate Beneficial Bacterium from the Human Microbiome. <i>MSystems</i> , 2021, 6, e0042521.	3.8	11
2998	Direct Metatranscriptomic Survey of the Sunflower Microbiome and Virome. <i>Viruses</i> , 2021, 13, 1867.	3.3	6
2999	Identification of Tick-Borne Pathogens and Genotyping of <i>Coxiella burnetii</i> in <i>Rhipicephalus microplus</i> in Yunnan Province, China. <i>Frontiers in Microbiology</i> , 2021, 12, 736484.	3.5	11
3000	Understanding Responses of Soil Microbiome to the Nitrogen and Phosphorus Addition in <i>Metasequoia glyptostroboides</i> Plantations of Different Ages. <i>Microbial Ecology</i> , 2022, 84, 565-579.	2.8	5
3001	Metagenomic insights into nitrogen and phosphorus cycling at the soil aggregate scale driven by organic material amendments. <i>Science of the Total Environment</i> , 2021, 785, 147329.	8.0	56
3002	Metagenomics-based insights into the microbial community profiling and flavor development potentiality of baijiu Daqu and huangjiu wheat Qu. <i>Food Research International</i> , 2022, 152, 110707.	6.2	38
3004	Elucidating gene expression adaptation of phylogenetically divergent coral holobionts under heat stress. <i>Nature Communications</i> , 2021, 12, 5731.	12.8	29
3006	OXA-900, a Novel OXA Sub-Family Carbapenemase Identified in <i>Citrobacter freundii</i> , Evades Detection by Commercial Molecular Diagnostics Tests. <i>Microorganisms</i> , 2021, 9, 1898.	3.6	4
3007	Exploring syntenic conservation across genomes for phylogenetic studies of organisms subjected to horizontal gene transfers: A case study with <i>Cyanobacteria</i> and <i>cyanolichens</i> . <i>Molecular Phylogenetics and Evolution</i> , 2021, 162, 107100.	2.7	8

#	ARTICLE	IF	CITATIONS
3009	Ectomycorrhizal fungal decay traits along a soil nitrogen gradient. <i>New Phytologist</i> , 2021, 232, 2152-2164.	7.3	14
3010	Microbial characterisation and Cold-Adapted Predicted Protein (CAPP) database construction from the active layer of Greenland's permafrost. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	2.7	2
3011	Blood Meals With Active and Heat-Inactivated Serum Modifies the Gene Expression and Microbiome of <i>Aedes albopictus</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 724345.	3.5	3
3012	<i>Novisyntrophococcus fermenticellae</i> gen. nov., sp. nov., isolated from an anaerobic fermentation cellar of Chinese strong-flavour baijiu. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	1.7	10
3013	Aquatic microbial community is partially functionally redundant: Insights from an in situ reciprocal transplant experiment. <i>Science of the Total Environment</i> , 2021, 786, 147433.	8.0	3
3014	<i>Pacificispira spongiicola</i> gen. nov., sp. nov., a nitrate-reducing bacterium isolated from tropical western Pacific. <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 2083-2090.	1.7	1
3016	Complete Genome Sequence of <i>Weissella confusa</i> LM1 and Comparative Genomic Analysis. <i>Frontiers in Microbiology</i> , 2021, 12, 749218.	3.5	6
3017	OrtSuite: from genomes to prediction of microbial interactions within targeted ecosystem processes. <i>Life Science Alliance</i> , 2021, 4, e202101167.	2.8	4
3018	Histamine-forming ability of <i>Lentilactobacillus parabuchneri</i> in reduced salt Cheddar cheese. <i>Food Microbiology</i> , 2021, 98, 103789.	4.2	5
3019	Genome sequencing of the neotype strain CBS 554.65 reveals the MAT1 α 2 locus of <i>Aspergillus niger</i> . <i>BMC Genomics</i> , 2021, 22, 679.	2.8	5
3020	MetaFunPrimer: an Environment-Specific, High-Throughput Primer Design Tool for Improved Quantification of Target Genes. <i>MSystems</i> , 2021, 6, e0020121.	3.8	2
3021	Transcriptional Activity of Predominant <i>Streptococcus</i> Species at Multiple Oral Sites Associate With Periodontal Status. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 752664.	3.9	7
3022	The chromosome-scale genome of <i>Magnolia officinalis</i> provides insight into the evolutionary position of magnoliids. <i>IScience</i> , 2021, 24, 102997.	4.1	14
3023	Metagenomics and metatranscriptomics uncover the microbial community associated with high S ₀ production in a denitrifying desulfurization granular sludge reactor. <i>Water Research</i> , 2021, 203, 117505.	11.3	12
3024	Tracing the fate of wastewater viruses reveals catchment-scale virome diversity and connectivity. <i>Water Research</i> , 2021, 203, 117568.	11.3	17
3025	The First Whole Genome Sequencing of <i>Sanghuangporus sanghuang</i> Provides Insights into Its Medicinal Application and Evolution. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 787.	3.5	15
3026	Adaptation of Fig Wasps (Agaodinae) to Their Host Revealed by Large-Scale Transcriptomic Data. <i>Insects</i> , 2021, 12, 815.	2.2	5
3027	Comparative metabolomic and transcriptomic analyses revealed the differential accumulation of secondary metabolites during the ripening process of acerola cherry (<i>Malpighia</i>) Tj ETQq1 1 0.784314 rgBT.4 Overlock 10 Tf 50		

#	ARTICLE	IF	CITATIONS
3028	Comparative transcriptome analysis at the onset of speciation in a mimetic butterfly—The Ithomiini <i>Melinaea marsaeus</i> . <i>Journal of Evolutionary Biology</i> , 2021, 34, 1704-1721.	1.7	2
3029	Long-read metagenomics of multiple displacement amplified DNA of low-biomass human gut phageomes by SACRA preprocessing chimeric reads. <i>DNA Research</i> , 2021, 28, .	3.4	11
3030	Diel-Regulated Transcriptional Cascades of Microbial Eukaryotes in the North Pacific Subtropical Gyre. <i>Frontiers in Microbiology</i> , 2021, 12, 682651.	3.5	6
3031	Ecological diversification reveals routes of pathogen emergence in endemic <i>Vibrio vulnificus</i> populations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	14
3032	RNA virome abundance and diversity is associated with host age in a bird species. <i>Virology</i> , 2021, 561, 98-106.	2.4	19
3034	Molecular and evolutionary basis for survival, its failure, and virulence factors of the zoonotic nematode <i>Anisakis pegreffii</i> . <i>Genomics</i> , 2021, 113, 2891-2905.	2.9	11
3035	Bacteria and Archaea Synergistically Convert Glycine Betaine to Biogenic Methane in the Formosa Cold Seep of the South China Sea. <i>MSystems</i> , 2021, 6, e0070321.	3.8	15
3036	Improved Large-Scale Homology Search by Two-Step Seed Search Using Multiple Reduced Amino Acid Alphabets. <i>Genes</i> , 2021, 12, 1455.	2.4	1
3037	Shotgun metagenomics assessment of the resistome, mobilome, pathogen dynamics and their ecological control modes in full-scale urban wastewater treatment plants. <i>Journal of Hazardous Materials</i> , 2021, 418, 126387.	12.4	20
3038	The regulatory role of gibberellin related genes DKGA2ox1 and MIR171f_3 in persimmon dwarfism. <i>Plant Science</i> , 2021, 310, 110958.	3.6	9
3040	MetaPlatanus: a metagenome assembler that combines long-range sequence links and species-specific features. <i>Nucleic Acids Research</i> , 2021, 49, e130-e130.	14.5	6
3041	MINTIA: a metagenomic INserT integrated assembly and annotation tool. <i>PeerJ</i> , 2021, 9, e11885.	2.0	0
3042	Genome Evolution of Filamentous Cyanobacterium Nostoc Species: From Facultative Symbiosis to Free Living. <i>Microorganisms</i> , 2021, 9, 2015.	3.6	4
3043	Genomic and Phenotypic Analysis of COVID-19-Associated Pulmonary Aspergillosis Isolates of <i>Aspergillus fumigatus</i> . <i>Microbiology Spectrum</i> , 2021, 9, e0001021.	3.0	31
3044	Comparison of DNA and RNA sequencing of total nucleic acids from human cervix for metagenomics. <i>Scientific Reports</i> , 2021, 11, 18852.	3.3	9
3045	Prokaryotic viruses impact functional microorganisms in nutrient removal and carbon cycle in wastewater treatment plants. <i>Nature Communications</i> , 2021, 12, 5398.	12.8	49
3046	Identification of <i>Faecalibacterium prausnitzii</i> strains for gut microbiome-based intervention in Alzheimer's-type dementia. <i>Cell Reports Medicine</i> , 2021, 2, 100398.	6.5	42
3047	Antibiotic-induced disturbances of the gut microbiota result in accelerated breast tumor growth. <i>IScience</i> , 2021, 24, 103012.	4.1	41

#	ARTICLE	IF	CITATIONS
3048	Periodontitis associates with species-specific gene expression of the oral microbiota. <i>Npj Biofilms and Microbiomes</i> , 2021, 7, 76.	6.4	18
3049	Different ways to play it cool: Transcriptomic analysis sheds light on different activity patterns of three amphipod species under long-term cold exposure. <i>Molecular Ecology</i> , 2021, 30, 5735-5751.	3.9	11
3050	Metagenomic Analysis: A Pathway Toward Efficiency Using High-Performance Computing. <i>Lecture Notes in Networks and Systems</i> , 2022, , 555-565.	0.7	0
3051	Struo2: efficient metagenome profiling database construction for ever-expanding microbial genome datasets. <i>PeerJ</i> , 2021, 9, e12198.	2.0	24
3053	Ectomycorrhizal access to organic nitrogen mediates CO2 fertilization response in a dominant temperate tree. <i>Nature Communications</i> , 2021, 12, 5403.	12.8	20
3055	Comparative Phylogenomic Analysis Reveals Evolutionary Genomic Changes and Novel Toxin Families in Endophytic <i>Liberibacter</i> Pathogens. <i>Microbiology Spectrum</i> , 2021, 9, e0050921.	3.0	6
3056	Genomic Insights into the Ecological Role and Evolution of a Novel <i>Thermoplasmata</i> Order, <i>“Candidatus</i> <i>Sysuiplasmatales</i> . <i>Applied and Environmental Microbiology</i> , 2021, 87, e0106521.	3.1	3
3057	Mining nematode protein secretomes to explain lifestyle and host specificity. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009828.	3.0	11
3059	Enhanced dewatering of activated sludge by acid assisted Heat-CaO2 treatment: Simultaneously removing heavy metals and mitigating antibiotic resistance genes. <i>Journal of Hazardous Materials</i> , 2021, 418, 126248.	12.4	24
3060	The Human Gut Resistome up to Extreme Longevity. <i>MSphere</i> , 2021, 6, e0069121.	2.9	12
3061	Analysis of Microorganism Diversity in <i>Haemaphysalis longicornis</i> From Shaanxi, China, Based on Metagenomic Sequencing. <i>Frontiers in Genetics</i> , 2021, 12, 723773.	2.3	1
3062	Telomere-to-telomere gapless chromosomes of banana using nanopore sequencing. <i>Communications Biology</i> , 2021, 4, 1047.	4.4	86
3063	Regulation of carbon assimilation in <i>Skeletonema costatum</i> under diel variations. <i>Science of the Total Environment</i> , 2021, 786, 147533.	8.0	2
3065	Metagenomic Insights Into the Microbial Iron Cycle of Subseafloor Habitats. <i>Frontiers in Microbiology</i> , 2021, 12, 667944.	3.5	4
3066	Cell wall proteomic analysis of the cnidarian photosymbionts <i>Breviolum minutum</i> and <i>Cladocodium goreau</i> . <i>Journal of Eukaryotic Microbiology</i> , 2021, , e12870.	1.7	7
3067	De novo Assembly, Annotation, and Analysis of Transcriptome Data of the Ladakh Ground Skink Provide Genetic Information on High-Altitude Adaptation. <i>Genes</i> , 2021, 12, 1423.	2.4	0
3068	Seasonality and Geography Have a Greater Influence than the Use of Chlorine-Based Cleaning Agents on the Microbiota of Bulk Tank Raw Milk. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0108121.	3.1	8
3069	Metabolomics integrated with transcriptomics reveals the distribution of iridoid and crocin metabolic flux in <i>Gardenia jasminoides</i> Ellis. <i>PLoS ONE</i> , 2021, 16, e0256802.	2.5	15

#	ARTICLE	IF	CITATIONS
3070	Bacterial Transformation of Aromatic Monomers in Softwood Black Liquor. <i>Frontiers in Microbiology</i> , 2021, 12, 735000.	3.5	9
3071	Metagenomics reveals contrasting energy utilization efficiencies of captive and wild camels (<i>Camelus</i>) Tj ETQq1 1 0.784314 rgBT /Over	2.6	11
3072	Characteristics of steroidogenesis-related factors in the musk gland of Chinese forest musk deer (<i>Moschus berezovskii</i>). <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2021, 212, 105916.	2.5	8
3073	An in vitro model for studies of attenuation of antibioticâ€inhibited growth of <i>Aggregatibacter actinomycetemcomitans</i> Y4 by polyamines. <i>Molecular Oral Microbiology</i> , 2021, 36, 308-315.	2.7	1
3074	Chromosome-Level Genome Sequence of <i>Aspergillus puulaauensis</i> MK2, a Fungus Isolated from a Dead Hard Tick. <i>Microbiology Resource Announcements</i> , 2021, 10, e0037221.	0.6	1
3075	Evaluating the Efficiency of DNA Metabarcoding to Analyze the Diet of <i>Hippocampus guttulatus</i> (Teleostea: Syngnathidae). <i>Life</i> , 2021, 11, 998.	2.4	9
3076	Microbial Phylogenetic Context Using Phylogenetic Outlines. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	6
3077	The influence of alfalfaâ€switchgrass intercropping on microbial community structure and function. <i>Environmental Microbiology</i> , 2021, 23, 6828-6843.	3.8	5
3078	Development of Genome-Wide Functional Markers Using Draft Genome Assembly of Guava (<i>Psidium</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 708332.	3.6	8
3079	Probiotics maintain the gut microbiome homeostasis during Indian Antarctic expedition by ship. <i>Scientific Reports</i> , 2021, 11, 18793.	3.3	6
3080	Diversity of microbial communities and genes involved in nitrous oxide emissions in Antarctic soils impacted by marine animals as revealed by metagenomics and 100 metagenome-assembled genomes. <i>Science of the Total Environment</i> , 2021, 788, 147693.	8.0	12
3081	The role of pollination in controlling <i>Ginkgo biloba</i> ovule development. <i>New Phytologist</i> , 2021, 232, 2353-2368.	7.3	8
3082	Hydrodynamic disturbance controls microbial community assembly and biogeochemical processes in coastal sediments. <i>ISME Journal</i> , 2022, 16, 750-763.	9.8	38
3083	Metagenomic Analysis of Saliva Reveals Disease-Associated Microbiotas in Patients With Periodontitis and Crohnâ€™s Disease-Associated Periodontitis. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 719411.	3.9	9
3084	Novel Freshwater Cyanophages Provide New Insights into Evolutionary Relationships between Freshwater and Marine Cyanophages. <i>Microbiology Spectrum</i> , 2021, 9, e0059321.	3.0	10
3085	The first chromosomeâ€level genome assembly of a green lacewing <i>Chrysopa pallens</i> and its implication for biological control. <i>Molecular Ecology Resources</i> , 2022, 22, 755-767.	4.8	7
3087	Effects of Rotations With Legume on Soil Functional Microbial Communities Involved in Phosphorus Transformation. <i>Frontiers in Microbiology</i> , 2021, 12, 661100.	3.5	19
3088	Activity and structure of methanogenic microbial communities in sediments of cascade hydropower reservoirs, Southwest China. <i>Science of the Total Environment</i> , 2021, 786, 147515.	8.0	7

#	ARTICLE	IF	CITATIONS
3090	Unraveling Gene Content Variation Across Eukaryotic Giant Viruses Based on Network Analyses and Host Associations. <i>Virus Evolution</i> , 2021, 7, veab081.	4.9	5
3091	Arms race in a cell: genomic, transcriptomic, and proteomic insights into intracellular phageâ€“bacteria interplay in deep-sea snail holobionts. <i>Microbiome</i> , 2021, 9, 182.	11.1	7
3092	Comprehensive metagenomic and enzyme activity analysis reveals the negatively influential and potentially toxic mechanism of polystyrene nanoparticles on nitrogen transformation in constructed wetlands. <i>Water Research</i> , 2021, 202, 117420.	11.3	77
3093	Increasing the power of interpretation for soil metaproteomics data. <i>Microbiome</i> , 2021, 9, 195.	11.1	25
3094	High Prevalence of Coinfecting Enteropathogens in Suspected Rotavirus Vaccine Breakthrough Cases. <i>Journal of Clinical Microbiology</i> , 2021, 59, e0123621.	3.9	9
3095	Soil type shapes the antibiotic resistome profiles of long-term manured soil. <i>Science of the Total Environment</i> , 2021, 786, 147361.	8.0	39
3096	Microbial river-to-sea continuum: gradients in benthic and planktonic diversity, osmoregulation and nutrient cycling. <i>Microbiome</i> , 2021, 9, 190.	11.1	29
3097	Differences between diploid donors are the main contributing factor for subgenome asymmetry measured in either gene ratio or relative diversity in allopolyploids. <i>Genome</i> , 2021, 64, 847-856.	2.0	1
3098	Infants with cystic fibrosis have altered fecal functional capacities with potential clinical and metabolic consequences. <i>BMC Microbiology</i> , 2021, 21, 247.	3.3	6
3099	Disease-induced changes in plant microbiome assembly and functional adaptation. <i>Microbiome</i> , 2021, 9, 187.	11.1	157
3102	Eight Metagenome-Assembled Genomes Provide Evidence for Microbial Adaptation in 20,000- to 1,000,000-Year-Old Siberian Permafrost. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0097221.	3.1	13
3103	Discovery of Novel Viruses Associated With the Invasive Cane Toad (<i>Rhinella marina</i>) in Its Native and Introduced Ranges. <i>Frontiers in Microbiology</i> , 2021, 12, 733631.	3.5	7
3104	Belowground responses of bacterial communities to foliar SA application over four plant generations. <i>Plant and Soil</i> , 2022, 470, 65-79.	3.7	2
3107	Effect of rice (<i>Oryza sativa</i> L.) genotype on yield: Evidence from recruiting spatially consistent rhizosphere microbiome. <i>Soil Biology and Biochemistry</i> , 2021, 161, 108395.	8.8	27
3108	Dual-chamber differs from single-chamber microbial electrosynthesis in biogas production performance under low temperature (15â„ƒ). <i>Bioresource Technology</i> , 2021, 337, 125377.	9.6	19
3109	Soil aeration rather than methanotrophic community drives methane uptake under drought in a subtropical forest. <i>Science of the Total Environment</i> , 2021, 792, 148292.	8.0	9
3110	Genes associated with antibiotic tolerance and synthesis of antimicrobial compounds in a mangrove with contrasting salinities. <i>Marine Pollution Bulletin</i> , 2021, 171, 112740.	5.0	7
3111	Metagenomic insights into the effect of thermal hydrolysis pre-treatment on microbial community of an anaerobic digestion system. <i>Science of the Total Environment</i> , 2021, 791, 148096.	8.0	31

#	ARTICLE	IF	CITATIONS
3112	Plants exert beneficial influence on soil microbiome in a HCH contaminated soil revealing advantage of microbe-assisted plant-based HCH remediation of a dumpsite. <i>Chemosphere</i> , 2021, 280, 130690.	8.2	24
3113	Effects of drift algae accumulation and nitrate loading on nitrogen cycling in a eutrophic coastal sediment. <i>Science of the Total Environment</i> , 2021, 790, 147749.	8.0	14
3114	A metatranscriptomic analysis of changing dynamics in the plankton communities adjacent to aquaculture leases in southern Tasmania, Australia. <i>Marine Genomics</i> , 2021, 59, 100858.	1.1	1
3115	Elevated colonic microbiota-associated paucimannosidic and truncated N-glycans in pediatric ulcerative colitis. <i>Journal of Proteomics</i> , 2021, 249, 104369.	2.4	4
3116	Improving the quality of Suancai by inoculating with <i>Lactobacillus plantarum</i> and <i>Pediococcus pentosaceus</i> . <i>Food Research International</i> , 2021, 148, 110581.	6.2	22
3117	Rapid start-up strategy of partial denitrification and microbially driven mechanism of nitrite accumulation mediated by dissolved organic matter. <i>Bioresource Technology</i> , 2021, 340, 125663.	9.6	39
3118	Antimicrobial resistance bacteria and genes detected in hospital sewage provide valuable information in predicting clinical antimicrobial resistance. <i>Science of the Total Environment</i> , 2021, 795, 148815.	8.0	24
3119	Simultaneous ammonium and sulfate biotransformation driven by aeration: Nitrogen/sulfur metabolism and metagenome-based microbial ecology. <i>Science of the Total Environment</i> , 2021, 794, 148650.	8.0	10
3120	Aminirod propionatiphilus gen. nov., sp. nov., an isolated secondary fermenter in methanogenic hydrocarbon-degrading communities. <i>International Biodeterioration and Biodegradation</i> , 2021, 165, 105323.	3.9	3
3121	Unraveling the metabolic pathway of choline-TMA-TMAO: Effects of gypenosides and implications for the therapy of TMAO related diseases. <i>Pharmacological Research</i> , 2021, 173, 105884.	7.1	9
3122	Comprehensive analysis of miRNA-mRNA/lncRNA during gonadal development of triploid female rainbow trout (<i>Oncorhynchus mykiss</i>). <i>Genomics</i> , 2021, 113, 3533-3543.	2.9	10
3123	Micro-nano aeration is a promising alternative for achieving high-rate partial nitrification. <i>Science of the Total Environment</i> , 2021, 795, 148899.	8.0	15
3124	A haploid diamondback moth (<i>Plutella xylostella</i> L.) genome assembly resolves 31 chromosomes and identifies a diamide resistance mutation. <i>Insect Biochemistry and Molecular Biology</i> , 2021, 138, 103622.	2.7	19
3125	Intercrop mulch affects soil biology and microbial diversity in rainfed transgenic Bt cotton hybrids. <i>Science of the Total Environment</i> , 2021, 794, 148787.	8.0	14
3126	Mitogenomics of Cladocera (Branchiopoda): Marked gene order rearrangements and independent predation roots. <i>Molecular Phylogenetics and Evolution</i> , 2021, 164, 107275.	2.7	12
3127	Anti-oxidant mechanisms of <i>Chlorella pyrenoidosa</i> under acute GenX exposure. <i>Science of the Total Environment</i> , 2021, 797, 149005.	8.0	24
3128	Antibiotics adaptation costs alter carbon sequestration strategies of microorganisms in karst river. <i>Environmental Pollution</i> , 2021, 288, 117819.	7.5	9
3129	The salmon louse genome: Copepod features and parasitic adaptations. <i>Genomics</i> , 2021, 113, 3666-3680.	2.9	17

#	ARTICLE	IF	CITATIONS
3130	Contrasting transcriptomic responses of a microbial eukaryotic community to oil and dispersant. <i>Environmental Pollution</i> , 2021, 288, 117774.	7.5	1
3131	Transcriptomics reveals that the caudal neurosecretory system in the olive flounder (<i>Paralichthys</i>) Tj ETQq1 1 0.784314 rgBT /Overlode 2021, 544, 737032.	3.5	7
3132	Co-occurring microorganisms regulate the succession of cyanobacterial harmful algal blooms. <i>Environmental Pollution</i> , 2021, 288, 117682.	7.5	39
3133	Comparative transcriptome analysis reveals changes in gene expression in sea cucumber (<i>Holothuria</i>) Tj ETQq1 1 0.784314 rgBT /Overlode D: Genomics and Proteomics, 2021, 40, 100883.	1.0	12
3134	Transcriptome-wide study in the green microalga <i>Messastrum gracile</i> SE-MC4 identifies prominent roles of photosynthetic integral membrane protein genes during exponential growth stage. <i>Phytochemistry</i> , 2021, 192, 112936.	2.9	4
3135	Neurotoxins in the venom gland of <i>Calommata signata</i> , a burrowing spider. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2021, 40, 100871.	1.0	2
3136	Phylogenomics, divergence time estimation and trait evolution provide a new look into the Gracilariales (Rhodophyta). <i>Molecular Phylogenetics and Evolution</i> , 2021, 165, 107294.	2.7	22
3137	Bimetallic nitrogen-doped porous carbon derived from ZIF-L&FeTPP@ZIF-8 as electrocatalysis and application for antibiotic wastewater treatment. <i>Separation and Purification Technology</i> , 2021, 276, 119259.	7.9	22
3138	Distinct metabolic strategies of the dominant heterotrophic bacterial groups associated with marine <i>Synechococcus</i> . <i>Science of the Total Environment</i> , 2021, 798, 149208.	8.0	10
3139	Contribution of enrofloxacin and Cu ²⁺ to the antibiotic resistance of bacterial community in a river biofilm. <i>Environmental Pollution</i> , 2021, 291, 118156.	7.5	12
3140	Impact of chicken litter pre-application treatment on the abundance, field persistence, and transfer of antibiotic resistant bacteria and antibiotic resistance genes to vegetables. <i>Science of the Total Environment</i> , 2021, 801, 149718.	8.0	13
3141	Increase of N ₂ O production during nitrate reduction after long-term sulfide addition in lake sediment microcosms. <i>Environmental Pollution</i> , 2021, 291, 118231.	7.5	17
3142	Three-compartment septic tanks as sustainable on-site treatment facilities? Watch out for the potential dissemination of human-associated pathogens and antibiotic resistance. <i>Journal of Environmental Management</i> , 2021, 300, 113709.	7.8	12
3143	Genetic authentication: Differentiation of hazelnut cultivars using polymorphic sites of the chloroplast genome. <i>Food Control</i> , 2021, 130, 108344.	5.5	7
3144	Transcriptomic profiling of <i>Paulownia elongata</i> in response to heat stress. <i>Plant Gene</i> , 2021, 28, 100330.	2.3	0
3145	Identification of pigment genes (melanin, carotenoid and pteridine) associated with skin color variant in red tilapia using transcriptome analysis. <i>Aquaculture</i> , 2022, 547, 737429.	3.5	27
3146	Squash root microbiome transplants and metagenomic inspection for in situ arid adaptations. <i>Science of the Total Environment</i> , 2022, 805, 150136.	8.0	12
3147	Gut interkingdom predator-prey interactions are key determinants of shrimp health. <i>Aquaculture</i> , 2022, 546, 737304.	3.5	15

#	ARTICLE	IF	CITATIONS
3148	Metagenomic evidence for co-occurrence of antibiotic, biocide and metal resistance genes in pigs. Environment International, 2022, 158, 106899.	10.0	40
3149	Enhanced survival of multi-species biofilms under stress is promoted by low-abundant but antimicrobial-resistant keystone species. Journal of Hazardous Materials, 2022, 422, 126836.	12.4	17
3150	Fate, mobility, and pathogenicity of drinking water treatment plant resistomes deciphered by metagenomic assembly and network analyses. Science of the Total Environment, 2022, 804, 150095.	8.0	13
3151	Effects of spatially heterogeneous warming on gut microbiota, nutrition and gene flow of a heat-sensitive ungulate population. Science of the Total Environment, 2022, 806, 150537.	8.0	3
3152	Insights into the molecular basis of biocontrol of Botrytis cinerea by Clonostachys rosea in tomato. Scientia Horticulturae, 2022, 291, 110547.	3.6	19
3153	LC-MS/MS targeting analysis of terpenoid metabolism in Carya cathayensis at different developmental stages. Food Chemistry, 2022, 366, 130583.	8.2	10
3154	A multi-omic screening approach for the discovery of thermoactive glycoside hydrolases. Extremophiles, 2021, 25, 101-114.	2.3	6
3155	Nanopore-based metagenomics analysis reveals prevalence of mobile antibiotic and heavy metal resistome in wastewater. Ecotoxicology, 2021, 30, 1572-1585.	2.4	18
3156	At Least Seven Distinct Rotavirus Genotype Constellations in Bats with Evidence of Reassortment and Zoonotic Transmissions. MBio, 2021, 12, .	4.1	31
3157	Comparative metagenomic discovery of the dynamic cellulose-degrading process from a synergistic cellulolytic microbiota. Cellulose, 2021, 28, 2105-2123.	4.9	8
3158	Chromosomal scale assembly of parasitic wasp genome reveals symbiotic virus colonization. Communications Biology, 2021, 4, 104.	4.4	27
3159	Functional plasticity in oyster gut microbiomes along a eutrophication gradient in an urbanized estuary. Animal Microbiome, 2021, 3, 5.	3.8	22
3160	<i>De novo</i> genome assembly of the tobacco hornworm moth (<i>Manduca sexta</i>). G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	20
3161	Coastal Bacterial Community Response to Glacier Melting in the Western Antarctic Peninsula. Microorganisms, 2021, 9, 88.	3.6	10
3162	Fly-over phylogeny across invertebrate to vertebrate: The giant panda and insects share a highly similar gut microbiota. Computational and Structural Biotechnology Journal, 2021, 19, 4676-4683.	4.1	7
3163	The Functional Evolution of Termite Gut Microbiota. SSRN Electronic Journal, 0, , .	0.4	0
3164	A new emu genome illuminates the evolution of genome configuration and nuclear architecture of avian chromosomes. Genome Research, 2021, 31, 497-511.	5.5	30
3165	Developing SNPs and Strategies for Genomic Analysis in Alfalfa. Compendium of Plant Genomes, 2021, , 159-175.	0.5	0

#	ARTICLE	IF	CITATIONS
3166	Effect of host breeds on gut microbiome and serum metabolome in meat rabbits. BMC Veterinary Research, 2021, 17, 24.	1.9	20
3167	Gene variations in Autism Spectrum Disorder are associated with alternation of gut microbiota, metabolites and cytokines. Gut Microbes, 2021, 13, 1-16.	9.8	28
3168	BRAKER2: automatic eukaryotic genome annotation with GeneMark-EP+ and AUGUSTUS supported by a protein database. NAR Genomics and Bioinformatics, 2021, 3, lqaa108.	3.2	803
3169	Barley Anther and Meiocyte Transcriptome Dynamics in Meiotic Prophase I. Frontiers in Plant Science, 2020, 11, 619404.	3.6	19
3170	A microbial gene catalog of anaerobic digestion from full-scale biogas plants. GigaScience, 2021, 10, .	6.4	23
3171	Giant lungfish genome elucidates the conquest of land by vertebrates. Nature, 2021, 590, 284-289.	27.8	132
3172	Potato Virus A Isolates from Three Continents: Their Biological Properties, Phylogenetics, and Prehistory. Phytopathology, 2021, 111, 217-226.	2.2	24
3173	Accurate Annotation of Microbial Metagenomic Genes and Identification of Core Sets. Methods in Molecular Biology, 2021, 2242, 115-138.	0.9	0
3174	Parallel algorithm for the unsupervised binning of metagenomic sequences. , 2021, , .		0
3175	High-Throughput Analysis to Decipher Bacterial Diversity and their Functional Properties in Freshwater Bodies. , 2021, , 511-542.		0
3176	Identification and characterization of CONSTANS-like genes from Curcuma alismatifolia. Horticulture Environment and Biotechnology, 2021, 62, 279-286.	2.1	5
3177	Nutrient-imbalanced conditions shift the interplay between zooplankton and gut microbiota. BMC Genomics, 2021, 22, 37.	2.8	5
3178	Metagenome Analysis of a Hydrocarbon-Degrading Bacterial Consortium Reveals the Specific Roles of BTEX Biodegraders. Genes, 2021, 12, 98.	2.4	20
3180	Genomic Analyses of Phenotypic Differences Between Native and Invasive Populations of Diffuse Knapweed (Centaurea diffusa). Frontiers in Ecology and Evolution, 2021, 8, .	2.2	7
3181	Induction of the glycolysis product methylglyoxal on trimethylamine lyase synthesis in the intestinal microbiota from mice fed with choline and dietary fiber. Food and Function, 2021, 12, 9880-9893.	4.6	3
3182	A combination of fecal calprotectin and human beta-defensin 2 facilitates diagnosis and monitoring of inflammatory bowel disease. Gut Microbes, 2021, 13, 1943288.	9.8	4
3183	The <i>Cymbidium goeringii</i> genome provides insight into organ development and adaptive evolution in orchids. Ornamental Plant Research, 2021, 1, 1-13.	0.9	7
3184	Resistance to pirimiphos-methyl in West African Anopheles is spreading via duplication and introgression of the Ace1 locus. PLoS Genetics, 2021, 17, e1009253.	3.5	33

#	ARTICLE	IF	CITATIONS
3185	<i>Clostridium fessum</i> sp. nov., isolated from human faeces. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	1.7	10
3186	Antimicrobial-specific response from resistance gene carriers studied in a natural, highly diverse microbiome. Microbiome, 2021, 9, 29.	11.1	13
3187	A roadmap for metagenomic enzyme discovery. Natural Product Reports, 2021, 38, 1994-2023.	10.3	76
3188	Trace gas oxidizers are widespread and active members of soil microbial communities. Nature Microbiology, 2021, 6, 246-256.	13.3	97
3189	Transcriptomic analysis of <i>Chlorella</i> sp. HS2 suggests the overflow of acetyl-CoA and NADPH cofactor induces high lipid accumulation and halotolerance. Food and Energy Security, 2021, 10, e267.	4.3	7
3190	Inferring Orthology and Paralogy. Methods in Molecular Biology, 2019, 1910, 149-175.	0.9	84
3191	Advancements in Microbial Genome Sequencing and Microbial Community Characterization. , 2019, , 87-113.		1
3192	Metagenomic insights into the influence of salinity and cytostatic drugs on the composition and functional genes of microbial community in forward osmosis anaerobic membrane bioreactors. Chemical Engineering Journal, 2017, 326, 462-469.	12.7	46
3193	De novo transcriptome analysis of the mussel <i>Perna viridis</i> after exposure to the toxic dinoflagellate <i>Prorocentrum lima</i> . Ecotoxicology and Environmental Safety, 2020, 192, 110265.	6.0	25
3194	Homogeneous selection drives antibiotic resistome in two adjacent sub-watersheds, China. Journal of Hazardous Materials, 2020, 398, 122820.	12.4	46
3195	De novo assembly and functional annotation of the heart+hemolymph transcriptome in the Caribbean spiny lobster <i>Panulirus argus</i> . Marine Genomics, 2020, 54, 100783.	1.1	6
3196	De novo assembly and annotation of the transcriptome of <i>Astyanax lacustris</i> liver unveil candidate genes to monitor response to environmental stress. Marine Genomics, 2020, 54, 100784.	1.1	4
3197	A complex virome including two distinct emaraviruses associated with virus-like symptoms in <i>Camellia japonica</i> . Virus Research, 2020, 286, 197964.	2.2	16
3198	Will a Non-antibiotic Metalloid Enhance the Spread of Antibiotic Resistance Genes: The Selenate Story. Environmental Science & Technology, 2021, 55, 1004-1014.	10.0	42
3199	Verrucomicrobia use hundreds of enzymes to digest the algal polysaccharide fucoidan. Nature Microbiology, 2020, 5, 1026-1039.	13.3	182
3200	Single cell genomes of <i>Prochlorococcus</i> , <i>Synechococcus</i> , and sympatric microbes from diverse marine environments. Scientific Data, 2018, 5, 180154.	5.3	81
3201	Seasonal and diel patterns of abundance and activity of viruses in the Red Sea. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 29738-29747.	7.1	27
3202	Effects of fecal microbiota transplantation in subjects with irritable bowel syndrome are mirrored by changes in gut microbiome. Gut Microbes, 2020, 12, 1794263.	9.8	31

#	ARTICLE	IF	CITATIONS
3203	RNA based mNGS approach identifies a novel human coronavirus from two individual pneumonia cases in 2019 Wuhan outbreak. <i>Emerging Microbes and Infections</i> , 2020, 9, 313-319.	6.5	471
3204	Exploring the abundance, metabolic potential and gene expression of subseafloor <i>Chloroflexi</i> in million-year-old oxic and anoxic abyssal clay. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	2.7	34
3205	A high-quality genome assembly and annotation of the gray mangrove, <i>Avicennia marina</i> . <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	16
3206	Comparative Genomics of Strictly Vertically Transmitted, Feminizing Microsporidia Endosymbionts of Amphipod Crustaceans. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	12
3207	Evolutionary Plasticity of Mating-Type Determination Mechanisms in <i>Paramecium aurelia</i> Sibling Species. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	13
3208	PanACoTA: a modular tool for massive microbial comparative genomics. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqaa106.	3.2	26
3209	Novel hepatitis D-like agents in vertebrates and invertebrates. <i>Virus Evolution</i> , 2019, 5, vez021.	4.9	63
3210	Prevalence of Yellow Leaf Disease (YLD) and its Associated Areca Palm Velarivirus 1 (APV1) in Betel Palm (<i>Areca catechu</i>) Plantations in Hainan, China. <i>Plant Disease</i> , 2020, 104, 2556-2562.	1.4	14
3211	<i>Schaedlerella arabinosiphila</i> gen. nov., sp. nov., a D-arabinose-utilizing bacterium isolated from faeces of C57BL/6J mice that is a close relative of <i>Clostridium</i> species ASF 502. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 3616-3622.	1.7	12
3212	A taxonomic note on the genus <i>Lactobacillus</i> : Description of 23 novel genera, emended description of the genus <i>Lactobacillus</i> Beijerinck 1901, and union of <i>Lactobacillaceae</i> and <i>Leuconostocaceae</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 2782-2858.	1.7	2,775
3213	Proposal to reclassify the proteobacterial classes Deltaproteobacteria and Oligoflexia, and the phylum Thermodesulfobacteria into four phyla reflecting major functional capabilities. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 5972-6016.	1.7	830
3214	<i>Sporofaciens musculi</i> gen. nov., sp. nov., a novel bacterium isolated from the caecum of an obese mouse. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 71, .	1.7	15
3215	Complete genome of <i>Aedes aegypti</i> anphevirus in the Aag2 mosquito cell line. <i>Journal of General Virology</i> , 2018, 99, 832-836.	2.9	13
3216	Sequencing detects human papillomavirus in some apparently HPV-negative invasive cervical cancers. <i>Journal of General Virology</i> , 2020, 101, 265-270.	2.9	16
3217	Exploration of the virome of the European brown shrimp (<i>Crangon crangon</i>). <i>Journal of General Virology</i> , 2020, 101, 651-666.	2.9	13
3218	Metagenomic assembly of new (sub)polar Cyanobacteria and their associated microbiome from non-axenic cultures. <i>Microbial Genomics</i> , 2018, 4, .	2.0	23
3219	SynerClust: a highly scalable, synteny-aware orthologue clustering tool. <i>Microbial Genomics</i> , 2018, 4, .	2.0	18
3220	Genomic analysis of bacteria in the Acute Oak Decline pathobiome. <i>Microbial Genomics</i> , 2019, 5, .	2.0	31

#	ARTICLE	IF	CITATIONS
3221	Comparison of long-read sequencing technologies in the hybrid assembly of complex bacterial genomes. <i>Microbial Genomics</i> , 2019, 5, .	2.0	171
3222	Whole-genome sequencing of dog-specific assemblages C and D of <i>Giardia duodenalis</i> from single and pooled cysts indicates host-associated genes. <i>Microbial Genomics</i> , 2019, 5, .	2.0	16
3223	An assessment of genome annotation coverage across the bacterial tree of life. <i>Microbial Genomics</i> , 2020, 6, .	2.0	55
3224	Mycoparasitism illuminated by genome and transcriptome sequencing of <i>Coniothyrium minitans</i> , an important biocontrol fungus of the plant pathogen <i>Sclerotinia sclerotiorum</i> . <i>Microbial Genomics</i> , 2020, 6, .	2.0	15
3225	Preterm infants harbour diverse <i>Klebsiella</i> populations, including atypical species that encode and produce an array of antimicrobial resistance- and virulence-associated factors. <i>Microbial Genomics</i> , 2020, 6, .	2.0	35
3226	Platon: identification and characterization of bacterial plasmid contigs in short-read draft assemblies exploiting protein sequence-based replicon distribution scores. <i>Microbial Genomics</i> , 2020, 6, .	2.0	87
3227	Metagenomic approaches in microbial ecology: an update on whole-genome and marker gene sequencing analyses. <i>Microbial Genomics</i> , 2020, 6, .	2.0	69
3228	Comprehensive genome data analysis establishes a triple whammy of carbapenemases, ICEs and multiple clinically relevant bacteria. <i>Microbial Genomics</i> , 2020, 6, .	2.0	17
3229	Metagenome-assembled genome binning methods with short reads disproportionately fail for plasmids and genomic Islands. <i>Microbial Genomics</i> , 2020, 6, .	2.0	67
3230	Comprehensive screening of genomic and metagenomic data reveals a large diversity of tetracycline resistance genes. <i>Microbial Genomics</i> , 2020, 6, .	2.0	19
3526	Genome and time-of-day transcriptome of <i>Wolffia australiana</i> link morphological minimization with gene loss and less growth control. <i>Genome Research</i> , 2021, 31, 225-238.	5.5	56
3527	Distributed Many-to-Many Protein Sequence Alignment using Sparse Matrices. , 2020, , .		9
3528	Environment and host species identity shape gut microbiota diversity in sympatric herbivorous mammals. <i>Microbial Biotechnology</i> , 2021, 14, 1300-1315.	4.2	24
3529	A region of the sex chromosome associated with population differences in diapause induction contains highly divergent alleles at clock genes. <i>Evolution; International Journal of Organic Evolution</i> , 2021, 75, 490-500.	2.3	5
3530	Horizontal Gene Transfer to a Defensive Symbiont with a Reduced Genome in a Multipartite Beetle Microbiome. <i>MBio</i> , 2020, 11, .	4.1	52
3531	Genome Sequences of Novel Members of Previously Described DNA and RNA Virus Families, Isolated from Feces of a Drill Monkey in Nigeria. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	3
3532	Genome Sequences of Seven <i>Megrivirus</i> Strains from Chickens in The Netherlands. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	4
3533	Staphylococcal Protein A (<i>spa</i>) Locus Is a Hot Spot for Recombination and Horizontal Gene Transfer in <i>Staphylococcus pseudintermedius</i> . <i>MSphere</i> , 2020, 5, .	2.9	16

#	ARTICLE	IF	CITATIONS
3534	The Evolutionary Success of the Marine Bacterium SAR11 Analyzed through a Metagenomic Perspective. <i>MSystems</i> , 2020, 5, .	3.8	22
3535	Stability of the Virome in Lab- and Field-Collected <i>Aedes albopictus</i> Mosquitoes across Different Developmental Stages and Possible Core Viruses in the Publicly Available Virome Data of <i>Aedes</i> Mosquitoes. <i>MSystems</i> , 2020, 5, .	3.8	40
3536	Genomes of the <i>Candidatus</i> Actinomarinales Order: Highly Streamlined Marine Epipelagic Actinobacteria. <i>MSystems</i> , 2020, 5, .	3.8	24
3537	Lifestyle and the presence of helminths is associated with gut microbiome composition in Cameroonians. <i>Genome Biology</i> , 2020, 21, 122.	8.8	48
3538	Harnessing the strategy of metagenomics for exploring the intestinal microecology of sable (Martes) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	3.0	5
3539	The microbiome as a biosensor: functional profiles elucidate hidden stress in hosts. <i>Microbiome</i> , 2020, 8, 71.	11.1	24
3540	BlobTools: Interrogation of genome assemblies. <i>F1000Research</i> , 0, 6, 1287.	1.6	600
3541	Draft genomes of two Australian strains of the plant pathogen, <i>Phytophthora cinnamomi</i> . <i>F1000Research</i> , 2017, 6, 1972.	1.6	10
3542	Draft genomes of two Australian strains of the plant pathogen, <i>Phytophthora cinnamomi</i> . <i>F1000Research</i> , 2017, 6, 1972.	1.6	7
3543	Metagenomic analysis of an ecological wastewater treatment plant's microbial communities and their potential to metabolize pharmaceuticals. <i>F1000Research</i> , 2016, 5, 1881.	1.6	49
3544	Expansion of RiPP biosynthetic space through integration of pan-genomics and machine learning uncovers a novel class of lanthipeptides. <i>PLoS Biology</i> , 2020, 18, e3001026.	5.6	75
3545	MEGAN Community Edition - Interactive Exploration and Analysis of Large-Scale Microbiome Sequencing Data. <i>PLoS Computational Biology</i> , 2016, 12, e1004957.	3.2	1,500
3546	rasbhari: Optimizing Spaced Seeds for Database Searching, Read Mapping and Alignment-Free Sequence Comparison. <i>PLoS Computational Biology</i> , 2016, 12, e1005107.	3.2	36
3547	Genome diversity of marine phages recovered from Mediterranean metagenomes: Size matters. <i>PLoS Genetics</i> , 2017, 13, e1007018.	3.5	82
3548	Identification of chironomid species as natural reservoirs of toxigenic <i>Vibrio cholerae</i> strains with pandemic potential. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008959.	3.0	9
3549	Dual Transcriptomic Profiling of Host and Microbiota during Health and Disease in Pediatric Asthma. <i>PLoS ONE</i> , 2015, 10, e0131819.	2.5	87
3550	Microbial Communities Can Be Described by Metabolic Structure: A General Framework and Application to a Seasonally Variable, Depth-Stratified Microbial Community from the Coastal West Antarctic Peninsula. <i>PLoS ONE</i> , 2015, 10, e0135868.	2.5	146
3551	COGNIZER: A Framework for Functional Annotation of Metagenomic Datasets. <i>PLoS ONE</i> , 2015, 10, e0142102.	2.5	87

#	ARTICLE	IF	CITATIONS
3552	The Intestinal Eukaryotic Virome in Healthy and Diarrhoeic Neonatal Piglets. PLoS ONE, 2016, 11, e0151481.	2.5	28
3553	MetLab: An In Silico Experimental Design, Simulation and Analysis Tool for Viral Metagenomics Studies. PLoS ONE, 2016, 11, e0160334.	2.5	14
3554	Discovery and Partial Genomic Characterisation of a Novel Nidovirus Associated with Respiratory Disease in Wild Shingleback Lizards (<i>Tiliqua rugosa</i>). PLoS ONE, 2016, 11, e0165209.	2.5	43
3555	Unbiased RNA Shotgun Metagenomics in Social and Solitary Wild Bees Detects Associations with Eukaryote Parasites and New Viruses. PLoS ONE, 2016, 11, e0168456.	2.5	46
3556	PanWeb: A web interface for pan-genomic analysis. PLoS ONE, 2017, 12, e0178154.	2.5	23
3557	Impact of maintenance immunosuppressive therapy on the fecal microbiome of renal transplant recipients: Comparison between an everolimus- and a standard tacrolimus-based regimen. PLoS ONE, 2017, 12, e0178228.	2.5	44
3558	On the core bacterial flora of <i>Ixodes persulcatus</i> (Taiga tick). PLoS ONE, 2017, 12, e0180150.	2.5	18
3559	Single primer isothermal amplification (SPIA) combined with next generation sequencing provides complete bovine coronavirus genome coverage and higher sequence depth compared to sequence-independent single primer amplification (SISPA). PLoS ONE, 2017, 12, e0187780.	2.5	14
3560	Variability in metagenomic samples from the Puget Sound: Relationship to temporal and anthropogenic impacts. PLoS ONE, 2018, 13, e0192412.	2.5	9
3561	Viruses in unexplained encephalitis cases in American black bears (<i>Ursus americanus</i>). PLoS ONE, 2020, 15, e0244056.	2.5	11
3562	The blood DNA virome in 8,000 humans. PLoS Pathogens, 2017, 13, e1006292.	4.7	259
3563	Beyond the sea: <i>Crepidula atrasolea</i> as a spiralian model system. International Journal of Developmental Biology, 2017, 61, 479-493.	0.6	13
3564	Genetically engineered distal airway stem cell transplantation protects mice from pulmonary infection. EMBO Molecular Medicine, 2020, 12, e10233.	6.9	20
3565	RNA-Seq: the Early Response of the Snail <i>Physella acuta</i> to the Digenetic Trematode <i>Echinostoma paraensei</i> . Journal of Parasitology, 2020, 106, 490.	0.7	7
3566	The whole transcriptome regulation as a function of mitochondrial polymorphisms and aging in <i>Caenorhabditis elegans</i> . Aging, 2020, 12, 2453-2470.	3.1	12
3569	Functional and Transcriptomic Characterization of a Dye-decolorizing Fungus from <i>Taxus</i> Rhizosphere. Polish Journal of Microbiology, 2018, 67, 417-430.	1.7	6
3570	Recovery of the Gut Microbiota after Antibiotics Depends on Host Diet and Environmental Reservoirs. SSRN Electronic Journal, 0, , .	0.4	4
3571	Using Metagenomics to Connect Microbial Community Biodiversity and Functions. Current Issues in Molecular Biology, 2017, 24, 103-118.	2.4	47

#	ARTICLE	IF	CITATIONS
3572	Next-generation sequencing to elucidate adaptive stress response and plantaricin genes among <i>Lactobacillus plantarum</i> strains. <i>Future Microbiology</i> , 2020, 15, 333-348.	2.0	8
3573	Longitudinal Changes in Skin Microbiome Associated with Change in Skin Status in Patients with Psoriasis. <i>Acta Dermato-Venereologica</i> , 2020, 100, adv00329.	1.3	5
3574	Chlorovirus and myovirus diversity in permafrost thaw ponds. <i>Aquatic Microbial Ecology</i> , 2018, 82, 209-224.	1.8	5
3575	Uncovering cryptochrome/photolyase gene diversity in aquatic microbiomes exposed to diverse UV-B regimes. <i>Aquatic Microbial Ecology</i> , 2020, 85, 141-154.	1.8	10
3576	The Progress of Multi-Omics Technologies: Determining Function in Lactic Acid Bacteria Using a Systems Level Approach. <i>Frontiers in Microbiology</i> , 2019, 10, 3084.	3.5	54
3577	CusS-CusR Two-Component System Mediates Tigecycline Resistance in Carbapenem-Resistant <i>Klebsiella pneumoniae</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 3159.	3.5	19
3578	The Developmental Transcriptome of Bagworm, <i>Metisa plana</i> (Lepidoptera: Psychidae) and Insights into Chitin Biosynthesis Genes. <i>Genes</i> , 2021, 12, 7.	2.4	4
3579	Metatranscriptome Analysis of Sympatric Bee Species Identifies Bee Virus Variants and a New Virus, <i>Andrena</i> -Associated Bee Virus-1. <i>Viruses</i> , 2021, 13, 291.	3.3	15
3580	Structure and Functions of Hydrocarbon-Degrading Microbial Communities in Bioelectrochemical Systems. <i>Water (Switzerland)</i> , 2020, 12, 343.	2.7	16
3581	Long non-coding RNA expression profiling following treatment with resveratrol to improve insulin resistance. <i>Molecular Medicine Reports</i> , 2020, 22, 1303-1316.	2.4	8
3582	Three new subfamilies of skipper butterflies (Lepidoptera, HesperIIDae). <i>ZooKeys</i> , 2019, 861, 91-105.	1.1	29
3583	A new and improved genome sequence of <i>Cannabis sativa</i> . <i>GigaByte</i> , 0, 2020, 1-13.	0.0	7
3584	Lake mixing regime selects apparent methane oxidation kinetics of the methanotroph assemblage. <i>Biogeosciences</i> , 2020, 17, 4247-4259.	3.3	12
3585	Microbial functional signature in the atmospheric boundary layer. <i>Biogeosciences</i> , 2020, 17, 6081-6095.	3.3	12
3587	The genomes of polyextremophilic cyanidiales contain 1% horizontally transferred genes with diverse adaptive functions. <i>ELife</i> , 2019, 8, .	6.0	50
3588	Endangered wild salmon infected by newly discovered viruses. <i>ELife</i> , 2019, 8, .	6.0	66
3589	A molecular filter for the cnidarian stinging response. <i>ELife</i> , 2020, 9, .	6.0	18
3590	Global landscape of phenazine biosynthesis and biodegradation reveals species-specific colonization patterns in agricultural soils and crop microbiomes. <i>ELife</i> , 2020, 9, .	6.0	44

#	ARTICLE	IF	CITATIONS
3591	Metage2Metabo, microbiota-scale metabolic complementarity for the identification of key species. <i>ELife</i> , 2020, 9, .	6.0	44
3592	Reconstructing ecosystem functions of the active microbial community of the Baltic Sea oxygen depleted sediments. <i>PeerJ</i> , 2016, 4, e1593.	2.0	25
3593	Validation of picogram- and femtogram-input DNA libraries for microscale metagenomics. <i>PeerJ</i> , 2016, 4, e2486.	2.0	64
3594	Antibiotic resistance potential of the healthy preterm infant gut microbiome. <i>PeerJ</i> , 2017, 5, e2928.	2.0	34
3595	Metabolic marker gene mining provides insight in global <i>mcrA</i> diversity and, coupled with targeted genome reconstruction, sheds further light on metabolic potential of the <i>Methanomassiliicoccales</i> . <i>PeerJ</i> , 2018, 6, e5614.	2.0	34
3596	Relative abundance and molecular evolution of Lake Sinai Virus (Sinaivirus) clades. <i>PeerJ</i> , 2019, 7, e6305.	2.0	18
3597	Human gut resistome can be country-specific. <i>PeerJ</i> , 2019, 7, e6389.	2.0	13
3598	Assessing alignment-based taxonomic classification of ancient microbial DNA. <i>PeerJ</i> , 2019, 7, e6594.	2.0	23
3599	Identification and characterization of hirudin-HN, a new thrombin inhibitor, from the salivary glands of <i>Hirudo nipponia</i> . <i>PeerJ</i> , 2019, 7, e7716.	2.0	18
3600	Co-expression clustering across flower development identifies modules for diverse floral forms in <i>Achimenes</i> (Gesneriaceae). <i>PeerJ</i> , 2020, 8, e8778.	2.0	8
3601	The level of putative carotenoid-binding proteins determines the body color in two species of endemic Lake Baikal amphipods. <i>PeerJ</i> , 2020, 8, e9387.	2.0	5
3602	Understanding genomic diversity, pan-genome, and evolution of SARS-CoV-2. <i>PeerJ</i> , 2020, 8, e9576.	2.0	19
3603	<i>Gluconobacter</i> dominates the gut microbiome of the Asian palm civet <i>Paradoxurus hermaphroditus</i> that produces kopi luwak. <i>PeerJ</i> , 2020, 8, e9579.	2.0	10
3604	Evaluation of computational methods for human microbiome analysis using simulated data. <i>PeerJ</i> , 2020, 8, e9688.	2.0	14
3605	Needles in haystacks: reevaluating old paradigms for the discovery of bacterial secondary metabolites. <i>Natural Product Reports</i> , 2021, 38, 2083-2099.	10.3	14
3606	dbAMP 2.0: updated resource for antimicrobial peptides with an enhanced scanning method for genomic and proteomic data. <i>Nucleic Acids Research</i> , 2022, 50, D460-D470.	14.5	49
3607	PhylomeDB V5: an expanding repository for genome-wide catalogues of annotated gene phylogenies. <i>Nucleic Acids Research</i> , 2022, 50, D1062-D1068.	14.5	30
3610	EXAGRAPH: Graph and combinatorial methods for enabling exascale applications. <i>International Journal of High Performance Computing Applications</i> , 2021, 35, 553-571.	3.7	9

#	ARTICLE	IF	CITATIONS
3611	Comparison of virulence-related determinants between the ST59-t437 and ST239-t030 genotypes of methicillin-resistant <i>Staphylococcus aureus</i> . BMC Microbiology, 2021, 21, 264.	3.3	2
3612	Functions predict horizontal gene transfer and the emergence of antibiotic resistance. Science Advances, 2021, 7, eabj5056.	10.3	44
3613	High-quality genome assembly of an important biodiesel plant, <i>Euphorbia lathyris</i> L. DNA Research, 2021, 28, .	3.4	11
3614	Virus diversity in metagenomes of a lichen symbiosis (<i>Umbilicaria phaea</i>): complete viral genomes, putative hosts and elevational distributions. Environmental Microbiology, 2021, 23, 6637-6650.	3.8	11
3615	Predominant Biphenyl Dioxygenase From Legacy Polychlorinated Biphenyl (PCB)-Contaminated Soil Is a Part of Unusual Gene Cluster and Transforms Flavone and Flavanone. Frontiers in Microbiology, 2021, 12, 644708.	3.5	4
3617	Evolutionary Implications of the RNA N ⁶ -Methyladenosine Methylome in Plants. Molecular Biology and Evolution, 2022, 39, .	8.9	26
3618	Genomic insights into biocontrol potential of <i>Bacillus stercoris</i> LJBS06. 3 Biotech, 2021, 11, 458.	2.2	3
3619	Differential pathogenesis of closely related 2018 Nigerian outbreak clade III Lassa virus isolates. PLoS Pathogens, 2021, 17, e1009966.	4.7	6
3620	The importance of age in compositional and functional profiling of the human intestinal microbiome. PLoS ONE, 2021, 16, e0258505.	2.5	10
3621	Microbial population genomes from the Amazon River reveal possible modulation of the organic matter degradation process in tropical freshwaters. Molecular Ecology, 2022, 31, 206-219.	3.9	2
3622	Better detection of Torque teno virus in children with leukemia by metagenomic sequencing than by quantitative PCR. Journal of Medical Virology, 2022, 94, 634-641.	5.0	10
3623	Transcriptome analysis of <i>Clavibacter michiganensis</i> subsp. <i>michiganensis</i> -infected tomatoes: a role of salicylic acid in the host response. BMC Plant Biology, 2021, 21, 476.	3.6	17
3624	Prediction of Genes That Function in Methanogenesis and CO ₂ Pathways in Extremophiles. Microorganisms, 2021, 9, 2211.	3.6	3
3627	Discovery and Evolution of a Divergent Coronavirus in the Plateau Pika From China That Extends the Host Range of Alphacoronaviruses. Frontiers in Microbiology, 2021, 12, 755599.	3.5	9
3628	Drought Stress Triggers Shifts in the Root Microbial Community and Alters Functional Categories in the Microbial Gene Pool. Frontiers in Microbiology, 2021, 12, 744897.	3.5	26
3629	SMRT Sequencing of the Full-Length Transcriptome of the <i>Coelomactra antiquata</i> . Frontiers in Genetics, 2021, 12, 741243.	2.3	9
3631	<i>Rhodocaloribacter litoris</i> gen. nov., sp. nov., isolated from an intertidal hot spring. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	1.7	9
3632	Chromosome-level genome assembly reveals homologous chromosomes and recombination in asexual rotifer <i>Adineta vaga</i> . Science Advances, 2021, 7, eabg4216.	10.3	30

#	ARTICLE	IF	CITATIONS
3634	Metagenomic Sequencing Reveals that High-Grain Feeding Alters the Composition and Metabolism of Cecal Microbiota and Induces Cecal Mucosal Injury in Sheep. <i>MSystems</i> , 2021, 6, e0091521.	3.8	13
3635	Assessing the Impact of a Viral Infection on the Expression of Transposable Elements in the Cabbage Looper Moth (<i>Trichoplusia ni</i>). <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	2
3636	Removal of large viruses and their dispersal through fecal pellets of the appendicularian <i>Oikopleura dioica</i> during <i>Emiliana huxleyi</i> bloom conditions. <i>Limnology and Oceanography</i> , 2021, 66, 3963.	3.1	1
3637	A chromosome-level genome sequence of <i>Chrysanthemum seticuspe</i> , a model species for hexaploid cultivated chrysanthemum. <i>Communications Biology</i> , 2021, 4, 1167.	4.4	32
3638	Successional dynamics and alternative stable states in a saline activated sludge microbial community over 9 years. <i>Microbiome</i> , 2021, 9, 199.	11.1	33
3639	The Adaptive Evolution and Gigantism Mechanisms of the Hadal "Supergiant" Amphipod <i>Alicella gigantea</i> . <i>Frontiers in Marine Science</i> , 2021, 8, .	2.5	4
3640	Contamination in Reference Sequence Databases: Time for Divide-and-Rule Tactics. <i>Frontiers in Microbiology</i> , 2021, 12, 755101.	3.5	25
3641	A versatile genetic toolbox for <i>Prevotella copri</i> enables studying polysaccharide utilization systems. <i>EMBO Journal</i> , 2021, 40, e108287.	7.8	18
3642	Characterization of the First Cultured Psychrotolerant Representative of <i>Legionella</i> from Antarctica Reveals Its Unique Genome Structure. <i>Microbiology Spectrum</i> , 2021, 9, e0042421.	3.0	7
3643	Evaluating the Distribution of Bacterial Natural Product Biosynthetic Genes across Lake Huron Sediment. <i>ACS Chemical Biology</i> , 2021, 16, 2623-2631.	3.4	4
3644	Prolonged Impairment of Short-Chain Fatty Acid and L-Isoleucine Biosynthesis in Gut Microbiome in Patients With COVID-19. <i>Gastroenterology</i> , 2022, 162, 548-561.e4.	1.3	131
3645	Utilizing the VirIdAI Pipeline to Search for Viruses in the Metagenomic Data of Bat Samples. <i>Viruses</i> , 2021, 13, 2006.	3.3	3
3647	Microbial colonization and resistome dynamics in food processing environments of a newly opened pork cutting industry during 1.5 years of activity. <i>Microbiome</i> , 2021, 9, 204.	11.1	20
3648	Comparative transcriptomic analysis of races 1, 2, 5 and 6 of <i>Fusarium oxysporum</i> f.sp. <i>pisi</i> in a susceptible pea host identifies differential pathogenicity profiles. <i>BMC Genomics</i> , 2021, 22, 734.	2.8	7
3649	Global Analysis of the Zinc Homeostasis Network in <i>Pseudomonas aeruginosa</i> and Its Gene Expression Dynamics. <i>Frontiers in Microbiology</i> , 2021, 12, 739988.	3.5	11
3650	Hybrid Sequencing in Different Types of Goat Skeletal Muscles Reveals Genes Regulating Muscle Development and Meat Quality. <i>Animals</i> , 2021, 11, 2906.	2.3	4
3652	Western and non-western gut microbiomes reveal new roles of <i>Prevotella</i> in carbohydrate metabolism and mouth-gut axis. <i>Npj Biofilms and Microbiomes</i> , 2021, 7, 77.	6.4	28
3653	Biological Mitigation of Antibiotic Resistance Gene Dissemination by Antioxidant-Producing Microorganisms in Activated Sludge Systems. <i>Environmental Science & Technology</i> , 2021, 55, 15831-15842.	10.0	24

#	ARTICLE	IF	CITATIONS
3654	Predicting drug targets by homology modelling of <i>Pseudomonas aeruginosa</i> proteins of unknown function. <i>PLoS ONE</i> , 2021, 16, e0258385.	2.5	0
3655	Genomic and transcriptomic dissection of Theionarchaea in marine ecosystem. <i>Science China Life Sciences</i> , 2021, , 1.	4.9	2
3656	Structure and Functional Attributes of Bacterial Communities in Premise Plumbing Across the United States. <i>Environmental Science & Technology</i> , 2021, 55, 14105-14114.	10.0	15
3657	Music of metagenomicsâ€”a review of its applications, analysis pipeline, and associated tools. <i>Functional and Integrative Genomics</i> , 2022, 22, 3-26.	3.5	3
3658	Phylogenomics of SAR116 Clade Reveals Two Subclades with Different Evolutionary Trajectories and an Important Role in the Ocean Sulfur Cycle. <i>MSystems</i> , 2021, 6, e0094421.	3.8	12
3659	A Previously Undescribed Highly Prevalent Phage Identified in a Danish Enteric Virome Catalog. <i>MSystems</i> , 2021, 6, e0038221.	3.8	22
3660	Cytokinin Inhibits Fungal Development and Virulence by Targeting the Cytoskeleton and Cellular Trafficking. <i>MBio</i> , 2021, 12, e0306820.	4.1	10
3661	Transcriptome and de novo analysis of <i>Rosa xanthina</i> f. <i>spontanea</i> in response to cold stress. <i>BMC Plant Biology</i> , 2021, 21, 472.	3.6	7
3662	MetaMLP: A Fast Word Embedding Based Classifier to Profile Target Gene Databases in Metagenomic Samples. <i>Journal of Computational Biology</i> , 2021, 28, 1063-1074.	1.6	2
3663	A Comparative Transcriptional Landscape of Two Castor Cultivars Obtained by Single-Molecule Sequencing Comparative Analysis. <i>Frontiers in Genetics</i> , 2021, 12, 749340.	2.3	0
3664	The Bioinformatics Virtual Coordination Network: An Open-Source and Interactive Learning Environment. <i>Frontiers in Education</i> , 2021, 6, .	2.1	2
3665	Comparative Transcriptome Sequencing of Taro Corm Development With a Focus on the Starch and Sucrose Metabolism Pathway. <i>Frontiers in Genetics</i> , 2021, 12, 771081.	2.3	5
3666	The Depletion of Carbohydrate Metabolic Genes in the Gut Microbiome Contributes to the Transition From Central Obesity to Type 2 Diabetes. <i>Frontiers in Endocrinology</i> , 2021, 12, 747646.	3.5	6
3667	Transcriptome profiling of <i>Arabidopsis thaliana</i> roots in response to allelopathic effects of <i>Conyza canadensis</i> . <i>Ecotoxicology</i> , 2022, 31, 53-63.	2.4	5
3669	MCRL: using a reference library to compress a metagenome into a non-redundant list of sequences, considering viruses as a case study. <i>Bioinformatics</i> , 2022, 38, 631-647.	4.1	3
3671	FiberGrowth Pipeline: A Framework Toward Predicting Fiber-Specific Growth From Human Gut Bacteroidetes Genomes. <i>Frontiers in Microbiology</i> , 2021, 12, 632567.	3.5	1
3672	Biogeographical distributions of nitrogenâ€”cycling functional genes in a subtropical estuary. <i>Functional Ecology</i> , 2022, 36, 187-201.	3.6	23
3673	Transcriptomic and Coexpression Network Analyses Revealed Pine Chalcone Synthase Genes Associated with Pine Wood Nematode Infection. <i>International Journal of Molecular Sciences</i> , 2021, 22, 11195.	4.1	11

#	ARTICLE	IF	CITATIONS
3674	Fecal Putative Uropathogen Abundance and Antibiotic Resistance Gene Carriage in Women With Refractory Recurrent Urinary Tract Infection Treated With Fecal Microbiota Transplantation. Female Pelvic Medicine and Reconstructive Surgery, 2022, 28, 213-219.	1.1	1
3675	Spatiotemporal dynamics of the resistome and virulome of riverine microbiomes disturbed by a mining mud tsunami. Science of the Total Environment, 2022, 806, 150936.	8.0	6
3676	Phytoplankton exudates and lysates support distinct microbial consortia with specialized metabolic and ecophysiological traits. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	37
3677	Chromosome-Level Genome Assembly of <i>Nephotettix cincticeps</i> (Uhler, 1896) (Hemiptera: Tj ETQq1 1 0.784314 rgBT ₇ /Overlook	2.5	7
3678	Mobile Antimicrobial Resistance Genes in Probiotics. Antibiotics, 2021, 10, 1287.	3.7	22
3679	Genome-wide analysis of <i>Claviceps paspali</i> : insights into the secretome of the main species causing ergot disease in <i>Paspalum</i> spp. BMC Genomics, 2021, 22, 766.	2.8	1
3680	Phage-Mediated Explosive Cell Lysis Induces the Formation of a Different Type of O-IMV in <i>Shewanella vesiculosa</i> M7T. Frontiers in Microbiology, 2021, 12, 713669.	3.5	12
3683	New Arsenite Oxidase Gene (<i>aioA</i>) PCR Primers for Assessing Arsenite-Oxidizer Diversity in the Environment Using High-Throughput Sequencing. Frontiers in Microbiology, 2021, 12, 691913.	3.5	2
3685	Lactitol Supplementation Modulates Intestinal Microbiome in Liver Cirrhotic Patients. Frontiers in Medicine, 2021, 8, 762930.	2.6	9
3686	Metagenomic Sequencing of Multiple Soil Horizons and Sites in Close Vicinity Revealed Novel Secondary Metabolite Diversity. MSystems, 2021, 6, e0101821.	3.8	16
3687	Comprehensive analysis of hub mRNA, lncRNA and miRNA, and associated ceRNA networks implicated in grass carp (<i>Ctenopharyngodon idella</i>) growth traits. Genomics, 2021, 113, 4004-4014.	2.9	9
3688	Virome analysis of three Ixodidae ticks species from Colombia: A potential strategy for discovering and surveying tick-borne viruses. Infection, Genetics and Evolution, 2021, 96, 105103.	2.3	5
3689	Genome-resolved metagenomics reveals how soil bacterial communities respond to elevated H ₂ availability. Soil Biology and Biochemistry, 2021, 163, 108464.	8.8	12
3690	Shedding light on the functional role of the Ignavibacteria in Italian rice field soil: A meta-genomic/transcriptomic analysis. Soil Biology and Biochemistry, 2021, 163, 108444.	8.8	12
3691	Genome survey of sago palm (<i>Metroxylon sagu</i> Rottboll). Plant Gene, 2021, 28, 100341.	2.3	8
3692	Spatial-temporal targeted and non-targeted surveys to assess microbiological composition of drinking water in Puerto Rico following Hurricane Maria. Water Research X, 2021, 13, 100123.	6.1	9
3714	Five life stage-specific transcriptome assemblies for the reniform nematode, <i>Rotylenchulus reniformis</i> Linford & Oliveira. Journal of Nematology, 2018, 50, 1-2.	0.9	0
3716	The Use of Distributed Data Storage and Processing Systems in Bioinformatic Data Analysis. Communications in Computer and Information Science, 2018, , 18-32.	0.5	0

#	ARTICLE	IF	CITATIONS
3717	The Transcriptome of <i>Paraphelidium Tribonemae</i> Illuminates the Ancestry of Fungi and Opisthosporidia. SSRN Electronic Journal, 0, , .	0.4	0
3754	Theoretical and Practical Analyses in Metagenomic Sequence Classification. Communications in Computer and Information Science, 2019, , 27-37.	0.5	0
3755	Transcriptome Analysis of the Effect of Cutting Age on Adventitious Root Formation of Populus. Botanical Research, 2019, 08, 293-306.	0.0	0
3812	Complete Genome Sequences of Three Rabbit Endogenous Lentivirus Type K Viruses Obtained from Commercial Meat Rabbits in Italy. Microbiology Resource Announcements, 2019, 8, .	0.6	0
3820	Exploring Toxin Evolution: Venom Protein Transcript Sequencing and Transcriptome-Guided High-Throughput Proteomics. Methods in Molecular Biology, 2020, 2068, 97-127.	0.9	3
3824	Biological Sequence Analysis. , 0, , 55-69.		2
3845	Draft Genome Sequence of Clostridium sp. Strain FP1, with Similarity to Clostridium tagluense , Isolated from Spoiled Lamb. Microbiology Resource Announcements, 2020, 9, .	0.6	3
3853	Lysinibacillus antri sp. nov., isolated from cave soil. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 3295-3299.	1.7	5
3860	Whole-Genome Sequence of an Indian Group A Streptococcus emm Type 1-2 Strain Isolated from a Blood Sample in North India. Microbiology Resource Announcements, 2020, 9, .	0.6	1
3869	Cyclobacterium salsum sp. nov. and Cyclobacterium roseum sp. nov., isolated from a saline lake. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 3785-3793.	1.7	9
3874	Comprehensive analysis and identification of heat-responsive genes in <i>Agarophyton vermiculophyllum</i> by RNA-sequencing. Botanica Marina, 2020, 63, 479-490.	1.2	3
3878	Investigation of stalk formation, frequency of dividing cells and gene expression in periphyton mats dominated by <i>Didymosphenia geminata</i> . Aquatic Ecosystem Health and Management, 2020, 23, 302-312.	0.6	0
3889	Orthologous Revelation between Elaeis guineensis, Arabidopsis thaliana and Solanum lycopersicum. International Journal of Life Sciences and Biotechnology, 2020, 3, 164-179.	0.7	0
3895	A Feasibility Study for MPI over HDFS. , 2020, , .		0
3896	MinION sequencing from sea ice cryoconites leads to de novo genome reconstruction from metagenomes. Scientific Reports, 2021, 11, 21041.	3.3	9
3897	Biogeography of Bacterial Communities and Specialized Metabolism in Human Aerodigestive Tract Microbiomes. Microbiology Spectrum, 2021, 9, e0166921.	3.0	3
3898	The Dynamic Codon Biased: calculating prokaryotic codon usage biases. Microbial Genomics, 2021, 7, .	2.0	3
3899	Unbiased Antimicrobial Resistance Detection from Clinical Bacterial Isolates Using Proteomics. Analytical Chemistry, 2021, 93, 14599-14608.	6.5	6

#	ARTICLE	IF	CITATIONS
3900	Functional metagenomic analysis of quorum sensing signaling in a nitrifying community. <i>Npj Biofilms and Microbiomes</i> , 2021, 7, 79.	6.4	8
3901	Long-read sequencing to interrogate strain-level variation among adherent-invasive <i>Escherichia coli</i> isolated from human intestinal tissue. <i>PLoS ONE</i> , 2021, 16, e0259141.	2.5	7
3903	Transcriptomic and Metabolomic Differences Between Two <i>Saposhnikovia divaricata</i> (Turcz.) Schischk Phenotypes With Single- and Double-Headed Roots. <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 764093.	4.1	3
3904	Patterns in the Microbial Community of Salt-Tolerant Plants and the Functional Genes Associated with Salt Stress Alleviation. <i>Microbiology Spectrum</i> , 2021, 9, e0076721.	3.0	27
3906	RNA virome diversity and <i>Wolbachia</i> infection in individual <i>Drosophila simulans</i> flies. <i>Journal of General Virology</i> , 2021, 102, .	2.9	4
3907	Comparison of different valent iron on anaerobic sludge digestion: Focusing on oxidation reduction potential, dissolved organic nitrogen and microbial community. <i>Frontiers of Environmental Science and Engineering</i> , 2022, 16, 1.	6.0	11
3909	Non-vernalization requirement in Chinese kale caused by loss of <i>BoFLC</i> and low expressions of its paralogs. <i>Theoretical and Applied Genetics</i> , 2022, 135, 473-483.	3.6	4
3910	Analysis of Sex Chromosome Evolution in the Clade <i>Palaeognathae</i> from Phased Genome Assembly. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	2
3911	<i>Blautia liquoris</i> sp. nov., isolated from the mud in a fermentation cellar used for the production of Chinese strong-flavour liquor. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	1.7	4
3913	Improved method for the extraction of high-quality DNA from lignocellulosic compost samples for metagenomic studies. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 8881-8893.	3.6	9
3914	Comprehensive functional core microbiome comparison in genetically obese and lean hosts under the same environment. <i>Communications Biology</i> , 2021, 4, 1246.	4.4	14
3915	Metagenomic Analysis of Biocide-Treated Neotropical Oil Reservoir Water Unveils Microdiversity of Thermophile <i>Tepidiphilus</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 741555.	3.5	4
3916	Ammonium regulates the development of pine roots through hormonal crosstalk and differential expression of transcription factors in the apex. <i>Plant, Cell and Environment</i> , 2022, 45, 915-935.	5.7	11
3917	Histology and transcriptomic analyses of barnacles with different base materials and habitats shed lights on the duplication and chemical diversification of barnacle cement proteins. <i>BMC Genomics</i> , 2021, 22, 783.	2.8	12
3919	HoSelN: A Workflow for Integrating Various Homology Search Results from Metagenomic and Metatranscriptomic Sequence Datasets. <i>Bio-protocol</i> , 2020, 10, e3679.	0.4	0
3920	The Complete Genome of Probiotic <i>Lactobacillus sakei</i> Derived from Plateau Yak Feces. <i>Genes</i> , 2020, 11, 1527.	2.4	8
3922	Utilization of low-molecular-weight organic compounds by the filterable fraction of a lotic microbiome. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	2.7	0
3924	Genomic analysis of dibenzofuran-degrading <i>Pseudomonas veronii</i> strain Pvy reveals its biodegradative versatility. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	5

#	ARTICLE	IF	CITATIONS
3925	The First Draft Genome of a Cold-Water Coral <i>Trachythela</i> sp. (Alcyonacea: Stolonifera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 74	2.5	5
3926	Taxonomic Binning Approaches and Functional Characteristics of the Microbial Community during the Anaerobic Digestion of Hydrolyzed Corncob. <i>Energies</i> , 2021, 14, 66.	3.1	3
3931	Marine Ultrasmall Prokaryotes Likely Affect the Cycling of Carbon, Methane, Nitrogen, and Sulfur. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	6
3933	Mycobacterial and Plasmodium ovale-associated destruction of the jaw bones. <i>Oral Diseases</i> , 2022, 28, 452-468.	3.0	1
3934	Comparative Analysis of Carbohydrate Active Enzymes in the <i>Flammulina velutipes</i> var. <i>lupinicola</i> Genome. <i>Microorganisms</i> , 2021, 9, 20.	3.6	3
3935	Genome analysis of <i>Plectus murrayi</i> , a nematode from continental Antarctica. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, 1-9.	1.8	4
3936	Bioinformatics Pre-Processing of Microbiome Data with An Application to Metagenomic Forensics. <i>Frontiers in Probability and the Statistical Sciences</i> , 2021, , 45-78.	0.1	1
3937	Elucidation of the biochemical pathways involved in two distinct cut-surface discolouration phenotypes of lettuce. <i>Postharvest Biology and Technology</i> , 2022, 183, 111753.	6.0	5
3938	Study on the differences in sludge toxicity and microbial community structure caused by catechol, resorcinol and hydroquinone with metagenomic analysis. <i>Journal of Environmental Management</i> , 2022, 302, 114027.	7.8	16
3939	Low strength wastewater anammox start-up by stepwise decrement in influent nitrogen: Biofilm formation mechanism and mathematical modelling. <i>Environment International</i> , 2022, 158, 106929.	10.0	32
3940	Transcriptomic evidences for microbial carbon and nitrogen cycles in the deoxygenated seawaters of Bohai Sea. <i>Environment International</i> , 2022, 158, 106889.	10.0	12
3941	Denitrification and dissimilatory nitrate reduction to ammonia in long-term lake sediment microcosms with iron(II). <i>Science of the Total Environment</i> , 2022, 807, 150835.	8.0	20
3942	Carbon sources driven supernatant micro-particles differentiate in submerged anaerobic membrane bioreactors (AnMBRs). <i>Chemical Engineering Journal</i> , 2022, 430, 133020.	12.7	10
3946	The Mucosally-Adherent Rectal Microbiota Contains Features Unique to Alcohol-Related Cirrhosis. <i>Gut Microbes</i> , 2021, 13, 1987781.	9.8	10
3950	Computational Metagenomics: State-of-the-Art, Facts and Artifacts. , 2020, , 199-227.		0
3951	Orthology: Promises and Challenges. , 2020, , 203-228.		10
3953	A Comprehensive Analysis of the Global Human Gut Archaeome from a Thousand Genome Catalogue. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
3954	RNN-VirSeeker: a deep learning method for identification of short viral sequences from metagenomes. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, PP, 1-1.	3.0	15

#	ARTICLE	IF	CITATIONS
3965	InsectBase 2.0: a comprehensive gene resource for insects. <i>Nucleic Acids Research</i> , 2022, 50, D1040-D1045.	14.5	74
3966	Bacterial adaptation by a transposition burst of an invading IS element. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	6
3970	<i>Vulcaniibacterium gelatinicum</i> sp. nov., a moderately thermophilic bacterium isolated from a hot spring. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 1571-1577.	1.7	5
3975	Identification and characterization of the glycoside hydrolase family 18 genes from the entomopathogenic fungus <i>Isaria cicadae</i> genome. <i>Canadian Journal of Microbiology</i> , 2020, 66, 274-287.	1.7	3
3981	Deep (Meta)genomics and (Meta)transcriptome Analyses of Fungal and Bacteria Consortia From Aircraft Tanks and Kerosene Identify Key Genes in Fuel and Tank Corrosion. <i>Frontiers in Microbiology</i> , 2021, 12, 722259.	3.5	5
3982	Metagenomic Identification of Viral Sequences in Laboratory Reagents. <i>Viruses</i> , 2021, 13, 2122.	3.3	21
3984	L-Cysteine Synthase Enhanced Sulfide Biotransformation in Subtropical Marine Mangrove Sediments as Revealed by Metagenomics Analysis. <i>Water (Switzerland)</i> , 2021, 13, 3053.	2.7	2
3985	BioProv - A provenance library for bioinformatics workflows. <i>Journal of Open Source Software</i> , 2021, 6, 3622.	4.6	1
3986	Expression analyses in <i>Ginkgo biloba</i> provide new insights into the evolution and development of the seed. <i>Scientific Reports</i> , 2021, 11, 21995.	3.3	8
3987	Integrative analysis of Iso-Seq and RNA-seq data reveals transcriptome complexity and differentially expressed transcripts in sheep tail fat. <i>PeerJ</i> , 2021, 9, e12454.	2.0	16
3988	A Novel Subtype of Bovine Hepacivirus Identified in Ticks Reveals the Genetic Diversity and Evolution of Bovine Hepacivirus. <i>Viruses</i> , 2021, 13, 2206.	3.3	11
3989	Virulent Bacteria as Inflammatory and Immune Co-Factor in Colon Carcinogenesis: Evidence From Two Monozygotic Patients and Validation in CRC Patient and Healthy Cohorts. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 749750.	3.9	1
3990	Identification of heat responsive genes in pea stipules and anthers through transcriptional profiling. <i>PLoS ONE</i> , 2021, 16, e0251167.	2.5	4
3991	The Role Transition of Dietary Species Richness in Modulating the Gut Microbial Assembly and Postweaning Performance of a Generalist Herbivore. <i>MSystems</i> , 2021, 6, e0097921.	3.8	6
3992	An internal recycling mechanism between ammonia/ammonium and nitrate driven by ammonia-oxidizing archaea and bacteria (AOA, AOB, and Comammox) and DNRA on Angkor sandstone monuments. <i>International Biodeterioration and Biodegradation</i> , 2021, 165, 105328.	3.9	24
3993	DNA Viral Diversity, Abundance, and Functional Potential Vary across Grassland Soils with a Range of Historical Moisture Regimes. <i>MBio</i> , 2021, 12, e0259521.	4.1	24
3994	Evaluating <i>de Novo</i> Assembly and Binning Strategies for Time Series Drinking Water Metagenomes. <i>Microbiology Spectrum</i> , 2021, 9, e0143421.	3.0	16
3995	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, .	7.1	68

#	ARTICLE	IF	CITATIONS
3996	A novel SARS-CoV-2 related coronavirus in bats from Cambodia. Nature Communications, 2021, 12, 6563.	12.8	127
3997	The origin and impeded dissemination of the DNA phosphorothioation system in prokaryotes. Nature Communications, 2021, 12, 6382.	12.8	14
3998	Environmental Factors Influencing Phyllosphere Bacterial Communities in Giant Pandasâ€™ Staple Food Bamboos. Frontiers in Microbiology, 2021, 12, 748141.	3.5	2
3999	Spike Formation Is a Turning Point Determining Wheat Root Microbiome Abundance, Structures and Functions. International Journal of Molecular Sciences, 2021, 22, 11948.	4.1	2
4000	Glycan Biosynthesis Ability of Gut Microbiota Increased in Primary Hypertension Patients Taking Antihypertension Medications and Potentially Promoted by Macrophage-Adenosine Monophosphate-Activated Protein Kinase. Frontiers in Microbiology, 2021, 12, 719599.	3.5	6
4001	Transcriptome profiling reveals the developmental regulation of NaCl-treated Forcipomyia taiwana eggs. BMC Genomics, 2021, 22, 792.	2.8	2
4003	The rumen microbiome inhibits methane formation through dietary choline supplementation. Scientific Reports, 2021, 11, 21761.	3.3	3
4004	Bakta: rapid and standardized annotation of bacterial genomes via alignment-free sequence identification. Microbial Genomics, 2021, 7, .	2.0	168
4005	Comparative hologenomics of two <i>Ixodes scapularis</i> tick populations in New Jersey. PeerJ, 2021, 9, e12313.	2.0	3
4006	How to resist soil desiccation: Transcriptional changes in a Mediterranean earthworm during aestivation. Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology, 2022, 264, 111112.	1.8	5
4007	Draft genome of the blister beetle, <i>Epicauta chinensis</i> . International Journal of Biological Macromolecules, 2021, 193, 1694-1694.	7.5	4
4008	<i>Burkholderiaceae</i> and Multidrug Resistance Genes Are Key Players in Resistome Development in a Germfree Soil Model. MSystems, 2021, 6, e0098821.	3.8	7
4015	Isolation and sequence-based characterization of a koala symbiont: <i>Lonepinella koalarum</i> . PeerJ, 2020, 8, e10177.	2.0	5
4016	Transcriptome analysis of diploid and triploid <i>Populus tomentosa</i> . PeerJ, 2020, 8, e10204.	2.0	4
4044	Ancestral state reconstruction of metabolic pathways across pangenome ensembles. Microbial Genomics, 2020, 6, .	2.0	3
4045	A glimpse of antimicrobial resistance gene diversity in kefir and yoghurt. Scientific Reports, 2020, 10, 22458.	3.3	27
4055	Draft Genome Sequence of <i>Bifidobacterium longum</i> subsp. <i>infantis</i> BI-G201, a Commercialization Strain. Microbiology Resource Announcements, 2020, 9, .	0.6	1
4056	KELSA: A Knowledge-Enriched Local Sequence Alignment Algorithm for Comparing Patient Medical Records. Studies in Computational Intelligence, 2021, , 227-240.	0.9	0

#	ARTICLE	IF	CITATIONS
4057	Comparative Genome Analysis Reveals Natural Variations in the Genomes of <i>Erwinia pyrifoliae</i> , a Black Shoot Blight Pathogen in Apple and Pear. <i>Plant Pathology Journal</i> , 2020, 36, 428-439.	1.7	5
4060	Resveratrol improves high-fat diet-induced insulin resistance in mice by downregulating the lncRNA NONMMUT008655.2. <i>American Journal of Translational Research (discontinued)</i> , 2020, 12, 1-18.	0.0	7
4061	Viral metagenomics in blood donations with post-donation illness reports from Brazil. <i>Blood Transfusion</i> , 2021, 19, 93-101.	0.4	1
4062	Dysbiotic gut microbiota in pancreatic cancer patients form correlation networks with the oral microbiota and prognostic factors. <i>American Journal of Cancer Research</i> , 2021, 11, 3163-3175.	1.4	4
4063	A chromosome-level genome assembly for the eastern fence lizard (<i>Sceloporus undulatus</i>), a reptile model for physiological and evolutionary ecology. <i>GigaScience</i> , 2021, 10, .	6.4	3
4064	Taxonomic and functional characterization of the rumen microbiome of Japanese Black cattle revealed by 16S rRNA gene amplicon and metagenome shotgun sequencing. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	2.7	9
4065	Genome-resolved metagenomics provides insights into the functional complexity of microbial mats in Blue Holes, Shark Bay. <i>FEMS Microbiology Ecology</i> , 2022, 98, .	2.7	10
4066	An integrated workflow for enhanced taxonomic and functional coverage of the mouse fecal metaproteome. <i>Cut Microbes</i> , 2021, 13, 1994836.	9.8	6
4067	Higher abundance of core antimicrobial resistant genes in effluent from wastewater treatment plants. <i>Water Research</i> , 2022, 208, 117882.	11.3	51
4068	Biological sequence analysis. , 2022, , 33-47.		0
4069	Introduction to basics of bioinformatics. , 2022, , 1-15.		5
4070	The male and female gonad transcriptome of the edible sea urchin, <i>Paracentrotus lividus</i> : Identification of sex-related and lipid biosynthesis genes. <i>Aquaculture Reports</i> , 2022, 22, 100936.	1.7	6
4071	Effect of bioaugmentation on the growth and rhizosphere microbiome assembly of hydroponic cultures of <i>Mentha aquatica</i> . <i>Ecological Genetics and Genomics</i> , 2022, 22, 100107.	0.5	1
4072	Evaluating DNA metabarcoding to analyze diet composition of wild long-snouted seahorse <i>Hippocampus guttulatus</i> . , 2021, , .		1
4073	Utilization Efficiency of Human Milk Oligosaccharides by Human-Associated <i>Akkermansia</i> Is Strain Dependent. <i>Applied and Environmental Microbiology</i> , 2022, 88, AEM0148721.	3.1	29
4074	A resource for improved predictions of <i>Trypanosoma</i> and <i>Leishmania</i> protein three-dimensional structure. <i>PLoS ONE</i> , 2021, 16, e0259871.	2.5	29
4075	Xylan alleviates dietary fiber deprivation-induced dysbiosis by selectively promoting <i>Bifidobacterium pseudocatenulatum</i> in pigs. <i>Microbiome</i> , 2021, 9, 227.	11.1	28
4076	Genomic characterization of silvergrass cryptic virus 1, a novel partitivirus infecting <i>Miscanthus sinensis</i> . <i>Archives of Virology</i> , 2022, 167, 261-265.	2.1	4

#	ARTICLE	IF	CITATIONS
4077	Molecular Identification and Selection of Probiotic Strains Able to Reduce the Serum TMAO Level in Mice Challenged with Choline. <i>Foods</i> , 2021, 10, 2931.	4.3	6
4078	Gut microbiome drives individual memory variation in bumblebees. <i>Nature Communications</i> , 2021, 12, 6588.	12.8	34
4081	RFPlasmid: predicting plasmid sequences from short-read assembly data using machine learning. <i>Microbial Genomics</i> , 2021, 7, .	2.0	31
4082	Highly flexible metabolism of the marine euglenozoan protist <i>Diplonema papillatum</i> . <i>BMC Biology</i> , 2021, 19, 251.	3.8	19
4083	A comparative study of pan-genome methods for microbial organisms: <i>Acinetobacter baumannii</i> pan-genome reveals structural variation in antimicrobial resistance-carrying plasmids. <i>Microbial Genomics</i> , 2021, 7, .	2.0	4
4084	Fucosylated Human Milk Oligosaccharide Foraging within the Species <i>Bifidobacterium pseudocatenulatum</i> Is Driven by Glycosyl Hydrolase Content and Specificity. <i>Applied and Environmental Microbiology</i> , 2022, 88, AEM0170721.	3.1	18
4085	PangenomeNet: a pan-genome-based network reveals functional modules on antimicrobial resistome for <i>Escherichia coli</i> strains. <i>BMC Bioinformatics</i> , 2021, 22, 548.	2.6	7
4087	Genome-wide understanding of evolutionary and functional relationships of rice Yellow Stripe-Like (YSL) transporter family in comparison with other plant species. <i>Biologia (Poland)</i> , 2022, 77, 39-53.	1.5	11
4088	Circadian dynamics of the teleost skin immune-microbiome interface. <i>Microbiome</i> , 2021, 9, 222.	11.1	20
4089	Single cell genomics reveals plastid-lacking Picozoa are close relatives of red algae. <i>Nature Communications</i> , 2021, 12, 6651.	12.8	40
4090	Transcriptional responses of <i>Trichodesmium</i> to natural inverse gradients of Fe and P availability. <i>ISME Journal</i> , 2022, 16, 1055-1064.	9.8	18
4091	Metagenomic analysis to identify novel infectious agents in systemic anaplastic large cell lymphoma. <i>Infectious Agents and Cancer</i> , 2021, 16, 65.	2.6	0
4092	Bacteria.guru: Comparative Transcriptomics and Co-Expression Database for Bacterial Pathogens. <i>Journal of Molecular Biology</i> , 2022, 434, 167380.	4.2	4
4093	Genome of the estuarine oyster provides insights into climate impact and adaptive plasticity. <i>Communications Biology</i> , 2021, 4, 1287.	4.4	29
4094	Origins and evolution of extreme life span in Pacific Ocean rockfishes. <i>Science</i> , 2021, 374, 842-847.	12.6	71
4095	Metagenomics Analysis to Investigate the Microbial Communities and Their Functional Profile During Cyanobacterial Blooms in Lake Varese. <i>Microbial Ecology</i> , 2022, 83, 850-868.	2.8	15
4097	The highly diverse Antarctic Peninsula soil microbiota as a source of novel resistance genes. <i>Science of the Total Environment</i> , 2022, 810, 152003.	8.0	18
4098	Study of Heavy Metals and Microbial Communities in Contaminated Sediments Along an Urban Estuary. <i>Frontiers in Marine Science</i> , 2021, 8, .	2.5	12

#	ARTICLE	IF	CITATIONS
4099	Unveiling Ecological and Genetic Novelty within Lytic and Lysogenic Viral Communities of Hot Spring Phototrophic Microbial Mats. <i>Microbiology Spectrum</i> , 2021, , e0069421.	3.0	4
4102	Evaluations of biochar amendment on anaerobic co-digestion of pig manure and sewage sludge: waste-to-methane conversion, microbial community, and antibiotic resistance genes. <i>Bioresource Technology</i> , 2022, 346, 126400.	9.6	15
4103	Current understanding and perspectives in anaerobic digestion based on genome-resolved metagenomic approaches. <i>Bioresource Technology</i> , 2022, 344, 126350.	9.6	23
4104	Transcriptome-wide deregulation of gene expression by artificial light at night in tadpoles of common toads. <i>Science of the Total Environment</i> , 2022, 818, 151734.	8.0	5
4105	Comparison of gastrointestinal microbiota in golden snub-nosed monkey (<i>Rhinopithecus roxellanae</i>), green monkey (<i>Chlorocebus aethiops sabaeus</i>), and ring-tailed lemur (<i>Lemur catta</i>) by high throughput sequencing. <i>Global Ecology and Conservation</i> , 2022, 33, e01946.	2.1	3
4106	Protoplast isolation and transcriptome analysis of developing xylem in <i>Pinus massoniana</i> (Pinaceae). <i>Molecular Biology Reports</i> , 2022, 49, 1857-1869.	2.3	1
4108	Virome Analysis of Signal Crayfish (<i>Pacifastacus leniusculus</i>) along Its Invasion Range Reveals Diverse and Divergent RNA Viruses. <i>Viruses</i> , 2021, 13, 2259.	3.3	6
4109	Cocaine esterase occurrence in global wastewater microbiomes and potential for biotransformation of novel psychoactive substances. <i>Environmental Microbiology Reports</i> , 2022, 14, 96-109.	2.4	1
4110	The potential of family-free rearrangements towards gene orthology inference. <i>Journal of Bioinformatics and Computational Biology</i> , 2021, 19, 2140014.	0.8	3
4113	Phylogenetic Relatedness and Genome Structure of <i>Yersinia ruckeri</i> Revealed by Whole Genome Sequencing and a Comparative Analysis. <i>Frontiers in Microbiology</i> , 2021, 12, 782415.	3.5	1
4114	Human and Animal RNA Virus Diversity Detected by Metagenomics in Cameroonian Clams. <i>Frontiers in Microbiology</i> , 2021, 12, 770385.	3.5	8
4115	Unexpected Mechanism of Biodegradation and Defluorination of 2,2-Difluoro-1,3-Benzodioxole by <i>Pseudomonas putida</i> F1. <i>MBio</i> , 2021, 12, e0300121.	4.1	10
4116	Comparative Transcriptome Analysis of the Phototrophic Dinoflagellate <i>Biecheleriopsis adriatica</i> Grown Under Optimal Temperature and Cold and Heat Stress. <i>Frontiers in Marine Science</i> , 2021, 8, .	2.5	7
4117	Increased microbial expression of organic nitrogen cycling genes in long-term warmed grassland soils. <i>ISME Communications</i> , 2021, 1, .	4.2	14
4118	Hybrid de novo genome-reassembly reveals new insights on pathways and pathogenicity determinants in rice blast pathogen <i>Magnaporthe oryzae</i> RMg_DI. <i>Scientific Reports</i> , 2021, 11, 22922.	3.3	8
4119	Compendium of 530 metagenome-assembled bacterial and archaeal genomes from the polar Arctic Ocean. <i>Nature Microbiology</i> , 2021, 6, 1561-1574.	13.3	57
4120	A primer and discussion on DNA-based microbiome data and related bioinformatics analyses. , 0, 1, .		6
4121	Commensal <i>Bifidobacterium</i> Strains Enhance the Efficacy of Neo-Epitope Based Cancer Vaccines. <i>Vaccines</i> , 2021, 9, 1356.	4.4	10

#	ARTICLE	IF	CITATIONS
4122	Hundreds of Out-of-Frame Remodeled Gene Families in the <i>Escherichia coli</i> Pangenome. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	6
4124	Ecological generalism drives hyperdiversity of secondary metabolite gene clusters in xylarialean endophytes. <i>New Phytologist</i> , 2022, 233, 1317-1330.	7.3	23
4125	Metagenomics of Antarctic Marine Sediment Reveals Potential for Diverse Chemolithoautotrophy. <i>MSphere</i> , 2021, 6, e0077021.	2.9	5
4127	Wolbachia reduces virus infection in a natural population of <i>Drosophila</i> . <i>Communications Biology</i> , 2021, 4, 1327.	4.4	26
4128	Genome sequencing of the multicellular alga <i>Astrephomene</i> provides insights into convergent evolution of germ-soma differentiation. <i>Scientific Reports</i> , 2021, 11, 22231.	3.3	7
4129	A review of the resistome within the digestive tract of livestock. <i>Journal of Animal Science and Biotechnology</i> , 2021, 12, 121.	5.3	17
4132	Searching for New Microbiome-Targeted Therapeutics through a Drug Repurposing Approach. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 17277-17286.	6.4	4
4133	Leave no stone unturned: individually adapted xerotolerant <i>Thaumarchaeota</i> sheltered below the boulders of the Atacama Desert hyperarid core. <i>Microbiome</i> , 2021, 9, 234.	11.1	18
4134	The draft chromosome-level genome assembly of tetraploid ground cherry (<i>Prunus fruticosa</i> Pall.) from long reads. <i>Genomics</i> , 2021, 113, 4173-4183.	2.9	14
4135	Single-molecule real-time transcript sequencing of developing cotton anthers facilitates genome annotation and fertility restoration candidate gene discovery. <i>Genomics</i> , 2021, 113, 4245-4253.	2.9	5
4136	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.	8.0	7
4137	TSEBRA: transcript selector for BRAKER. <i>BMC Bioinformatics</i> , 2021, 22, 566.	2.6	91
4138	Chromosome-level genome assembly of the Chinese three-keeled pond turtle (<i>Mauremys reevesii</i>) provides insights into freshwater adaptation. <i>Molecular Ecology Resources</i> , 2022, 22, 1596-1605.	4.8	8
4141	ASER: Animal Sex Reversal Database. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 873-881.	6.9	5
4142	Interspecies variation in hominid gut microbiota controls host gene regulation. <i>Cell Reports</i> , 2021, 37, 110057.	6.4	9
4143	Vaccine Hyporesponse Induced by Individual Antibiotic Treatment in Mice and Non-Human Primates Is Diminished upon Recovery of the Gut Microbiome. <i>Vaccines</i> , 2021, 9, 1340.	4.4	5
4145	Novel Insights into the Stemness and Immune Privilege of Mesenchymal Stem Cells from Human Wharton Jelly by Single-Cell RNA Sequencing. <i>Medical Science Monitor</i> , 2022, 28, e934660.	1.1	2
4146	Developmental series of gene expression clarifies maternal mRNA provisioning and maternal-to-zygotic transition in a reef-building coral. <i>BMC Genomics</i> , 2021, 22, 815.	2.8	11

#	ARTICLE	IF	CITATIONS
4147	Cross-regional scale pollution of freshwater biofilms unveiled by antibiotic resistance genes. <i>Science of the Total Environment</i> , 2022, 818, 151835.	8.0	11
4148	Love bites: male frogs (<i>Plectrohyla</i> , <i>Hylidae</i>) use teeth scratching to deliver sodefrin precursor-like factors to females during amplexus. <i>Frontiers in Zoology</i> , 2021, 18, 59.	2.0	7
4149	Genomic Characterization of Imipenem- and Imipenem-Relebactam-Resistant Clinical Isolates of <i>Pseudomonas aeruginosa</i> . <i>MSphere</i> , 2021, 6, e0083621.	2.9	5
4150	Active and Covert Infections of Cricket Iridovirus and <i>Acheta domesticus</i> Densovirus in Reared <i>Gryllobates sigillatus</i> Crickets. <i>Frontiers in Microbiology</i> , 2021, 12, 780796.	3.5	8
4151	Comparative morphological, physiological, biochemical and genomic studies reveal novel genes of <i>Dunaliella bioculata</i> and <i>D. quatolecta</i> in response to salt stress. <i>Molecular Biology Reports</i> , 2022, 49, 1749-1761.	2.3	4
4152	Weaning Age and Its Effect on the Development of the Swine Gut Microbiome and Resistome. <i>MSystems</i> , 2021, 6, e0068221.	3.8	26
4153	High viral abundance and low diversity are associated with increased CRISPR-Cas prevalence across microbial ecosystems. <i>Current Biology</i> , 2022, 32, 220-227.e5.	3.9	23
4154	Toward the Heterologous Biosynthesis of Plant Natural Products: Gene Discovery and Characterization. <i>ACS Synthetic Biology</i> , 2021, 10, 2784-2795.	3.8	12
4155	Metagenomic analysis reveals microbiome and resistome in the seawater and sediments of Kongsfjorden (Svalbard, High Arctic). <i>Science of the Total Environment</i> , 2022, 809, 151937.	8.0	16
4157	Telomere-to-telomere genome assembly of asparaginase-producing <i>Trichoderma simmonsii</i> . <i>BMC Genomics</i> , 2021, 22, 830.	2.8	9
4159	Alteration of the gut microbiota in rhesus monkey with spontaneous osteoarthritis. <i>BMC Microbiology</i> , 2021, 21, 328.	3.3	10
4160	Multi-species host range of staphylococcal phages isolated from wastewater. <i>Nature Communications</i> , 2021, 12, 6965.	12.8	50
4161	Safety Evaluation of <i>Weissella cibaria</i> JW15 by Phenotypic and Genotypic Property Analysis. <i>Microorganisms</i> , 2021, 9, 2450.	3.6	12
4162	<i>Muribaculaceae</i> Genomes Assembled from Metagenomes Suggest Genetic Drivers of Differential Response to Acarbose Treatment in Mice. <i>MSphere</i> , 2021, 6, e0085121.	2.9	53
4163	The <i>Cymbidium</i> genome reveals the evolution of unique morphological traits. <i>Horticulture Research</i> , 2021, 8, 255.	6.3	33
4165	Gastrointestinal tract microbial community of <i>Babylonia areolata</i> and its diversity are closely correlated with the outbreak of disease. <i>Aquaculture Research</i> , 2022, 53, 1636-1648.	1.8	1
4166	An integrated metagenomic and metabolite profiling study of hydrocarbon biodegradation and corrosion in navy ships. <i>Npj Materials Degradation</i> , 2021, 5, .	5.8	7
4167	Scalingâ€“up a fragmentâ€“based proteinâ€“protein interaction method using a human reference interaction set. <i>Proteins: Structure, Function and Bioinformatics</i> , 2022, 90, 959-972.	2.6	5

#	ARTICLE	IF	CITATIONS
4168	Characterization of antimicrobial resistance genes and virulence factor genes in an Arctic permafrost region revealed by metagenomics. <i>Environmental Pollution</i> , 2022, 294, 118634.	7.5	26
4169	Saline lakes on the Qinghai-Tibet Plateau harbor unique viral assemblages mediating microbial environmental adaption. <i>IScience</i> , 2021, 24, 103439.	4.1	13
4170	Time-restricted feeding induces <i>Lactobacillus</i> - and <i>Akkermansia</i> -specific functional changes in the rat fecal microbiota. <i>Npj Biofilms and Microbiomes</i> , 2021, 7, 85.	6.4	14
4172	The Underrated Salivary Virome of Men Who Have Sex With Men Infected With HIV. <i>Frontiers in Immunology</i> , 2021, 12, 759253.	4.8	7
4174	The Chemosensory Transcriptome of a Diving Beetle. <i>Frontiers in Ecology and Evolution</i> , 2021, 9, .	2.2	1
4176	A Catalogue of 48,425 Nonredundant Viruses From Oral Metagenomes Expands the Horizon of the Human Oral Virome. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
4177	Advanced Simultaneous Nitrogen and Phosphorus Removal for Non-Sterile Wastewater Through a Novel Coupled Yeast-Sludge System: Performance, Microbial Interaction, and Mechanism. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
4178	Metagenomic Insights of the Microbial Community from a Polluted River in Brazil 2020. <i>Lecture Notes in Computer Science</i> , 2021, , 137-144.	1.3	0
4180	The bone-degrading enzyme machinery: From multi-component understanding to the treatment of residues from the meat industry. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 6328-6342.	4.1	2
4181	Overproduction of medicinal ergot alkaloids based on a fungal platform. <i>Metabolic Engineering</i> , 2022, 69, 198-208.	7.0	15
4182	Defining the Sensitivity Landscape of 74,389 <i>EGFR</i> Variants to Tyrosine Kinase Inhibitors. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
4183	Shotgun metagenomics of Cheonggukjang, a fermented soybean food of Korea: Community structure, predictive functionalities and amino acids profile. <i>Food Research International</i> , 2022, 151, 110904.	6.2	22
4184	Increased circulating butyrate and ursodeoxycholate during probiotic intervention in humans with type 2 diabetes. <i>BMC Microbiology</i> , 2022, 22, 19.	3.3	14
4185	Transcriptome analyses of the Chinese white pine beetle-fungal symbiont <i>Leptographium qinlingensis</i> under terpene stress or growth on host pine sawdust. <i>Symbiosis</i> , 2022, 86, 17-31.	2.3	10
4186	SpeciesRax: A Tool for Maximum Likelihood Species Tree Inference from Gene Family Trees under Duplication, Transfer, and Loss. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	29
4187	Rapidly Deployable Algae Cleaning System for Applications in Freshwater Reservoirs and Water Bodies. <i>Phycology</i> , 2022, 2, 60-75.	3.6	0
4188	Profiling Signal Transduction in Global Marine Biofilms. <i>Frontiers in Microbiology</i> , 2021, 12, 768926.	3.5	9
4189	Structure and Function of Rhizosphere Soil and Root Endophytic Microbial Communities Associated With Root Rot of <i>Panax notoginseng</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 752683.	3.6	13

#	ARTICLE	IF	CITATIONS
4191	The influence of planting <i>Carex praeclara</i> and <i>Leymus secalinus</i> on soil properties and microbial community in a Zoige desertified alpine grassland. <i>Global Ecology and Conservation</i> , 2022, 34, e02002.	2.1	8
4192	Isolation and Characterization of the First Temperate Virus Infecting <i>Psychrobacillus</i> from Marine Sediments. <i>Viruses</i> , 2022, 14, 108.	3.3	6
4193	Population genomics provides insights into lineage divergence and local adaptation within the cotton bollworm. <i>Molecular Ecology Resources</i> , 2022, 22, 1875-1891.	4.8	18
4194	Genome-Resolved Metagenomics Reveals Distinct Phosphorus Acquisition Strategies between Soil Microbiomes. <i>MSystems</i> , 2022, 7, e0110721.	3.8	64
4195	Novel putative pathogenic viruses identified in pangolins by mining metagenomic data. <i>Journal of Medical Virology</i> , 2022, 94, 2500-2509.	5.0	6
4196	The anammox coupled partial-denitrification process in an integrated granular sludge and fixed-biofilm reactor developed for mainstream wastewater treatment: Performance and community structure. <i>Water Research</i> , 2022, 210, 117964.	11.3	52
4197	New insights into the functioning and structure of the PE and PP plastispheres from the Mediterranean Sea. <i>Environmental Pollution</i> , 2022, 295, 118678.	7.5	20
4198	Virulent phage vB_CpeP_HN02 inhibits <i>Clostridium perfringens</i> on the surface of the chicken meat. <i>International Journal of Food Microbiology</i> , 2022, 363, 109514.	4.7	13
4199	Toward shotgun metagenomic approaches for microbial source tracking sewage spills based on laboratory mesocosms. <i>Water Research</i> , 2022, 210, 117993.	11.3	12
4200	Abundance and diversity of n-alkane and PAH-degrading bacteria and their functional genes “Potential for use in detection of marine oil pollution. <i>Science of the Total Environment</i> , 2022, 810, 152238.	8.0	12
4201	Diversity, abundances and distribution of antibiotic resistance genes and virulence factors in the South China Sea revealed by metagenomic sequencing. <i>Science of the Total Environment</i> , 2022, 814, 152803.	8.0	15
4202	Contribution of plasmidome, metal resistome and integrases to the persistence of the antibiotic resistome in aquatic environments. <i>Environmental Pollution</i> , 2022, 297, 118774.	7.5	6
4203	Cropping system exerts stronger influence on antibiotic resistance gene assemblages in greenhouse soils than reclaimed wastewater irrigation. <i>Journal of Hazardous Materials</i> , 2022, 425, 128046.	12.4	12
4204	Integrated transcriptomic and proteomic analysis of the physiological changes of the liver in domesticated Eurasian perch, <i>Perca fluviatilis</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2022, 41, 100957.	1.0	3
4205	Carboxylesterases from bacterial enrichment culture degrade strobilurin fungicides. <i>Science of the Total Environment</i> , 2022, 814, 152751.	8.0	6
4206	Water microbiome dynamics of Pacific white shrimp <i>Penaeus vannamei</i> infected with <i>Vibrio parahaemolyticus</i> strains responsible for acute hepatopancreatic necrosis disease. <i>Aquaculture</i> , 2022, 551, 737871.	3.5	6
4207	Metagenomics revealed the mobility and hosts of antibiotic resistance genes in typical pesticide wastewater treatment plants. <i>Science of the Total Environment</i> , 2022, 817, 153033.	8.0	26
4208	Performance characteristics and community analysis of a single-stage partial nitrification, anammox and denitrification (SPANADA) integrated process for treating low C/N ratio wastewater. <i>Chemical Engineering Journal</i> , 2022, 433, 134452.	12.7	10

#	ARTICLE	IF	CITATIONS
4209	Efficient Microcystis removal and sulfonamide-resistance gene propagation mitigation by constructed wetlands and functional genes analysis. Chemosphere, 2022, 292, 133481.	8.2	7
4213	Prot2GO: Predicting GO Annotations From Protein Sequences and Interactions. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2023, 20, 2772-2780.	3.0	2
4214	Population genomics reveals historical and ongoing recombination in the <i>Fusarium oxysporum</i> species complex. Studies in Mycology, 2021, 99, 100132-100132.	7.2	8
4216	The Capability of Utilizing Abiotic Enantiomers of Amino Acids by Halomonas sp. LMO_D1 Derived From the Mariana Trench. Frontiers in Astronomy and Space Sciences, 2021, 8, .	2.8	3
4217	First Description of the Mitogenome and Phylogeny of Culicinae Species from the Amazon Region. Genes, 2021, 12, 1983.	2.4	12
4218	Gut microbiome is associated with the clinical response to anti-PD-1 based immunotherapy in hepatobiliary cancers. , 2021, 9, e003334.		101
4219	StartLink and StartLink+: Prediction of Gene Starts in Prokaryotic Genomes. Frontiers in Bioinformatics, 2021, 1, .	2.1	1
4220	Unstable Relationship Between Braarudosphaera bigelowii (= Chrysochromulina parkeae) and Its Nitrogen-Fixing Endosymbiont. Frontiers in Plant Science, 2021, 12, 749895.	3.6	6
4221	Biome-specific distribution of Ni-containing carbon monoxide dehydrogenases. Extremophiles, 2022, 26, 9.	2.3	5
4222	Investigation of fiber utilization in the rumen of dairy cows based on metagenome-assembled genomes and single-cell RNA sequencing. Microbiome, 2022, 10, 11.	11.1	24
4223	De Novo Transcriptome Assembly and SNP Discovery for the Development of dCAPS Markers in Oat. Agronomy, 2022, 12, 184.	3.0	3
4224	Organochlorine contamination enriches virus-encoded metabolism and pesticide degradation associated auxiliary genes in soil microbiomes. ISME Journal, 2022, 16, 1397-1408.	9.8	45
4225	The genome of low-chill Chinese plum 'Sanyueli' (<i>Prunus salicina</i> Lindl.) provides insights into the regulation of the chilling requirement of flower buds. Molecular Ecology Resources, 2022, 22, 1919-1938.	4.8	11
4226	Microbiomes of air dust collected during the ground-based closed bioregenerative life support experiment "Lunar Palace 365". Environmental Microbiomes, 2022, 17, 4.	5.0	4
4227	Phylogenomic Analysis of the Phylum Nematoda: Conflicts and Congruences With Morphology, 18S rRNA, and Mitogenomes. Frontiers in Ecology and Evolution, 2022, 9, .	2.2	28
4229	Multi-omics analyses of the ulcerative colitis gut microbiome link Bacteroides vulgatus proteases with disease severity. Nature Microbiology, 2022, 7, 262-276.	13.3	110
4230	Long Intergenic Noncoding RNA (lincRNA) Discovery from Non-Strand-Specific RNA-Seq Data. Methods in Molecular Biology, 2022, 2443, 465-482.	0.9	2
4231	Virome Analysis Reveals Diverse and Divergent RNA Viruses in Wild Insect Pollinators in Beijing, China. Viruses, 2022, 14, 227.	3.3	4

#	ARTICLE	IF	CITATIONS
4232	Multi-omics analysis reveals metabolism of okadaic acid in gut lumen of rat. Archives of Toxicology, 2022, 96, 831-843.	4.2	6
4233	Assembly of 97 Novel Bacterial Genomes in the Microbial Community Affiliated with Polyvinyl Alcohol in Soil of Northern China. BioMed Research International, 2022, 2022, 1-14.	1.9	1
4234	Effects of activated sludge and UV disinfection processes on the bacterial community and antibiotic resistance profile in a municipal wastewater treatment plant. Environmental Science and Pollution Research, 2022, 29, 36088-36099.	5.3	4
4235	Long-term degradation from marshes into meadows shifts microbial functional diversity of soil phosphorus cycling in an alpine wetland of the Tibetan Plateau. Land Degradation and Development, 2022, 33, 628-637.	3.9	13
4236	Significance of gene variants for the functional biogeography of the near-surface Atlantic Ocean microbiome. Nature Communications, 2022, 13, 456.	12.8	18
4237	Identification of a Novel Hepacivirus in Mongolian Gerbil (<i>Meriones unguiculatus</i>) from Shaanxi, China. Virologica Sinica, 2022, 37, 307-307.	3.0	4
4239	Characterization of the Gut Microbiome and Resistomes of Wild and Zoo-Captive Macaques. Frontiers in Veterinary Science, 2021, 8, 778556.	2.2	3
4240	Understanding nutritive need in <i>Harmonia axyridis</i> larvae: Insights from nutritional geometry. Insect Science, 2022, 29, 1433-1444.	3.0	4
4241	METAGENOMIC NEXT-GENERATION SEQUENCING DETECTS PATHOGENS IN ENDOPHTHALMITIS PATIENTS. Retina, 2022, 42, 992-1000.	1.7	11
4244	Gut-microbial adaptation and transformation of silver nanoparticles mediated the detoxification of <i>Daphnia magna</i> and their offspring. Environmental Science: Nano, 2022, 9, 361-374.	4.3	4
4245	Microbial Mercury Methylation Potential in a Large-Scale Municipal Solid Waste (Msw) Landfill, China. SSRN Electronic Journal, 0, , .	0.4	0
4246	The rumen liquid metatranscriptome of post-weaned dairy calves differed by pre-weaning ruminal administration of differentially-enriched, rumen-derived inocula. Animal Microbiome, 2022, 4, 4.	3.8	5
4247	Genetic diversity in terrestrial subsurface ecosystems impacted by geological degassing. Nature Communications, 2022, 13, 284.	12.8	11
4248	SARS-like Coronaviruses in Horseshoe Bats (<i>Rhinolophus</i> spp.) in Russia, 2020. Viruses, 2022, 14, 113.	3.3	41
4249	Communities of T4-like bacteriophages associated with bacteria in Lake Baikal: diversity and biogeography. PeerJ, 0, 10, e12748.	2.0	3
4251	Molecular Characterization of <i>Candida auris</i> Isolates at a Major Tertiary Care Center in Lebanon. Frontiers in Microbiology, 2021, 12, 770635.	3.5	8
4252	Sporophyte Stage Genes Exhibit Stronger Selection Than Gametophyte Stage Genes in Haplodiplontic Giant Kelp. Frontiers in Marine Science, 2022, 8, .	2.5	5
4254	Inhalable Antibiotic Resistome from Wastewater Treatment Plants to Urban Areas: Bacterial Hosts, Dissemination Risks, and Source Contributions. Environmental Science & Technology, 2022, 56, 7040-7051.	10.0	38

#	ARTICLE	IF	CITATIONS
4255	Genome-wide analysis reveals a rhamnolipid-dependent modulation of flagellar genes in <i>Pseudomonas aeruginosa</i> PAO1. <i>Current Genetics</i> , 2022, 68, 289-304.	1.7	0
4256	Discovery and Evolutionary Analysis of a Novel Bat-Borne Paramyxovirus. <i>Viruses</i> , 2022, 14, 288.	3.3	8
4257	Microbial Survival in an Extreme Martian Analog Ecosystem: Poás Volcano, Costa Rica. <i>Frontiers in Astronomy and Space Sciences</i> , 2022, 9, .	2.8	3
4259	Clinical Tick-Borne Encephalitis in a Roe Deer (<i>Capreolus capreolus</i> L.). <i>Viruses</i> , 2022, 14, 300.	3.3	8
4261	The <i>Chrysanthemum lavandulifolium</i> genome and the molecular mechanism underlying diverse capitulum types. <i>Horticulture Research</i> , 2022, 9, .	6.3	24
4263	Enrichment of phosphate-accumulating organisms (PAOs) in a microfluidic model biofilm system by mimicking a typical aerobic granular sludge feast/famine regime. <i>Applied Microbiology and Biotechnology</i> , 2022, 106, 1313-1324.	3.6	6
4264	Comparative genomics reveals electron transfer and syntrophic mechanisms differentiating methanotrophic and methanogenic archaea. <i>PLoS Biology</i> , 2022, 20, e3001508.	5.6	62
4266	Polysaccharide utilization loci in <i>Bacteroides</i> determine population fitness and community-level interactions. <i>Cell Host and Microbe</i> , 2022, 30, 200-215.e12.	11.0	40
4267	Metagenomic analysis reveals wide distribution of phototrophic bacteria in hydrothermal vents on the ultraslow-spreading Southwest Indian Ridge. <i>Marine Life Science and Technology</i> , 2022, 4, 255-267.	4.6	4
4268	Ontology-aware neural network: a general framework for pattern mining from microbiome data. <i>Briefings in Bioinformatics</i> , 2022, , .	6.5	1
4269	In-situ sequencing reveals the effect of storage on lacustrine sediment microbiome demographics and functionality. <i>Environmental Microbiomes</i> , 2022, 17, 5.	5.0	5
4270	Pre-SARS-CoV-2 Human Sera Reacts with Peptides from All the 7 Human Coronaviruses: Peptide Microarray IgM and IgG Screening. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
4271	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.	9.8	27
4272	Genomic insight into the scale specialization of the biological control agent <i>Novius pumilus</i> (Weise,) Tj ETQq1 1 0.784314 rgBT / Overl	2.8	6
4274	Microbiota of the prostate tumor environment investigated by whole-transcriptome profiling. <i>Genome Medicine</i> , 2022, 14, 9.	8.2	14
4275	Metatranscriptome Profiling of a Specialized Microbial Consortium during the Degradation of Nixtamalized Maize Pericarp. <i>Microbiology Spectrum</i> , 2022, 10, e0231821.	3.0	4
4276	CANT-HYD: A Curated Database of Phylogeny-Derived Hidden Markov Models for Annotation of Marker Genes Involved in Hydrocarbon Degradation. <i>Frontiers in Microbiology</i> , 2021, 12, 764058.	3.5	21
4278	Sustainable treatment of nitrate-containing wastewater by an autotrophic hydrogen-oxidizing bacterium. <i>Environmental Science and Ecotechnology</i> , 2022, 9, 100146.	13.5	13

#	ARTICLE	IF	CITATIONS
4280	De novo assembly and functional annotation of the nervous system transcriptome in the Caribbean spiny lobster <i>Panulirus argus</i> . <i>Coral Reefs</i> , 2022, 41, 191.	2.2	0
4281	Genome sequence and transcriptome of <i>Sorbus pohuashanensis</i> provide insights into population evolution and leaf sunburn response. <i>Journal of Genetics and Genomics</i> , 2022, 49, 547-558.	3.9	9
4282	Novel pegiviruses infecting wild birds and rodents. <i>Virologica Sinica</i> , 2022, 37, 208-214.	3.0	3
4283	Neurological infection by chikungunya and a triple Arbovirus co-infection in Mato Grosso, Central Western Brazil during 2019. <i>Journal of Clinical Virology</i> , 2022, 146, 105056.	3.1	4
4284	ORTHOSKIM: In silico sequence capture from genomic and transcriptomic libraries for phylogenomic and barcoding applications. <i>Molecular Ecology Resources</i> , 2022, 22, 2018-2037.	4.8	7
4285	Pepper Fruit Elongation Is Controlled by <i>Capsicum annuum</i> Ovate Family Protein 20. <i>Frontiers in Plant Science</i> , 2021, 12, 815589.	3.6	12
4286	Metagenomic Analysis of Bacterial Communities and Antibiotic Resistance Genes in <i>Penaeus monodon</i> Biofloc-Based Aquaculture Environments. <i>Frontiers in Marine Science</i> , 2022, 8, .	2.5	6
4287	Chromosome-level genome assembly of <i>Zizania latifolia</i> provides insights into its seed shattering and phytocassane biosynthesis. <i>Communications Biology</i> , 2022, 5, 36.	4.4	11
4288	Endophytic fungus <i>Pseudodidymocyrtis lobariellae</i> KL27 promotes taxol biosynthesis and accumulation in <i>Taxus chinensis</i> . <i>BMC Plant Biology</i> , 2022, 22, 12.	3.6	10
4290	Elevational Constraints on the Composition and Genomic Attributes of Microbial Communities in Antarctic Soils. <i>MSystems</i> , 2022, 7, e0133021.	3.8	9
4291	Differential priority effects impact taxonomy and functionality of host-associated microbiomes. <i>Molecular Ecology</i> , 2023, 32, 6278-6293.	3.9	6
4292	Thermal stress triggers productive viral infection of a key coral reef symbiont. <i>ISME Journal</i> , 2022, 16, 1430-1441.	9.8	15
4293	Unique mobile elements and scalable gene flow at the prokaryote-eukaryote boundary revealed by circularized Asgard archaea genomes. <i>Nature Microbiology</i> , 2022, 7, 200-212.	13.3	29
4294	MCycDB: A curated database for comprehensively profiling methane cycling processes of environmental microbiomes. <i>Molecular Ecology Resources</i> , 2022, 22, 1803-1823.	4.8	16
4295	N ₂ fixation in the Mediterranean Sea related to the composition of the diazotrophic community and impact of dust under present and future environmental conditions. <i>Biogeosciences</i> , 2022, 19, 415-435.	3.3	5
4296	EST-SSR Marker Development and Full-Length Transcriptome Sequence Analysis of Tiger Lily (<i>Lilium</i>) Tj ETQq1 1 0.784314 6gBT /Over	1.1	1
4297	The hidden world within plants: metatranscriptomics unveils the complexity of wood microbiomes. <i>Journal of Experimental Botany</i> , 2022, 73, 2682-2697.	4.8	24
4298	Revisiting the intrageneric structure of the genus <i>Pseudomonas</i> with complete whole genome sequence information: Insights into diversity and pathogen-related genetic determinants. <i>Infection, Genetics and Evolution</i> , 2022, 97, 105183.	2.3	6

#	ARTICLE	IF	CITATIONS
4299	Chromosome-level assembly of the common vetch (<i>Vicia sativa</i>) reference genome. <i>GigaByte</i> , 0, 2022, 1-20.	0.0	10
4300	Commensal Bacteria in the Cystic Fibrosis Airway Microbiome Reduce <i>P. aeruginosa</i> Induced Inflammation. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 824101.	3.9	11
4302	Landâ€use type temporarily affects active pond community structure but not gene expression patterns. <i>Molecular Ecology</i> , 2022, 31, 1716-1734.	3.9	5
4303	Site-and-branch-heterogeneous analyses of an expanded dataset favour mitochondria as sister to known Alphaproteobacteria. <i>Nature Ecology and Evolution</i> , 2022, 6, 253-262.	7.8	48
4304	Oceanic Crustal Fluid Single Cell Genomics Complements Metagenomic and Metatranscriptomic Surveys With Orders of Magnitude Less Sample Volume. <i>Frontiers in Microbiology</i> , 2021, 12, 738231.	3.5	1
4305	Dysbiotic microbes and how to find them: a review of microbiome profiling in prostate cancer. <i>Journal of Experimental and Clinical Cancer Research</i> , 2022, 41, 31.	8.6	8
4306	Accumulation of Anthocyanidins Determines Leaf Color of Liquidambar Formosana as Revealed by Transcriptome Sequencing and Metabolism Analysis. <i>Current Issues in Molecular Biology</i> , 2022, 44, 242-256.	2.4	1
4307	RNA Virosphere in a Marine Zooplankton Community in the Subtropical Western North Pacific. <i>Microbes and Environments</i> , 2022, 37, n/a.	1.6	3
4308	PANDA2: protein function prediction using graph neural networks. <i>NAR Genomics and Bioinformatics</i> , 2022, 4, lqac004.	3.2	8
4309	Archaeal and Bacterial Metagenome-Assembled Genome Sequences Derived from Pig Feces. <i>Microbiology Resource Announcements</i> , 2022, 11, e0114221.	0.6	6
4310	Comparative Genomics of <i>Clostridium baratii</i> Reveals Strain-Level Diversity in Toxin Abundance. <i>Microorganisms</i> , 2022, 10, 213.	3.6	6
4312	Novel Viral Communities Potentially Assisting in Carbon, Nitrogen, and Sulfur Metabolism in the Upper Slope Sediments of Mariana Trench. <i>MSystems</i> , 2022, 7, e0135821.	3.8	22
4313	Seasonal variations in the composition and functional profiles of gut microbiota reflect dietary changes in plateau pikas. <i>Integrative Zoology</i> , 2022, 17, 379-395.	2.6	30
4314	Genomic Characterization of a Novel Freshwater Cyanophage Reveals a New Lineage of Cyanopodovirus. <i>Frontiers in Microbiology</i> , 2021, 12, 768868.	3.5	8
4315	Comparative Genome Analysis Reveals Accumulation of Single-Nucleotide Repeats in Pathogenic <i>Escherichia</i> Lineages. <i>Current Issues in Molecular Biology</i> , 2022, 44, 498-504.	2.4	0
4317	Theabrownin isolated from <sc>Puâ€erh</sc> tea regulates <sc><i>Bacteroidetes</i></sc> to improve metabolic syndrome of rats induced by <sc>highâ€fat, highâ€sugar and highâ€salt diet</sc>. <i>Journal of the Science of Food and Agriculture</i> , 2022, 102, 4250-4265.	3.5	12
4318	Integrative RNA-Seq analysis of <i>Capsicum annuum</i> L.- <i>Phytophthora capsici</i> L. pathosystem reveals molecular cross-talk and activation of host defence response. <i>Physiology and Molecular Biology of Plants</i> , 2022, 28, 171-188.	3.1	7
4319	Long-read metagenomic sequencing reveals shifts in associations of antibiotic resistance genes with mobile genetic elements from sewage to activated sludge. <i>Microbiome</i> , 2022, 10, 20.	11.1	52

#	ARTICLE	IF	CITATIONS
4321	Nuclear genome of a pedinophyte pinpoints genomic innovation and streamlining in the green algae. <i>New Phytologist</i> , 2022, 233, 2144-2154.	7.3	5
4325	Functional convergence of Yunnan snub-nosed monkey and bamboo-eating panda gut microbiomes revealing the driving by dietary flexibility on mammal gut microbiome. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 685-699.	4.1	13
4326	Partitivirus-like viruses from African armyworm increase larval and pupal mortality of a novel host: the Egyptian cotton leafworm. <i>Pest Management Science</i> , 2022, 78, 1529-1537.	3.4	4
4327	Multimodal deep learning applied to classify healthy and disease states of human microbiome. <i>Scientific Reports</i> , 2022, 12, 824.	3.3	13
4328	Molecular Responses to Thermal and Osmotic Stress in Arctic Intertidal Mussels (<i>Mytilus edulis</i>): The Limits of Resilience. <i>Genes</i> , 2022, 13, 155.	2.4	14
4329	Insights into agar and secondary metabolite pathways from the genome of the red alga <i>Gracilaria domingensis</i> (Rhodophyta, Gracilariaceae). <i>Journal of Phycology</i> , 2022, 58, 406-423.	2.3	10
4331	A Chromosome-Level Genome Assembly of the Parasitic Wasp <i>Chelonus formosanus</i> (Hymenoptera: Braconidae). <i>Genome Biology and Evolution</i> , 2022, 14, .	2.5	1
4332	A Broad Survey of Gene Body and Repeat Methylation in Cnidaria Reveals a Complex Evolutionary History. <i>Genome Biology and Evolution</i> , 2022, 14, .	2.5	1
4333	The MicroRNAs-Transcription Factors-mRNA Regulatory Network Plays an Important Role in Resistance to Cold Stress in the Pearl Gentian Grouper. <i>Frontiers in Marine Science</i> , 2022, 8, .	2.5	5
4334	Multi-omics analyses revealed key factors involved in fluorescent carbon-dots-regulated secondary metabolism in <i>Tetrastigma hemsleyanum</i> . <i>Journal of Nanobiotechnology</i> , 2022, 20, 63.	9.1	4
4335	Biosynthetic Potential of the Endophytic Fungus <i>Helotiales</i> sp. BL73 Revealed via Compound Identification and Genome Mining. <i>Applied and Environmental Microbiology</i> , 2022, 88, aem0251021.	3.1	7
4338	Changes in Gut Microbiota of Patients with Atopic Dermatitis During Balneotherapy. <i>Clinical, Cosmetic and Investigational Dermatology</i> , 2022, Volume 15, 163-176.	1.8	6
4339	Spotlight on alternative frame coding: Two long overlapping genes in <i>Pseudomonas aeruginosa</i> are translated and under purifying selection. <i>IScience</i> , 2022, 25, 103844.	4.1	13
4340	Impact of dietary fructooligosaccharides (FOS) on murine gut microbiota and intestinal IgA secretion. <i>3 Biotech</i> , 2022, 12, 56.	2.2	2
4341	A time-series meta-transcriptomic analysis reveals the seasonal, host, and gender structure of mosquito viromes. <i>Virus Evolution</i> , 2022, 8, veac006.	4.9	20
4342	Differential Response of Bacterial Microdiversity to Simulated Global Change. <i>Applied and Environmental Microbiology</i> , 2022, 88, aem0242921.	3.1	7
4343	Transcriptomic analysis of interactions between <i>Lymantria dispar</i> larvae and carvacrol. <i>Pesticide Biochemistry and Physiology</i> , 2022, 181, 105012.	3.6	2
4345	Response behavior of antibiotic resistance genes to zinc oxide nanoparticles in cattle manure thermophilic anaerobic digestion process: A metagenomic analysis. <i>Bioresource Technology</i> , 2022, 347, 126709.	9.6	11

#	ARTICLE	IF	CITATIONS
4346	Phylogenomic classification and synteny network analyses deciphered the evolutionary landscape of aldol-keto reductase (AKR) gene superfamily in the plant kingdom. <i>Gene</i> , 2022, 816, 146169.	2.2	4
4347	High-specificity targets in SARS-CoV-2 N protein for serological detection and distinction from SARS-CoV. <i>Computers in Biology and Medicine</i> , 2022, 143, 105272.	7.0	5
4348	Metagenomics insights into the profiles of antibiotic resistome in combined sewage overflows from reads to metagenome assembly genomes. <i>Journal of Hazardous Materials</i> , 2022, 429, 128277.	12.4	20
4349	Microbial regulation of nitrous oxide emissions from chloropicrin-fumigated soil amended with biochar. <i>Journal of Hazardous Materials</i> , 2022, 429, 128060.	12.4	8
4350	Metagenomic assemblage genomes analyses reveal the polysaccharides hydrolyzing potential of marine group II euryarchaea. <i>Environmental Research</i> , 2022, 209, 112865.	7.5	6
4351	Host Adaptation in <i>Legionellales</i> Is 1.9 Ga, Coincident with Eukaryogenesis. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	15
4352	Disrupted Circadian Rest-Activity Cycles in Inflammatory Bowel Disease Are Associated With Aggressive Disease Phenotype, Subclinical Inflammation, and Dysbiosis. <i>Frontiers in Medicine</i> , 2021, 8, 770491.	2.6	7
4353	Current and Emerging Tools of Computational Biology To Improve the Detoxification of Mycotoxins. <i>Applied and Environmental Microbiology</i> , 2022, 88, AEM0210221.	3.1	9
4355	Metagenomics of the midgut microbiome of <i>Rhipicephalus microplus</i> from China. <i>Parasites and Vectors</i> , 2022, 15, 48.	2.5	10
4356	Shenlian (SL) Decoction, a Traditional Chinese Medicine Compound, May Ameliorate Blood Glucose via Mediating the Gut Microbiota in db/db Mice. <i>Journal of Diabetes Research</i> , 2022, 2022, 1-20.	2.3	7
4357	The dynamic trophic architecture of open-ocean protist communities revealed through machine-guided metatranscriptomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	27
4358	Developmental Regulation and Functional Prediction of microRNAs in an Expanded <i>Fasciola hepatica</i> miRNome. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 811123.	3.9	9
4359	Insights into the proteomic profile of newly harvested corn and metagenomic analysis of the broiler intestinal microbiota. <i>Journal of Animal Science and Biotechnology</i> , 2022, 13, 26.	5.3	6
4360	TransPi—a comprehensive TRanscriptome ANalysis Pipeline for <i>de novo</i> transcriptome assembly. <i>Molecular Ecology Resources</i> , 2022, 22, 2070-2086.	4.8	14
4361	Quantifying cumulative phenotypic and genomic evidence for procedural generation of metabolic network reconstructions. <i>PLoS Computational Biology</i> , 2022, 18, e1009341.	3.2	3
4363	Chromosome-Level Genome Assembly of <i>Anthidium xuezhongi</i> Niu & Zhu, 2020 (Hymenoptera: Apoidea): TJ ETQq1 _{2.5} 1 _{0.7843} 14 rgBT	2.5	1
4364	Chromosome-level genome assembly of <i>Aristolochia contorta</i> provides insights into the biosynthesis of benzyloquinoline alkaloids and aristolochic acids. <i>Horticulture Research</i> , 2022, 9, .	6.3	11
4365	Effect of host genetics on the gut microbiome in 7,738 participants of the Dutch Microbiome Project. <i>Nature Genetics</i> , 2022, 54, 143-151.	21.4	132

#	ARTICLE	IF	CITATIONS
4366	Complete Genome Sequencing and Comparative Analysis of the Clinically-Derived <i>Apiotrichum mycotoxinivorans</i> Strain GMU1709. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 834015.	3.9	3
4368	A Genome Sequence Resource of <i>Nigrospora sphaerica</i> Causing Fruit Dried-Shrink Disease in <i>Akebia trifoliata</i> . <i>Plant Disease</i> , 2022, 106, 745-747.	1.4	1
4370	Feeding Practice and Delivery Mode Are Determinants of Vitamin K in the Infant Gut: An Exploratory Analysis. <i>Current Developments in Nutrition</i> , 2022, 6, nza019.	0.3	1
4373	A Chromosome-Level Genome Assembly of the European Beech (<i>Fagus sylvatica</i>) Reveals Anomalies for Organelle DNA Integration, Repeat Content and Distribution of SNPs. <i>Frontiers in Genetics</i> , 2021, 12, 691058.	2.3	17
4374	Full Genome of batCoV/MinFul/2018/SriLanka, a Novel Alpha-Coronavirus Detected in <i>Miniopterus fuliginosus</i> , Sri Lanka. <i>Viruses</i> , 2022, 14, 337.	3.3	8
4375	Seasonal changes in the expression of insulin-like androgenic hormone (IAG) in the androgenic gland of the Jonah crab, <i>Cancer borealis</i> . <i>PLoS ONE</i> , 2022, 17, e0261206.	2.5	4
4376	First Multi-Organ Full-Length Transcriptome of Tree Fern <i>Alsophila spinulosa</i> Highlights the Stress-Resistant and Light-Adapted Genes. <i>Frontiers in Genetics</i> , 2021, 12, 784546.	2.3	4
4378	Identification of Bacterial Populations and Functional Mechanisms Potentially Involved in Biochar-Facilitated Antagonism of the Soilborne Pathogen <i>Fusarium oxysporum</i> . <i>Phytobiomes Journal</i> , 2022, 6, 139-150.	2.7	5
4379	Complete genome sequence of the kiwifruit bacterial canker pathogen <i>Pseudomonas savastanoi</i> strain MHT1. <i>BMC Microbiology</i> , 2022, 22, 44.	3.3	0
4382	The gut microbiome and antibiotic resistome of chronic diarrhea rhesus macaques (<i>Macaca mulatta</i>) and its similarity to the human gut microbiome. <i>Microbiome</i> , 2022, 10, 29.	11.1	24
4383	Morphological and Comparative Transcriptome Analysis of Three Species of Five-Needle Pines: Insights Into Phenotypic Evolution and Phylogeny. <i>Frontiers in Plant Science</i> , 2022, 13, 795631.	3.6	3
4384	Molecular characterization of the gastrointestinal eukaryotic virome in elderly people in Belem, Para, Brazil. <i>Infection, Genetics and Evolution</i> , 2022, 99, 105241.	2.3	1
4385	PredicTF: prediction of bacterial transcription factors in complex microbial communities using deep learning. <i>Environmental Microbiomes</i> , 2022, 17, 7.	5.0	6
4386	Metagenomic Analysis Reveals a Changing Microbiome Associated With the Depth of Invasion of Oral Squamous Cell Carcinoma. <i>Frontiers in Microbiology</i> , 2022, 13, 795777.	3.5	15
4388	Comparison of Transcriptome Responses between <i>Sogatella furcifera</i> Females That Acquired Southern Rice Black-Streaked Dwarf Virus and Not. <i>Insects</i> , 2022, 13, 182.	2.2	1
4390	Soil phytoremediation reveals alteration in soil microbial metabolic activities along time gradient of cover crop mulching. <i>Environmental Research</i> , 2022, 209, 112884.	7.5	7
4391	Metagenomic analysis further extends the role of Chloroflexi in fundamental biogeochemical cycles. <i>Environmental Research</i> , 2022, 209, 112888.	7.5	38
4392	HSDFinder: A BLAST-Based Strategy for Identifying Highly Similar Duplicated Genes in Eukaryotic Genomes. <i>Frontiers in Bioinformatics</i> , 2021, 1, .	2.1	5

#	ARTICLE	IF	CITATIONS
4393	Carbon assimilating fungi from surface ocean to subseafloor revealed by coupled phylogenetic and stable isotope analysis. <i>ISME Journal</i> , 2022, 16, 1245-1261.	9.8	22
4394	A catalogue of 1,167 genomes from the human gut archaeome. <i>Nature Microbiology</i> , 2022, 7, 48-61.	13.3	72
4395	Towards the biogeography of prokaryotic genes. <i>Nature</i> , 2022, 601, 252-256.	27.8	85
4396	GEnView: a gene-centric, phylogeny-based comparative genomics pipeline for bacterial genomes and plasmids. <i>Bioinformatics</i> , 2022, 38, 1727-1728.	4.1	6
4398	Immunological tolerance in the evolution of male pregnancy. <i>Molecular Ecology</i> , 2023, 32, 819-840.	3.9	13
4399	Metagenomic Study on Chinese Homemade Paocai: The Effects of Raw Materials and Fermentation Periods on the Microbial Ecology and Volatile Components. <i>Foods</i> , 2022, 11, 62.	4.3	16
4401	A Mitosome With Distinct Metabolism in the Uncultured Protist Parasite <i>Paramikrocytos cancri</i> (Rhizaria, Ascetosporea). <i>SSRN Electronic Journal</i> , 0, , .	0.4	1
4402	Exploring the Impact of Biochar on Antibiotics and Antibiotics Resistance Genes in Pig Manure Aerobic Composting Through Untargeted Metabolomics and Metagenomics. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
4403	Co-Infection of Peruvian Horse Sickness Virus and West Nile Virus Associated with Neurological Diseases in Horses from Brazil. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
4404	A Five-Fold Expansion of the Global RNA Virome Reveals Multiple New Clades of RNA Bacteriophages. <i>SSRN Electronic Journal</i> , 0, , .	0.4	4
4405	New Insights into the Physiology of Fruit Ripening of Apricot (<i>Prunus Armeniaca</i> L.) and Japanese Plum (<i>P. Salicina</i> L.) Using Rna-Seq Analysis. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
4406	The Faecal Microbial Taxonomic Composition and Antimicrobial Resistance Gene Profile S ÅOf Three Different Pig Breeds. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
4407	Microbial Mechanisms for Methane Source-to-Sink Transition after Wetland Conversion to Cropland. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
4408	OMARU: a robust and multifaceted pipeline for metagenome-wide association study. <i>NAR Genomics and Bioinformatics</i> , 2022, 4, lqac019.	3.2	3
4409	<i>Desulfovulcanus ferrireducens</i> gen. nov., sp. nov., a thermophilic autotrophic iron and sulfate-reducing bacterium from subseafloor basalt that grows on akaganite and lepidocrocite minerals. <i>Extremophiles</i> , 2022, 26, 13.	2.3	2
4410	Convergent consequences of parthenogenesis on stick insect genomes. <i>Science Advances</i> , 2022, 8, eabg3842.	10.3	27
4411	Spatial distribution and community structure of microbiota associated with cowpea aphid (<i>Aphis</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	2.2	2
4412	Co-infecting pathogens can contribute to inflammatory responses and severe symptoms in COVID-19. <i>Journal of Thoracic Disease</i> , 2022, 14, 355-370.	1.4	5

#	ARTICLE	IF	CITATIONS
4413	Occurrence of Wheat Curl Mite and Mite-Vectored Viruses of Wheat in Colorado and Insights into the Wheat Virome. <i>Plant Disease</i> , 2022, 106, 2678-2688.	1.4	6
4414	RNA Virus Diversity in Birds and Small Mammals From Qinghaiâ€“Tibet Plateau of China. <i>Frontiers in Microbiology</i> , 2022, 13, 780651.	3.5	7
4415	Gut metagenome associations with extensive digital health data in a volunteer-based Estonian microbiome cohort. <i>Nature Communications</i> , 2022, 13, 869.	12.8	12
4416	Contributions of Human-Associated Archaeal Metabolites to Tumor Microenvironment and Carcinogenesis. <i>Microbiology Spectrum</i> , 2022, 10, e0236721.	3.0	15
4417	Comparative analysis of differential gene expression indicates divergence in ontogenetic strategies of leaves in two conifer genera. <i>Ecology and Evolution</i> , 2022, 12, e8611.	1.9	3
4418	Investigation and characterization of human gut phageome in advanced liver cirrhosis of defined etiologies. <i>Gut Pathogens</i> , 2022, 14, 9.	3.4	1
4419	Comparative analyses of parasites with a comprehensive database of genome-scale metabolic models. <i>PLoS Computational Biology</i> , 2022, 18, e1009870.	3.2	5
4420	Niche partitioning of the ubiquitous and ecologically relevant NS5 marine group. <i>ISME Journal</i> , 2022, 16, 1570-1582.	9.8	11
4421	Microbial Functional Diversity Correlates with Species Diversity along a Temperature Gradient. <i>MSystems</i> , 2022, 7, e0099121.	3.8	14
4422	Protist.guru: A Comparative Transcriptomics Database for Protists. <i>Journal of Molecular Biology</i> , 2022, 434, 167502.	4.2	4
4423	Sequencing Depth Has a Stronger Effect than DNA Extraction on Soil Bacterial Richness Discovery. <i>Biomolecules</i> , 2022, 12, 364.	4.0	3
4424	Wei2GO: weighted sequence similarity-based protein function prediction. <i>PeerJ</i> , 2022, 10, e12931.	2.0	5
4426	A Highly Divergent Hepacivirus Identified in Domestic Ducks Further Reveals the Genetic Diversity of Hepaciviruses. <i>Viruses</i> , 2022, 14, 371.	3.3	5
4427	Taxonomic and functional diversity of <i>Dendrobium officinale</i> microbiome in Danxia habitat. <i>Journal of Applied Microbiology</i> , 2022, 132, 3758-3770.	3.1	4
4428	Annual transcriptome of a key zooplankton species, the copepod <i>Calanus finmarchicus</i> . <i>Ecology and Evolution</i> , 2022, 12, e8605.	1.9	6
4429	Using AnnoTree to Get More Assignments, Faster, in DIAMOND+MEGAN Microbiome Analysis. <i>MSystems</i> , 2022, 7, e0140821.	3.8	11
4430	The novel genus, <i>Candidatus</i> Phosphoribacterâ„“™, previously identified as <i>Tetrasphaera</i> , is the dominant polyphosphate accumulating lineage in EBPR wastewater treatment plants worldwide. <i>ISME Journal</i> , 2022, 16, 1605-1616.	9.8	41
4431	Chromosome-level genome assembly of a xerophytic plant, <i>Haloxylon ammodendron</i> . <i>DNA Research</i> , 2022, 29, .	3.4	15

#	ARTICLE	IF	CITATIONS
4432	Positive Priming Effects Induced by Allochthonous and Autochthonous Organic Matter Input in the Lake Sediments With Different Salinity. <i>Geophysical Research Letters</i> , 2022, 49, .	4.0	6
4433	Contamination detection in genomic data: more is not enough. <i>Genome Biology</i> , 2022, 23, 60.	8.8	37
4434	Microbial Biomass, Composition, and Functions Are Responsible for the Differential Removal of Trace Organic Chemicals in Biofiltration Systems: A Batch Study. <i>Frontiers in Water</i> , 2022, 4, .	2.3	4
4435	Gut Microbiome Characteristics in feral and domesticated horses from different geographic locations. <i>Communications Biology</i> , 2022, 5, 172.	4.4	20
4436	Microbial Community and Metabolite Dynamics During Soy Sauce Koji Making. <i>Frontiers in Microbiology</i> , 2022, 13, 841529.	3.5	14
4437	Comparative transcriptomes of three different skin sites for the Asiatic toad (<i>Bufo</i>) Tj ETQq1 1 0.784314 rgBT / Overlock 10 Tf 50 942	2.0	1
4438	Data Filtering Algorithm for DNA Metabarcoding Studies of Ecological Communities. <i>Russian Journal of Genetics</i> , 2022, 58, 223-234.	0.6	0
4439	Phylotranscriptomic and Evolutionary Analyses of Oedogoniales (Chlorophyceae, Chlorophyta). <i>Diversity</i> , 2022, 14, 157.	1.7	2
4440	Total infectome characterization of respiratory infections in pre-COVID-19 Wuhan, China. <i>PLoS Pathogens</i> , 2022, 18, e1010259.	4.7	16
4441	An estimate of the deepest branches of the tree of life from ancient vertically evolving genes. <i>ELife</i> , 2022, 11, .	6.0	43
4442	A genome assembly of the Atlantic chub mackerel (<i>Scomber colias</i>): a valuable teleost fishing resource. <i>GigaByte</i> , 0, 2022, 1-21.	0.0	3
4443	Multi-Omic Analysis in a Metabolic Syndrome Porcine Model Implicates Arachidonic Acid Metabolism Disorder as a Risk Factor for Atherosclerosis. <i>Frontiers in Nutrition</i> , 2022, 9, 807118.	3.7	5
4444	Cultivation and metabolic insights of an uncultured clade, Bacteroidetes <i>VC2</i> Bac22 (<i>Candidatus</i> Sulfidibacteriales ord. nov.), from deep-sea hydrothermal vents. <i>Environmental Microbiology</i> , 2022, 24, 2484-2501.	3.8	7
4445	Alphaflexivirus Genomes in Stony Coral Tissue Loss Disease-Affected, Disease-Exposed, and Disease-Unexposed Coral Colonies in the U.S. Virgin Islands. <i>Microbiology Resource Announcements</i> , 2022, 11, e0119921.	0.6	10
4447	A Microbial Signature for Paediatric Perianal Crohn's Disease. <i>Journal of Crohn's and Colitis</i> , 2022, 16, 1281-1292.	1.3	8
4448	Nuclear genome of <i>Bulinus truncatus</i> , an intermediate host of the carcinogenic human blood fluke <i>Schistosoma haematobium</i> . <i>Nature Communications</i> , 2022, 13, 977.	12.8	14
4449	Full-length transcriptome analysis of multiple organs and identification of adaptive genes and pathways in <i>Mikania micrantha</i> . <i>Scientific Reports</i> , 2022, 12, 3272.	3.3	0
4452	Butterfly eyespots evolved via cooption of an ancestral gene-regulatory network that also patterns antennae, legs, and wings. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	39

#	ARTICLE	IF	CITATIONS
4453	Integrated meta-omics reveals new ruminal microbial features associated with feed efficiency in dairy cattle. <i>Microbiome</i> , 2022, 10, 32.	11.1	36
4454	A cattle graph genome incorporating global breed diversity. <i>Nature Communications</i> , 2022, 13, 910.	12.8	35
4455	METABOLIC: high-throughput profiling of microbial genomes for functional traits, metabolism, biogeochemistry, and community-scale functional networks. <i>Microbiome</i> , 2022, 10, 33.	11.1	168
4457	The <i>Bacillus</i> phage ϕ SP1 ² and its relatives: a temperate phage model system reveals new strains, species, prophage integration loci, conserved proteins and lysogeny management components. <i>Environmental Microbiology</i> , 2022, 24, 2098-2118.	3.8	19
4458	Beta-Amylase and Phosphatidic Acid Involved in Recalcitrant Seed Germination of Chinese Chestnut. <i>Frontiers in Plant Science</i> , 2022, 13, 828270.	3.6	1
4459	In silico evaluation of a targeted metaproteomics strategy for broad screening of cellulolytic enzyme capacities in anaerobic microbiome bioreactors. , 2022, 15, 32.		3
4461	Disentangle genus microdiversity within a complex microbial community by using a multi-distance long-read binning method: example of <i>Candidatus</i> <i>Accumulibacter</i> . <i>Environmental Microbiology</i> , 2022, 24, 2136-2156.	3.8	4
4463	Genome-based reclassification of the genus <i>Meiothermus</i> along with the proposal of a new genus <i>Allomeiothermus</i> gen. nov. <i>Antonie Van Leeuwenhoek</i> , 2022, 115, 645.	1.7	12
4464	Extensive metagenomic analysis of the porcine gut resistome to identify indicators reflecting antimicrobial resistance. <i>Microbiome</i> , 2022, 10, 39.	11.1	19
4465	Functional Traits Resolve Mechanisms Governing the Assembly and Distribution of Nitrogen-Cycling Microbial Communities in the Global Ocean. <i>MBio</i> , 2022, 13, e0383221.	4.1	31
4466	PHISDetector: A Tool to Detect Diverse <i>In Silico</i> Phage-Host Interaction Signals for Virome Studies. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 508-523.	6.9	20
4467	Transcriptomic and Physiological Responses of <i>Chlorella pyrenoidosa</i> during Exposure to 17 β -Ethinylestradiol. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3583.	4.1	8
4469	Pan-Genome Analysis of <i>Delftia tsuruhatensis</i> Reveals Important Traits Concerning the Genetic Diversity, Pathogenicity, and Biotechnological Properties of the Species. <i>Microbiology Spectrum</i> , 2022, 10, e0207221.	3.0	13
4470	Anthocyanin and Flavonol Glycoside Metabolic Pathways Underpin Floral Color Mimicry and Contrast in a Sexually Deceptive Orchid. <i>Frontiers in Plant Science</i> , 2022, 13, 860997.	3.6	11
4471	Intrinsic variation in the vertically transmitted core virome of the mosquito <i>Aedes aegypti</i> . <i>Molecular Ecology</i> , 2022, 31, 2545-2561.	3.9	18
4472	Analysis of Competing Endogenous RNAs and MicroRNAs in Tea (<i>Camellia sinensis</i>) Leaves During Infection by the Leaf Spot Pathogen <i>Pestalotiopsis trachicarpicola</i> . <i>Molecular Plant-Microbe Interactions</i> , 2022, 35, 432-438.	2.6	2
4473	Novel canine high-quality metagenome-assembled genomes, prophages and host-associated plasmids provided by long-read metagenomics together with Hi-C proximity ligation. <i>Microbial Genomics</i> , 2022, 8, .	2.0	4
4474	Draft Genome Sequence of <i>Pediococcus pentosaceus</i> IMI 507024. <i>Microbiology Resource Announcements</i> , 2022, 11, e0121621.	0.6	2

#	ARTICLE	IF	CITATIONS
4475	A step towards validation of high-throughput sequencing for the identification of plant pathogenic oomycetes. <i>Phytopathology</i> , 2022, , .	2.2	8
4476	Down-regulation of the bacterial protein biosynthesis machinery in response to weeks, years, and decades of soil warming. <i>Science Advances</i> , 2022, 8, eabm3230.	10.3	18
4478	Exposure to <i>Trypanosoma</i> parasites induces changes in the microbiome of the Chagas disease vector <i>Rhodnius prolixus</i> . <i>Microbiome</i> , 2022, 10, 45.	11.1	10
4479	Enzymatic Verification and Comparative Analysis of Carrageenan Metabolism Pathways in Marine Bacterium <i>Flavobacterium algicola</i> . <i>Applied and Environmental Microbiology</i> , 2022, , e0025622.	3.1	3
4480	Performance of Five Metagenomic Classifiers for Virus Pathogen Detection Using Respiratory Samples from a Clinical Cohort. <i>Pathogens</i> , 2022, 11, 340.	2.8	4
4481	Benchmarking metagenomics classifiers on ancient viral DNA: a simulation study. <i>PeerJ</i> , 2022, 10, e12784.	2.0	4
4482	The methyl phosphate capping enzyme Bmc1/Bin3 is a stable component of the fission yeast telomerase holoenzyme. <i>Nature Communications</i> , 2022, 13, 1277.	12.8	8
4483	Long-read genome sequencing of bread wheat facilitates disease resistance gene cloning. <i>Nature Genetics</i> , 2022, 54, 227-231.	21.4	63
4484	Detection and Analysis of Syntenic Quantitative Trait Loci Controlling Cell Wall Quality in Angiosperms. <i>Frontiers in Plant Science</i> , 2022, 13, 855093.	3.6	2
4485	The virota and its transkingdom interactions in the healthy infant gut. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2114619119.	7.1	30
4486	Genomics-based higher classification of the species-rich hairstreaks (Lepidoptera: Lycaenidae: Eumaeini). <i>Systematic Entomology</i> , 2022, 47, 445-469.	3.9	5
4487	Increasing the diversity of dietary fibers in a daily-consumed bread modifies gut microbiota and metabolic profile in subjects at cardiometabolic risk. <i>Gut Microbes</i> , 2022, 14, 2044722.	9.8	28
4488	Multi-Omics Strategies for Investigating the Microbiome in Toxicology Research. <i>Toxicological Sciences</i> , 2022, 187, 189-213.	3.1	6
4489	Comprehensive and functional analyses reveal the genomic diversity and potential toxicity of <i>Microcystis</i> . <i>Harmful Algae</i> , 2022, 113, 102186.	4.8	8
4490	Transcriptome Sequencing Reveals the Antiviral Innate Immunity by IFN- λ 3 in Chinese Sturgeon Macrophages. <i>Frontiers in Immunology</i> , 2022, 13, 854689.	4.8	2
4491	New Insights into the Toxin Diversity and Antimicrobial Activity of the "Fire Coral" <i>Millepora complanata</i> . <i>Toxins</i> , 2022, 14, 206.	3.4	5
4492	Environmental Potential for Microbial 1,4-Dioxane Degradation Is Sparse despite Mobile Elements Playing a Role in Trait Distribution. <i>Applied and Environmental Microbiology</i> , 2022, 88, e0209121.	3.1	8
4493	The ER membrane complex (EMC) can functionally replace the Oxa1 insertase in mitochondria. <i>PLoS Biology</i> , 2022, 20, e3001380.	5.6	18

#	ARTICLE	IF	CITATIONS
4494	Symbiotic bacteria of the gall-inducing mite <i>Fragariocoptes setiger</i> (Eriophyoidea) and phylogenomic resolution of the eriophyoid position among Acari. <i>Scientific Reports</i> , 2022, 12, 3811.	3.3	19
4496	Positive Interventional Effect of Engineered Butyrate-Producing Bacteria on Metabolic Disorders and Intestinal Flora Disruption in Obese Mice. <i>Microbiology Spectrum</i> , 2022, 10, e0114721.	3.0	15
4497	Chromosomal-level genome assembly of the springtail <i>Tomocerus qinae</i> (Collembola). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 662</i>	2.5	2
4498	The Macronutrient Composition of Infant Formula Produces Differences in Gut Microbiota Maturation That Associate with Weight Gain Velocity and Weight Status. <i>Nutrients</i> , 2022, 14, 1241.	4.1	8
4499	Discovery of the non- <i>€</i> cosmopolitan lineages in <i>Candidatus</i> Thermoprofundales. <i>Environmental Microbiology</i> , 2022, 24, 3063-3080.	3.8	3
4501	Interaction of bacterial genera associated with therapeutic response to immune checkpoint PD-1 blockade in a United States cohort. <i>Genome Medicine</i> , 2022, 14, 35.	8.2	29
4503	A chromosome-scale genome assembly of the false clownfish, <i>Amphiprion ocellaris</i> . <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	11
4504	Viral diversity and potential environmental risk in microplastic at watershed scale: Evidence from metagenomic analysis of plastisphere. <i>Environment International</i> , 2022, 161, 107146.	10.0	23
4505	MEDUSA: A Pipeline for Sensitive Taxonomic Classification and Flexible Functional Annotation of Metagenomic Shotgun Sequences. <i>Frontiers in Genetics</i> , 2022, 13, 814437.	2.3	5
4506	Genome-wide identification and characterization of <i>Fusarium circinatum</i> -responsive lncRNAs in <i>Pinus radiata</i> . <i>BMC Genomics</i> , 2022, 23, 194.	2.8	4
4508	Quantifying and Cataloguing Unknown Sequences within Human Microbiomes. <i>MSystems</i> , 2022, 7, e0146821.	3.8	2
4510	Reverse Genomics: Design of Universal Epitope Sets to Isolate All Saccharibacteria Members from the Human Oral Cavity. <i>Microorganisms</i> , 2022, 10, 602.	3.6	3
4511	Transcriptome Analysis of Immune Responses and Metabolic Regulations of Chinese Soft-Shelled Turtle (<i>Pelodiscus sinensis</i>) against <i>Edwardsiella tarda</i> Infection. <i>Fishes</i> , 2022, 7, 79.	1.7	3
4512	Positively selected genes in the hoary bat (<i>Lasiurus cinereus</i>) lineage: prominence of thymus expression, immune and metabolic function, and regions of ancient synten. <i>PeerJ</i> , 2022, 10, e13130.	2.0	0
4513	SHOOT: phylogenetic gene search and ortholog inference. <i>Genome Biology</i> , 2022, 23, 85.	8.8	28
4514	Global population structure of the <i>Serratia marcescens</i> complex and identification of hospital-adapted lineages in the complex. <i>Microbial Genomics</i> , 2022, 8, .	2.0	8
4515	The genome sequence of the lesser marbled fritillary, <i>Brenthis ino</i> , and evidence for a segregating neo-Z chromosome. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	8
4516	Genome-Wide Transcriptional Response of <i>Mycobacterium smegmatis</i> MC2155 to G-Quadruplex Ligands BRACO-19 and TMPyP4. <i>Frontiers in Microbiology</i> , 2022, 13, 817024.	3.5	8

#	ARTICLE	IF	CITATIONS
4517	Effects of Short-Chain Fatty Acid Modulation on Potentially Diarrhea-Causing Pathogens in Yaks Through Metagenomic Sequencing. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 805481.	3.9	9
4518	Finding the right fit: evaluation of short-read and long-read sequencing approaches to maximize the utility of clinical microbiome data. <i>Microbial Genomics</i> , 2022, 8, .	2.0	15
4519	Genomics-Based Reconstruction and Predictive Profiling of Amino Acid Biosynthesis in the Human Gut Microbiome. <i>Microorganisms</i> , 2022, 10, 740.	3.6	15
4520	Selection drives convergent gene expression changes during transitions to co-sexuality in haploid sexual systems. <i>Nature Ecology and Evolution</i> , 2022, 6, 579-589.	7.8	12
4521	Computational Tools for the Analysis of Uncultivated Phage Genomes. <i>Microbiology and Molecular Biology Reviews</i> , 2022, 86, e0000421.	6.6	13
4522	Microbiomes in the Challenger Deep slope and bottom-axis sediments. <i>Nature Communications</i> , 2022, 13, 1515.	12.8	31
4523	Methods for the targeted sequencing and analysis of integrons and their gene cassettes from complex microbial communities. <i>Microbial Genomics</i> , 2022, 8, .	2.0	9
4524	Taxonomy of Rhizobiaceae revisited: proposal of a new framework for genus delimitation. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	1.7	125
4525	Comparative transcriptome profiling of <i>Polianthes tuberosa</i> during a compatible interaction with root-knot nematode <i>Meloidogyne incognita</i> . <i>Molecular Biology Reports</i> , 2022, , 1.	2.3	1
4526	Correlation Analysis of the Microbiome and Immune Function in the Lung-Gut Axis of Critically Ill Patients in the ICU. <i>Frontiers in Medicine</i> , 2022, 9, 808302.	2.6	4
4528	Ethylmalonyl-CoA pathway involved in polyhydroxyvalerate synthesis in <i>Candidatus Contendobacter</i> . <i>AMB Express</i> , 2022, 12, 39.	3.0	2
4529	The phylogeny of the Anderson's White-bellied Rat (<i>Niviventer andersoni</i>) based on complete mitochondrial genomes. <i>Ecology and Evolution</i> , 2022, 12, e8663.	1.9	4
4530	Full-length transcriptome analysis of <i>Adiantum flabellulatum</i> gametophyte. <i>PeerJ</i> , 2022, 10, e13079.	2.0	5
4532	Habitat-adapted microbial communities mediate <i>Sphagnum</i> peatmoss resilience to warming. <i>New Phytologist</i> , 2022, 234, 2111-2125.	7.3	18
4533	Transcriptome Profiling and Functional Validation of RING-Type E3 Ligases in Halophyte <i>Sesuvium verrucosum</i> under Salinity Stress. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2821.	4.1	3
4534	High quality genome assembly of the anhydrobiotic midge provides insights on a single chromosome-based emergence of extreme desiccation tolerance. <i>NAR Genomics and Bioinformatics</i> , 2022, 4, lqac029.	3.2	6
4535	Chromosomal-level genome of a sheet-web spider provides insight into the composition and evolution of venom. <i>Molecular Ecology Resources</i> , 2022, 22, 2333-2348.	4.8	10
4537	A Systematic Phylogenomic Classification of the Multidrug and Toxic Compound Extrusion Transporter Gene Family in Plants. <i>Frontiers in Plant Science</i> , 2022, 13, 774885.	3.6	8

#	ARTICLE	IF	CITATIONS
4538	Structure and function of the soil microbiome underlying N ₂ O emissions from global wetlands. <i>Nature Communications</i> , 2022, 13, 1430.	12.8	72
4539	Metaproteomics as a tool for studying the protein landscape of human-gut bacterial species. <i>PLoS Computational Biology</i> , 2022, 18, e1009397.	3.2	8
4541	Metagenomic insights to the functional potential of sediment microbial communities in freshwater lakes. <i>Metabarcoding and Metagenomics</i> , 0, 6, .	0.0	6
4542	Phosphonate production by marine microbes: Exploring new sources and potential function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2113386119.	7.1	31
4543	Metatranscriptomic Analyses Unravel Dynamic Changes in the Microbial and Metabolic Transcriptional Profiles in Artisanal Austrian Hard-Cheeses During Ripening. <i>Frontiers in Microbiology</i> , 2022, 13, 813480.	3.5	4
4544	Integration of the Human Gut Microbiome and Serum Metabolome Reveals Novel Biological Factors Involved in the Regulation of Bone Mineral Density. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 853499.	3.9	9
4545	Haplotype-resolved Chinese male genome assembly based on high-fidelity sequencing. <i>Fundamental Research</i> , 2022, 2, 946-953.	3.3	11
4546	High-Quality, Phased Genomes of <i>Phytophthora ramorum</i> Clonal Lineages NA1 and EU1. <i>Molecular Plant-Microbe Interactions</i> , 2022, 35, 360-363.	2.6	4
4547	Antimicrobial resistance determinants in silage. <i>Scientific Reports</i> , 2022, 12, 5243.	3.3	2
4548	Characterization of the Ocular Surface Microbiome in Keratitis Patients after Repeated Ophthalmic Antibiotic Exposure. <i>Microbiology Spectrum</i> , 2022, 10, e0216221.	3.0	5
4549	Species composition and overall diversity are significantly correlated between the tongue coating and gastric fluid microbiomes in gastritis patients. <i>BMC Medical Genomics</i> , 2022, 15, 60.	1.5	5
4550	Complete genome sequence of a novel arivirus from a yellow spotted stink bug (<i>Erthesina fullo</i>) Tj ETQq1 1 0.784314 rgBT /Overlock	2.1	3
4551	Machine Learning and Deep Learning Applications in Metagenomic Taxonomy and Functional Annotation. <i>Frontiers in Microbiology</i> , 2022, 13, 811495.	3.5	8
4552	Host-microbiome protein-protein interactions capture disease-relevant pathways. <i>Genome Biology</i> , 2022, 23, 72.	8.8	10
4553	Comparative Analysis of the Gut Microbiota of Mongolian Gazelle (<i>Procapra gutturosa</i>) Under Fragmented Habitats. <i>Frontiers in Microbiology</i> , 2022, 13, 830321.	3.5	1
4554	Changes to gut amino acid transporters and microbiome associated with increased E/I ratio in Chd8+/+ mouse model of ASD-like behavior. <i>Nature Communications</i> , 2022, 13, 1151.	12.8	35
4555	House crickets (Othoptera: Gryllidae: <i>Acheta domesticus</i>) reared in small-scale laboratory conditions harbour limited viral flora. <i>Journal of Insects As Food and Feed</i> , 2022, 8, 1149-1155.	3.9	0
4556	Loss of Plastid Developmental Genes Coincides With a Reversion to Monoplastidy in Hornworts. <i>Frontiers in Plant Science</i> , 2022, 13, 863076.	3.6	6

#	ARTICLE	IF	CITATIONS
4557	Comparative Respiratory Tract Microbiome Between Carbapenem-Resistant <i>Acinetobacter baumannii</i> Colonization and Ventilator Associated Pneumonia. <i>Frontiers in Microbiology</i> , 2022, 13, 782210.	3.5	5
4558	Microbial communities of Auka hydrothermal sediments shed light on vent biogeography and the evolutionary history of thermophily. <i>ISME Journal</i> , 2022, 16, 1750-1764.	9.8	16
4559	Insights into carbon-fixation pathways through metagenomics in the sediments of deep-sea cold seeps. <i>Marine Pollution Bulletin</i> , 2022, 176, 113458.	5.0	15
4560	Experimental evidence for the impact of soil viruses on carbon cycling during surface plant litter decomposition. <i>ISME Communications</i> , 2022, 2, .	4.2	26
4561	Metagenomic and Functional Characterization of Two Chilean Kefir Beverages Reveals a Dairy Beverage Containing Active Enzymes, Short-Chain Fatty Acids, Microbial Î²-Amyloids, and Bio-Film Inhibitors. <i>Foods</i> , 2022, 11, 900.	4.3	8
4562	Metabolome and transcriptome analyses identify the plant immunity systems that facilitate sesquiterpene and lignan biosynthesis in <i>Syringa pinnatifolia</i> Hemsl.. <i>BMC Plant Biology</i> , 2022, 22, 132.	3.6	6
4563	Record-Breaking Rain Event Altered Estuarine Viral Assemblages. <i>Microorganisms</i> , 2022, 10, 729.	3.6	5
4564	Constructing benchmark test sets for biological sequence analysis using independent set algorithms. <i>PLoS Computational Biology</i> , 2022, 18, e1009492.	3.2	10
4565	Gentamicin at sub-inhibitory concentrations selects for antibiotic resistance in the environment. <i>ISME Communications</i> , 2022, 2, .	4.2	11
4566	Exploration of the Potential Relationship Between Gut Microbiota Remodeling Under the Influence of High-Protein Diet and Crohn's Disease. <i>Frontiers in Microbiology</i> , 2022, 13, 831176.	3.5	6
4568	The Broad Host Range Phage vB_CpeS_BG3P Is Able to Inhibit <i>Clostridium perfringens</i> Growth. <i>Viruses</i> , 2022, 14, 676.	3.3	7
4569	Clinical and In Vitro Evidence Favoring Immunoglobulin Treatment of a Chronic Norovirus Infection in a Patient With Common Variable Immunodeficiency. <i>Journal of Infectious Diseases</i> , 2022, 226, 1781-1789.	4.0	12
4570	Comparative Genomics of Seasonal Senescence in Forest Trees. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3761.	4.1	4
4572	Novel viruses discovered in the transcriptomes of agnathan fish. <i>Journal of Fish Diseases</i> , 2022, 45, 931-938.	1.9	3
4574	A mouse model of occult intestinal colonization demonstrating antibiotic-induced outgrowth of carbapenem-resistant <i>Enterobacteriaceae</i> . <i>Microbiome</i> , 2022, 10, 43.	11.1	8
4575	Simultaneous Hospital Outbreaks of New Delhi Metallo-Î²-Lactamase-Producing <i>Enterobacteriales</i> Unraveled Using Whole-Genome Sequencing. <i>Microbiology Spectrum</i> , 2022, 10, e0228721.	3.0	4
4576	Characterization and Genomic Analysis of the First Podophage Infecting <i>Shewanella</i> , Representing a Novel Viral Cluster. <i>Frontiers in Microbiology</i> , 2022, 13, 853973.	3.5	3
4577	Preliminary Results about Lamb Meat Tenderness Based on the Study of Novel Isoforms and Alternative Splicing Regulation Pathways Using Iso-seq, RNA-seq and CTCF ChIP-seq Data. <i>Foods</i> , 2022, 11, 1068.	4.3	7

#	ARTICLE	IF	CITATIONS
4578	Metagenomic survey of the microbiome of ancient Siberian permafrost and modern Kamchatkan cryosols. <i>MicroLife</i> , 2022, 3, .	2.1	5
4579	Characterization of a rare clinical isolate of <i>A.Âspinulosporus</i> following a central nervous system infection. <i>Microbes and Infection</i> , 2022, 24, 104973.	1.9	1
4580	The medusa of <i>Aurelia coerulea</i> is similar to its polyp in molecular composition and different from the medusa of <i>Stomolophus meleagris</i> in toxicity. <i>Toxicon</i> , 2022, 210, 89-99.	1.6	1
4581	The adjustment of life history strategies drives the ecological adaptations of soil microbiota to aridity. <i>Molecular Ecology</i> , 2022, 31, 2920-2934.	3.9	18
4583	Genome Sequences of Five Arenaviruses from Pygmy Mice (<i>Mus minutoides</i>) in Sierra Leone. <i>Microbiology Resource Announcements</i> , 2022, 11, e0009522.	0.6	3
4584	The genomic basis of host and vector specificity in non-pathogenic trypanosomatids. <i>Biology Open</i> , 2022, 11, .	1.2	4
4585	Picornavirus-Like Viruses of the Havel River, Germany. <i>Frontiers in Microbiology</i> , 2022, 13, 865287.	3.5	6
4586	Novel insight into the formation mechanism of umami peptides based on microbial metabolism in Chouguiyu, a traditional Chinese fermented fish. <i>Food Research International</i> , 2022, 157, 111211.	6.2	24
4587	Complete Genome Sequences of Five Isolated <i>Pseudomonas</i> Strains that Catabolize Pentose Sugars and Aromatic Compounds Obtained from Lignocellulosic Biomass. <i>Microbiology Resource Announcements</i> , 2022, 11, e0098721.	0.6	4
4588	Chromosome-Level Genome Assembly Reveals Dynamic Sex Chromosomes in Neotropical Leaf-Litter Geckos (<i>Sphaerodactylidae</i> : <i>Sphaerodactylus</i>). <i>Journal of Heredity</i> , 2022, 113, 272-287.	2.4	19
4589	Diet Supplementation with NUTRIOSE, a Resistant Dextrin, Increases the Abundance of <i>Parabacteroides distasonis</i> in the Human Gut. <i>Molecular Nutrition and Food Research</i> , 2022, 66, e2101091.	3.3	8
4590	From rags to enriched: metagenomic insights into ammonia-oxidizing archaea following ammonia enrichment of a denuded oligotrophic soil ecosystem. <i>Environmental Microbiology</i> , 2022, 24, 3097-3110.	3.8	4
4591	Linking transcriptional dynamics of CH ₄ -cycling grassland soil microbiomes to seasonal gas fluxes. <i>ISME Journal</i> , 2022, 16, 1788-1797.	9.8	12
4594	The phyllosphere microbiome shifts toward combating melanose pathogen. <i>Microbiome</i> , 2022, 10, 56.	11.1	54
4595	Phylogeny-Aware Analysis of Metagenome Community Ecology Based on Matched Reference Genomes while Bypassing Taxonomy. <i>MSystems</i> , 2022, 7, e0016722.	3.8	35
4596	Genome-wide analysis of the hard clam mitogen-activated protein kinase kinase gene family and their transcriptional profiles under abiotic stress. <i>Marine Environmental Research</i> , 2022, 176, 105606.	2.5	5
4597	Soil microbial metabolism on carbon and nitrogen transformation links the crop-residue contribution to soil organic carbon. <i>Npj Biofilms and Microbiomes</i> , 2022, 8, 14.	6.4	12
4598	Genome Sequence Resource for <i>Bipolaris zeicola</i> , the Cause of Northern Corn Leaf Spot Disease. <i>Phytopathology</i> , 2022, , PHYTO05210196A.	2.2	2

#	ARTICLE	IF	CITATIONS
4599	Encounter With a Selfish Virus Sabotages Its Vector to Orient Toward Requisite Host Plant: A Case Study With Chili Leaf Curl Virus-Whitefly. <i>Frontiers in Ecology and Evolution</i> , 2022, 10, .	2.2	4
4600	Draft Genome Sequence of <i>Lactocaseibacillus rhamnosus</i> IMI 507023. <i>Microbiology Resource Announcements</i> , 2022, 11, e0121721.	0.6	2
4602	Not all permafrost microbiomes are created equal: Influence of permafrost thaw on the soil microbiome in a laboratory incubation study. <i>Soil Biology and Biochemistry</i> , 2022, 167, 108605.	8.8	7
4603	Cryptic and abundant marine viruses at the evolutionary origins of Earth's RNA virome. <i>Science</i> , 2022, 376, 156-162.	12.6	124
4605	Positron-emitting radiotracers spatially resolve unexpected biogeochemical relationships linked with methane oxidation in Arctic soils. <i>Global Change Biology</i> , 2022, , .	9.5	0
4606	Current progress and open challenges for applying deep learning across the biosciences. <i>Nature Communications</i> , 2022, 13, 1728.	12.8	105
4607	Genome Sequence of <i>Streptomyces</i> sp. Strain GQFP Isolated from Soil Near the Roots of Pharmaceutical Plant <i>Elaeagnus pungens</i> . <i>Microbiology Resource Announcements</i> , 2022, , e0000222.	0.6	0
4609	Inter-species Metabolic Interactions in an In-vitro Minimal Human Gut Microbiome of Core Bacteria. <i>Npj Biofilms and Microbiomes</i> , 2022, 8, 21.	6.4	26
4610	MTD: a unique pipeline for host and meta-transcriptome joint and integrative analyses of RNA-seq data. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	1
4611	Identification of Differentially Expressed Genes Reveal Conserved Mechanisms in the Rice-Magnaporthe oryzae Interaction. <i>Frontiers in Plant Science</i> , 2022, 13, 723356.	3.6	2
4612	Higher Phytohormone Contents and Weaker Phytohormone Signal Transduction Were Observed in Cold-Tolerant Cucumber. <i>Plants</i> , 2022, 11, 961.	3.5	2
4613	De novo transcriptome analysis of gonads reveals the sex-associated genes in Chinese hook snout carp <i>Opsariichthys bidens</i> . <i>Aquaculture Reports</i> , 2022, 23, 101068.	1.7	5
4614	RNA-viromics reveals diverse communities of soil RNA viruses with the potential to affect grassland ecosystems across multiple trophic levels. <i>ISME Communications</i> , 2022, 2, .	4.2	32
4615	Halophilic <i>Marteella</i> sp. AD-3 enhanced phenanthrene degradation in a bioaugmented activated sludge system through syntrophic interaction. <i>Water Research</i> , 2022, 218, 118432.	11.3	7
4616	<i>Natronosporangium hydrolyticum</i> gen. nov., sp. nov., a haloalkaliphilic polyhydrolytic actinobacterium from a soda solonchak soil in Central Asia. <i>Systematic and Applied Microbiology</i> , 2022, 45, 126307.	2.8	2
4617	A mixed blessing of viruses in wastewater treatment plants. <i>Water Research</i> , 2022, 215, 118237.	11.3	21
4618	Population-based variations of a core resistome revealed by urban sewage metagenome surveillance. <i>Environment International</i> , 2022, 163, 107185.	10.0	19
4619	Metagenomic insights into direct interspecies electron transfer and quorum sensing in blackwater anaerobic digestion reactors supplemented with granular activated carbon. <i>Bioresource Technology</i> , 2022, 352, 127113.	9.6	26

#	ARTICLE	IF	CITATIONS
4620	Exploring the impact of biochar on antibiotics and antibiotics resistance genes in pig manure aerobic composting through untargeted metabolomics and metagenomics. <i>Bioresource Technology</i> , 2022, 352, 127118.	9.6	24
4621	Microbial functional genes influenced by short-term experimental drought across European agricultural fields. <i>Soil Biology and Biochemistry</i> , 2022, 168, 108650.	8.8	6
4622	Identification and molecular characterization of highly divergent RNA viruses in cattle, Uganda.. <i>Virus Research</i> , 2022, 313, 198739.	2.2	4
4623	Biodegradation and potential effect of ranitidine during aerobic composting of human feces. <i>Chemosphere</i> , 2022, 296, 134062.	8.2	8
4624	Whole genome sequence data of <i>Lactiplantibacillus plantarum</i> IMI 507027. <i>Data in Brief</i> , 2022, 42, 108025.	1.0	5
4625	Insight into the genome data of commercially important giant kelp <i>Macrocystis pyrifera</i> . <i>Data in Brief</i> , 2022, 42, 108068.	1.0	2
4626	The host-specific resistome in environmental feces of Eurasian otters (<i>Lutra lutra</i>) and leopard cats (<i>Prionailurus bengalensis</i>) revealed by metagenomic sequencing. <i>One Health</i> , 2022, 14, 100385.	3.4	1
4627	Dark carbon fixation in intertidal sediments: Controlling factors and driving microorganisms. <i>Water Research</i> , 2022, 216, 118381.	11.3	18
4628	Nitrogen input promotes denitrifying methanotrophs' abundance and contribution to methane emission reduction in coastal wetland and paddy soil. <i>Environmental Pollution</i> , 2022, 302, 119090.	7.5	20
4629	Unraveling microbe-mediated degradation of lignin and lignin-derived aromatic fragments in the Pearl River Estuary sediments. <i>Chemosphere</i> , 2022, 296, 133995.	8.2	2
4630	Metagenomics reveals bacterioplankton community adaptation to long-term thermal pollution through the strategy of functional regulation in a subtropical bay. <i>Water Research</i> , 2022, 216, 118298.	11.3	11
4631	Metagenomic evidence for the microbial transformation of carboxyl-rich alicyclic molecules: A long-term macrocosm experiment. <i>Water Research</i> , 2022, 216, 118281.	11.3	11
4632	Impact of nitrate addition on the resistome and mobilome from a full-scale sewer. <i>Chemical Engineering Journal</i> , 2022, 439, 135653.	12.7	3
4633	Shifts of lipid metabolites help decode immobilization of soil cadmium under reductive soil disinfestation. <i>Science of the Total Environment</i> , 2022, 829, 154592.	8.0	2
4634	Comparing resistome profiles from anthropogenically impacted and non-impacted areas of two South Shetland Islands " Maritime Antarctica. <i>Environmental Pollution</i> , 2022, 304, 119219.	7.5	10
4635	New insights of bacterial communities in fermented vegetables from shotgun metagenomics and identification of antibiotic resistance genes and probiotic bacteria. <i>Food Research International</i> , 2022, 157, 111190.	6.2	18
4636	Microbial habitat specificity largely affects microbial co-occurrence patterns and functional profiles in wetland soils. <i>Geoderma</i> , 2022, 418, 115866.	5.1	20
4637	Viral diversity and biogeochemical potential revealed in different prawn-culture sediments by virus-enriched metagenome analysis. <i>Environmental Research</i> , 2022, 210, 112901.	7.5	7

#	ARTICLE	IF	CITATIONS
4638	Electrochemically active microorganisms sense charge transfer resistance for regulating biofilm electroactivity, spatio-temporal distribution, and catabolic pathway. Chemical Engineering Journal, 2022, 442, 136248.	12.7	14
4640	Full Issue PDF. Molecular Plant-Microbe Interactions, 2021, 34, 1228-1333.	2.6	0
4643	High resolution proteomics of Aedes aegypti salivary glands infected with either dengue, Zika or chikungunya viruses identify new virus specific and broad antiviral factors. Scientific Reports, 2021, 11, 23696.	3.3	20
4645	Transcriptomic and Proteomic Characterizations of the Molecular Response to Blue Light and Salicylic Acid in Haematococcus pluvialis. Marine Drugs, 2022, 20, 1.	4.6	20
4647	Phenotypic and genetic analyses of two <i>Campylobacter fetus</i> isolates from a patient with relapsed prosthetic valve endocarditis. Pathogens and Disease, 2022, 79, .	2.0	3
4648	Evolutionary assembly of cooperating cell types in an animal chemical defense system. Cell, 2021, 184, 6138-6156.e28.	28.9	13
4649	Genomic and transcriptomic evidence for the diverse adaptations of <i>Synechococcus</i> subclusters 5.2 and 5.3 to mesoscale eddies. New Phytologist, 2022, 233, 1828-1842.	7.3	4
4650	Acidovorax pan-genome reveals specific functional traits for plant beneficial and pathogenic plant-associations. Microbial Genomics, 2021, 7, .	2.0	6
4651	Systematic evaluation of horizontal gene transfer between eukaryotes and viruses. Nature Microbiology, 2022, 7, 327-336.	13.3	87
4653	Meta-transcriptomic analysis of the virome and microbiome of the invasive Indian myna (Acridotheres tristis) in the United States. BMC Genomics, 2022, 23, 11.	3.4	11
4656	Metagenomic Analysis Reveals Previously Undescribed Bat Coronavirus Strains in Eswatini. EcoHealth, 2021, 18, 421-428.	2.0	6
4658	Incremental and Semi-Supervised Learning of 16S-rRNA Genes For Taxonomic Classification. , 2021, , .		3
4659	Cross-Kingdom Gene Coexpression Analysis Using <i>Stemphylium botryosum</i> "Lens ervoides" System Revealed Plasticity of Intercommunication Between the Pathogen Secretome and the Host Immune Systems. Molecular Plant-Microbe Interactions, 2021, 34, 1365-1377.	2.6	1
4660	A variety of highly divergent eukaryotic ssDNA viruses in sera of pigs. Journal of General Virology, 2021, 102, .	2.9	3
4661	An Interplay between Viruses and Bacteria Associated with the White Sea Sponges Revealed by Metagenomics. Life, 2022, 12, 25.	2.4	3
4662	Single-Larva RNA Sequencing Identifies Markers of Copper Toxicity and Exposure in Early Mytilus californianus Larvae. Frontiers in Physiology, 2021, 12, 647482.	2.8	1
4663	Gut microbiota modulates weight gain in mice after discontinued smoke exposure. Nature, 2021, 600, 713-719.	27.8	35
4664	An optimized FM-index library for nucleotide and amino acid search. Algorithms for Molecular Biology, 2021, 16, 25.	1.2	1

#	ARTICLE	IF	CITATIONS
4665	Cold Acclimation in <i>Brachypodium</i> Is Accompanied by Changes in Above-Ground Bacterial and Fungal Communities. <i>Plants</i> , 2021, 10, 2824.	3.5	7
4666	The genetic basis of phage susceptibility, cross-resistance and host-range in <i>Salmonella</i> . <i>Microbiology (United Kingdom)</i> , 2021, 167, .	1.8	20
4667	Phylogenomic and Microsynteny Analysis Provides Evidence of Genome Arrangements of High-Affinity Nitrate Transporter Gene Families of Plants. <i>International Journal of Molecular Sciences</i> , 2021, 22, 13036.	4.1	6
4670	Streptozotocin-induced hyperglycemia alters the cecal metabolome and exacerbates antibiotic-induced dysbiosis. <i>Cell Reports</i> , 2021, 37, 110113.	6.4	11
4672	Captivity Influences the Gut Microbiome of <i>Rhinopithecus roxellana</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 763022.	3.5	15
4673	Virtifier: a deep learning-based identifier for viral sequences from metagenomes. <i>Bioinformatics</i> , 2022, 38, 1216-1222.	4.1	20
4674	A Large-Scale Multiple Genome Comparison of Acidophilic Archaea (pH \approx 5.0) Extends Our Understanding of Oxidative Stress Responses in Polyextreme Environments. <i>Antioxidants</i> , 2022, 11, 59.	5.1	3
4675	Multi-Omics Reveal the Efficient Phosphate-Solubilizing Mechanism of Bacteria on Rocky Soil. <i>Frontiers in Microbiology</i> , 2021, 12, 761972.	3.5	15
4676	Pangenomics in crop improvement—“from coding structural variations to finding regulatory variants with pangenome graphs. <i>Plant Genome</i> , 2022, 15, e20177.	2.8	33
4677	The hidden genomic diversity of ciliated protists revealed by single-cell genome sequencing. <i>BMC Biology</i> , 2021, 19, 264.	3.8	11
4678	A high-throughput multiplexing and selection strategy to complete bacterial genomes. <i>GigaScience</i> , 2021, 10, .	6.4	13
4680	Diel Protein Regulation of Marine Picoplanktonic Communities Assessed by Metaproteomics. <i>Microorganisms</i> , 2021, 9, 2621.	3.6	2
4681	Genome sequence of the English grain aphid, <i>Sitobion avenae</i> and its endosymbiont <i>Buchnera aphidicola</i> . <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	4
4682	Adapting Macroecology to Microbiology: Using Occupancy Modeling To Assess Functional Profiles across Metagenomes. <i>MSystems</i> , 2021, 6, e0079021.	3.8	1
4683	Salivary and Intestinal Transcriptomes Reveal Differential Gene Expression in Starving, Fed and <i>Trypanosoma cruzi</i> -Infected <i>Rhodnius neglectus</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 773357.	3.9	1
4685	First Insights Into the Virus and Viroid Communities in Hemp (<i>Cannabis sativa</i>). <i>Frontiers in Agronomy</i> , 2021, 3, .	3.3	21
4686	Taxon-Specific Shifts in Bacterial and Archaeal Transcription of Dissolved Organic Matter Cycling Genes in a Stratified Fjord. <i>MSystems</i> , 2021, 6, e0057521.	3.8	1
4688	Full Issue PDF. <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 1336-1464.	2.6	0

#	ARTICLE	IF	CITATIONS
4689	Genome-Wide Identification, Primary Functional Characterization of the NHX Gene Family in <i>Canavalia rosea</i> , and Their Possible Roles for Adaptation to Tropical Coral Reefs. <i>Genes</i> , 2022, 13, 33.	2.4	4
4690	Full Genome Sequence of a <i>Methanomassiliicoccales</i> Representative Enriched from Peat Soil. <i>Microbiology Resource Announcements</i> , 2021, 10, e0044321.	0.6	4
4691	Reproductive health and endocrine disruption in smallmouth bass (<i>Micropterus dolomieu</i>) from the Lake Erie drainage, Pennsylvania, USA. <i>Environmental Monitoring and Assessment</i> , 2022, 194, 3.	2.7	10
4692	Worldwide distribution and environmental origin of the Adelaide imipenemase (AIM-1), a potent carbapenemase in <i>Pseudomonas aeruginosa</i> . <i>Microbial Genomics</i> , 2021, 7, .	2.0	3
4693	Comparative Metagenomic and Metabolomic Profiling of Rhizospheres of <i>Panax notoginseng</i> Grown under Forest and Field Conditions. <i>Agronomy</i> , 2021, 11, 2488.	3.0	14
4694	Rotavirus NSP1 Contributes to Intestinal Viral Replication, Pathogenesis, and Transmission. <i>MBio</i> , 2021, 12, e0320821.	4.1	10
4695	The Genome of the "Sea Vomit" <i>Didemnum vexillum</i> . <i>Life</i> , 2021, 11, 1377.	2.4	0
4696	A novel enterovirus in lambs with poliomyelitis and brain stem encephalitis. <i>Transboundary and Emerging Diseases</i> , 2022, 69, 227-234.	3.0	2
4697	A guide to phylotranscriptomic analysis for phycologists. <i>Algae</i> , 2021, 36, 333-340.	2.3	4
4699	Incremental & Semi-Supervised Learning for Functional Analysis of Protein Sequences. , 2021, , .		1
4702	Pelagic N_2 fixation dominated by sediment diazotrophic communities in a shallow temperate estuary. <i>Limnology and Oceanography</i> , 2022, 67, 364-378.	3.1	9
4703	Risk and protection strategies of <i>Amolops wuyiensis</i> intestine against gastrointestinal nematode (<i>Cosmocercoides wuyiensis</i> n. sp.) infection. <i>Environmental Microbiology</i> , 2022, 24, 1454-1466.	3.8	2
4704	Specific gut microbiome signatures and the associated pro-inflammatory functions are linked to pediatric allergy and acquisition of immune tolerance. <i>Nature Communications</i> , 2021, 12, 5958.	12.8	77
4705	Enhanced Ethanol Production From Carbon Monoxide by Enriched <i>Clostridium</i> Bacteria. <i>Frontiers in Microbiology</i> , 2021, 12, 754713.	3.5	5
4706	Transcriptome and metabolome changes in Chinese cedar during cold acclimation reveal the roles of flavonoids in needle discoloration and cold resistance. <i>Tree Physiology</i> , 2022, 42, 1858-1875.	3.1	7
4707	DeepGOZero: improving protein function prediction from sequence and zero-shot learning based on ontology axioms. <i>Bioinformatics</i> , 2022, 38, i238-i245.	4.1	23
4708	Three new clades of putative viral RNA-dependent RNA polymerases with rare or unique catalytic triads discovered in libraries of ORFans from powdery mildews and the yeast of oenological interest <i>Starmarella bacillari</i> s. <i>Virus Evolution</i> , 2022, 8, .	4.9	12
4709	Metagenomic analysis reveals mixed <i>Mycobacterium tuberculosis</i> infection in a 18th century Hungarian midwife. <i>Tuberculosis</i> , 2022, , 102181.	1.9	3

#	ARTICLE	IF	CITATIONS
4710	Evaluation of Potential Probiotic Properties of a Strain of <i>Lactobacillus plantarum</i> for Shrimp Farming: From Beneficial Functions to Safety Assessment. <i>Frontiers in Microbiology</i> , 2022, 13, 854131.	3.5	7
4711	Metagenomic investigation of the equine faecal microbiome reveals extensive taxonomic diversity. <i>PeerJ</i> , 2022, 10, e13084.	2.0	18
4712	Oogenesis and lipid metabolism in the deep-sea sponge <i>Phakellia ventilabrum</i> (Linnaeus, 1767). <i>Scientific Reports</i> , 2022, 12, 6317.	3.3	8
4716	Chemotaxis shapes the microscale organization of the ocean's microbiome. <i>Nature</i> , 2022, 605, 132-138.	27.8	51
4718	Lifestyle, mating type and mitochondrial genome features of the plant pathogen <i>Calonectria hawksworthii</i> (Hypocreales, Nectriaceae) as revealed by genome analyses. <i>Canadian Journal of Plant Pathology</i> , 2022, 44, 723-736.	1.4	1
4720	DBSCAN-SWA: An Integrated Tool for Rapid Prophage Detection and Annotation. <i>Frontiers in Genetics</i> , 2022, 13, 885048.	2.3	10
4721	Comparative genomics analysis of genus <i>Leuconostoc</i> resolves its taxonomy and elucidates its biotechnological importance. <i>Food Microbiology</i> , 2022, 106, 104039.	4.2	11
4723	Full Issue PDF. <i>Molecular Plant-Microbe Interactions</i> , 2022, 35, 300-367.	2.6	0
4724	Genomic Architecture and Evolution of the Cellulose synthase Gene Superfamily as Revealed by Phylogenomic Analysis. <i>Frontiers in Plant Science</i> , 2022, 13, 870818.	3.6	6
4725	Fungal dye-decolorizing peroxidase diversity: roles in either intra- or extracellular processes. <i>Applied Microbiology and Biotechnology</i> , 2022, 106, 2993-3007.	3.6	3
4726	Phylogeny and Metabolic Potential of the Candidate Phylum SAR324. <i>Biology</i> , 2022, 11, 599.	2.8	8
4727	A Capsidless Virus Is -Encapsidated by a Bisegmented Botybirnavirus. <i>Journal of Virology</i> , 2022, 96, e0029622.	3.4	11
4728	Single cell genome sequencing of laboratory mouse microbiota improves taxonomic and functional resolution of this model microbial community. <i>PLoS ONE</i> , 2022, 17, e0261795.	2.5	3
4729	A <i>Solanum lycopersicoides</i> reference genome facilitates insights into tomato specialized metabolism and immunity. <i>Plant Journal</i> , 2022, 110, 1791-1810.	5.7	16
4730	Metatranscriptomic Assessment of the Microbial Community Associated With the Flavescence dorée Phytoplasma Insect Vector <i>Scaphoideus titanus</i> . <i>Frontiers in Microbiology</i> , 2022, 13, 866523.	3.5	4
4731	Microbial Activities and Selection from Surface Ocean to Subseafloor on the Namibian Continental Shelf. <i>Applied and Environmental Microbiology</i> , 2022, 88, e0021622.	3.1	4
4732	Environmental factors shaping the gut microbiome in a Dutch population. <i>Nature</i> , 2022, 604, 732-739.	27.8	239
4733	Changes in gut microbiota, metabolite SCFAs, and GPR43 expression in obese diabetic mice after sleeve gastrectomy. <i>Journal of Applied Microbiology</i> , 2022, 133, 555-568.	3.1	3

#	ARTICLE	IF	CITATIONS
4735	Precise genotyping of circular mobile elements from metagenomic data uncovers human-associated plasmids with recent common ancestors. <i>Genome Research</i> , 2022, , gr.275894.121.	5.5	0
4736	The Microbial Metagenome of Eluates Obtained From the Surface of Broccoli Heads Subjected to Different Light Treatments. <i>Frontiers in Microbiology</i> , 2022, 13, 820419.	3.5	0
4737	Gene expression profiles provide insights into the survival strategies in deep-sea mussel (<i>Bathymodiolus platifrons</i>) of different developmental stages. <i>BMC Genomics</i> , 2022, 23, 311.	2.8	2
4739	Heterophil/Lymphocyte Ratio Level Modulates Salmonella Resistance, Cecal Microbiota Composition and Functional Capacity in Infected Chicken. <i>Frontiers in Immunology</i> , 2022, 13, 816689.	4.8	13
4740	Comparative Genomic Analysis of <i>Vibrio cincinnatiensis</i> Provides Insights into Genetic Diversity, Evolutionary Dynamics, and Pathogenic Traits of the Species. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4520.	4.1	3
4741	Integrative Transcriptomics and Proteomics Elucidate the Regulatory Mechanism of <i>Hydrangea macrophylla</i> Flower-Color Changes Induced by Exogenous Aluminum. <i>Agronomy</i> , 2022, 12, 969.	3.0	3
4742	Prediction and Inferred Evolution of Acid Tolerance Genes in the Biotechnologically Important <i>Acidihalobacter</i> Genus. <i>Frontiers in Microbiology</i> , 2022, 13, 848410.	3.5	6
4743	Comparative Genomics of Members of the Genus <i>DeFluviicoccus</i> With Insights Into Their Ecophysiological Importance. <i>Frontiers in Microbiology</i> , 2022, 13, 834906.	3.5	8
5454	Population genomics confirms acquisition of drug-resistant <i>Aspergillus fumigatus</i> infection by humans from the environment. <i>Nature Microbiology</i> , 2022, 7, 663-674.	13.3	82
5455	Shotgun metagenomic sequencing revealed the prebiotic potential of a grain-based diet in mice. <i>Scientific Reports</i> , 2022, 12, 6748.	3.3	2
5457	Genome of the ramshorn snail <i>Biomphalaria straminea</i> -an obligate intermediate host of schistosomiasis.. <i>GigaScience</i> , 2022, 11, .	6.4	11
5458	Early branching arbuscular mycorrhizal fungus <i>Paraglomus occultum</i> carries a small and repeat-poor genome compared to relatives in the Glomeromycotina. <i>Microbial Genomics</i> , 2022, 8, .	2.0	14
5459	Prophage-mediated genome differentiation of the <i>Salmonella</i> Derby ST71 population. <i>Microbial Genomics</i> , 2022, 8, .	2.0	1
5460	Metagenomic tracking of antibiotic resistance genes through a pre-harvest vegetable production system: an integrated lab-microcosm and greenhouse scale analysis. <i>Environmental Microbiology</i> , 2022, 24, 3705-3721.	3.8	6
5461	Into the darkness: the ecologies of novel "microbial dark matter" phyla in an Antarctic lake. <i>Environmental Microbiology</i> , 2022, 24, 2576-2603.	3.8	9
5462	Chromosome-level genome assembly for takin (<i>Budorcas taxicolor</i>) provides insights into its taxonomic status and genetic diversity. <i>Molecular Ecology</i> , 2023, 32, 1323-1334.	3.9	5
5464	Reevaluation of the Phylogenetic Diversity and Global Distribution of the Genus "Candidatus" <i>Accumulibacter</i> . <i>MSystems</i> , 2022, 7, e0001622.	3.8	22
5465	Precision Probiotics in Agroecosystems: Multiple Strategies of Native Soil Microbiotas for Conquering the Competitor <i>Ralstonia solanacearum</i> . <i>MSystems</i> , 2022, 7, e0115921.	3.8	4

#	ARTICLE	IF	CITATIONS
5466	Comparison of SARS-CoV-2 sequencing using the ONT GridION and the Illumina MiSeq. BMC Genomics, 2022, 23, 319.	2.8	19
5467	Distinctive signatures of pathogenic and antibiotic resistant potentials in the hadal microbiome. Environmental Microbiomes, 2022, 17, 19.	5.0	6
5469	Optimizing the Parametrization of Homologue Classification in the Pan-Genome Computation for a Bacterial Species: Case Study Streptococcus pyogenes. Methods in Molecular Biology, 2022, 2449, 299-324.	0.9	1
5470	A chromosome-level reference genome of <i>Ensete glaucum</i> gives insight into diversity and chromosomal and repetitive sequence evolution in the Musaceae. GigaScience, 2022, 11, .	6.4	19
5471	ProTranslator: Zero-Shot Protein Function Prediction Using Textual Description. Lecture Notes in Computer Science, 2022, , 279-294.	1.3	6
5472	CHERRY: a Computational methoD for accuratE pRediction of virusâ€“pRokaryotic interactions using a graph encoderâ€“decoder model. Briefings in Bioinformatics, 2022, 23, .	6.5	21
5473	Taxonomic and functional diversity from Antarctic ice-tephra microbial community: ecological insights and potential for bioprospection. Anais Da Academia Brasileira De Ciencias, 2022, 94, e20210621.	0.8	0
5474	A Deep Learning Framework for Predicting Protein Functions With Co-Occurrence of GO Terms. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2023, 20, 833-842.	3.0	4
5475	ANI analysis of poxvirus genomes reveals its potential application to viral species rank demarcation. Virus Evolution, 2022, 8, .	4.9	7
5476	Enhanced Cultured Diversity of the Mouse Gut Microbiota Enables Custom-Made Synthetic Communities. SSRN Electronic Journal, 0, , .	0.4	1
5477	FUNAGE-Pro: comprehensive web server for gene set enrichment analysis of prokaryotes. Nucleic Acids Research, 2022, 50, W330-W336.	14.5	17
5478	Longitudinal and Comparative Analysis of Gut Microbiota of Tunisian Newborns According to Delivery Mode. Frontiers in Microbiology, 2022, 13, 780568.	3.5	4
5479	The Pomegranate Deciduous Trait Is Genetically Controlled by a PgPolyQ-MADS Gene. Frontiers in Plant Science, 2022, 13, 870207.	3.6	1
5480	Identification of a New Endo-Î²-1,4-xylanase Prospected from the Microbiota of the Termite Heterotermes tenuis. Microorganisms, 2022, 10, 906.	3.6	1
5481	Fleshy or dry: transcriptome analyses reveal the genetic mechanisms underlying bract development in Ephedra. EvoDevo, 2022, 13, 10.	3.2	1
5482	Metagenomics Reveals the Diversity and Taxonomy of Carbohydrate-Active Enzymes and Antibiotic Resistance Genes in Suancai Bacterial Communities. Genes, 2022, 13, 773.	2.4	3
5483	Identification of pellicle formation related microorganisms in traditional Sichuan paocai through metagenomic sequence and the effects of Baijiu/Salt on pellicle and volatile components. Food Research International, 2022, 159, 111130.	6.2	8
5484	The Regulatory Network and Role of the circRNA-miRNA-mRNA ceRNA Network in the Progression and the Immune Response of Wilms Tumor Based on RNA-Seq. Frontiers in Genetics, 2022, 13, 849941.	2.3	5

#	ARTICLE	IF	CITATIONS
5485	Diagnosis and analysis of unexplained cases of childhood encephalitis in Australia using metatranscriptomic sequencing. <i>Journal of General Virology</i> , 2022, 103, .	2.9	2
5486	Parallel Evolution of C-Type Lectin Domain Gene Family Sizes in Insect-Vectored Nematodes. <i>Frontiers in Plant Science</i> , 2022, 13, 856826.	3.6	2
5487	Comprehensive Genomic Analysis of Marine Strain <i>Streptomyces</i> sp. 891, an Excellent Producer of Chrysomycin A with Therapeutic Potential. <i>Marine Drugs</i> , 2022, 20, 287.	4.6	5
5488	kmtricks: efficient and flexible construction of Bloom filters for large sequencing data collections. <i>Bioinformatics Advances</i> , 2022, 2, .	2.4	19
5489	The genome of <i>Corydalis</i> reveals the evolution of benzyloquinoline alkaloid biosynthesis in Ranunculales. <i>Plant Journal</i> , 2022, 111, 217-230.	5.7	19
5490	Metagenomic analysis reveals the different characteristics of microbial communities inside and outside the karst tiankeng. <i>BMC Microbiology</i> , 2022, 22, 115.	3.3	12
5491	Full-Length Transcriptome Data for the White Cloud Mountain Minnow (<i>Tanichthys albonubes</i>) From a Wild Population Based on Isoform Sequencing. <i>Frontiers in Marine Science</i> , 2022, 9, .	2.5	0
5492	Fecal microbiota transfer between young and aged mice reverses hallmarks of the aging gut, eye, and brain. <i>Microbiome</i> , 2022, 10, 68.	11.1	107
5493	Metagenomic investigation of the seasonal distribution of bacterial community and antibiotic-resistant genes in Day River Downstream, Ninh Binh, Vietnam. <i>Applied Biological Chemistry</i> , 2022, 65, .	1.9	5
5494	Metagenomic-Metabolomic Mining of Kinema, a Naturally Fermented Soybean Food of the Eastern Himalayas. <i>Frontiers in Microbiology</i> , 2022, 13, 868383.	3.5	17
5495	Comparative genomic analysis of <i>Thermus</i> provides insights into the evolutionary history of an incomplete denitrification pathway. , 0, , .		3
5497	Comprehensive Genome-Wide Identification, Characterization, and Expression Analysis of CCHC-Type Zinc Finger Gene Family in Wheat (<i>Triticum aestivum</i> L.). <i>Frontiers in Plant Science</i> , 2022, 13, 892105.	3.6	6
5498	Slope aspect affects the soil microbial communities in karst tiankeng negative landforms. <i>Bmc Ecology and Evolution</i> , 2022, 22, 54.	1.6	9
5499	Metagenomic Insights Into Competition Between Denitrification and Dissimilatory Nitrate Reduction to Ammonia Within One-Stage and Two-Stage Partial-Nitritation Anammox Bioreactor Configurations. <i>Frontiers in Microbiology</i> , 2022, 13, 825104.	3.5	9
5500	Nasopharyngeal airway dual-transcriptome of infants with severe bronchiolitis and risk of childhood asthma: A multicenter prospective study. <i>Journal of Allergy and Clinical Immunology</i> , 2022, 150, 806-816.	2.9	19
5501	The Genome-Wide Identification of Long Non-Coding RNAs Involved in Floral Thermogenesis in <i>Nelumbo nucifera</i> Gaertn. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4901.	4.1	0
5502	Flavonoid Synthesis and Metabolism During the Fruit Development in Hickory (<i>Carya cathayensis</i>). <i>Frontiers in Plant Science</i> , 2022, 13, .	3.6	4
5503	Bioprospecting of Plant Growth-Promoting Traits of <i>Pseudomonas</i> sp. Strain C3 Isolated from the Atacama Desert: Molecular and Culture-Based Analysis. <i>Diversity</i> , 2022, 14, 388.	1.7	5

#	ARTICLE	IF	CITATIONS
5504	<i>Occultella gossypii</i> sp. nov., an alkali-resistant isolate from soil sampled in a cotton field. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	1.7	0
5505	Sugars dominate the seagrass rhizosphere. Nature Ecology and Evolution, 2022, 6, 866-877.	7.8	27
5506	Microbial mercury methylation potential in a large-scale municipal solid waste landfill, China. Waste Management, 2022, 145, 102-111.	7.4	3
5507	Chromosome-Scale, Haplotype-Resolved Genome Assembly of Suaeda Glauca. Frontiers in Genetics, 2022, 13, .	2.3	3
5508	Parental origins of the cultivated tetraploid sour cherry (<scp><i>Prunus cerasus</i></scp> L.). Plants People Planet, 2022, 4, 444-450.	3.3	5
5509	Hybrid Assembly and Annotation of the Genome of the Indian Punica granatum, a Superfood. Frontiers in Genetics, 2022, 13, .	2.3	4
5510	The cytochrome P450s of Leptographium qinlingensis: Gene characteristics, phylogeny, and expression in response to terpenoids. Fungal Biology, 2022, 126, 395-406.	2.5	2
5511	Interactive analysis of biosurfactants in fruit-waste fermentation samples using BioSurfDB and MEGAN. Scientific Reports, 2022, 12, 7769.	3.3	3
5512	Whole genome resequencing reveals signatures of rapid selection in a virus-affected commercial fishery. Molecular Ecology, 2022, 31, 3658-3671.	3.9	3
5513	The in-situ release of algal bloom populations and the role of prokaryotic communities in their establishment and growth. Water Research, 2022, 219, 118565.	11.3	13
5514	Third Generation Genome Sequencing Reveals That Endobacteria in Nematophagous Fungi Esteya vermicola Contain Multiple Genes Encoding for Nematicidal Proteins. Frontiers in Microbiology, 2022, 13, 842684.	3.5	1
5515	Compendium of specialized metabolite biosynthetic diversity encoded in bacterial genomes. Nature Microbiology, 2022, 7, 726-735.	13.3	106
5516	Integrated small RNA profiling and degradome analysis of Anthurium andraeanum cultivars with different-colored spathes. Journal of Plant Research, 2022, 135, 609-626.	2.4	1
5517	Functional repertoire convergence of distantly related eukaryotic plankton lineages abundant in the sunlit ocean. Cell Genomics, 2022, 2, 100123.	6.5	70
5518	A total infectome approach to understand the etiology of infectious disease in pigs. Microbiome, 2022, 10, 73.	11.1	11
5519	<i>Escherichia coli</i> Strains from Patients with Inflammatory Bowel Diseases have Disease-specific Genomic Adaptations. Journal of Crohn's and Colitis, 2022, 16, 1584-1597.	1.3	5
5520	The Complete Genome Resource of <i>Xanthomonas axonopodis</i> pv. <i>glycines</i> ICMP5732 Causing Pustule Disease on Soybean. Plant Disease, 2022, , PDIS11212512A.	1.4	0
5521	A De Novo Chromosome-Level Genome Assembly of the White-Tailed Deer, <i>Odocoileus Virginianus</i>. Journal of Heredity, 2022, 113, 479-489.	2.4	3

#	ARTICLE	IF	CITATIONS
5522	Tissue remodeling by an opportunistic pathogen triggers allergic inflammation. <i>Immunity</i> , 2022, 55, 895-911.e10.	14.3	19
5523	Comprehensive Analysis Reveals the Genetic and Pathogenic Diversity of <i>Ralstonia solanacearum</i> Species Complex and Benefits Its Taxonomic Classification. <i>Frontiers in Microbiology</i> , 2022, 13, .	3.5	3
5525	Comparative Transcriptome Analysis Provides Insights into the Resistance in <i>Pueraria</i> [<i>Pueraria lobata</i> (Willd.) Ohwi] in Response to Pseudo-Rust Disease. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5223.	4.1	5
5526	vRhyme enables binning of viral genomes from metagenomes. <i>Nucleic Acids Research</i> , 2022, 50, e83-e83.	14.5	30
5527	Deep learning of a bacterial and archaeal universal language of life enables transfer learning and illuminates microbial dark matter. <i>Nature Communications</i> , 2022, 13, 2606.	12.8	21
5528	Gene expression changes in <i>Epinephelus marginatus</i> (Teleostei, Serranidae) liver reveals candidate molecular biomarker of iron ore contamination. <i>Chemosphere</i> , 2022, , 134899.	8.2	1
5529	Metatranscriptomic profiling reveals diverse tick-borne bacteria, protozoans and viruses in ticks and wildlife from Australia. <i>Transboundary and Emerging Diseases</i> , 2022, 69, .	3.0	9
5530	Full Issue PDF. <i>Molecular Plant-Microbe Interactions</i> , 2022, 35, 368-438.	2.6	0
5531	The Virome of Healthy Honey Bee Colonies: Ubiquitous Occurrence of Known and New Viruses in Bee Populations. <i>MSystems</i> , 2022, 7, e0007222.	3.8	7
5532	Diet and Host Genetics Drive the Bacterial and Fungal Intestinal Metatranscriptome of Gilthead Sea Bream. <i>Frontiers in Microbiology</i> , 2022, 13, .	3.5	12
5533	Genome-Wide Identification and Evolution Analysis of the Gibberellin Oxidase Gene Family in Six Gramineae Crops. <i>Genes</i> , 2022, 13, 863.	2.4	9
5534	A neural network-based framework to understand the type 2 diabetes-related alteration of the human gut microbiome. , 2022, 1, .		5
5535	Microbially promoted calcite precipitation in the pelagic redoxcline: Elucidating the formation of the turbid layer. <i>Geobiology</i> , 2022, 20, 498-517.	2.4	5
5536	Discovery of lignin-transforming bacteria and enzymes in thermophilic environments using stable isotope probing. <i>ISME Journal</i> , 2022, 16, 1944-1956.	9.8	16
5537	Host-Associated Phages Disperse across the Extraterrestrial Analogue Antarctica. <i>Applied and Environmental Microbiology</i> , 2022, 88, e0031522.	3.1	7
5538	Marine Sponge Endosymbionts: Structural and Functional Specificity of the Microbiome within <i>Eurypongia arenaria</i> Cells. <i>Microbiology Spectrum</i> , 2022, 10, e0229621.	3.0	5
5539	Integrated transcriptome and endogenous hormone analysis provides new insights into callus proliferation in <i>Osmanthus fragrans</i> . <i>Scientific Reports</i> , 2022, 12, 7609.	3.3	5
5540	Inferring antibiotic susceptibility from metagenomic data: dream or reality?. <i>Clinical Microbiology and Infection</i> , 2022, 28, 1225-1229.	6.0	3

#	ARTICLE	IF	CITATIONS
5541	VirHunter: A Deep Learning-Based Method for Detection of Novel RNA Viruses in Plant Sequencing Data. <i>Frontiers in Bioinformatics</i> , 2022, 2, .	2.1	11
5542	The potential for bacteria from carbon-limited deep terrestrial environments to participate in chlorine cycling. <i>FEMS Microbiology Ecology</i> , 2022, 98, .	2.7	3
5543	Evolution, Expression Patterns, and Distribution of Novel Ribbon Worm Predatory and Defensive Toxins. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	8
5544	Comparative Genomics Unveils the Habitat Adaptation and Metabolic Profiles of <i>Clostridium</i> in an Artificial Ecosystem for Liquor Production. <i>MSystems</i> , 2022, 7, e0029722.	3.8	13
5545	Physiological Effects and Transcriptomic Analysis of sbGnRH on the Liver in Pompano (<i>Trachinotus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	3.5	4
5546	Genetic and Epigenetic Differentiation Across Intertidal Gradients in the Foundation Plant <i>Spartina alterniflora</i> . <i>Frontiers in Ecology and Evolution</i> , 2022, 10, .	2.2	2
5547	Systematic Comparison of Nanopore and Illumina Sequencing for the Detection of Plant Viruses and Viroids Using Total RNA Sequencing Approach. <i>Frontiers in Microbiology</i> , 2022, 13, .	3.5	14
5548	Daily patterns in parasite processes: diel variation in fish louse transcriptomes. <i>International Journal for Parasitology</i> , 2022, 52, 509-518.	3.1	1
5549	The Relationship Between Gut Microbiome and Bile Acids in Primates With Diverse Diets. <i>Frontiers in Microbiology</i> , 2022, 13, .	3.5	3
5550	Active assimilators of soluble microbial products produced by wastewater anammox bacteria and their roles revealed by DNA-SIP coupled to metagenomics. <i>Environment International</i> , 2022, 164, 107265.	10.0	23
5551	Sustainability assessment of topsoil ecology in Chongqing, China based on the application of livestock and poultry manure. <i>Journal of Cleaner Production</i> , 2022, 358, 131969.	9.3	16
5552	Metagenomic assembly reveals the circadian oscillations of the microbiome and antibiotic resistance genes in a model of laying hens. <i>Science of the Total Environment</i> , 2022, 836, 155692.	8.0	4
5553	Description of mitochon genome and phylogenetic considerations of <i>Sabethes bipartipes</i> , <i>Sabethes cyaneus</i> , <i>Sabethes quasicyaneus</i> , and <i>Sabethes tarsopus</i> (Diptera: Culicidae). <i>Acta Tropica</i> , 2022, 232, 106493.	2.0	2
5554	Weighted gene Co-expression network analysis (WGCNA) reveals a set of hub genes related to chlorophyll metabolism process in chlorella (<i>Chlorella vulgaris</i>) response androstenedione. <i>Environmental Pollution</i> , 2022, 306, 119360.	7.5	9
5555	Single-cell metagenomics and metagenomics approaches reveal extracellular electron transfer of psychrophilic electroactive biofilms. <i>Science of the Total Environment</i> , 2022, 836, 155606.	8.0	4
5556	Multi-omics analysis reveals the influence of tetracycline on the growth of ryegrass root. <i>Journal of Hazardous Materials</i> , 2022, 435, 129019.	12.4	10
5557	Dynamic patterns of quorum sensing signals in phycospheric microbes during a marine algal bloom. <i>Environmental Research</i> , 2022, 212, 113443.	7.5	13
5558	Comparative transcriptome profiling of high and low oil yielding <i>Santalum album</i> L. <i>PLoS ONE</i> , 2022, 17, e0252173.	2.5	0

#	ARTICLE	IF	CITATIONS
5559	Deep insights into the anaerobic co-digestion of waste activated sludge with concentrated leachate under different salinity stresses. <i>Science of the Total Environment</i> , 2022, 838, 155922.	8.0	20
5560	Identification and genome characterization of novel parechovirus sequences from <i>Hipposideros armiger</i> in China. <i>Virology Journal</i> , 2022, 19, 80.	3.4	0
5561	Tracing RNA viruses associated with Nudibranchia gastropods. <i>PeerJ</i> , 2022, 10, e13410.	2.0	4
5562	Transcriptomic response of intertidal brittle star <i>Ophiothrix exigua</i> to seasonal variation. <i>Marine Genomics</i> , 2022, 64, 100957.	1.1	4
5563	Description of the mitogenome and phylogeny of <i>Aedes</i> spp. (Diptera: Culicidae) from the Amazon region. <i>Acta Tropica</i> , 2022, 232, 106500.	2.0	2
5564	Insights into Prokaryotic Community and Its Potential Functions in Nitrogen Metabolism in the Bay of Bengal, a Pronounced Oxygen Minimum Zone. <i>Microbiology Spectrum</i> , 2022, 10, e0089221.	3.0	9
5565	Appraisal of cytotoxicity and acrylamide mitigation potential of L-asparaginase SlpA from fish gut microbiome. <i>Applied Microbiology and Biotechnology</i> , 2022, 106, 3583-3598.	3.6	1
5566	Comparative transcriptomics of drought stress response of taproot meristem region of contrasting purple carrot breeding lines supported by physio-biochemical parameters. <i>Functional and Integrative Genomics</i> , 2022, 22, 697-710.	3.5	2
5567	Genome-wide DNA methylation and gene expression patterns of androgenetic haploid tiger pufferfish (<i>Takifugu rubripes</i>) provide insights into haploid syndrome. <i>Scientific Reports</i> , 2022, 12, 8252.	3.3	1
5568	AMR-meta: a k-mer and metafeature approach to classify antimicrobial resistance from high-throughput short-read metagenomics data. <i>GigaScience</i> , 2022, 11, .	6.4	8
5569	Giant Starship Elements Mobilize Accessory Genes in Fungal Genomes. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	39
5570	Bee foraging preferences, microbiota and pathogens revealed by direct shotgun metagenomics of honey. <i>Molecular Ecology Resources</i> , 2022, 22, 2506-2523.	4.8	6
5571	The Isolation and Characterization of Rare Mycobiome Associated With Spacecraft Assembly Cleanrooms. <i>Frontiers in Microbiology</i> , 2022, 13, 777133.	3.5	7
5572	A Deep Embedded Clustering Algorithm for the Binning of Metagenomic Sequences. <i>IEEE Access</i> , 2022, 10, 54348-54357.	4.2	5
5580	Gene Co-expression Network and Regression Analysis Identify the Transcriptomic, Physiological, and Biochemical Indicators of the Response of Alpine Woody Plant <i>Rhododendron rex</i> to Drought Stress. <i>Frontiers in Plant Science</i> , 2022, 13, .	3.6	2
5581	A catalog of 48,425 nonredundant viruses from oral metagenomes expands the horizon of the human oral virome. <i>IScience</i> , 2022, 25, 104418.	4.1	20
5582	From head to rootlet: comparative transcriptomic analysis of a rhizocephalan barnacle <i>Peltogaster reticulata</i> (Crustacea: Rhizocephala). <i>F1000Research</i> , 0, 11, 583.	1.6	4
5583	Effects of <i>Spartina alterniflora</i> Invasion on Nitrogen Fixation and Phosphorus Solubilization in a Subtropical Marine Mangrove Ecosystem. <i>Microbiology Spectrum</i> , 2022, 10, .	3.0	9

#	ARTICLE	IF	CITATIONS
5585	Exploration of the metabolic flexibility of glycogen accumulating organisms through metatranscriptome analysis and metabolic characterization. Journal of Environmental Sciences, 2023, 126, 234-248.	6.1	4
5586	Metagenomic Analysis Reveals a Mitigating Role for <i>Lactobacillus paracasei</i> and <i>Bifidobacterium animalis</i> in Experimental Periodontitis. Nutrients, 2022, 14, 2125.	4.1	10
5587	Nodules of wild legumes as unique natural hotspots of antibiotic resistance genes. Science of the Total Environment, 2022, 839, 156036.	8.0	1
5588	Viral communities in the parasite <i>Varroa destructor</i> and in colonies of their honey bee host (<i>Apis mellifera</i>). Tj ETQq1 1 0.784314 rgBT /Overlock 12	3.3	12
5589	Global landscape of gut microbiome diversity and antibiotic resistomes across vertebrates. Science of the Total Environment, 2022, 838, 156178.	8.0	10
5590	The functional evolution of termite gut microbiota. Microbiome, 2022, 10, .	11.1	35
5591	Antibiotic-producing Micrococcales govern the microbiome that inhabits the fur of two-toed sloths. Environmental Microbiology, 2022, 24, 3148-3163.	3.8	3
5594	Isolation and Genome Analysis of an Amoeba-Associated Bacterium <i>Dyella terrae</i> Strain Ely Copper Mine From Acid Rock Drainage in Vermont, United States. Frontiers in Microbiology, 2022, 13, .	3.5	1
5595	Triobinned genomes of the woodrats <i>Neotoma bryanti</i> and <i>Neotoma lepida</i> reveal novel gene islands and rapid copy number evolution of xenobiotic metabolizing genes. Molecular Ecology Resources, 2022, 22, 2713-2731.	4.8	13
5596	Genome of the lepidopleurid chiton <i>Hanleya hanleyi</i> (Mollusca, Polyplacophora). F1000Research, 0, 11, 555.	1.6	4
5597	Profiles of antibiotic- and heavy metal-related resistance genes in animal manure revealed using a metagenomic analysis. Ecotoxicology and Environmental Safety, 2022, 239, 113655.	6.0	21
5598	Community reassemblies of eukaryotes, prokaryotes, and viruses in the hexabromocyclododecanes-contaminated microcosms. Journal of Hazardous Materials, 2022, 436, 129159.	12.4	3
5599	Genome-Wide Identification and Functional Analysis of the Gasa Gene Family Responding to Multiple Stressors in <i>Canavalia Rosea</i> . SSRN Electronic Journal, 0, , .	0.4	2
5600	Plant pathogens provide clues to the potential origin of bat white-nose syndrome <i>Pseudogymnoascus destructans</i> . Virulence, 2022, 13, 1020-1031.	4.4	6
5601	Biological Characteristics of Infectious Laryngotracheitis Viruses Isolated in China. Viruses, 2022, 14, 1200.	3.3	3
5602	A chromosome-level genome assembly of the pollinating fig wasp <i>Valisia javana</i> . DNA Research, 2022, 29, .	3.4	3
5603	ROCKER Models for Reliable Detection and Typing of Short-Read Sequences Carrying Î²-Lactamase Genes. MSystems, 2022, 7, .	3.8	1
5604	Transcriptome Mining Expands Knowledge of RNA Viruses across the Plant Kingdom. Journal of Virology, 2022, 96, .	3.4	32

#	ARTICLE	IF	CITATIONS
5605	Whole-Genome Sequencing and Analysis of the White-Rot Fungus <i>Ceriporia lacerata</i> Reveals Its Phylogenetic Status and the Genetic Basis of Lignocellulose Degradation and Terpenoid Synthesis. <i>Frontiers in Microbiology</i> , 2022, 13, .	3.5	4
5606	Perception of a conserved family of plant signalling peptides by the receptor kinase HSL3. <i>ELife</i> , 0, 11, .	6.0	20
5607	De novo transcriptome assembly of the cotyledon of <i>Camellia oleifera</i> for discovery of genes regulating seed germination. <i>BMC Plant Biology</i> , 2022, 22, .	3.6	6
5608	Metagenomic mining of Indian river confluence reveal functional microbial community with lignocellulolytic potential. <i>3 Biotech</i> , 2022, 12, .	2.2	1
5610	Unearthing Shifts in Microbial Communities Across a Soil Disturbance Gradient. <i>Frontiers in Microbiology</i> , 2022, 13, .	3.5	3
5611	Massive Heat Shock Protein 70 Genes Expansion and Transcriptional Signatures Uncover Hard Clam Adaptations to Heat and Hypoxia. <i>Frontiers in Marine Science</i> , 2022, 9, .	2.5	10
5613	Community structure and function of microbiomes in polluted stretches of river Yamuna in New Delhi, India, using shotgun metagenomics. <i>Environmental Science and Pollution Research</i> , 2022, 29, 71311-71325.	5.3	12
5614	Comparative Analyses of Antibiotic Resistance Genes in Jejunal Microbiota of Pigs in Different Areas. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, .	3.9	1
5615	Time-series transcriptomic screening of factors contributing to the cross-tolerance to UV radiation and anhydrobiosis in tardigrades. <i>BMC Genomics</i> , 2022, 23, .	2.8	7
5616	A global analysis of alternative splicing of <i>Dichocarpum</i> medicinal plants, Ranunculales. <i>Current Genomics</i> , 2022, 23, .	1.6	0
5617	Myriapod genomes reveal ancestral horizontal gene transfer and hormonal gene loss in millipedes. <i>Nature Communications</i> , 2022, 13, .	12.8	12
5620	Lysophosphatidylserines derived from microbiota in Crohn's disease elicit pathological Th1 response. <i>Journal of Experimental Medicine</i> , 2022, 219, .	8.5	12
5625	<i>Sphingomonas</i> Relies on Chemotaxis to Degrade Polycyclic Aromatic Hydrocarbons and Maintain Dominance in Coking Sites. <i>Microorganisms</i> , 2022, 10, 1109.	3.6	16
5626	Genomic insights into evolution and control of <i>Wohlfahrtia magnifica</i> , a widely distributed myiasis-causing fly of warm-blooded vertebrates. <i>Molecular Ecology Resources</i> , 2022, 22, 2744-2757.	4.8	4
5628	Bioelectrochemically assisting anaerobic digestion enhanced methane production under low-temperature. <i>Renewable Energy</i> , 2022, 194, 1071-1083.	8.9	6
5629	Evolutionary targets of gene expression divergence in a complex of closely related pine species. <i>Journal of Systematics and Evolution</i> , 2023, 61, 198-212.	3.1	1
5630	Early life microbial exposures shape the <i>Crassostrea gigas</i> immune system for lifelong and intergenerational disease protection. <i>Microbiome</i> , 2022, 10, .	11.1	24
5632	Flexible protein database based on amino acid k-mers. <i>Scientific Reports</i> , 2022, 12, .	3.3	4

#	ARTICLE	IF	CITATIONS
5633	Analysis of Gut Microbiota Signature and Microbe-Disease Progression Associations in Locally Advanced Non-Small Cell Lung Cancer Patients Treated With Concurrent Chemoradiotherapy. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, .	3.9	5
5634	Genome of <i>Malassezia arunalokei</i> and Its Distribution on Facial Skin. <i>Microbiology Spectrum</i> , 2022, 10, .	3.0	7
5635	HT-ARGfinder: A Comprehensive Pipeline for Identifying Horizontally Transferred Antibiotic Resistance Genes and Directionality in Metagenomic Sequencing Data. <i>Frontiers in Environmental Science</i> , 2022, 10, .	3.3	2
5636	Expressions of resistome is linked to the key functions and stability of active rumen microbiome. <i>Animal Microbiome</i> , 2022, 4, .	3.8	7
5637	The plant rhizosphere "root niche is an edaphic "mini-oasis" in hyperarid deserts with enhanced microbial competition. <i>ISME Communications</i> , 2022, 2, .	4.2	18
5638	Genome Sequencing of <i>Amomum tsao-ko</i> Provides Novel Insight Into Its Volatile Component Biosynthesis. <i>Frontiers in Plant Science</i> , 2022, 13, .	3.6	1
5639	Longitudinal Evaluation of Gut Bacteriomes and Viromes after Fecal Microbiota Transplantation for Eradication of Carbapenem-Resistant <i>Enterobacteriaceae</i> . <i>MSystems</i> , 2022, 7, .	3.8	5
5640	Environmental factors influence yak milk composition by modulating short-chain fatty acid metabolism in intestinal microorganisms. <i>LWT - Food Science and Technology</i> , 2022, 163, 113608.	5.2	3
5641	Genome sequencing and evolutionary analysis of a new endophytic <i>Trichoderma</i> species isolated from orchid roots with reduced repertoire of protein-coding genes. <i>Mycological Progress</i> , 2022, 21, .	1.4	0
5642	Performance Characteristics of Next-Generation Sequencing for the Detection of Antimicrobial Resistance Determinants in <i>Escherichia coli</i> Genomes and Metagenomes. <i>MSystems</i> , 2022, 7, .	3.8	5
5643	Microbial and genes diversity analysis: Relationship between starch conversion and carbohydrate metabolism during Niandoubao fermentation via the glutinous proso millet (GPM) process. <i>Food Control</i> , 2022, 140, 109154.	5.5	4
5644	Invasive earthworms alter forest soil microbiomes and nitrogen cycling. <i>Soil Biology and Biochemistry</i> , 2022, 171, 108724.	8.8	11
5645	Extreme freeze-tolerance in cryophilic tardigrades relies on controlled ice formation but does not involve significant change in transcription. <i>Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology</i> , 2022, 271, 111245.	1.8	8
5646	Tobacco straw biochar improved the growth of Chinese cherry (<i>Prunus pseudocerasus</i>) via altering plant physiology and shifting the rhizosphere bacterial community. <i>Scientia Horticulturae</i> , 2022, 303, 111244.	3.6	7
5647	Comparative transcriptome analysis reveals the molecular mechanism underlying lily double flowering. <i>Scientia Horticulturae</i> , 2022, 303, 111221.	3.6	1
5649	PON-All: Amino Acid Substitution Tolerance Predictor for All Organisms. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	3.5	7
5651	Influence of Tire Wear Particle Input on Water Purification Efficiency of Bioretention System. <i>SSRN Electronic Journal</i> , 0, .	0.4	0
5653	Metagenomic and Metabolomic Insights Into the Mechanism Underlying the Disparity in Milk Yield of Holstein Cows. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	3

#	ARTICLE	IF	CITATIONS
5654	The Gut Microbiota Composition of <i>Cnaphalocrocis medinalis</i> and Their Predicted Contribution to Larval Nutrition. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	3
5655	Mechanisms of Pine Disease Susceptibility Under Experimental Climate Change. <i>Frontiers in Forests and Global Change</i> , 0, 5, .	2.3	3
5656	Old genes in new places: A taxon-rich analysis of interdomain lateral gene transfer events. <i>PLoS Genetics</i> , 2022, 18, e1010239.	3.5	6
5657	Structured Framework and Genome Analysis of <i>Magnaporthe grisea</i> Inciting Pearl Millet Blast Disease Reveals Versatile Metabolic Pathways, Protein Families, and Virulence Factors. <i>Journal of Fungi (Basel, Tj ETQq1 1 0 3784314 rgBT /Overl</i>		
5658	Reference nodule transcriptomes for <i>Melilotus officinalis</i> and <i>Medicago sativa</i> cv. Algonquin. <i>Plant Direct</i> , 2022, 6, .	1.9	4
5660	Dynamic metabolic interactions and trophic roles of human gut microbes identified using a minimal microbiome exhibiting ecological properties. <i>ISME Journal</i> , 2022, 16, 2144-2159.	9.8	16
5662	Metabolic pathways of CO ₂ fixing microorganisms determined C-fixation rates in grassland soils along the precipitation gradient. <i>Soil Biology and Biochemistry</i> , 2022, 172, 108764.	8.8	18
5663	Metagenomic analysis of the gut microbiota in piglets either challenged or not with enterotoxigenic <i>Escherichia coli</i> reveals beneficial effects of probiotics on microbiome composition, resistome, digestive function and oxidative stress responses. <i>PLoS ONE</i> , 2022, 17, e0269959.	2.5	7
5664	Molecular basis of intraspecific differentiation for heavy metal tolerance in the copper moss <i>Scopelophila cataractae</i> . <i>Environmental and Experimental Botany</i> , 2022, 201, 104970.	4.2	4
5665	Alaskan palaeosols in modern times: Deciphering unique microbial diversity within the late-Holocene. <i>Holocene</i> , 0, , 095968362211012.	1.7	0
5666	The evolution of multi-gene families and metabolic pathways in the evening primroses (<i>Oenothera</i>): Tj ETQq0 0 0 rgBT /Overl	2.5	3
5667	Transcriptome Profiling of the Leaf Spot Pathogen, <i>Pestalotiopsis trachicarpicola</i> , and Its Host, Tea (<i>Camellia sinensis</i>), During Infection. <i>Plant Disease</i> , 2022, 106, 2247-2252.	1.4	4
5669	A metagenomic portrait of the microbial community responsible for two decades of bioremediation of poly-contaminated groundwater. <i>Water Research</i> , 2022, 221, 118767.	11.3	11
5670	Comparative Single-Cell Transcriptomics Reveals Novel Genes Involved in Bivalve Embryonic Shell Formation and Questions Ontogenetic Homology of Molluscan Shell Types. <i>Frontiers in Cell and Developmental Biology</i> , 0, 10, .	3.7	7
5671	A phylogenetic and proteomic reconstruction of eukaryotic chromatin evolution. <i>Nature Ecology and Evolution</i> , 2022, 6, 1007-1023.	7.8	26
5672	A high-quality de novo genome assembly based on nanopore sequencing of a wild-caught coconut rhinoceros beetle (<i>Oryctes rhinoceros</i>). <i>BMC Genomics</i> , 2022, 23, .	2.8	6
5673	Identification of diverse viruses associated with grasshoppers unveils the parallel relationship between host phylogeny and virome composition. <i>Virus Evolution</i> , 2022, 8, .	4.9	5
5675	Islet autoantibody seroconversion in type-1 diabetes is associated with metagenome-assembled genomes in infant gut microbiomes. <i>Nature Communications</i> , 2022, 13, .	12.8	8

#	ARTICLE	IF	CITATIONS
5676	Nanopore sequencing of a monkeypox virus strain isolated from a pustular lesion in the Central African Republic. <i>Scientific Reports</i> , 2022, 12, .	3.3	42
5677	Detection of <i>Salmonella enterica</i> serovar Montevideo in food products using specific PCR primers developed by comparative genomics. <i>LWT - Food Science and Technology</i> , 2022, 165, 113677.	5.2	5
5678	Wild and Captive Environments Drive the Convergence of Gut Microbiota and Impact Health in Threatened Equids. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	4
5679	Gut microbiota alternation under the intestinal epithelium-specific knockout of mouse Piga gene. <i>Scientific Reports</i> , 2022, 12, .	3.3	3
5680	Ecology of <i>Methanonatronarchaeia</i> . <i>Environmental Microbiology</i> , 2022, 24, 5217-5229.	3.8	5
5681	PIMGAVir and Vir-MinION: Two Viral Metagenomic Pipelines for Complete Baseline Analysis of 2nd and 3rd Generation Data. <i>Viruses</i> , 2022, 14, 1260.	3.3	3
5682	Global, highly specific and fast filtering of alignment seeds. <i>BMC Bioinformatics</i> , 2022, 23, .	2.6	1
5683	SeqScreen: accurate and sensitive functional screening of pathogenic sequences via ensemble learning. <i>Genome Biology</i> , 2022, 23, .	8.8	13
5684	Complete genome sequence of the <i>Pogostemon cablin</i> bacterial wilt pathogen <i>Ralstonia solanacearum</i> strain SY1. <i>Genes and Genomics</i> , 0, , .	1.4	1
5685	Genetic and genomic architecture of species-specific cuticular hydrocarbon variation in parasitoid wasps. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2022, 289, .	2.6	3
5686	Functional and phylogenetic analyses of camel rumen microbiota associated with different lignocellulosic substrates. <i>Npj Biofilms and Microbiomes</i> , 2022, 8, .	6.4	15
5687	Global leaf and root transcriptome in response to cadmium reveals tolerance mechanisms in <i>Arundo donax</i> L. <i>BMC Genomics</i> , 2022, 23, .	2.8	7
5689	Transcriptome of the synganglion in the tick <i>Ixodes ricinus</i> and evolution of the cys-loop ligand-gated ion channel family in ticks. <i>BMC Genomics</i> , 2022, 23, .	2.8	4
5690	Global and seasonal variation of marine phosphonate metabolism. <i>ISME Journal</i> , 2022, 16, 2198-2212.	9.8	22
5691	<i>Sedimentimonas flavescens</i> gen. nov., sp. nov., isolated from sediment of Clam Island, Liaoning Province. <i>Antonie Van Leeuwenhoek</i> , 0, , .	1.7	0
5692	Globally distributed mining-impacted environments are underexplored hotspots of multidrug resistance genes. <i>ISME Journal</i> , 2022, 16, 2099-2113.	9.8	35
5693	Robust variation in infant gut microbiome assembly across a spectrum of lifestyles. <i>Science</i> , 2022, 376, 1220-1223.	12.6	63
5694	DeepPhageTP: a convolutional neural network framework for identifying phage-specific proteins from metagenomic sequencing data. <i>PeerJ</i> , 0, 10, e13404.	2.0	3

#	ARTICLE	IF	CITATIONS
5696	Obligate sexual reproduction of a homothallic fungus closely related to the <i>Cryptococcus</i> pathogenic species complex. <i>ELife</i> , 0, 11, .	6.0	4
5697	Environmental and Anthropogenic Factors Shape the Snow Microbiome and Antibiotic Resistome. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	4
5698	Detection of Ancient Viruses and Long-Term Viral Evolution. <i>Viruses</i> , 2022, 14, 1336.	3.3	8
5699	Effects of 5-azaC on Iridoid Glycoside Accumulation and DNA Methylation in <i>Rehmannia glutinosa</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	0
5700	Substrate complexity affects the prevalence and interconnections of antibiotic, metal and biocide resistance genes, integron-integrase genes, human pathogens and virulence factors in anaerobic digestion. <i>Journal of Hazardous Materials</i> , 2022, 438, 129441.	12.4	5
5701	Spatial Patterns and Composition Traits of Soil Microbial Nitrogen-Metabolism Genes in the <i>Robinia pseudoacacia</i> Forests at a Regional Scale. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	2
5702	Narrow-Headed Voles Species Complex (Cricetidae, Rodentia): Evidence for Species Differentiation Inferred from Transcriptome Data. <i>Diversity</i> , 2022, 14, 512.	1.7	2
5704	Genome-Scale Mutational Analysis of Cathode-Oxidizing <i>Thioclava electrotropha</i> ELOx9T. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	0
5705	Gut virome profiling identifies a widespread bacteriophage family associated with metabolic syndrome. <i>Nature Communications</i> , 2022, 13, .	12.8	32
5706	Transcriptome and Metabonomics Combined Analysis Revealed the Defense Mechanism Involved in Hydrogen-Rich Water-Regulated Cold Stress Response of <i>Tetrastigma hemsleyanum</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	4
5707	Genome sequence for the blue-flowered Andean shrub <i>Lochroma cyaneum</i> reveals extensive discordance across the berry clade of Solanaceae. <i>Plant Genome</i> , 2022, 15, .	2.8	2
5708	Combined read- and assembly-based metagenomics to reconstruct a <i>Dehalococcoides mccartyi</i> genome from PCB-contaminated sediments and evaluate functional differences among organohalide-respiring consortia in the presence of different halogenated contaminants. <i>FEMS Microbiology Ecology</i> , 2022, 98, .	2.7	3
5711	Application of Next Generation Sequencing on Norovirus-contaminated oyster samples. <i>EFSA Supporting Publications</i> , 2022, 19, .	0.7	5
5712	The Machine-Learning-Mediated Interface of Microbiome and Genetic Risk Stratification in Neuroblastoma Reveals Molecular Pathways Related to Patient Survival. <i>Cancers</i> , 2022, 14, 2874.	3.7	4
5713	Resolving deep evolutionary relationships within the RNA virus phylum <i>Lenarviricota</i> . <i>Virus Evolution</i> , 2022, 8, .	4.9	11
5714	Transcript Complexity and New Insights of Restorer Line in CMS-D8 Cotton Through Full-Length Transcriptomic Analysis. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	1
5715	Metatranscriptomic Comparison of Viromes in Endemic and Introduced Passerines in New Zealand. <i>Viruses</i> , 2022, 14, 1364.	3.3	9
5716	De novo transcriptome assembly and annotation of the third stage larvae of the zoonotic parasite <i>Anisakis pegreffii</i> . <i>BMC Research Notes</i> , 2022, 15, .	1.4	4

#	ARTICLE	IF	CITATIONS
5717	<i>Candidatus</i> Nitrosopolaris, a genus of putative ammonia-oxidizing archaea with a polar/alpine distribution. FEMS Microbes, 2022, 3, .	2.1	10
5718	Improvement of eukaryotic protein predictions from soil metagenomes. Scientific Data, 2022, 9, .	5.3	1
5719	Co-Expression Analysis Reveals Differential Expression of Homologous Genes Associated with Specific Terpenoid Biosynthesis in Rehmannia glutinosa. Genes, 2022, 13, 1092.	2.4	3
5720	Growth rate determines prokaryote-provirus network modulated by temperature and host genetic traits. Microbiome, 2022, 10, .	11.1	0
5721	Introduction to the principles and methods underlying the recovery of metagenome-assembled genomes from metagenomic data. MicrobiologyOpen, 2022, 11, .	3.0	8
5722	Differentiated Evolutionary Strategies of Genetic Diversification in Atlantic and Pacific Thaumarchaeal Populations. MSystems, 2022, 7, .	3.8	3
5723	Genetic and transcriptomic dissection of an artificially induced paired spikelets mutant of wheat (Triticum aestivum L.). Theoretical and Applied Genetics, 2022, 135, 2543-2554.	3.6	4
5724	Gut virome dysbiosis following focal cerebral ischemia in mice. Journal of Cerebral Blood Flow and Metabolism, 2022, 42, 1597-1602.	4.3	4
5725	Transcriptomic and proteomic profiling of peptidase expression in Fasciola hepatica eggs developing at host's body temperature. Scientific Reports, 2022, 12, .	3.3	4
5726	Recovery of High Quality Metagenome-Assembled Genomes From Full-Scale Activated Sludge Microbial Communities in a Tropical Climate Using Longitudinal Metagenome Sampling. Frontiers in Microbiology, 0, 13, .	3.5	8
5728	Key aspects of the past 30 Years of protein design. Reports on Progress in Physics, 0, , .	20.1	2
5729	Genome evolution and diversity of wild and cultivated potatoes. Nature, 2022, 606, 535-541.	27.8	125
5730	Long-Read Metagenomics Improves the Recovery of Viral Diversity from Complex Natural Marine Samples. MSystems, 2022, 7, .	3.8	11
5731	Comparative metagenomics reveals expanded insights into intra- and interspecific variation among wild bee microbiomes. Communications Biology, 2022, 5, .	4.4	12
5732	Biosynthetic potential of the global ocean microbiome. Nature, 2022, 607, 111-118.	27.8	128
5733	Distinct gut microbiota and health outcomes in asymptomatic infection, viral nucleic acid test re-positive, and convalescent COVID-19 cases. , 0, , .		3
5734	A Transcriptomic Atlas Underlying Developmental Plasticity of Seasonal Forms of <i>Bicyclus anynana</i> Butterflies. Molecular Biology and Evolution, 2022, 39, .	8.9	9
5735	Taxonomic profiling and functional gene annotation of microbial communities in sediment of river Ganga at Kanpur, India: insights from whole-genome metagenomics study. Environmental Science and Pollution Research, 2022, 29, 82309-82323.	5.3	15

#	ARTICLE	IF	CITATIONS
5736	Integrated metabolomic and transcriptomic analysis reveals variation in the metabolites and genes of <i>Platycodon grandiflorus</i> roots from different regions. <i>Phytochemical Analysis</i> , 2022, 33, 982-994.	2.4	3
5737	Evolutionary Divergence of <i>Marinobacter</i> Strains in Cryopeg Brines as Revealed by Pangenomics. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	6
5738	Reduction of microbial diversity in grassland soil is driven by long-term climate warming. <i>Nature Microbiology</i> , 2022, 7, 1054-1062.	13.3	86
5739	The Chromosome-Scale Assembly of the <i>Curcuma alismatifolia</i> Genome Provides Insight Into Anthocyanin and Terpenoid Biosynthesis. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	4
5740	Mycoviroomic Analysis Unveils Complex Virus Composition in a Hypovirulent Strain of <i>Sclerotinia sclerotiorum</i> . <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 649.	3.5	5
5741	Draft Genome Sequences of Five <i>Cystobasidium ongulense</i> Strains Isolated from Areas near Syowa Station, East Antarctica. <i>Microbiology Resource Announcements</i> , 2022, 11, .	0.6	4
5742	Another lesson from unmapped reads: in-depth analysis of RNA-Seq reads from various horse tissues. <i>Journal of Applied Genetics</i> , 2022, 63, 571-581.	1.9	2
5743	Composition and Ecological Roles of the Core Microbiome along the Abyssal-Hadal Transition Zone Sediments of the Mariana Trench. <i>Microbiology Spectrum</i> , 2022, 10, .	3.0	11
5744	Comparative Analysis of Microbiome Metagenomics in Reintroduced Wild Horses and Resident Asiatic Wild Asses in the Gobi Desert Steppe. <i>Microorganisms</i> , 2022, 10, 1166.	3.6	2
5746	Anthropogenic impacts on antibiotic resistance genes and their hosts from pristine to urban river using metagenomic and binning approaches. <i>Aquatic Toxicology</i> , 2022, 249, 106221.	4.0	13
5747	Metagenomic analysis of the abundances, diversity, and distribution of antibiotic resistance genes and their potential bacterial hosts in two types of shrimp-rearing farms in South China. <i>Ecotoxicology and Environmental Safety</i> , 2022, 241, 113801.	6.0	6
5748	Genome analysis uncovers the prolific antagonistic and plant growth-promoting potential of endophyte <i>Bacillus velezensis</i> K1. <i>Gene</i> , 2022, 836, 146671.	2.2	15
5749	Differential responses of bloom-forming <i>Ulva intestinalis</i> and economically important <i>Gracilariopsis lemaneiformis</i> to marine heatwaves under changing nitrate conditions. <i>Science of the Total Environment</i> , 2022, 840, 156591.	8.0	13
5750	A phylotranscriptome study using silica gel-dried leaf tissues produces an updated robust phylogeny of Ranunculaceae. <i>Molecular Phylogenetics and Evolution</i> , 2022, 174, 107545.	2.7	10
5751	Metagenomic assembly and binning analyses the prevalence and spread of antibiotic resistome in water and fish gut microbiomes along an environmental gradient. <i>Journal of Environmental Management</i> , 2022, 318, 115521.	7.8	13
5752	Insights into microbial contamination in multi-type manure-amended soils: The profile of human bacterial pathogens, virulence factor genes and antibiotic resistance genes. <i>Journal of Hazardous Materials</i> , 2022, 437, 129356.	12.4	34
5753	Fertilizing-induced changes in the nitrifying microbiota associated with soil nitrification and crop yield. <i>Science of the Total Environment</i> , 2022, 841, 156752.	8.0	12
5754	Renewable nitrogen-containing products by Maillard reaction of sewage sludge and glucose. Part I. Analysis of nitrogen composition and protein model based on AlphaFold2. <i>Fuel</i> , 2022, 325, 124968.	6.4	4

#	ARTICLE	IF	CITATIONS
5755	Comparative Genomics Reveals that Metabolism Underlies Evolution of Entomopathogenicity in Bee-Loving <i>Ascosphaera</i> Spp. Fungi. SSRN Electronic Journal, 0, , .	0.4	0
5759	Chromosome-level genome assembly and annotation of the native Chinese wild blueberry <i>Vaccinium bracteatum</i>. Fruit Research, 2022, 2, 1-14.	2.0	5
5760	Proteotranscriptomics “A facilitator in omics research. Computational and Structural Biotechnology Journal, 2022, 20, 3667-3675.	4.1	4
5761	Research progress of reduced amino acid alphabets in protein analysis and prediction. Computational and Structural Biotechnology Journal, 2022, 20, 3503-3510.	4.1	7
5762	A chromosome-level genome assembly and intestinal transcriptome of <i>Trypoxylus dichotomus</i> (Coleoptera: Scarabaeidae) to understand its lignocellulose digestion ability. GigaScience, 2022, 11, .	6.4	5
5763	Chromosome-level genome assembly of<i>Plazaster borealis</i> sheds light on the morphogenesis of multiarmed starfish and its regenerative capacity. GigaScience, 2022, 11, .	6.4	6
5764	Chromosome-level assembly and annotation of the blue catfish<i>Ictalurus furcatus</i>, an aquaculture species for hybrid catfish reproduction, epigenetics, and heterosis studies. GigaScience, 2022, 11, .	6.4	8
5765	Applying Synteny Networks (SynNet) to Study Genomic Arrangements of Protein-Coding Genes in Plants. Methods in Molecular Biology, 2022, , 199-215.	0.9	2
5766	Plasma Virome Reveals Blooms and Transmission of Anellovirus in Intravenous Drug Users with HIV-1, HCV, and/or HBV Infections. Microbiology Spectrum, 2022, 10, .	3.0	7
5767	Characterization of a new L-carnosine synthase mined from deep-sea sediment metagenome. Microbial Cell Factories, 2022, 21, .	4.0	2
5768	Insights into plastic biodegradation: community composition and functional capabilities of the superworm (<i>Zophobas morio</i>) microbiome in styrofoam feeding trials. Microbial Genomics, 2022, 8, .	2.0	11
5769	Accurate identification of bacteriophages from metagenomic data using Transformer. Briefings in Bioinformatics, 2022, 23, .	6.5	14
5770	Transcriptomic evidence for visual adaptation during the aquatic to terrestrial metamorphosis in leopard frogs. BMC Biology, 2022, 20, .	3.8	7
5771	In-depth characterization of denitrifier communities across different soil ecosystems in the tundra. Environmental Microbiomes, 2022, 17, .	5.0	25
5773	Marine Microeukaryote Metatranscriptomics: Sample Processing and Bioinformatic Workflow Recommendations for Ecological Applications. Frontiers in Marine Science, 0, 9, .	2.5	8
5775	Integrative Analysis of miRNAs and Their Targets Involved in Ray Floret Growth in <i>Gerbera hybrida</i> . International Journal of Molecular Sciences, 2022, 23, 7296.	4.1	0
5777	Biosynthesis and Metabolism of Garlic Odor Compounds in Cultivated Chinese Chives (<i>Allium</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 107 2022, 23, 7013.	4.1	4
5778	Virioplankton assemblages from challenger deep, the deepest place in the oceans. IScience, 2022, 25, 104680.	4.1	7

#	ARTICLE	IF	CITATIONS
5779	Genome of the bee <i>Holcopasites calliopsidis</i> a species showing the common apid trait of brood parasitism. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	2
5781	Genome-Resolved Metagenomic Analysis of Groundwater: Insights into Arsenic Mobilization in Biogeochemical Interaction Networks. <i>Environmental Science & Technology</i> , 2022, 56, 10105-10119.	10.0	25
5783	Genomes of six viruses that infect Asgard archaea from deep-sea sediments. <i>Nature Microbiology</i> , 2022, 7, 953-961.	13.3	17
5784	Antibiotic Resistance Genes Associated with Marine Surface Sediments: A Baseline from the Shores of Kuwait. <i>Sustainability</i> , 2022, 14, 8029.	3.2	15
5785	Potential metabolic and genetic interaction among viruses, methanogen and methanotrophic archaea, and their syntrophic partners. <i>ISME Communications</i> , 2022, 2, .	4.2	5
5787	The Gut Microbiome Composition Is Altered in Long-standing Type 1 Diabetes and Associates With Glycemic Control and Disease-Related Complications. <i>Diabetes Care</i> , 2022, 45, 2084-2094.	8.6	21
5788	Differentially Expressed Transcription Factors during Male and Female Cone Development in <i>Pinus halepensis</i> . <i>Agronomy</i> , 2022, 12, 1588.	3.0	2
5789	Identification and Expression Analysis of Chemosensory Genes in the Antennal Transcriptome of <i>Chrysanthemum Aphid Macrosiphoniella sanborni</i> . <i>Insects</i> , 2022, 13, 597.	2.2	6
5790	The RNA virome of echinoderms. <i>Journal of General Virology</i> , 2022, 103, .	2.9	1
5791	Protective Effects of Cinnamaldehyde on the Oxidative Stress, Inflammatory Response, and Apoptosis in the Hepatocytes of <i>Salmonella Gallinarum</i> -Challenged Young Chicks. <i>Oxidative Medicine and Cellular Longevity</i> , 2022, 2022, 1-21.	4.0	3
5792	Comparative physiology and transcriptome analysis reveals that chloroplast development influences silver-white leaf color formation in <i>Hydrangea macrophylla</i> var. <i>maculata</i> . <i>BMC Plant Biology</i> , 2022, 22, .	3.6	1
5793	<i>Halomonas salinarum</i> sp. nov., a moderately halophilic bacterium isolated from saline soil in Yingkou, China. <i>Archives of Microbiology</i> , 2022, 204, .	2.2	3
5794	Genome-Wide Analysis of miR159 Gene Family and Predicted Target Genes Associated with Environmental Stress in <i>Dendrobium officinale</i> : A Bioinformatics Study. <i>Genes</i> , 2022, 13, 1221.	2.4	3
5795	Ripening of Pomegranate Skin as Revealed by Developmental Transcriptomics. <i>Cells</i> , 2022, 11, 2215.	4.1	2
5796	Metagenomic Characterization of Resistance Genes in Deception Island and Their Association with Mobile Genetic Elements. <i>Microorganisms</i> , 2022, 10, 1432.	3.6	5
5798	Microbiomes Associated With the Surfaces of Northern Argentinian Fruits Show a Wide Species Diversity. <i>Frontiers in Microbiology</i> , 2022, 13, .	3.5	5
5799	Diversity of novel archaeal viruses infecting methanogens discovered through coupling of stable isotope probing and metagenomics. <i>Environmental Microbiology</i> , 2022, 24, 4853-4868.	3.8	12
5801	Exaggerated trans-membrane charge of ammonium transporters in nutrient-poor marine environments. <i>Open Biology</i> , 2022, 12, .	3.6	1

#	ARTICLE	IF	CITATIONS
5802	Both Disease Activity and HLA-B*27 Status Are Associated With Gut Microbiome Dysbiosis in Spondyloarthritis Patients. <i>Arthritis and Rheumatology</i> , 2023, 75, 41-52.	5.6	19
5803	Î±-cyanobacteria possessing form IA RuBisCO globally dominate aquatic habitats. <i>ISME Journal</i> , 2022, 16, 2421-2432.	9.8	14
5805	Rapid bacterioplankton transcription cascades regulate organic matter utilization during phytoplankton bloom progression in a coastal upwelling system. <i>ISME Journal</i> , 2022, 16, 2360-2372.	9.8	17
5806	Phylogenomics Resolves the Phylogeny of Theaceae by Using Low-Copy and Multi-Copy Nuclear Gene Makers and Uncovers a Fast Radiation Event Contributing to Tea Plants Diversity. <i>Biology</i> , 2022, 11, 1007.	2.8	8
5807	Oral and gut dysbiosis leads to functional alterations in Parkinson's disease. <i>Npj Parkinson's Disease</i> , 2022, 8, .	5.3	15
5808	Auxiliary Metabolic Gene Functions in Pelagic and Benthic Viruses of the Baltic Sea. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	21
5809	Diverse Genomic Traits Differentiate Sinking-Particle-Associated versus Free-Living Microbes throughout the Oligotrophic Open Ocean Water Column. <i>MBio</i> , 2022, 13, .	4.1	21
5810	Reducing plant-derived ethylene concentrations increases the resistance of temperate grassland to drought. <i>Science of the Total Environment</i> , 2022, 846, 157408.	8.0	3
5812	Integrated Metabolomic and Transcriptomic Analysis Reveals the Effect of Artificial Shading on Reducing the Bitter Taste of Bamboo Shoots. <i>Horticulturae</i> , 2022, 8, 594.	2.8	2
5813	Chromosome-scale genome assembly of <i>Rhododendron molle</i> provides insights into its evolution and terpenoid biosynthesis. <i>BMC Plant Biology</i> , 2022, 22, .	3.6	6
5814	Comprehensive Evaluation of RNA and DNA Viromic Methods Based on Species Richness and Abundance Analyses Using Marmot Rectal Samples. <i>MSystems</i> , 2022, 7, .	3.8	8
5815	A chromosome-level genome assembly of <i>Neotoxoptera formosana</i> (Takahashi, 1921) (Hemiptera: Tj ETQq1 1 0.784314 rgBT	1.8	0
5816	Use of Metagenomic Whole Genome Shotgun Sequencing Data in Taxonomic Assignment of <i>Dipterygium glaucum</i> Rhizosphere and Surrounding Bulk Soil Microbiomes, and Their Response to Watering. <i>Sustainability</i> , 2022, 14, 8764.	3.2	5
5817	Changes in the Species and Functional Composition of Activated Sludge Communities Revealed Mechanisms of Partial Nitrification Established by Ultrasonication. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	0
5818	The activity and functions of soil microbial communities in the Finnish sub-Arctic vary across vegetation types. <i>FEMS Microbiology Ecology</i> , 2022, 98, .	2.7	8
5819	Uncovering Hidden Members and Functions of the Soil Microbiome Using <i>De Novo</i> Metaproteomics. <i>Journal of Proteome Research</i> , 2022, 21, 2023-2035.	3.7	6
5820	Genomic Insights Into the Interspecific Diversity and Evolution of <i>Mobiluncus</i> , a Pathogen Associated With Bacterial Vaginosis. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	0
5821	Application of young maize plant residues alters the microbiome composition and its functioning in a soil under conservation agriculture: a metagenomics study. <i>Archives of Microbiology</i> , 2022, 204, .	2.2	1

#	ARTICLE	IF	CITATIONS
5822	Oxford Nanopore R10.4 long-read sequencing enables the generation of near-finished bacterial genomes from pure cultures and metagenomes without short-read or reference polishing. <i>Nature Methods</i> , 2022, 19, 823-826.	19.0	152
5823	Pseudofinder: Detection of Pseudogenes in Prokaryotic Genomes. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	38
5824	Cæsection increases cecal abundance of the archetypal bile acid and glucocorticoid modifying <i>Lachnoclostridium [clostridium] scindens</i> in mice. <i>Physiological Reports</i> , 2022, 10, .	1.7	3
5825	Dissemination of carbapenemase-producing Enterobacterales in the community of Rawalpindi, Pakistan. <i>PLoS ONE</i> , 2022, 17, e0270707.	2.5	8
5826	Bioavailable iron titrations reveal oceanic <i>Synechococcus</i> ecotypes optimized for different iron availabilities. <i>ISME Communications</i> , 2022, 2, .	4.2	8
5827	The clove (<i>Syzygium aromaticum</i>) genome provides insights into the eugenol biosynthesis pathway. <i>Communications Biology</i> , 2022, 5, .	4.4	6
5828	Characterization of the Putative Acylated Cellulose Synthase Operon in <i>Komagataeibacter xylinus</i> E25. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7851.	4.1	5
5829	Recovery of Lutacidiplasmatales archaeal order genomes suggests convergent evolution in Thermoplasmatota. <i>Nature Communications</i> , 2022, 13, .	12.8	10
5831	A super pan-genomic landscape of rice. <i>Cell Research</i> , 2022, 32, 878-896.	12.0	99
5832	Metagenomic insights into the antibiotic resistome in freshwater and seawater from an Antarctic ice-free area. <i>Environmental Pollution</i> , 2022, 309, 119738.	7.5	7
5833	Root-Associated Microbiota Response to Ecological Factors: Role of Soil Acidity in Enhancing Citrus Tolerance to Huanglongbing. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	2
5834	Effect of <i>Saccharomyces cerevisiae</i> culture mitigates heat stress-related dame in dairy cows by multi-omics. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	2
5836	Chromosome-level assembly and analysis of the <i>Thymus</i> genome provide insights into glandular secretory trichome formation and monoterpene biosynthesis in thyme. <i>Plant Communications</i> , 2022, 3, 100413.	7.7	20
5838	Genome and Transcriptome Sequence Resources and Effector Repertoire of <i>Pythium myriotylum</i> Drechsler. <i>Molecular Plant-Microbe Interactions</i> , 2022, 35, 715-718.	2.6	1
5839	Adaptation of the infant gut microbiome during the complementary feeding transition. <i>PLoS ONE</i> , 2022, 17, e0270213.	2.5	5
5840	Development of SSR Markers Based on Transcriptome Sequencing and Verification of Their Conservation across Species of Ornamental <i>Pennisetum</i> Rich. (Poaceae). <i>Agronomy</i> , 2022, 12, 1683.	3.0	2
5841	Stable carbon isotope values of syndeositional carbonate spherules and micrite record spatial and temporal changes in photosynthesis intensity. <i>Geobiology</i> , 2022, 20, 667-689.	2.4	2
5842	High-quality pan-genome of <i>Escherichia coli</i> generated by excluding confounding and highly similar strains reveals an association between unique gene clusters and genomic islands. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	5

#	ARTICLE	IF	CITATIONS
5843	Genomic Sequencing of Dengue Virus Strains Associated with Papua New Guinean Outbreaks in 2016 Reveals Endemic Circulation of DENV-1 and DENV-2. American Journal of Tropical Medicine and Hygiene, 2022, 107, 1234-1238.	1.4	2
5844	Selection of <i>Anabaena</i> sp. PCC 7938 as a Cyanobacterium Model for Biological ISRU on Mars. Applied and Environmental Microbiology, 2022, 88, .	3.1	10
5845	The Gut Microbiota Determines the High-Altitude Adaptability of Tibetan Wild Asses (<i>Equus kiang</i>) in Qinghai-Tibet Plateau. Frontiers in Microbiology, 0, 13, .	3.5	6
5846	Polycyclic Aromatic Hydrocarbon Degradation in the Sea-Surface Microlayer at Coastal Antarctica. Frontiers in Microbiology, 0, 13, .	3.5	9
5847	Extensive Non-Coding Sequence Divergence Between the Major Human Pathogen <i>Aspergillus fumigatus</i> and its Relatives. Frontiers in Fungal Biology, 0, 3, .	2.0	3
5848	Genomic surveillance of Rift Valley fever virus: from sequencing to lineage assignment. BMC Genomics, 2022, 23, .	2.8	8
5849	The evolutionary origin of host association in the Rickettsiales. Nature Microbiology, 2022, 7, 1189-1199.	13.3	29
5850	Genome sequencing reveals chromosome fusion and extensive expansion of genes related to secondary metabolism in <i>Artemisia argyi</i> . Plant Biotechnology Journal, 2022, 20, 1902-1915.	8.3	25
5851	Equilibrated evolution of the mixed auto-/allopolyploid haplotype-resolved genome of the invasive hexaploid Prussian carp. Nature Communications, 2022, 13, .	12.8	6
5852	Genome-centric metagenomics analysis revealed the metabolic function of abundant microbial communities in thermal hydrolysis-assisted thermophilic anaerobic digesters under propionate stress. Bioresource Technology, 2022, 360, 127574.	9.6	12
5853	Removal of organic micropollutants from municipal wastewater by aerobic granular sludge and conventional activated sludge. Journal of Hazardous Materials, 2022, 438, 129528.	12.4	15
5854	Localized intensification of arsenic methylation within landfill leachate-saturated zone. Science of the Total Environment, 2022, 842, 156979.	8.0	0
5855	Preliminary investigation of microorganisms potentially involved in microplastics degradation using an integrated metagenomic and biochemical approach. Science of the Total Environment, 2022, 843, 157017.	8.0	13
5856	Profiles and potential mobility of antibiotic resistance genes in different bioelectrochemistry-enhanced constructed wetlands. Chemical Engineering Journal, 2022, 450, 138005.	12.7	4
5858	Whole-body metabolic modelling predicts isoleucine dependency of SARS-CoV-2 replication. Computational and Structural Biotechnology Journal, 2022, 20, 4098-4109.	4.1	11
5859	<i>Caenorhabditis</i> nematodes colonize ephemeral resource patches in neotropical forests. Ecology and Evolution, 2022, 12, .	1.9	9
5860	Genetic redundancy of 4-hydroxybenzoate 3-hydroxylase genes ensures the catabolic safety of <i>Pigmentiphaga</i> sp. <i>scs</i> in 3-bromo-4-hydroxybenzoate-contaminated habitats. Environmental Microbiology, 2022, 24, 5123-5138.	3.8	3
5861	Systematic whole-genome sequencing reveals an unexpected diversity among actinomycetoma pathogens and provides insights into their antibacterial susceptibilities. PLoS Neglected Tropical Diseases, 2022, 16, e0010128.	3.0	4

#	ARTICLE	IF	CITATIONS
5863	Isolation and Characterization of a Lytic <i>Vibrio parahaemolyticus</i> Phage vB_VpaP_GHSM17 from Sewage Samples. <i>Viruses</i> , 2022, 14, 1601.	3.3	7
5864	Patient-derived <i>Enterococcus faecium</i> with inflammatory genotypes promote colitis. <i>Journal of Gastroenterology</i> , 2022, 57, 770-783.	5.1	2
5865	Metagenomics: An Approach for Unraveling the Community Structure and Functional Potential of Activated Sludge of a Common Effluent Treatment Plant. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	1
5866	Co-infection of mammarenaviruses in a wild mouse, Tanzania. <i>Virus Evolution</i> , 2022, 8, .	4.9	3
5867	The SWC4 subunit of the SWR1 chromatin remodeling complex is involved in varying virulence of <i>Metarhizium brunneum</i> isolates offering role of epigenetic regulation of pathogenicity. <i>Virulence</i> , 2022, 13, 1252-1269.	4.4	5
5868	An amateur gut microbial configuration formed in giant panda for striving to digest cellulose in bamboo: Systematic evidence from intestinal digestive enzymes, functional genes and microbial structures. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	0
5869	Discovery and Evolution of Six Positive-Sense RNA Viruses Co-infecting the Hypovirulent Strain SCH733 of <i>Sclerotinia sclerotiorum</i> . <i>Phytopathology</i> , 2022, 112, 2449-2461.	2.2	3
5872	Genome-Wide Identification, Characterisation and Phylogenetic Analysis of 52 Striped Catfish (<i>Pangasianodon hypophthalmus</i>) ATP-Binding Cassette (ABC) Transporter Genes. <i>Tropical Life Sciences Research</i> , 2022, 33, 257-293.	0.9	3
5873	Microbial Multitrophic Communities Drive the Variation of Antibiotic Resistome in the Gut of Soil Woodlice (Crustacea: Isopoda). <i>Environmental Science & Technology</i> , 2022, 56, 15034-15043.	10.0	8
5875	Chromosome-scale assembly of the <i>Moringa oleifera</i> Lam. genome uncovers polyploid history and evolution of secondary metabolism pathways through tandem duplication. <i>Plant Genome</i> , 2022, 15, .	2.8	8
5876	Adaptation to Environmental Extremes Structures Functional Traits in Biological Soil Crust and Hypolithic Microbial Communities. <i>MSystems</i> , 0, , .	3.8	3
5877	High-quality, chromosome-scale genome assemblies: comparisons of three <i>Diaphorina citri</i> (Asian citrus psyllid) geographic populations. <i>DNA Research</i> , 2022, 29, .	3.4	10
5878	Nanopore sequencing technology and its application in plant virus diagnostics. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	13
5879	Genomic divergence of <i>Stellera chamaejasme</i> through local selection across the Qinghai-Tibet plateau and northern China. <i>Molecular Ecology</i> , 2022, 31, 4782-4796.	3.9	15
5882	Rotavirus vaccine-derived cases in Belgium: Evidence for reversion of attenuating mutations and alternative causes of gastroenteritis. <i>Vaccine</i> , 2022, , .	3.8	3
5883	Metagenomic binning and assembled genome analysis revealed the distinct composition of resistome and mobilome in the Ili River. <i>Ecotoxicology and Environmental Safety</i> , 2022, 242, 113886.	6.0	5
5887	Local-scale virome depiction in Medellín, Colombia, supports significant differences between <i>Aedes aegypti</i> and <i>Aedes albopictus</i> . <i>PLoS ONE</i> , 2022, 17, e0263143.	2.5	9
5888	A comparative study of flow cytometry-sorted communities and shotgun viral metagenomics in a Singapore municipal wastewater treatment plant. , 2022, 1, .		2

#	ARTICLE	IF	CITATIONS
5890	Deep-Sea <i>In Situ</i> Insights into the Formation of Zero-Valent Sulfur Driven by a Bacterial Thiosulfate Oxidation Pathway. <i>MBio</i> , 2022, 13, .	4.1	9
5891	Divergent Host-Microbe Interaction and Pathogenesis Proteins Detected in Recently Identified <i>Liberibacter</i> Species. <i>Microbiology Spectrum</i> , 2022, 10, .	3.0	3
5892	RNA viromes from terrestrial sites across China expand environmental viral diversity. <i>Nature Microbiology</i> , 2022, 7, 1312-1323.	13.3	64
5893	Metagenomic insights into the microbe-mediated B and K2 vitamin biosynthesis in the gastrointestinal microbiome of ruminants. <i>Microbiome</i> , 2022, 10, .	11.1	18
5894	Population genomics of ancient and modern <i>Trichuris trichiura</i> . <i>Nature Communications</i> , 2022, 13, .	12.8	10
5896	An Age Effect of Rumen Microbiome in Dairy Buffaloes Revealed by Metagenomics. <i>Microorganisms</i> , 2022, 10, 1491.	3.6	2
5897	Genetic and genomic diversity in the sorghum gene bank collection of Uganda. <i>BMC Plant Biology</i> , 2022, 22, .	3.6	2
5898	microTrait: A Toolset for a Trait-Based Representation of Microbial Genomes. <i>Frontiers in Bioinformatics</i> , 0, 2, .	2.1	8
5899	Transcriptome and Metabolome Analyses Reveal Differences in Terpenoid and Flavonoid Biosynthesis in <i>Cryptomeria fortunei</i> Needles Across Different Seasons. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	3
5900	Characterizing Hox genes in mayflies (Ephemeroptera), with <i>Hexagenia limbata</i> as a new mayfly model. <i>EvoDevo</i> , 2022, 13, .	3.2	0
5901	Cytokinin Regulates Energy Utilization in <i>Botrytis cinerea</i> . <i>Microbiology Spectrum</i> , 2022, 10, .	3.0	4
5903	Comparative transcriptomics of tropical woody plants supports fast and furious strategy along the leaf economics spectrum in lianas. <i>Biology Open</i> , 2022, 11, .	1.2	3
5904	Gut Microbiome Is Associated With the Response to Chemoradiotherapy in Patients With Non-small Cell Lung Cancer. <i>International Journal of Radiation Oncology Biology Physics</i> , 2023, 115, 407-418.	0.8	4
5905	Activity-based protein profiling identifies alternating activation of enzymes involved in the bifidobacterium shunt pathway or mucin degradation in the gut microbiome response to soluble dietary fiber. <i>Npj Biofilms and Microbiomes</i> , 2022, 8, .	6.4	7
5906	A Genome for Editha™s Checkerspot Butterfly: An Insect with Complex Host-Adaptive Suites and Rapid Evolutionary Responses to Environmental Changes. <i>Genome Biology and Evolution</i> , 2022, 14, .	2.5	4
5907	Using HPV-meta for human papillomavirus RNA quality detection. <i>Scientific Reports</i> , 2022, 12, .	3.3	1
5908	Human mitochondrial protein complexes revealed by large-scale coevolution analysis and deep learning-based structure modeling. <i>Bioinformatics</i> , 2022, 38, 4301-4311.	4.1	14
5909	HelR is a helicase-like protein that protects RNA polymerase from rifamycin antibiotics. <i>Molecular Cell</i> , 2022, 82, 3151-3165.e9.	9.7	4

#	ARTICLE	IF	CITATIONS
5910	Competition-cooperation in the chemoautotrophic ecosystem of Movile Cave: first metagenomic approach on sediments. <i>Environmental Microbiomes</i> , 2022, 17, .	5.0	10
5911	Characterization of <i>Pipistrellus pygmaeus</i> Bat Virome from Sweden. <i>Viruses</i> , 2022, 14, 1654.	3.3	2
5913	Chromosomal-level assembly of <i>Bactericera cockerelli</i> reveals rampant gene family expansions impacting genome structure, function and insect-microbe-plant interactions. <i>Molecular Ecology Resources</i> , 2023, 23, 233-252.	4.8	5
5914	Chromosome-level Genome Assembly of the High-altitude Leopard (<i>Panthera pardus</i>) Sheds Light on Its Environmental Adaptation. <i>Genome Biology and Evolution</i> , 0, , .	2.5	1
5915	Drought Stress Stimulates the Terpenoid Backbone and Triterpenoid Biosynthesis Pathway to Promote the Synthesis of Saikosaponin in <i>Bupleurum chinense</i> DC. <i>Roots. Molecules</i> , 2022, 27, 5470.	3.8	4
5917	Comparative Metagenomics Highlight a Widespread Pathway Involved in Catabolism of Phosphonates in Marine and Terrestrial Serpentinizing Ecosystems. <i>MSystems</i> , 2022, 7, .	3.8	4
5918	Maize and peanut intercropping improves the nitrogen accumulation and yield per plant of maize by promoting the secretion of flavonoids and abundance of <i>Bradyrhizobium</i> in rhizosphere. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	14
5919	(Meta)Genomic Analysis Reveals Diverse Energy Conservation Strategies Employed by Globally Distributed <i>Gemmatimonadota</i> . <i>MSystems</i> , 2022, 7, .	3.8	6
5921	<i>Dysgonomonas mossii</i> Strain Shenzhen WH 0221, a New Member of the Genus <i>Dysgonomonas</i> Isolated from the Blood of a Patient with Diabetic Nephropathy, Exhibits Multiple Antibiotic Resistance. <i>Microbiology Spectrum</i> , 0, , .	3.0	1
5922	A Pipeline NanoTRF as a New Tool for De Novo Satellite DNA Identification in the Raw Nanopore Sequencing Reads of Plant Genomes. <i>Plants</i> , 2022, 11, 2103.	3.5	3
5923	A thousand metagenome-assembled genomes of <i>Akkermansia</i> reveal phylogroups and geographical and functional variations in the human gut. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	3.9	6
5925	Comparative Transcriptomic and Metabolic Analyses Reveal the Coordinated Mechanisms in <i>Pinus koraiensis</i> under Different Light Stress Conditions. <i>International Journal of Molecular Sciences</i> , 2022, 23, 9556.	4.1	6
5927	Differences in intestinal microflora of birds among different ecological types. <i>Frontiers in Ecology and Evolution</i> , 0, 10, .	2.2	2
5929	Metagenomic shotgun sequencing and metabolomic profiling identify specific human gut microbiota associated with diabetic retinopathy in patients with type 2 diabetes. <i>Frontiers in Immunology</i> , 0, 13, .	4.8	7
5931	Metagenome sequencing and 768 microbial genomes from cold seep in South China Sea. <i>Scientific Data</i> , 2022, 9, .	5.3	12
5932	The gill transcriptome of threatened European freshwater mussels. <i>Scientific Data</i> , 2022, 9, .	5.3	10
5933	Comparative Genomics of <i>Mortierellaceae</i> Provides Insights into Lipid Metabolism: Two Novel Types of Fatty Acid Synthase. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 891.	3.5	4
5934	Multi-omics analyses of airway host-microbe interactions in chronic obstructive pulmonary disease identify potential therapeutic interventions. <i>Nature Microbiology</i> , 2022, 7, 1361-1375.	13.3	43

#	ARTICLE	IF	CITATIONS
5935	Expanding the environmental virome: Infection profile in a native rainforest tree species. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	2
5936	Transcriptome Analysis and Intraspecific Variation in Spanish Fir (<i>Abies pinsapo</i> Boiss.). <i>International Journal of Molecular Sciences</i> , 2022, 23, 9351.	4.1	1
5937	Automated antimicrobial susceptibility testing and antimicrobial resistance genotyping using Illumina and Oxford Nanopore Technologies sequencing data among Enterobacteriaceae. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	2
5939	Genetic determinants of antimicrobial resistance in three multi-drug resistant strains of <i>Cutibacterium acnes</i> isolated from patients with acne: a predictive in silico study. <i>Access Microbiology</i> , 2022, 4, .	0.5	3
5940	Comparative transcriptome and adaptive evolution analysis on the main liver and attaching liver of <i>Pareuchiloglanis macrotrema</i> . <i>Journal of Applied Genetics</i> , 0, , .	1.9	0
5941	Metagenomic insights into environmental risk of field microplastics in an urban river. <i>Water Research</i> , 2022, 223, 119018.	11.3	24
5942	A diversified and segregated mRNA spliced-leader system in the parasitic Perkinsozoa. <i>Open Biology</i> , 2022, 12, .	3.6	3
5943	Long-Read-Resolved, Ecosystem-Wide Exploration of Nucleotide and Structural Microdiversity of Lake Bacterioplankton Genomes. <i>MSystems</i> , 2022, 7, .	3.8	11
5945	Comparative evaluation of the microbial diversity and metabolite profiles of Japanese-style and Cantonese-style soy sauce fermentation. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	14
5946	Slower antibiotics degradation and higher resistance genes enrichment in plastsphere. <i>Water Research</i> , 2022, 222, 118920.	11.3	22
5947	Phylogenetically and catabolically diverse diazotrophs reside in deep-sea cold seep sediments. <i>Nature Communications</i> , 2022, 13, .	12.8	29
5948	Taxonomic classification of DNA sequences beyond sequence similarity using deep neural networks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	22
5950	A Chromosome-Scale Genome Assembly of a <i>Helicoverpa zea</i> Strain Resistant to <i>Bacillus thuringiensis</i> Cry1Ac Insecticidal Protein. <i>Genome Biology and Evolution</i> , 2023, 15, .	2.5	4
5951	<i>Vibrio tetraodonis</i> subsp. <i>pristinus</i> subsp. nov., isolated from the coral <i>Acropora cytherea</i> at Palmyra Atoll, and creation and emended description of <i>Vibrio tetraodonis</i> subsp. <i>tetraodonis</i> subsp. nov. <i>Antonie Van Leeuwenhoek</i> , 2022, 115, 1215-1228.	1.7	3
5952	Genome analysis and 2- ⁶ -fucosyllactose utilization characteristics of a new <i>Akkermansia muciniphila</i> strain isolated from mice feces. <i>Molecular Genetics and Genomics</i> , 0, , .	2.1	3
5954	Trafficked Malayan pangolins contain viral pathogens of humans. <i>Nature Microbiology</i> , 2022, 7, 1259-1269.	13.3	25
5955	A taxonomic note on the genus <i>Prevotella</i> : Description of four novel genera and emended description of the genera <i>Hallella</i> and <i>Xylanibacter</i> . <i>Systematic and Applied Microbiology</i> , 2022, 45, 126354.	2.8	23
5956	Phylotranscriptomic and Evolutionary Analyses of the Green Algal Order Chaetophorales (Chlorophyceae, Chlorophyta). <i>Genes</i> , 2022, 13, 1389.	2.4	1

#	ARTICLE	IF	CITATIONS
5959	Transcriptomic and Behavioral Studies of Small Yellow Croaker (<i>Larimichthys polyactis</i>) in Response to Noise Exposure. <i>Animals</i> , 2022, 12, 2061.	2.3	4
5960	Whole-genome sequence of a high-temperature edible mushroom <i>Pleurotus giganteus</i> (zhudugu). <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	8
5961	Coupled Aerobic Methane Oxidation and Arsenate Reduction Contributes to Soil-Arsenic Mobilization in Agricultural Fields. <i>Environmental Science & Technology</i> , 2022, 56, 11845-11856.	10.0	8
5963	<i>Zanthoxylum bungeanum</i> root-rot associated shifts in microbiomes of root endosphere, rhizosphere, and soil. <i>PeerJ</i> , 0, 10, e13808.	2.0	6
5964	Systematic profiling of the chicken gut microbiome reveals dietary supplementation with antibiotics alters expression of multiple microbial pathways with minimal impact on community structure. <i>Microbiome</i> , 2022, 10, .	11.1	12
5965	Human supplementation with <i>Pediococcus acidilactici</i> GR-1 decreases heavy metals levels through modifying the gut microbiota and metabolome. <i>Npj Biofilms and Microbiomes</i> , 2022, 8, .	6.4	19
5966	Metaproteome plasticity sheds light on the ecology of the rumen microbiome and its connection to host traits. <i>ISME Journal</i> , 2022, 16, 2610-2621.	9.8	4
5967	Elucidating the picocyanobacteria salinity divide through ecogenomics of new freshwater isolates. <i>BMC Biology</i> , 2022, 20, .	3.8	7
5968	TALE-cmap: Protein function prediction based on a TALE-based architecture and the structure information from contact map. <i>Computers in Biology and Medicine</i> , 2022, 149, 105938.	7.0	2
5969	De Novo Long-Read Whole-Genome Assemblies and the Comparative Pan-Genome Analysis of <i>Ascochyta</i> Blight Pathogens Affecting Field Pea. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 884.	3.5	0
5970	Optimization and evaluation of viral metagenomic amplification and sequencing procedures toward a genome-level resolution of the human fecal DNA virome. <i>Journal of Advanced Research</i> , 2023, 48, 75-86.	9.5	10
5971	Antibacterial Property and Metagenomic Analysis of Milk Kefir. <i>Probiotics and Antimicrobial Proteins</i> , 2022, 14, 1170-1183.	3.9	6
5973	Intraintestinal Analysis of the Functional Activity of Microbiomes and Its Application to the Common Marmoset Intestine. <i>MSystems</i> , 0, , .	3.8	0
5974	A comparative study of RNA yields from museum specimens, including an optimized protocol for extracting RNA from formalin-fixed specimens. <i>Frontiers in Ecology and Evolution</i> , 0, 10, .	2.2	5
5975	Rumen Metaproteomics Highlight the Unique Contributions of Microbe-Derived Extracellular and Intracellular Proteins for In Vitro Ruminant Fermentation. <i>Fermentation</i> , 2022, 8, 394.	3.0	1
5976	StrainPanDA: Linked reconstruction of strain composition and gene content profiles via pangenome-based decomposition of metagenomic data. , 2022, 1, .		8
5977	Characterization of toxin-antitoxin systems from public sequencing data: A case study in <i>Pseudomonas aeruginosa</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	2
5979	Microbial functional genes are driven by gradients in sediment stoichiometry, oxygen, and salinity across the Baltic benthic ecosystem. <i>Microbiome</i> , 2022, 10, .	11.1	12

#	ARTICLE	IF	CITATIONS
5980	Cascading effects of prey identity on gene expression in a kleptoplastidic ciliate. <i>Journal of Eukaryotic Microbiology</i> , 0, , .	1.7	2
5981	Enhanced anaerobic reduction of nitrobenzene at high salinity by betaine acting as osmoprotectant and regulator of metabolism. <i>Water Research</i> , 2022, 223, 118982.	11.3	14
5983	Genome characterization of a uropathogenic <i>Pseudomonas aeruginosa</i> isolate PA_HN002 with cyclic di-GMP-dependent hyper-biofilm production. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	3.9	3
5984	Physiological, Transcriptomic and Metabolomic Analyses of Overwintering <i>Cryptomeria fortunei</i> Needles. <i>Forests</i> , 2022, 13, 1249.	2.1	1
5985	First detection of <i>Rickettsia aeschlimannii</i> in <i>Hyalomma marginatum</i> in Tibet, China. <i>Zoonoses</i> , 2022, 2, .	1.1	3
5987	Genomic reconstruction of short-chain fatty acid production by the human gut microbiota. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	3.5	18
5989	The genome sequence of the scarce swallowtail, <i>Ipliclides podalirius</i> . <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	5
5990	Evaluating the clinical relevance of the enterotypes in the Estonian microbiome cohort. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	1
5991	Dynamic succession of microbial compost communities and functions during <i>Pleurotus ostreatus</i> mushroom cropping on a short composting substrate. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	2
5992	Integrated analysis of small RNAs, transcriptome and degradome sequencing reveal the drought stress network in <i>Agropyron mongolicum</i> Keng. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	2
5993	<i>Agromyces cavernae</i> sp. nov., a novel member of the genus <i>Agromyces</i> isolated from a karstic cave in Shaoguan. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	1.7	0
5994	A pan-Zea genome map for enhancing maize improvement. <i>Genome Biology</i> , 2022, 23, .	8.8	21
5995	Maternal and neonatal viromes indicate the risk of offspring's gastrointestinal tract exposure to pathogenic viruses of vaginal origin during delivery. , 2022, 1, 303-310.		6
5996	Multi-omic analyses identify mucosa bacteria and fecal metabolites associated with weight loss after fecal microbiota transplantation. <i>Innovation(China)</i> , 2022, 3, 100304.	9.1	2
5997	<i>Oceanobacillus alkalisolis</i> sp. nov., an alkaliphilic bacterium isolated from saline-alkaline soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	1.7	0
5998	<i>Huaxiibacter chinensis</i> gen. nov., sp. nov., recovered from human sputum. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	1.7	3
6000	MinION Nanopore Sequencing Accelerates Progress towards Ubiquitous Genetics in Water Research. <i>Water (Switzerland)</i> , 2022, 14, 2491.	2.7	9
6002	The nearly complete assembly of the <i>Cercis chinensis</i> genome and Fabaceae phylogenomic studies provide insights into new gene evolution. <i>Plant Communications</i> , 2023, 4, 100422.	7.7	4

#	ARTICLE	IF	CITATIONS
6003	Antibiotic resistance genes correlate with metal resistances and accumulate in the deep water layers of the Black Sea. <i>Environmental Pollution</i> , 2022, 312, 120033.	7.5	4
6004	Genomic characterization and phylogenetic analysis of a novel Nairobi sheep disease genogroup Orthonairovirus from ticks, Southeastern China. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	0
6006	Soil metatranscriptome demonstrates a shift in C, N, and S metabolisms of a grassland ecosystem in response to elevated atmospheric CO ₂ . <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	6
6007	Evolution of zygomycete secretomes and the origins of terrestrial fungal ecologies. <i>IScience</i> , 2022, 25, 104840.	4.1	13
6008	Chromosome-level and graphic genomes provide insights into metabolism of bioactive metabolites and cold-adaption of <i>Pueraria lobata</i> var. <i>montana</i> . <i>DNA Research</i> , 2022, 29, .	3.4	7
6009	Chemotaxis may assist marine heterotrophic bacterial diazotrophs to find microzones suitable for N ₂ fixation in the pelagic ocean. <i>ISME Journal</i> , 2022, 16, 2525-2534.	9.8	12
6010	Virome of Giant Panda-Infesting Ticks Reveals Novel Bunyaviruses and Other Viruses That Are Genetically Close to Those from Giant Pandas. <i>Microbiology Spectrum</i> , 2022, 10, .	3.0	4
6011	Deciphering the Tissue Tropism of the RNA Viromes Harbored by Field-Collected <i>Anopheles sinensis</i> and <i>Culex quinquefasciatus</i> . <i>Microbiology Spectrum</i> , 2022, 10, .	3.0	1
6014	Divergent genomic trajectories predate the origin of animals and fungi. <i>Nature</i> , 2022, 609, 747-753.	27.8	32
6015	A Long-Read Genome Assembly of a Native Mite in China <i>Pyemotes zhonghuajia</i> Yu, Zhang & He (Prostigmata: Pyemotidae) Reveals Gene Expansion in Toxin-Related Gene Families. <i>Toxins</i> , 2022, 14, 571.	3.4	3
6016	Integrated Sequencing Data, Annotation, and Targeting Analysis of mRNAs and MicroRNAs from Tea Leaf During Infection by Tea Leaf Spot Pathogen, <i>Epicoccum nigrum</i> . <i>Plant Disease</i> , 2022, 106, 2741-2745.	1.4	2
6017	Transposons and non-coding regions drive the intrafamily differences of genome size in insects. <i>IScience</i> , 2022, 25, 104873.	4.1	9
6018	Comparative transcriptomics of two coral holobionts collected during the 2017 El Niño heat wave reveal differential stress response mechanisms. <i>Marine Pollution Bulletin</i> , 2022, 182, 114017.	5.0	8
6019	Transcriptional response of short-term nanoplastic exposure in <i>Monodonta labio</i> . <i>Marine Pollution Bulletin</i> , 2022, 182, 114005.	5.0	3
6020	Soil antibiotic abatement associates with the manipulation of soil microbiome via long-term fertilizer application. <i>Journal of Hazardous Materials</i> , 2022, 439, 129704.	12.4	11
6021	Comparative genomics reveals that metabolism underlies evolution of entomopathogenicity in bee-loving <i>Ascosphaera</i> spp. fungi. <i>Journal of Invertebrate Pathology</i> , 2022, 194, 107804.	3.2	0
6022	Nitrite oxidation in oxygen-deficient conditions during landfill leachate treatment. <i>Environmental Research</i> , 2022, 214, 114090.	7.5	3
6023	Bioremediation of degraded pit mud by indigenous microbes for Baijiu production. <i>Food Microbiology</i> , 2022, 108, 104096.	4.2	6

#	ARTICLE	IF	CITATIONS
6026	Massive expansion of P-selectin genes in two Venerida species, <i>Sinonovacula constricta</i> and <i>Mercenaria mercenaria</i> : evidence from comparative genomics of Bivalvia. <i>BMC Genomics</i> , 2022, 23, .	2.8	0
6027	Microbial carbon, sulfur, iron, and nitrogen cycling linked to the potential remediation of a meromictic acidic pit lake. <i>ISME Journal</i> , 2022, 16, 2666-2679.	9.8	11
6028	Full-Length Transcriptome Maps of Reef-Building Coral Illuminate the Molecular Basis of Calcification, Symbiosis, and Circadian Genes. <i>International Journal of Molecular Sciences</i> , 2022, 23, 11135.	4.1	0
6029	Metaomics unveils the contribution of <i>Alteromonas</i> bacteria to carbon cycling in marine oxygen minimum zones. <i>Frontiers in Marine Science</i> , 0, 9, .	2.5	3
6030	Viruses Ubiquity and Diversity in Atacama Desert Endolithic Communities. <i>Viruses</i> , 2022, 14, 1983.	3.3	3
6031	Single-molecule Real-time (SMRT) Sequencing Facilitates Transcriptome Research and Genome Annotation of the Fish <i>Sillago sinica</i> . <i>Marine Biotechnology</i> , 2022, 24, 1002-1013.	2.4	1
6032	The necrosis- and ethylene-inducing peptide 1-like protein (NLP) gene family of the plant pathogen <i>Corynespora cassiicola</i> . <i>Current Genetics</i> , 2022, 68, 645-659.	1.7	2
6033	Significant compositional and functional variation reveals the patterns of gut microbiota evolution among the widespread Asian honeybee populations. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	5
6034	Viromes of 15 Pepper (<i>Capsicum annuum</i> L.) Cultivars. <i>International Journal of Molecular Sciences</i> , 2022, 23, 10507.	4.1	5
6035	Genome Sequence Data Reveal at Least Two Distinct Incursions of the Tropical Race 4 Variant of <i>Fusarium Wilt</i> into South America. <i>Phytopathology</i> , 2023, 113, 90-97.	2.2	5
6038	Coping with harsh heat environments: molecular adaptation of metabolic depression in the intertidal snail <i>Echinolittorina radiata</i> . <i>Cell Stress and Chaperones</i> , 2023, 28, 477-491.	2.9	8
6039	Genome-centric metagenomics insights into functional divergence and horizontal gene transfer of denitrifying bacteria in anammox consortia. <i>Water Research</i> , 2022, 224, 119062.	11.3	10
6040	Deciphering a novel chloramphenicol resistance mechanism: Oxidative inactivation of the propanediol pharmacophore. <i>Water Research</i> , 2022, 225, 119127.	11.3	10
6041	Cloacal virome of an ancient host lineage “The tuatara (<i>Sphenodon punctatus</i>)” Reveals abundant and diverse diet-related viruses. <i>Virology</i> , 2022, 575, 43-53.	2.4	7
6042	Metagenomic insights into resistome coalescence in an urban sewage treatment plant-river system. <i>Water Research</i> , 2022, 224, 119061.	11.3	18
6043	Regional mutations in CHIKV-ECSA genomes and detection of other viruses in the serum of acute febrile patients by a metagenomic approach in Mato Grosso, Central-Western Brazil, 2018. <i>Virology</i> , 2022, 576, 18-29.	2.4	1
6044	Identification of genes involved in oleoresin biosynthesis in <i>Pinus massoniana</i> through the combination of SMRT and Illumina sequencing. <i>Industrial Crops and Products</i> , 2022, 188, 115553.	5.2	5
6045	Metagenomic analysis of microbial community and gene function of anodic biofilm for nonylphenol removal in microbial fuel cells. <i>Journal of Cleaner Production</i> , 2022, 374, 133895.	9.3	7

#	ARTICLE	IF	CITATIONS
6046	Plastisphere showing unique microbiome and resistome different from activated sludge. Science of the Total Environment, 2022, 851, 158330.	8.0	8
6047	Virome analysis in lakes of the South Shetland Islands, Antarctica - 2020. Science of the Total Environment, 2022, 852, 158537.	8.0	4
6048	The antibiotic resistance and risk heterogeneity between urban and rural rivers in a pharmaceutical industry dominated city in China: The importance of social-economic factors. Science of the Total Environment, 2022, 852, 158530.	8.0	3
6049	Modular structure of complex II: An evolutionary perspective. Biochimica Et Biophysica Acta - Bioenergetics, 2023, 1864, 148916.	1.0	5
6050	A proposed framework for the identification of indicator genes for monitoring antibiotic resistance in wastewater: Insights from metagenomic sequencing. Science of the Total Environment, 2023, 854, 158698.	8.0	6
6051	Antibiotic resistance genes are differentially mobilized according to resistance mechanism. GigaScience, 2022, 11, .	6.4	11
6052	Metagenomic Insights into the Effects of Benzyl Dodecyl Dimethyl Ammonium Bromide (Bdab) Shock on Bacterial-Driven Nitrogen Removal in Moving Bed Biofilm Reactor (Mbbr). SSRN Electronic Journal, 0, , .	0.4	0
6053	Testing Phylogenetic Stability with Variable Taxon Sampling. Methods in Molecular Biology, 2022, , 167-188.	0.9	1
6054	Assembling a Reference Phylogenomic Tree of Bacteria and Archaea by Summarizing Many Gene Phylogenies. Methods in Molecular Biology, 2022, , 137-165.	0.9	1
6055	Wild Birds-The Sentinel of Antibiotic Resistance for Urban River: Study on Egrets and Jinjiang River in Chengdu, China. SSRN Electronic Journal, 0, , .	0.4	0
6056	Metagenomic analysis reveals presence of different animal viruses in commercial fetal bovine serum and trypsin. Zoological Research, 2022, 43, 756-766.	2.1	6
6057	Metagenomic Sequencing and Histology on a Chronic Wound Identified Epstein-Barr Virus-Associated Lymphoma. Evolutionary Bioinformatics, 2022, 18, 117693432211106.	1.2	0
6058	Rooting Species Trees Using Gene Tree-Species Tree Reconciliation. Methods in Molecular Biology, 2022, , 189-211.	0.9	3
6059	Reconstruction of Archaeal Genomes from Short-Read Metagenomes. Methods in Molecular Biology, 2022, , 487-527.	0.9	0
6060	An α type <i>gluco</i> -oligosaccharide from brown algae <i>Laminaria japonica</i> stimulated the growth of lactic acid bacteria encoding specific ABC transport system components. Food and Function, 2022, 13, 11153-11168.	4.6	3
6061	Metagenomic Approaches for the Discovery of Pollutant-Remediating Enzymes: Recent Trends and Challenges. , 2022, , 571-604.		0
6062	A Chromosome-Level Genome Assembly of the <i>Rhus</i> Gall Aphid <i>Schlechtendalia chinensis</i> Provides Insight into the Endogenization of <i>Parvovirus</i> -Like DNA Sequences. SSRN Electronic Journal, 0, , .	0.4	0
6063	Comparative genome analysis of four <i>Leuconostoc</i> strains with a focus on carbohydrate-active enzymes and oligosaccharide utilization pathways. Computational and Structural Biotechnology Journal, 2022, 20, 4771-4785.	4.1	4

#	ARTICLE	IF	CITATIONS
6064	Relative Time Inference Using Lateral Gene Transfers. <i>Methods in Molecular Biology</i> , 2022, , 75-94.	0.9	0
6065	Different Horizontal Transfer Mechanisms of Intracellular and Extracellular Args in Sludge Compost Under Sulfamethoxazole Stress. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
6066	Robust 3D Modelling Reveals Spatiosyntenic Properties of Animal Genomes. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1
6067	Transient Colonising Microbes Promote Gut Dysbiosis and Disease Pathology. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
6068	Searching Metagenomes for New Rhodopsins. <i>Methods in Molecular Biology</i> , 2022, , 101-108.	0.9	0
6069	Cross-biome soil viruses as an important reservoir of virulence genes. <i>Journal of Hazardous Materials</i> , 2023, 442, 130111.	12.4	5
6070	Evaluation of FEAST for metagenomics-based source tracking of antibiotic resistance genes. <i>Journal of Hazardous Materials</i> , 2023, 442, 130116.	12.4	8
6071	Metagenomic approaches for understanding microbial communities in contaminated environments: Bioinformatic tools, case studies and future outlook. , 2023, , 103-156.		1
6072	Long-term partial substitution of chemical fertilizer by organic amendments influences soil microbial functional diversity of phosphorus cycling and improves phosphorus availability in greenhouse vegetable production. <i>Agriculture, Ecosystems and Environment</i> , 2023, 341, 108193.	5.3	17
6073	RdRp-scan: A bioinformatic resource to identify and annotate divergent RNA viruses in metagenomic sequence data. <i>Virus Evolution</i> , 2022, 8, .	4.9	22
6074	Dysbiotic Oral and Gut Viromes in Untreated and Treated Rheumatoid Arthritis Patients. <i>Microbiology Spectrum</i> , 2022, 10, .	3.0	12
6075	Non-synonymous to synonymous substitutions suggest that orthologs tend to keep their functions, while paralogs are a source of functional novelty. <i>PeerJ</i> , 0, 10, e13843.	2.0	3
6076	Community Dynamics in Structure and Function of Honey Bee Gut Bacteria in Response to Winter Dietary Shift. <i>MBio</i> , 2022, 13, .	4.1	17
6077	Genome architecture and diverged selection shaping pattern of genomic differentiation in wild barley. <i>Plant Biotechnology Journal</i> , 2023, 21, 46-62.	8.3	7
6078	In silico metatranscriptomic approach for tracking biofilm-related effectors in dairies and its importance for improving food safety. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	0
6079	Meta-Analysis and Validation of a Colorectal Cancer Risk Prediction Model Using Deep Sequenced Fecal Metagenomes. <i>Cancers</i> , 2022, 14, 4214.	3.7	3
6080	Bacteria-plant interactions synergistically enhance biodegradation of diesel fuel hydrocarbons. <i>Communications Earth & Environment</i> , 2022, 3, .	6.8	20
6081	Complete Genome Sequence of <i>Lactobacillus salivarius</i> AR809, a Probiotic Strain with Oropharyngeal Tract Resistance and Adhesion to the Oral Epithelial Cells. <i>Current Microbiology</i> , 2022, 79, .	2.2	5

#	ARTICLE	IF	CITATIONS
6082	Genomic diversity and biosynthetic capabilities of sponge-associated chlamydiae. ISME Journal, 2022, 16, 2725-2740.	9.8	8
6083	Deep evaluation of the evolutionary history of the Heat Shock Factor (HSF) gene family and its expansion pattern in seed plants. PeerJ, 0, 10, e13603.	2.0	3
6084	An Improved 1.5-Gigabase Draft Assembly of Massospora cicadina (Zoopagomycota), an Obligate Fungal Parasite of 13- and 17-Year Cicadas. Microbiology Resource Announcements, 2022, 11, .	0.6	4
6085	Adaptive biomineralization in two morphotypes of Sternaspidae (Annelida) from the Northern China Seas. Frontiers in Marine Science, 0, 9, .	2.5	1
6086	Reduced and Nonreduced Genomes in <i>Paraburkholderia</i> Symbionts of Social Amoebas. MSystems, 0, .	3.8	5
6087	The effect of 3-nitrooxypropanol, a potent methane inhibitor, on ruminal microbial gene expression profiles in dairy cows. Microbiome, 2022, 10, .	11.1	9
6088	Chromosome-level assembly of <i>Culex pipiens molestus</i> and improved reference genome of <i>Culex pipiens pallens</i> (Culicidae, Diptera). Molecular Ecology Resources, 2023, 23, 486-498.	4.8	2
6089	Congenital tremor and splay leg in piglets – insights into the virome, local cytokine response, and histology. BMC Veterinary Research, 2022, 18, .	1.9	1
6090	Isolation, Identification and Characterization of Growth Parameters of Pseudomonas putida HSM-C2 with Coumarin-Degrading Bacteria. Molecules, 2022, 27, 6007.	3.8	2
6092	Dissecting Light Sensing and Metabolic Pathways on the Millimeter Scale in High-Altitude Modern Stromatolites. Microbial Ecology, 2023, 86, 914-932.	2.8	2
6093	Divergent evolutionary trajectories of bryophytes and tracheophytes from a complex common ancestor of land plants. Nature Ecology and Evolution, 2022, 6, 1634-1643.	7.8	45
6094	Expansion of the global RNA virome reveals diverse clades of bacteriophages. Cell, 2022, 185, 4023-4037.e18.	28.9	96
6095	De novo metatranscriptomic exploration of gene function in the millipede holobiont. Scientific Reports, 2022, 12, .	3.3	4
6096	Target of Rapamycin Regulates Photosynthesis and Cell Growth in Auxenochlorella pyrenoidosa. International Journal of Molecular Sciences, 2022, 23, 11309.	4.1	2
6097	Detection of the role of intestinal flora and tryptophan metabolism involved in antidepressant-like actions of crocetin based on a multi-omics approach. Psychopharmacology, 2022, 239, 3657-3677.	3.1	5
6098	MetaPhage: an Automated Pipeline for Analyzing, Annotating, and Classifying Bacteriophages in Metagenomics Sequencing Data. MSystems, 2022, 7, .	3.8	15
6099	Genome-guided prediction of acid resistance mechanisms in acidophilic methanotrophs of phylogenetically deep-rooted Verrucomicrobia isolated from geothermal environments. Frontiers in Microbiology, 0, 13, .	3.5	1
6100	Comparative transcriptome analysis of leaves of sour jujube seedlings under salt stress. Acta Physiologiae Plantarum, 2022, 44, .	2.1	2

#	ARTICLE	IF	CITATIONS
6102	Novel bacterial taxa in a minimal lignocellulolytic consortium and their potential for lignin and plastics transformation. ISME Communications, 2022, 2, .	4.2	5
6104	A combined protein toxin screening based on the transcriptome and proteome of <i>Solenopsis invicta</i> . Proteome Science, 2022, 20, .	1.7	3
6105	Variability of strain engraftment and predictability of microbiome composition after fecal microbiota transplantation across different diseases. Nature Medicine, 2022, 28, 1913-1923.	30.7	81
6106	Gut metagenomic characteristics of ADHD reveal low <i>Bacteroides ovatus</i> -associated host cognitive impairment. Gut Microbes, 2022, 14, .	9.8	10
6107	Metatranscriptomic holobiont analysis of carbohydrate-active enzymes in the millipede <i>Telodeinopus aoutii</i> (Diplopoda, Spirostreptida). Frontiers in Ecology and Evolution, 0, 10, .	2.2	8
6108	Genomic analysis reveals cryptic diversity in aphelids and sheds light on the emergence of Fungi. Current Biology, 2022, 32, 4607-4619.e7.	3.9	10
6109	Evidence for Assimilatory Nitrate Reduction as a Previously Overlooked Pathway of Reactive Nitrogen Transformation in Estuarine Suspended Particulate Matter. Environmental Science & Technology, 2022, 56, 14852-14866.	10.0	16
6110	Structural and functional dysbiosis of gut microbiota in Tibetan subjects with coronary heart disease. Genomics, 2022, , 110483.	2.9	0
6111	High-quality metagenome-assembled genomes from proximal colonic microbiomes of synbiotic-treated korean native black pigs reveal changes in functional capacity. Scientific Reports, 2022, 12, .	3.3	2
6112	Microseek: A Protein-Based Metagenomic Pipeline for Virus Diagnostic and Discovery. Viruses, 2022, 14, 1990.	3.3	10
6113	The updated weeping forsythia genome reveals the genomic basis for the evolution and the forsythin and forsythoside A biosynthesis. Horticultural Plant Journal, 2023, 9, 1149-1161.	5.0	3
6114	Metagenome analysis using the Kraken software suite. Nature Protocols, 2022, 17, 2815-2839.	12.0	106
6116	Pain Interference in End Stage Kidney Disease is Associated with Changes in Gut Microbiome Features Before and After Kidney Transplantation. Pain Management Nursing, 2023, 24, 68-77.	0.9	2
6117	Hybrid metagenome assemblies link carbohydrate structure with function in the human gut microbiome. Communications Biology, 2022, 5, .	4.4	4
6118	Metagenomic evidence of suppressed methanogenic pathways along soil profile after wetland conversion to cropland. Frontiers in Microbiology, 0, 13, .	3.5	0
6119	Architect: A tool for aiding the reconstruction of high-quality metabolic models through improved enzyme annotation. PLoS Computational Biology, 2022, 18, e1010452.	3.2	3
6121	Unveiling Mycoviromes Using Fungal Transcriptomes. International Journal of Molecular Sciences, 2022, 23, 10926.	4.1	5
6122	The effects of Aronia berry (poly)phenol supplementation on arterial function and the gut microbiome in middle aged men and women: Results from a randomized controlled trial. Clinical Nutrition, 2022, 41, 2549-2561.	5.0	14

#	ARTICLE	IF	CITATIONS
6123	The effect of “Fishery-PV Integration” on <i>Penaeus monodon</i> culture and research on the micro-ecological environment. <i>Frontiers in Marine Science</i> , 0, 9, .	2.5	1
6124	Genome of elegance coral <i>Catalaphyllia jardinei</i> (Euphylliidae). <i>Frontiers in Marine Science</i> , 0, 9, .	2.5	3
6125	Niche specialization and ecophysiological adaptation strategies of salt-tolerant nitrite oxidizers in soil. <i>Biology and Fertility of Soils</i> , 2022, 58, 815-825.	4.3	3
6127	Meta-transcriptomic comparison of two sponge holobionts feeding on coral- and macroalgal-dissolved organic matter. <i>BMC Genomics</i> , 2022, 23, .	2.8	4
6128	Bidirectional Interactions between Arboviruses and the Bacterial and Viral Microbiota in <i>Aedes aegypti</i> and <i>Culex quinquefasciatus</i> . <i>MBio</i> , 2022, 13, .	4.1	13
6129	Metagenomic and metatranscriptomic insights into sulfate-reducing bacteria in a revegetated acidic mine wasteland. <i>Npj Biofilms and Microbiomes</i> , 2022, 8, .	6.4	2
6130	Correlation of gut microbiota and metabolic functions with the antibody response to the BBIBP-CorV vaccine. <i>Cell Reports Medicine</i> , 2022, 3, 100752.	6.5	14
6131	A global phylogenomic and metabolic reconstruction of the large intestine bacterial community of domesticated cattle. <i>Microbiome</i> , 2022, 10, .	11.1	6
6134	Effects of g-C ₃ N ₄ on bacterial community and tetracycline resistance genes in two typical sediments in tetracycline pollution remediation. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	1
6135	An Evolutionary Framework of Acanthaceae Based on Transcriptomes and Genome Skims. <i>Systematic Botany</i> , 2022, 47, 716-728.	0.5	0
6136	Giant pandas’ staple food bamboo phyllosphere fungal community and its influencing factors. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	1
6138	Seasonal microbial dynamics in the ocean inferred from assembled and unassembled data: a view on the unknown biosphere. <i>ISME Communications</i> , 2022, 2, .	4.2	1
6139	Functionally diverse microbial communities show resilience in response to a record-breaking rain event. <i>ISME Communications</i> , 2022, 2, .	4.2	4
6141	Extensive gut virome variation and its associations with host and environmental factors in a population-level cohort. <i>Nature Communications</i> , 2022, 13, .	12.8	31
6142	Whole-Genome Sequence Analysis of an Endophytic Fungus <i>Alternaria</i> sp. SPS-2 and Its Biosynthetic Potential of Bioactive Secondary Metabolites. <i>Microorganisms</i> , 2022, 10, 1789.	3.6	6
6145	Whole Transcriptome Analyses of Apricots and Japanese Plum Fruits after 1-MCP (Ethylene-Inhibitor) and Ethrel (Ethylene-Precursor) Treatments Reveal New Insights into the Physiology of the Ripening Process. <i>International Journal of Molecular Sciences</i> , 2022, 23, 11045.	4.1	7
6148	Metabolic framework of spontaneous and synthetic sourdough metacommunities to reveal microbial players responsible for resilience and performance. <i>Microbiome</i> , 2022, 10, .	11.1	15
6149	Global contribution of pelagic fungi to protein degradation in the ocean. <i>Microbiome</i> , 2022, 10, .	11.1	14

#	ARTICLE	IF	CITATIONS
6151	mobileOG-db: a Manually Curated Database of Protein Families Mediating the Life Cycle of Bacterial Mobile Genetic Elements. <i>Applied and Environmental Microbiology</i> , 2022, 88, .	3.1	64
6152	Mucus-degrading <i>Bacteroides</i> link carbapenems to aggravated graft-versus-host disease. <i>Cell</i> , 2022, 185, 3705-3719.e14.	28.9	37
6153	A Novel Carrageenan Metabolic Pathway in <i>Flavobacterium algicola</i> . <i>Applied and Environmental Microbiology</i> , 2022, 88, .	3.1	0
6154	The Viral Fraction Metatranscriptomes of Lake Baikal. <i>Microorganisms</i> , 2022, 10, 1937.	3.6	4
6155	Dynamic transcriptome and network-based analysis of yellow leaf mutant <i>Ginkgo biloba</i> . <i>BMC Plant Biology</i> , 2022, 22, .	3.6	3
6157	Phosphoproteome Dynamics of <i>Streptomyces rimosus</i> during Submerged Growth and Antibiotic Production. <i>MSystems</i> , 0, , .	3.8	2
6158	A chromosome-level assembly of the widely used Rockefeller strain of <i>Aedes aegypti</i> , the yellow fever mosquito. <i>G3: Genes, Genomes, Genetics</i> , 0, , .	1.8	1
6159	Evidence for evolutionary adaptation of mixotrophic nanoflagellates to warmer temperatures. <i>Global Change Biology</i> , 2022, 28, 7094-7107.	9.5	9
6160	Arboviruses in Free-Ranging Birds and Hematophagous Arthropods (Diptera, Nematocera) from Forest Remnants and Urbanized Areas of an Environmental Protection Area in the Amazon Biome. <i>Viruses</i> , 2022, 14, 2101.	3.3	2
6161	Deciphering microbial gene function using natural language processing. <i>Nature Communications</i> , 2022, 13, .	12.8	13
6163	Genome-wide identification and functional prediction of silicon (Si) transporters in poplar (<i>Populus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.5	1
6165	Discovery of two novel Torque Teno viruses in <i>Callithrix penicillata</i> provides insights on Anelloviridae diversification dynamics. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	3
6166	Decoding the formation of diverse petal colors of <i>Lagerstroemia indica</i> by integrating the data from transcriptome and metabolome. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	7
6168	Reference quality genome sequence of Indian pomegranate cv. "Bhagawa"™ (<i>Punica granatum</i> L.). <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	5
6169	Gut Microbiota Profiles in Dairy Cattle from Highland and Coastal Regions Using Shotgun Metagenomic Approach. <i>BioMed Research International</i> , 2022, 2022, 1-8.	1.9	1
6170	Valorization of Biomasses from Energy Crops for the Discovery of Novel Thermophilic Glycoside Hydrolases through Metagenomic Analysis. <i>International Journal of Molecular Sciences</i> , 2022, 23, 10505.	4.1	3
6171	Multi-omics analysis reveals the host-microbe interactions in aged rhesus macaques. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	4
6172	Non-photoperiodic transition of female cannabis seedlings from juvenile to adult reproductive stage. <i>Plant Reproduction</i> , 0, , .	2.2	6

#	ARTICLE	IF	CITATIONS
6174	Adaptation and evolution of the sea anemone <i>Alvinactis</i> sp. to deep-sea hydrothermal vents: A comparison using transcriptomes. <i>Ecology and Evolution</i> , 2022, 12, .	1.9	2
6175	Insights into the global freshwater virome. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	8
6176	Human Gut Microbiota and Its Metabolites Impact Immune Responses in COVID-19 and Its Complications. <i>Gastroenterology</i> , 2023, 164, 272-288.	1.3	47
6177	Intestinal microbiome-mediated resistance against vibriosis for <i>Cynoglossus semilaevis</i> . <i>Microbiome</i> , 2022, 10, .	11.1	13
6178	Antibiotic resistance and genomic features of <i>Clostridioides difficile</i> in southwest China. <i>PeerJ</i> , 0, 10, e14016.	2.0	2
6179	A chromosome-level genome assembly of the potato grouper (<i>Epinephelus tukula</i>). <i>Genomics</i> , 2022, 114, 110473.	2.9	2
6180	Whole genome sequence analysis of two subspecies of <i>Companilactobacillus Futsaii</i> and experimental verification of drug resistance and effect on the exploratory behavior of mice based on unique gene. <i>PLoS ONE</i> , 2022, 17, e0274244.	2.5	1
6181	The Natural Product Domain Seeker version 2 (NaPDoS2) webtool relates ketosynthase phylogeny to biosynthetic function. <i>Journal of Biological Chemistry</i> , 2022, 298, 102480.	3.4	27
6182	Reconfiguration of Gut Microbiota and Reprogramming of Liver Metabolism with Phycobiliproteins Bioactive Peptides to Rehabilitate Obese Rats. <i>Nutrients</i> , 2022, 14, 3635.	4.1	4
6183	Prediction of transcript isoforms in 19 chicken tissues by Oxford Nanopore long-read sequencing. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	8
6184	MATEdb, a data repository of high-quality metazoan transcriptome assemblies to accelerate phylogenomic studies. , 0, 2, .		10
6185	A resistome survey across hundreds of freshwater bacterial communities reveals the impacts of veterinary and human antibiotics use. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	9
6187	Microbially enhanced methane uptake under warming enlarges ecosystem carbon sink in a Tibetan alpine grassland. <i>Global Change Biology</i> , 2022, 28, 6906-6920.	9.5	7
6188	Coupled abiotic-biotic cycling of nitrous oxide in tropical peatlands. <i>Nature Ecology and Evolution</i> , 2022, 6, 1881-1890.	7.8	5
6190	Metagenomic evidence for increasing antibiotic resistance in progeny upon parental antibiotic exposure as the cost of hormesis. <i>Chemosphere</i> , 2022, 309, 136738.	8.2	3
6191	Metagenomic insights into the symbiotic relationship in anammox consortia at reduced temperature. <i>Water Research</i> , 2022, 225, 119184.	11.3	45
6192	Enhanced cultured diversity of the mouse gut microbiota enables custom-made synthetic communities. <i>Cell Host and Microbe</i> , 2022, 30, 1630-1645.e25.	11.0	26
6193	Dynamics of the gut microbiota in rats after hypobaric hypoxia exposure. <i>PeerJ</i> , 0, 10, e14090.	2.0	5

#	ARTICLE	IF	CITATIONS
6194	Transcriptional regulation underlying the temperature response of embryonic development rate in the winter moth. <i>Molecular Ecology</i> , 0, , .	3.9	2
6195	Chromosome-level genome of a leaf vegetable <i>Glebionis coronaria</i> provides insights into the biosynthesis of monoterpenoids contributing to its special aroma. <i>DNA Research</i> , 2022, 29, .	3.4	3
6196	Diverse RNA Viruses Associated with Diatom, Eustigmatophyte, Dinoflagellate, and Rhodophyte Microalgae Cultures. <i>Journal of Virology</i> , 2022, 96, .	3.4	3
6197	Revealing the uncharacterised diversity of amphibian and reptile viruses. <i>ISME Communications</i> , 2022, 2, .	4.2	15
6198	Comprehensive collection of genes and comparative analysis of full-length transcriptome sequences from Japanese larch (<i>Larix kaempferi</i>) and Kuril larch (<i>Larix gmelinii</i> var. <i>japonica</i>). <i>BMC Plant Biology</i> , 2022, 22, .	3.6	4
6199	Viruses direct carbon cycling in lake sediments under global change. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	8
6200	Production of biopolymer precursors beta-alanine and L-lactic acid from CO ₂ with metabolically versatile <i>Rhodococcus opacus</i> DSM 43205. <i>Frontiers in Bioengineering and Biotechnology</i> , 0, 10, .	4.1	6
6201	Phylogenomics of a <i>Saccharomyces cerevisiae</i> cocoa strain reveals adaptation to a West African fermented food population. <i>IScience</i> , 2022, 25, 105309.	4.1	1
6203	Phylogenetic and functional diverse ANME-1 thrive in Arctic hydrothermal vents. <i>FEMS Microbiology Ecology</i> , 2022, 98, .	2.7	1
6206	Molecular and developmental signatures of genital size macro-evolution in bugs. <i>Molecular Biology and Evolution</i> , 0, , .	8.9	0
6207	Metagenomic and genomic characterization of heavy metal tolerance and resistance genes in the rhizosphere microbiome of <i>Avicennia germinans</i> in a semi-arid mangrove forest in the tropics. <i>Marine Pollution Bulletin</i> , 2022, 184, 114204.	5.0	6
6208	Advanced simultaneous nitrogen and phosphorus removal for non-sterile wastewater through a novel coupled yeast-sludge system: Performance, microbial interaction, and mechanism. <i>Chemosphere</i> , 2022, 309, 136645.	8.2	3
6209	Honeybee (<i>Apis mellifera</i>) resistance to deltamethrin exposure by Modulating the gut microbiota and improving immunity. <i>Environmental Pollution</i> , 2022, 314, 120340.	7.5	9
6210	Genomic virulence genes profile analysis of <i>Salmonella enterica</i> isolates from animal and human in China from 2004 to 2019. <i>Microbial Pathogenesis</i> , 2022, 173, 105808.	2.9	5
6211	The <i>Capparis spinosa</i> var. <i>herbacea</i> genome provides the first genomic instrument for a diversity and evolution study of the Capparaceae family. <i>GigaScience</i> , 2022, 11, .	6.4	5
6212	Metagenomic and Bile Acid Metabolomic Analysis of Fecal Microbiota Transplantation for Recurrent <i>Clostridiodes Difficile</i> and/or Inflammatory Bowel Diseases. <i>Medical Research Archives</i> , 2022, 10, .	0.2	5
6213	The Perennial Horse Gram (<i>Macrotyloma axillare</i>) Genome, Phylogeny, and Selection Across the Fabaceae. <i>Compendium of Plant Genomes</i> , 2022, , 255-279.	0.5	2
6214	Chromosome-level genome assembly for the Aldabra giant tortoise enables insights into the genetic health of a threatened population. <i>GigaScience</i> , 2022, 11, .	6.4	5

#	ARTICLE	IF	CITATIONS
6215	Virome in healthy pangolins reveals compatibility with multiple potentially zoonotic viruses. <i>Zoological Research</i> , 2022, 43, 977-988.	2.1	2
6216	First Genomic Evidence of a Henipa-like Virus in Brazil. <i>Viruses</i> , 2022, 14, 2167.	3.3	9
6217	Development and Validation of a Bioinformatic Workflow for the Rapid Detection of Viruses in Biosecurity. <i>Viruses</i> , 2022, 14, 2163.	3.3	4
6218	The Structure and Function of the <i>Sargassum fusiforme</i> Microbiome under Different Conditions. <i>Journal of Marine Science and Engineering</i> , 2022, 10, 1401.	2.6	1
6219	Comparative Metagenomics and Metabolomes Reveals Abnormal Metabolism Activity Is Associated with Gut Microbiota in Alzheimer's Disease Mice. <i>International Journal of Molecular Sciences</i> , 2022, 23, 11560.	4.1	9
6220	First Polycipivirus and Unmapped RNA Virus Diversity in the Yellow Crazy Ant, <i>Anoplolepis gracilipes</i> . <i>Viruses</i> , 2022, 14, 2161.	3.3	1
6221	Pivotal interplays between fecal metabolome and gut microbiome reveal functional signatures in cerebral ischemic stroke. <i>Journal of Translational Medicine</i> , 2022, 20, .	4.4	9
6222	First brain de novo transcriptome of the Tyrrhenian tree frog, <i>Hyla sarda</i> , for the study of dispersal behavior. <i>Frontiers in Ecology and Evolution</i> , 0, 10, .	2.2	2
6223	Comparative transcriptome profiling and weighted gene co-expression network analysis to identify core genes in maize (<i>Zea mays</i> L.) silks infected by multiple fungi. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	4
6224	Insights on Microbial Communities Inhabiting Non-Volcanic Hot Springs. <i>International Journal of Molecular Sciences</i> , 2022, 23, 12241.	4.1	3
6225	Investigation of <i>Streptomyces</i> sp. Strain EMB24 Secondary Metabolite Profile Has Unraveled Its Extraordinary Antibacterial Potency Against Drug-Resistant Bacteria. <i>Marine Biotechnology</i> , 2022, 24, 1168-1175.	2.4	5
6226	Metatranscriptomics Reveals the Diversity of the Tick Virome in Northwest China. <i>Microbiology Spectrum</i> , 2022, 10, .	3.0	12
6227	Comparative transcriptomic analysis of normal and abnormal in vitro flowers in <i>Cymbidium nanulum</i> Y. S. Wu et S. C. Chen identifies differentially expressed genes and candidate genes involved in flower formation. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	1
6228	Brain de novo transcriptome assembly of a toad species showing polymorphic anti-predatory behavior. <i>Scientific Data</i> , 2022, 9, .	5.3	3
6229	Genomic evidence supports the genetic convergence of a supergene controlling the distylous floral syndrome. <i>New Phytologist</i> , 2023, 237, 601-614.	7.3	10
6231	Gut microbiome dysbiosis contributes to abdominal aortic aneurysm by promoting neutrophil extracellular trap formation. <i>Cell Host and Microbe</i> , 2022, 30, 1450-1463.e8.	11.0	59
6232	Gut Microbiome and Its Cofactors Are Linked to Lipoprotein Distribution Profiles. <i>Microorganisms</i> , 2022, 10, 2156.	3.6	4
6233	A reference-grade genome assembly for <i>Astragalus mongholicus</i> and insights into the biosynthesis and high accumulation of triterpenoids and flavonoids in its roots. <i>Plant Communications</i> , 2023, 4, 100469.	7.7	8

#	ARTICLE	IF	CITATIONS
6234	Genome-Wide Prediction and Analysis of <i>Oryza</i> Species NRP Genes in Rice Blast Resistance. International Journal of Molecular Sciences, 2022, 23, 11967.	4.1	0
6235	Multiple waves of viral invasions in Symbiodiniaceae algal genomes. Virus Evolution, 2022, 8, .	4.9	3
6236	Canine Saliva as a Possible Source of Antimicrobial Resistance Genes. Antibiotics, 2022, 11, 1490.	3.7	4
6237	AsgeneDB: a curated orthology arsenic metabolism gene database and computational tool for metagenome annotation. NAR Genomics and Bioinformatics, 2022, 4, .	3.2	2
6238	Functional and metabolic alterations of gut microbiota in children with new-onset type 1 diabetes. Nature Communications, 2022, 13, .	12.8	28
6240	Genetic Reassortment between Endemic and Introduced <i>Macrobrachium rosenbergii</i> Nodaviruses in the Murray-Darling Basin, Australia. Viruses, 2022, 14, 2186.	3.3	0
6241	Population genomics of an icefish reveals mechanisms of glacier-driven adaptive radiation in Antarctic notothenioids. BMC Biology, 2022, 20, .	3.8	5
6242	Novel viral and microbial species in a translocated <i>Toutouwai</i> (<i>Petroica longipes</i>) population from Aotearoa/New Zealand. One Health Outlook, 2022, 4, .	3.4	4
6244	<i>Arthrobacter polaris</i> sp. nov., a new cold-adapted member of the family Micrococcaceae isolated from Antarctic fellfield soil. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	1.7	1
6245	Functional differentiation determines the molecular basis of the symbiotic lifestyle of <i>Ca. Nanohaloarchaeota</i> . Microbiome, 2022, 10, .	11.1	8
6248	Regulatory network of ginsenoside biosynthesis under Ro stress in the hairy roots of <i>Panax ginseng</i> revealed by RNA sequencing. Frontiers in Bioengineering and Biotechnology, 0, 10, .	4.1	4
6250	PyunBBX18 Is Involved in the Regulation of Anthocyanins Biosynthesis under UV-B Stress. Genes, 2022, 13, 1811.	2.4	3
6251	The genome and lifestage-specific transcriptomes of a plant-parasitic nematode and its host reveal susceptibility genes involved in trans-kingdom synthesis of vitamin B5. Nature Communications, 2022, 13, .	12.8	28
6253	The origin and distribution of the main oxygen sensing mechanism across metazoans. Frontiers in Physiology, 0, 13, .	2.8	1
6254	Concerted expansion and contraction of immune receptor gene repertoires in plant genomes. Nature Plants, 2022, 8, 1146-1152.	9.3	37
6255	Conjugative transfer of multi-drug resistance IncN plasmids from environmental waterborne bacteria to <i>Escherichia coli</i> . Frontiers in Microbiology, 0, 13, .	3.5	4
6256	Complete genome of <i>Vibrio japonicus</i> strain JCM 31412 and assessment of the Nereis clade of the genus <i>Vibrio</i> . Antonie Van Leeuwenhoek, 0, , .	1.7	0
6257	Evolutionary Divergence between <i>Toona ciliata</i> and <i>Toona sinensis</i> Assayed with Their Whole Genome Sequences. Genes, 2022, 13, 1799.	2.4	8

#	ARTICLE	IF	CITATIONS
6260	Recent reconfiguration of an ancient developmental gene regulatory network in <i>Heliocidaris</i> sea urchins. <i>Nature Ecology and Evolution</i> , 2022, 6, 1907-1920.	7.8	12
6261	Impact of Stagnation on the Diversity of Cyanobacteria in Drinking Water Treatment Plant Sludge. <i>Toxins</i> , 2022, 14, 749.	3.4	1
6262	Analyses of adult transcriptomes from four different populations of the spongy moth, <i>Lymantria dispar</i> L., from China and the USA. <i>Scientific Reports</i> , 2022, 12, .	3.3	2
6263	Maize intercropping enriches plant growth-promoting rhizobacteria and promotes both the growth and volatile oil concentration of <i>Atractylodes lancea</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	8
6264	Benchmarking taxonomic classifiers with Illumina and Nanopore sequence data for clinical metagenomic diagnostic applications. <i>Microbial Genomics</i> , 2022, 8, .	2.0	7
6265	<i>Fontivita pretiosa</i> gen. nov., sp. nov., a thermophilic planctomycete of the order <i>Tepidisphaerales</i> from a hot spring of Baikal lake region. <i>Systematic and Applied Microbiology</i> , 2022, , 126375.	2.8	3
6266	VEBA: a modular end-to-end suite for in silico recovery, clustering, and analysis of prokaryotic, microeukaryotic, and viral genomes from metagenomes. <i>BMC Bioinformatics</i> , 2022, 23, .	2.6	7
6267	Multi-trial analysis of HIV-1 envelope gp41-reactive antibodies among global recipients of candidate HIV-1 vaccines. <i>Frontiers in Immunology</i> , 0, 13, .	4.8	4
6268	Telomere-to-telomere genome assembly of bitter melon (<i>Momordica charantia</i> L. var.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 427 7. <i>Horticulture Research</i> , 2023, 10, .	6.3	16
6269	Comparing the taxonomic and functional profiles of gut microbiota from three pig breeds by metagenomic sequencing. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	0
6270	Anaerobic oxidation of propane coupled to nitrate reduction by a lineage within the class <i>Symbiobacteriia</i> . <i>Nature Communications</i> , 2022, 13, .	12.8	9
6272	Prostaglandin E2 synchronizes lunar-regulated beach spawning in grass puffers. <i>Current Biology</i> , 2022, 32, 4881-4889.e5.	3.9	7
6274	Genetic and physiological insights into the diazotrophic activity of a non-cyanobacterial marine diazotroph. <i>Environmental Microbiology</i> , 2022, 24, 6510-6523.	3.8	3
6275	<i>binny</i> : an automated binning algorithm to recover high-quality genomes from complex metagenomic datasets. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	5
6276	Metabolomic and transcriptomic exploration of the uric acid-reducing flavonoids biosynthetic pathways in the fruit of <i>Actinidia arguta</i> Sieb. Zucc.. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	5
6277	Associations of the skin, oral and gut microbiome with aging, frailty and infection risk reservoirs in older adults. <i>Nature Aging</i> , 2022, 2, 941-955.	11.6	21
6278	Genome-Wide Identification and Functional Analysis of the GASA Gene Family Responding to Multiple Stressors in <i>Canavalia rosea</i> . <i>Genes</i> , 2022, 13, 1988.	2.4	4
6279	<i>Leptospira sanjuanensis</i> sp. nov., a pathogenic species of the genus <i>Leptospira</i> isolated from soil in Puerto Rico. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	1.7	15

#	ARTICLE	IF	CITATIONS
6280	An overview of online resources for intra-species detection of gene duplications. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	1
6281	Genome-centric insight into metabolically active microbial population in shallow-sea hydrothermal vents. <i>Microbiome</i> , 2022, 10, .	11.1	2
6282	Pan-Genome Analysis Reveals Functional Divergences in Gut-Restricted <i>Gilliamella</i> and <i>Snodgrassella</i> . <i>Bioengineering</i> , 2022, 9, 544.	3.5	5
6283	Wild birds-the sentinel of antibiotic resistance for urban river: Study on egrets and Jinjiang river in Chengdu, China. <i>Environmental Research</i> , 2023, 216, 114566.	7.5	2
6284	Tree2GD: a phylogenomic method to detect large-scale gene duplication events. <i>Bioinformatics</i> , 2022, 38, 5317-5321.	4.1	5
6285	The mitochondrial genome of the red icefish (<i>Channichthys rugosus</i>) casts doubt on its species status. <i>Polar Biology</i> , 2022, 45, 1541-1552.	1.2	0
6286	Massive genome investigations reveal insights of prevalent introgression for environmental adaptation and triterpene biosynthesis in <i>Ganoderma</i> . <i>Molecular Ecology Resources</i> , 0, , .	4.8	4
6287	The novel distribution of intracellular and extracellular flavonoids produced by <i>Aspergillus</i> sp. Gbtc 2, an endophytic fungus from <i>Ginkgo biloba</i> root. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	2
6288	Integrated Analysis of Transcriptome and microRNA Profile Reveals the Toxicity of Euphorbia Factors toward Human Colon Adenocarcinoma Cell Line Caco-2. <i>Molecules</i> , 2022, 27, 6931.	3.8	2
6289	Draft Genome Resource for the Forest Pathogen <i>Coniferiporia weirii</i> – a Pathogen of <i>Thuja plicata</i> and <i>Callitropsis nootkatensis</i> . <i>Plant Disease</i> , 0, , .	1.4	0
6290	High-Quality Genome Resource of <i>Gilbertella persicaria</i> Causing Peach Soft Rot. <i>Plant Disease</i> , 2023, 107, 908-910.	1.4	1
6292	Insights from the genome sequence of <i>Bacillus tropicus</i> EMB20, an efficient β -lactamase-producing bacterium. <i>3 Biotech</i> , 2022, 12, .	2.2	1
6293	Metagenomics of Virus Diversities in Solid-State Brewing Process of Traditional Chinese Vinegar. <i>Foods</i> , 2022, 11, 3296.	4.3	5
6295	Multiple sources of aerobic methane production in aquatic ecosystems include bacterial photosynthesis. <i>Nature Communications</i> , 2022, 13, .	12.8	15
6296	Declining metal availability in the Mesozoic seawater reflected in phytoplankton succession. <i>Nature Geoscience</i> , 2022, 15, 932-941.	12.9	5
6297	Serological and Molecular Evidence of the Circulation of the Venezuelan Equine Encephalitis Virus Subtype IIIA in Humans, Wild Vertebrates and Mosquitos in the Brazilian Amazon. <i>Viruses</i> , 2022, 14, 2391.	3.3	1
6298	FunOrder 2.0 – a method for the fully automated curation of co-evolved genes in fungal biosynthetic gene clusters. <i>Frontiers in Fungal Biology</i> , 0, 3, .	2.0	0
6299	Transcriptome analysis reveals the proline metabolic pathway and its potential regulation TF-hub genes in salt-stressed potato. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	4

#	ARTICLE	IF	CITATIONS
6300	Transposable element expansion and low-level piRNA silencing in grasshoppers may cause genome gigantism. BMC Biology, 2022, 20, .	3.8	9
6301	Gene family expansions in Antarctic winged midge as a strategy for adaptation to cold environments. Scientific Reports, 2022, 12, .	3.3	7
6303	Whole-genome characterization of avian picornaviruses from diarrheic broiler chickens co-infected with multiple picornaviruses in Iran. Virus Genes, 2023, 59, 79-90.	1.6	1
6304	Changes of rhizosphere microbiome and metabolites in Meloidogyne incognita infested soil. Plant and Soil, 2023, 483, 331-353.	3.7	6
6306	HiFi chromosome-scale diploid assemblies of the grape rootstocks 110R, Kober 5BB, and 101â€™14 Mgt. Scientific Data, 2022, 9, .	5.3	6
6307	Lactacisobacillus rhamnosus HN001 alters the microbiota composition in the cecum but not the feces in a piglet model. Frontiers in Nutrition, 0, 9, .	3.7	3
6308	Comparative Genomic Analysis of 31 <i>Phytophthora</i> Genomes Reveals Genome Plasticity and Horizontal Gene Transfer. Molecular Plant-Microbe Interactions, 2023, 36, 26-46.	2.6	6
6310	The genome sequence of <i>Hirschfeldia incana</i> , a new Brassicaceae model to improve photosynthetic light-use efficiency. Plant Journal, 0, , .	5.7	2
6311	Investigating the relationship between the skin microbiome and flame retardant exposure of the endangered St. Lawrence Estuary beluga. Frontiers in Environmental Science, 0, 10, .	3.3	1
6313	Large-scale investigation of zoonotic viruses in the era of high-throughput sequencing. Microbiology and Immunology, 2023, 67, 1-13.	1.4	3
6315	Fusarium oxysporum effector clustering version 2: An updated pipeline to infer host range. Frontiers in Plant Science, 0, 13, .	3.6	2
6316	Distributional Pattern of Bacteria, Protists, and Diatoms in Ocean according to Water Depth in the Northern South China Sea. Microbiology Spectrum, 2022, 10, .	3.0	3
6318	Database of space life investigations and bioinformatics of microbiology in extreme environments. Frontiers in Microbiology, 0, 13, .	3.5	4
6319	Genome-wide scan for potential CD4+ T-cell vaccine candidates in Candida auris by exploiting reverse vaccinology and evolutionary information. Frontiers in Medicine, 0, 9, .	2.6	3
6320	Comammox biogeography subject to anthropogenic interferences along a high-altitude river. Water Research, 2022, 226, 119225.	11.3	5
6321	Complex host/symbiont integration of a multi-partner symbiotic system in the eusocial aphid Ceratovacuna japonica. IScience, 2022, 25, 105478.	4.1	8
6322	Impact of host age on viral and bacterial communities in a waterbird population. ISME Journal, 2023, 17, 215-226.	9.8	6
6323	Deciphering the potential of a plant growth promoting endophyte Rhizobium sp. WYJ-E13, and functional annotation of the genes involved in the metabolic pathway. Frontiers in Microbiology, 0, 13, .	3.5	1

#	ARTICLE	IF	CITATIONS
6324	CRAMdb: a comprehensive database for composition and roles of microbiome in animals. <i>Nucleic Acids Research</i> , 2023, 51, D700-D707.	14.5	5
6325	A Catalog of over 5,000 Metagenome-Assembled Microbial Genomes from the Caprinae Gut Microbiota. <i>Microbiology Spectrum</i> , 2022, 10, .	3.0	3
6326	Ensembl 2023. <i>Nucleic Acids Research</i> , 2023, 51, D933-D941.	14.5	153
6327	Frequency of occurrence and habitat selection shape the spatial variation in the antibiotic resistome in riverine ecosystems in eastern China. <i>Environmental Microbiomes</i> , 2022, 17, .	5.0	5
6328	Bacterial Community and Antibiotic Resistance Gene Profiles of Fish Gut Contents and Their Aquaculture Environment in Tianjin, China. <i>Aquaculture Journal</i> , 2022, 2, 269-284.	1.8	2
6329	Spatial turnover of soil viral populations and genotypes overlain by cohesive responses to moisture in grasslands. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	27
6330	Metatranscriptomics reveals contrasting effects of elevation on the activity of bacteria and bacterial viruses in soil. <i>Molecular Ecology</i> , 2023, 32, 6552-6563.	3.9	5
6331	Methanotrophy by a <i>Mycobacterium</i> species that dominates a cave microbial ecosystem. <i>Nature Microbiology</i> , 2022, 7, 2089-2100.	13.3	22
6332	Change in composition and potential functional genes of microbial communities on carbonatite rinds with different weathering times. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	7
6333	Simultaneous oxygen and nitrate respiration for nitrogen removal driven by aeration: Carbon/nitrogen metabolism and metagenome-based microbial ecology. <i>Journal of Water Process Engineering</i> , 2022, 50, 103196.	5.6	6
6334	Methylobacter couples methane oxidation and N ₂ O production in hypoxic wetland soil. <i>Soil Biology and Biochemistry</i> , 2022, 175, 108863.	8.8	6
6335	Metagenomic insight into the distribution of metal resistance genes within cascade reservoir waters: Synergic impacts of geographic variation and anthropogenic pollution. <i>Environmental Research</i> , 2023, 216, 114682.	7.5	4
6336	Dissecting the genome, secretome, and effectome repertoires of <i>Monilinia</i> spp.: The causal agent of brown rot disease: A comparative analysis. <i>Postharvest Biology and Technology</i> , 2023, 195, 112120.	6.0	8
6337	Uranium triggers ferroptosis-like cell death in <i>Vicia faba</i> roots by increasing iron accumulation and inhibiting glutathione peroxidase activity. <i>Environmental and Experimental Botany</i> , 2023, 205, 105122.	4.2	1
6338	Microbial mechanisms for methane source-to-sink transition after wetland conversion to cropland. <i>Geoderma</i> , 2023, 429, 116229.	5.1	4
6339	Phytostabilization mitigates antibiotic resistance gene enrichment in a copper mine tailings pond. <i>Journal of Hazardous Materials</i> , 2023, 443, 130255.	12.4	3
6340	Long-term high-P fertilizer input shifts soil P cycle genes and microorganism communities in dryland wheat production systems. <i>Agriculture, Ecosystems and Environment</i> , 2023, 342, 108226.	5.3	17
6341	Transcriptome responses to salt stress in roots and leaves of <i>Lilium pumilum</i> . <i>Scientia Horticulturae</i> , 2023, 309, 111622.	3.6	5

#	ARTICLE	IF	CITATIONS
6342	Horizontal transfer of intracellular and extracellular ARGs in sludge compost under sulfamethoxazole stress. <i>Chemical Engineering Journal</i> , 2023, 454, 139968.	12.7	14
6343	De novo transcriptome assembly and identification of G-Protein-Coupled-Receptors (GPCRs) in two species of monogenean parasites of fish. <i>Parasite</i> , 2022, 29, 51.	2.0	4
6344	PSPGO: Cross-Species Heterogeneous Network Propagation for Protein Function Prediction. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2023, 20, 1713-1724.	3.0	1
6345	Food provisioning results in functional, but not compositional, convergence of the gut microbiomes of two wild <i>Rhinopithecus</i> species: Evidence of functional redundancy in the gut microbiome. <i>Science of the Total Environment</i> , 2023, 858, 159957.	8.0	7
6346	Metabolic and metatranscriptional characteristics of corals bleaching induced by the most severe marine heatwaves in the South China Sea. <i>Science of the Total Environment</i> , 2023, 858, 160019.	8.0	4
6347	Simultaneous removal of sediment and water contaminants in a microbial electrochemical system with embedded active electrode by in-situ utilization of electrons. <i>Journal of Hazardous Materials</i> , 2023, 443, 130172.	12.4	3
6349	Transcriptome profiling revealed salt stress-responsive genes in <i>Lilium pumilum</i> bulbs. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	2
6350	Identification and Expression Analysis of Odorant-Binding and Chemosensory Protein Genes in Virus Vector <i>Nephotettix cincticeps</i> . <i>Insects</i> , 2022, 13, 1024.	2.2	0
6351	Comparative Genomics of the Genus <i>Pseudomonas</i> Reveals Host- and Environment-Specific Evolution. <i>Microbiology Spectrum</i> , 2022, 10, .	3.0	11
6352	Placing human gene families into their evolutionary context. <i>Human Genomics</i> , 2022, 16, .	2.9	6
6353	The Characterization of Three Novel Insect-Specific Viruses Discovered in the Bean Bug, <i>Riptortus pedestris</i> . <i>Viruses</i> , 2022, 14, 2500.	3.3	2
6354	Function-Based Rhizosphere Assembly along a Gradient of Desiccation in the Former Aral Sea. <i>MSystems</i> , 2022, 7, .	3.8	6
6355	Sequencing and Variant Detection of Eight Abundant Plant-Infecting Tobamoviruses across Southern California Wastewater. <i>Microbiology Spectrum</i> , 2022, 10, .	3.0	10
6356	Genome-partitioning strategy, plastid and nuclear phylogenomic discordance, and its evolutionary implications of <i>Clematis</i> (Ranunculaceae). <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	2
6357	Comparing adventitious root-formation and graft-unification abilities in clones of <i>Argania spinosa</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	2
6358	Genome-wide survey reveals the phylogenomic relationships of <i>Chirolophis japonicus</i> Herzenstein, 1890 (Stichaeidae, Perciformes). <i>ZooKeys</i> , 0, 1129, 55-72.	1.1	2
6359	Seasonal dynamics of the wild rodent faecal virome. <i>Molecular Ecology</i> , 2023, 32, 4763-4776.	3.9	6
6361	Frequent Occurrence and Metabolic Versatility of <i>Marinifilaceae</i> Bacteria as Key Players in Organic Matter Mineralization in Global Deep Seas. <i>MSystems</i> , 2022, 7, .	3.8	7

#	ARTICLE	IF	CITATIONS
6362	Metagenomic characterization of sphingomyelinase C in the microbiome of humans and environments. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	3.9	1
6363	Asynchronous responses of microbial CAZymes genes and the net CO ₂ exchange in alpine peatland following 5 years of continuous extreme drought events. <i>ISME Communications</i> , 2022, 2, .	4.2	3
6364	Diet-derived metabolites and mucus link the gut microbiome to fever after cytotoxic cancer treatment. <i>Science Translational Medicine</i> , 2022, 14, .	12.4	13
6365	Co-circulation of alpha- and beta-coronaviruses in <i>Pteropus vampyrus</i> flying foxes from Indonesia. <i>Transboundary and Emerging Diseases</i> , 2022, 69, 3917-3925.	3.0	1
6366	Contrasting modes of macro and microsynteny evolution in a eukaryotic subphylum. <i>Current Biology</i> , 2022, 32, 5335-5343.e4.	3.9	8
6367	Novel RNA viruses in oysters revealed by virome. , 2022, 1, .		6
6368	Metagenomic Insights into Microbial Community Structure, Function, and Salt Adaptation in Saline Soils of Arid Land, China. <i>Microorganisms</i> , 2022, 10, 2183.	3.6	2
6369	Comparative genomics of Lactobacillaceae from the gut of honey bees, <i>Apis mellifera</i> , from the Eastern United States. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	3
6370	Vetinformatics from functional genomics to drug discovery: Insights into decoding complex molecular mechanisms of livestock systems in veterinary science. <i>Frontiers in Veterinary Science</i> , 0, 9, .	2.2	7
6371	CoreGenes5.0: An Updated User-Friendly Webserver for the Determination of Core Genes from Sets of Viral and Bacterial Genomes. <i>Viruses</i> , 2022, 14, 2534.	3.3	6
6372	Effects of Microplastic on Human Gut Microbiome: Detection of Plastic-Degrading Genes in Human Gut Exposed to Microplastics—Preliminary Study. <i>Environments - MDPI</i> , 2022, 9, 140.	3.3	6
6376	Comparison and Functional Analysis of Odorant-Binding Proteins and Chemosensory Proteins in Two Closely Related Thrips Species, <i>Frankliniella occidentalis</i> and <i>Frankliniella intonsa</i> (Thysanoptera:) Tj ETQq1 1 0.784314 rgBT /Overlock 1 2022, 23, 13900.	4.1	2
6378	Comparative transcriptome sequencing analysis of female and male <i>Decapterus macrosoma</i> . <i>PeerJ</i> , 0, 10, e14342.	2.0	0
6379	MTSv: rapid alignment-based taxonomic classification and high-confidence metagenomic analysis. <i>PeerJ</i> , 0, 10, e14292.	2.0	1
6380	Multi-kingdom gut microbiota analyses define COVID-19 severity and post-acute COVID-19 syndrome. <i>Nature Communications</i> , 2022, 13, .	12.8	30
6381	Physiological and Transcriptomic Analysis Revealed the Molecular Mechanism of <i>Pinus koraiensis</i> Responses to Light. <i>International Journal of Molecular Sciences</i> , 2022, 23, 13608.	4.1	1
6382	Investigation of the halophilic <i>PET</i> hydrolase <i>PET6</i> from <i>Vibrio gazogenes</i> . <i>Protein Science</i> , 2022, 31, .	7.6	8
6383	Improved assembly and annotation of the sesame genome. <i>DNA Research</i> , 2022, 29, .	3.4	11

#	ARTICLE	IF	CITATIONS
6384	Nitrification Regulates the Spatiotemporal Variability of N ₂ O Emissions in a Eutrophic Lake. <i>Environmental Science & Technology</i> , 2022, 56, 17430-17442.	10.0	12
6385	Disulfiram ameliorates nonalcoholic steatohepatitis by modulating the gut microbiota and bile acid metabolism. <i>Nature Communications</i> , 2022, 13, .	12.8	19
6386	Selection for Translational Efficiency in Genes Associated with Alphaproteobacterial Gene Transfer Agents. <i>MSystems</i> , 2022, 7, .	3.8	4
6387	Defining the sensitivity landscape of EGFR variants to tyrosine kinase inhibitors. <i>Translational Research</i> , 2023, 255, 14-25.	5.0	8
6388	Decoding the microbiome and metabolome of the <i>Panchagavya</i> —An indigenous fermented bio- <i>formulation</i> . , 2022, 1, .		4
6389	Gene family evolution and natural selection signatures in <i>Datura</i> spp. (Solanaceae). <i>Frontiers in Ecology and Evolution</i> , 0, 10, .	2.2	1
6390	Single-cell transcriptome analysis of the <i>in vivo</i> response to viral infection in the cave nectar bat <i>Eonycteris spelaea</i> . <i>Immunity</i> , 2022, 55, 2187-2205.e5.	14.3	7
6392	Inactivation of the MSTN gene expression changes the composition and function of the gut microbiome in sheep. <i>BMC Microbiology</i> , 2022, 22, .	3.3	4
6393	Explaining the resistomes in a megacity's water supply catchment: Roles of microbial assembly-dominant taxa, niched environments and pathogenic bacteria. <i>Water Research</i> , 2023, 228, 119359.	11.3	8
6394	Exploring clade differentiation of the <i>Faecalibacterium prausnitzii</i> complex. <i>IScience</i> , 2022, 25, 105533.	4.1	0
6395	Integrated next-generation sequencing and comparative transcriptomic analysis of leaves provides novel insights into the ethylene pathway of <i>Chrysanthemum morifolium</i> in response to a Chinese isolate of chrysanthemum virus B. <i>Virology Journal</i> , 2022, 19, .	3.4	6
6396	Integrated Genomic and Transcriptomic Elucidation of Flowering in Garlic. <i>International Journal of Molecular Sciences</i> , 2022, 23, 13876.	4.1	1
6398	HGTtree v2.0: a comprehensive database update for horizontal gene transfer (HGT) events detected by the tree-reconciliation method. <i>Nucleic Acids Research</i> , 2023, 51, D1010-D1018.	14.5	5
6399	Complete Genome Sequence and Comparative Genome Analysis of <i>Variovorax</i> sp. Strains PAMC28711, PAMC26660, and PAMC28562 and Trehalose Metabolic Pathways in Antarctica Isolates. <i>International Journal of Microbiology</i> , 2022, 2022, 1-13.	2.3	3
6401	Discovery of integrons in Archaea: Platforms for cross-domain gene transfer. <i>Science Advances</i> , 2022, 8, .	10.3	8
6402	Effect of Shading on the Morphological, Physiological, and Biochemical Characteristics as Well as the Transcriptome of Matcha Green Tea. <i>International Journal of Molecular Sciences</i> , 2022, 23, 14169.	4.1	8
6404	The cancer chemotherapeutic 5-fluorouracil is a potent <i>Fusobacterium nucleatum</i> inhibitor and its activity is modified by intratumoral microbiota. <i>Cell Reports</i> , 2022, 41, 111625.	6.4	38
6405	AvP: A software package for automatic phylogenetic detection of candidate horizontal gene transfers. <i>PLoS Computational Biology</i> , 2022, 18, e1010686.	3.2	5

#	ARTICLE	IF	CITATIONS
6407	Dynamic Changes of Rhizosphere Soil Microbiome and Functional Genes Involved in Carbon and Nitrogen Cycling in Chinese Fir Monoculture. <i>Forests</i> , 2022, 13, 1906.	2.1	1
6408	Metagenomics revealing molecular profiles of microbial community structure and metabolic capacity in Bamucuo lake, Tibet. <i>Environmental Research</i> , 2023, 217, 114847.	7.5	2
6409	Metagenomic insights into the changes in the rhizosphere microbial community caused by the root-knot nematode <i>Meloidogyne incognita</i> in tobacco. <i>Environmental Research</i> , 2023, 216, 114848.	7.5	8
6410	Adaptation of a microbial community to demand-oriented biological methanation. , 2022, 15, .		4
6411	Wood feeding and social living: Draft genome of the subterranean termite <i>Reticulitermes lucifugus</i> (Blattodea; Termitoidae). <i>Insect Molecular Biology</i> , 2023, 32, 118-131.	2.0	4
6412	Effects of vegetation type differences induced by human disturbance on the nutrition strategy and gut microbiota of Siberian roe deer. <i>Molecular Ecology</i> , 2023, 32, 2534-2550.	3.9	2
6413	Viral community-wide auxiliary metabolic genes differ by lifestyles, habitats, and hosts. <i>Microbiome</i> , 2022, 10, .	11.1	35
6414	OrthoDB v11: annotation of orthologs in the widest sampling of organismal diversity. <i>Nucleic Acids Research</i> , 2023, 51, D445-D451.	14.5	76
6415	Genomic remnants of ancestral methanogenesis and hydrogenotrophy in Archaea drive anaerobic carbon cycling. <i>Science Advances</i> , 2022, 8, .	10.3	17
6416	In vitro fermentation of fructooligosaccharide and galactooligosaccharide and their effects on gut microbiota and SCFAs in infants. <i>Journal of Functional Foods</i> , 2022, 99, 105329.	3.4	6
6417	Dissection of <i>Besnoitia besnoiti</i> intermediate host life cycle stages: From morphology to gene expression. <i>PLoS Pathogens</i> , 2022, 18, e1010955.	4.7	3
6418	Antarctic <i>Sphingomonas</i> sp. So64.6b showed evolutive divergence within its genus, including new biosynthetic gene clusters. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	2
6419	Betalain accumulation and de novo transcriptome sequencing reveal the potential to increase bioactive compounds in <i>Alternanthera sessilis</i> elicited by methyl jasmonate. <i>Acta Physiologiae Plantarum</i> , 2023, 45, .	2.1	3
6420	Batch-mode stimulation of hydrocarbons biodegradation in freshwater sediments from historically contaminated AlÅksne lake. <i>Journal of Contaminant Hydrology</i> , 2023, 253, 104103.	3.3	2
6421	Spatiotemporal heterogeneity of nitrogen transformation potentials in a freshwater estuarine system. <i>Science of the Total Environment</i> , 2023, 859, 160335.	8.0	1
6423	Metagenomics reveals the response of antibiotic resistance genes to elevated temperature in the Yellow River. <i>Science of the Total Environment</i> , 2023, 859, 160324.	8.0	8
6425	The pan-genome of <i>Aspergillus fumigatus</i> provides a high-resolution view of its population structure revealing high levels of lineage-specific diversity driven by recombination. <i>PLoS Biology</i> , 2022, 20, e3001890.	5.6	21
6426	Parallel evolution of amphioxus and vertebrate small-scale gene duplications. <i>Genome Biology</i> , 2022, 23, .	8.8	14

#	ARTICLE	IF	CITATIONS
6428	The first complete genome of the simian malaria parasite <i>Plasmodium brasilianum</i> . <i>Scientific Reports</i> , 2022, 12, .	3.3	5
6429	Virome and nrVEEome diversity of <i>Aedes albopictus</i> mosquitoes from La Reunion Island and China. <i>Virology Journal</i> , 2022, 19, .	3.4	3
6431	Antibiotic sulfadiazine degradation by persulfate oxidation: Intermediates dependence of ecotoxicity and the induction of antibiotic resistance genes. <i>Bioresource Technology</i> , 2023, 368, 128306.	9.6	9
6432	Dietary citrus flavonoid extract improves lactational performance through modulating rumen microbiome and metabolites in dairy cows. <i>Food and Function</i> , 2023, 14, 94-111.	4.6	9
6433	Transcriptional profiling reveals a critical role of <i>GmFT2a</i> in soybean staygreen syndrome caused by the pest <i>Riptortus pedestris</i> . <i>New Phytologist</i> , 2023, 237, 1876-1890.	7.3	19
6434	Phenylalanine induces mango fruit resistance against chilling injuries during storage at suboptimal temperature. <i>Food Chemistry</i> , 2023, 405, 134909.	8.2	9
6435	Haplotype-phased and chromosome-level genome assembly of <i>Puccinia polysora</i> , a gigascale fungal pathogen causing southern corn rust. <i>Molecular Ecology Resources</i> , 2023, 23, 601-620.	4.8	7
6437	BDBlast: A Memory Efficient Architecture for Pairwise Alignments. <i>Lecture Notes in Computer Science</i> , 2022, , 1-13.	1.3	0
6438	Metagenomic insights into feasibility of agricultural wastes on optimizing water quality and natural bait by regulating microbial loop. <i>Environmental Research</i> , 2023, 217, 114941.	7.5	1
6439	Community-integrated multi-omics facilitates the isolation of an organohalide dehalogenation microorganism. <i>Innovation(China)</i> , 2023, 4, 100355.	9.1	2
6440	Identification of the key metabolites and related genes network modules highly associated with the nutrients and taste components among different Pepino (<i>Solanum muricatum</i>) cultivars. <i>Food Research International</i> , 2023, 163, 112287.	6.2	4
6441	Interactions among deep-sea mussels and their epibiotic and endosymbiotic chemoautotrophic bacteria: Insights from multi-omics analysis. <i>Zoological Research</i> , 2023, 44, 106-125.	2.1	4
6442	Coexistence of microplastics alters the inhibitory effect of antibiotics on sludge anaerobic digestion. <i>Chemical Engineering Journal</i> , 2023, 455, 140754.	12.7	25
6443	Metagenomics reveals that temperature predicts a small proportion of antibiotic resistomes and mobile genetic elements in polluted water. <i>Environmental Pollution</i> , 2023, 317, 120793.	7.5	5
6444	The impact of exclusive enteral nutrition on the gut microbiome and bile acid metabolism in pediatric Crohn's disease. <i>Clinical Nutrition</i> , 2023, 42, 116-128.	5.0	6
6445	Natural formation of copper sulfide nanoparticles via microbially mediated organic sulfur mineralization in soil: Processes and mechanisms. <i>Geoderma</i> , 2023, 430, 116300.	5.1	1
6446	Nitrogen-fixing sulfate reducing bacteria in shallow coastal sediments under simulated resuspension. <i>Estuarine, Coastal and Shelf Science</i> , 2023, 280, 108165.	2.1	5
6447	Transcriptome assemblies of two deep-sea octocorals <i>Calyptraphora lyra</i> and <i>Chrysogorgia stellata</i> from West Pacific seamount, Godin Guyot. <i>Marine Genomics</i> , 2023, 67, 101006.	1.1	1

#	ARTICLE	IF	CITATIONS
6448	Metabolomics and transcriptomics analyses provides insights into S-alk(en)yl cysteine sulfoxides (CSOs) accumulation in onion (<i>Allium cepa</i>). <i>Scientia Horticulturae</i> , 2023, 310, 111727.	3.6	2
6449	Metagenomic insights into the effects of organic and inorganic agricultural managements on soil phosphorus cycling. <i>Agriculture, Ecosystems and Environment</i> , 2023, 343, 108281.	5.3	8
6450	Composition and function of viruses in sauce-flavor baijiu fermentation. <i>International Journal of Food Microbiology</i> , 2023, 387, 110055.	4.7	4
6451	Taxonomic and functional dynamics of the soil microbiome from a tropical dry forest in kraft lignin-amended microcosms. <i>Applied Soil Ecology</i> , 2023, 183, 104766.	4.3	0
6452	Cold-adapted amphipod species upon heat stress: Proteomic responses and their correlation with transcriptomic responses. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2023, 45, 101048.	1.0	0
6453	Plant invasion by <i>Chromolaena odorata</i> alters the soil microbiome and provides insight into the role of copiotrophs. <i>Ecological Genetics and Genomics</i> , 2023, 26, 100157.	0.5	1
6454	Genetic diversity and known virulence genes in <i>Listeria innocua</i> strains isolated from cattle abortions and farm environment. <i>Veterinary and Animal Science</i> , 2023, 19, 100276.	1.5	3
6455	Reducing the number of accepted species in <i>Aspergillus</i> series <i>Nigri</i> . <i>Studies in Mycology</i> , 2022, 102, 95-132.	7.2	11
6456	Comparison of functional classification systems. <i>NAR Genomics and Bioinformatics</i> , 2022, 4, .	3.2	1
6457	Assessment of <i>Hippocampus guttulatus</i> diet using DNA metabarcoding of faeces. , 2022, , .		1
6458	Distinct evolutionary trajectories in the <i>Escherichia coli</i> pangenome occur within sequence types. <i>Microbial Genomics</i> , 2022, 8, .	2.0	10
6459	Draft Genome Sequence of Carrot Alternaria Leaf Blight Pathogen <i>Alternaria dauci</i> . <i>Plant Disease</i> , 2023, 107, 2197-2200.	1.4	1
6460	Pea-Tea Intercropping Improves Tea Quality through Regulating Amino Acid Metabolism and Flavonoid Biosynthesis. <i>Foods</i> , 2022, 11, 3746.	4.3	5
6461	Influence of salinity on the diversity and composition of carbohydrate metabolism, nitrogen and sulfur cycling genes in lake surface sediments. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	7
6463	Molecular detection and characterisation of the first Japanese encephalitis virus belonging to genotype IV acquired in Australia. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010754.	3.0	14
6464	Genome sequence and silkomics of the spindle ermine moth, <i>Yponomeuta cagnagella</i> , representing the early diverging lineage of the ditrysian Lepidoptera. <i>Communications Biology</i> , 2022, 5, .	4.4	3
6465	Transposable elements drive intron gain in diverse eukaryotes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	15
6466	Higher N ₂ O production in sequencing batch reactors compared to continuous stirred tank reactors: effect of feast-famine cycles. <i>Frontiers of Environmental Science and Engineering</i> , 2023, 17, .	6.0	0

#	ARTICLE	IF	CITATIONS
6467	Unravelling the genetic potential for hydrocarbon degradation in the sediment microbiome of Antarctic islands. <i>FEMS Microbiology Ecology</i> , 2022, 99, .	2.7	1
6469	MORBIDITY AND MORTALITY OF HAWAIIAN GEESE (<i>BRANTA SANDVICENSIS</i>) AND LAYSAN ALBATROSS (<i>PHOEBASTRIA IMMUTABILIS</i>) ASSOCIATED WITH RETICULOENDOTHELIOSIS VIRUS. <i>Journal of Wildlife Diseases</i> , 2022, 58, .	0.8	0
6470	Genomic signatures of recent convergent transitions to social life in spiders. <i>Nature Communications</i> , 2022, 13, .	12.8	7
6471	Characteristics of the Genome, Transcriptome and Ganoderic Acid of the Medicinal Fungus <i>Ganoderma lingzhi</i> . <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 1257.	3.5	3
6473	Genome-Scale Investigation of GARP Family Genes Reveals Their Pivotal Roles in Nutrient Stress Resistance in Allotetraploid Rapeseed. <i>International Journal of Molecular Sciences</i> , 2022, 23, 14484.	4.1	3
6474	The effects of elemene emulsion injection on rat fecal microbiota and metabolites: Evidence from metagenomic exploration and liquid chromatography-mass spectrometry. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	0
6476	Plasmid Genomes Reveal the Distribution, Abundance, and Organization of Mercury-Related Genes and Their Co-Distribution with Antibiotic Resistant Genes in Gammaproteobacteria. <i>Genes</i> , 2022, 13, 2149.	2.4	4
6477	Deep-sea sediment metagenome from Bay of Bengal reveals distinct microbial diversity and functional significance. <i>Genomics</i> , 2022, 114, 110524.	2.9	9
6478	Community characteristics and functional gene response analysis of phosphorus-metabolizing bacteria in plateau saline lake sediments. <i>Frontiers in Environmental Science</i> , 0, 10, .	3.3	2
6479	Rhizosphere microorganisms of <i>Crocus sativus</i> as antagonists against pathogenic <i>Fusarium oxysporum</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	0
6480	PhaTYP: predicting the lifestyle for bacteriophages using BERT. <i>Briefings in Bioinformatics</i> , 2023, 24, .	6.5	27
6481	Genome Sequence Resource for <i>Cercospora rodmanii</i> J1, a Potential Biological Control Agent for Water Hyacinth. <i>Phytopathology</i> , 2022, 112, 2462-2465.	2.2	0
6483	Fecal microbiota transplantation restores normal fecal composition and delays malignant development of mild chronic kidney disease in rats. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	5
6484	The profile and persistence of clinically critical antibiotic resistance genes and human pathogenic bacteria in manure-amended farmland soils. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	3.9	1
6486	Metabolome and transcriptome associated analysis of sesquiterpenoid metabolism in <i>Nardostachys jatamansi</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	2
6487	A large-scale benchmark study of tools for the classification of protein-coding and non-coding RNAs. <i>Nucleic Acids Research</i> , 2022, 50, 12094-12111.	14.5	2
6488	Glutathione Plays a Positive Role in the Proliferation of <i>Pinus koraiensis</i> Embryogenic Cells. <i>International Journal of Molecular Sciences</i> , 2022, 23, 14679.	4.1	1
6490	Influence of Geochemistry in the Tropical Hot Springs on Microbial Community Structure and Function. <i>Current Microbiology</i> , 2023, 80, .	2.2	1

#	ARTICLE	IF	CITATIONS
6491	Genomic Characteristics of Elite Maize Inbred Line 18-599 and Its Transcriptional Response to Drought and Low-Temperature Stresses. <i>Plants</i> , 2022, 11, 3242.	3.5	0
6492	Nanopore long-read-only metagenomics enables complete and high-quality genome reconstruction from mock and complex metagenomes. <i>Microbiome</i> , 2022, 10, .	11.1	28
6493	Chromosome-Level Genome Assembly of the Speckled Blue Grouper (<i>Epinephelus cyanopodus</i>) Provides Insight into Its Adaptive Evolution. <i>Biology</i> , 2022, 11, 1810.	2.8	1
6494	Co-infection of Peruvian horse sickness virus and West Nile virus associated with neurological diseases in horses from Brazil. <i>Heliyon</i> , 2022, 8, e12097.	3.2	0
6495	Discovering novel reproductive genes in a non-model fly using de novo GridION transcriptomics. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	1
6496	Comparison of Metagenomics and Metatranscriptomics Tools: A Guide to Making the Right Choice. <i>Genes</i> , 2022, 13, 2280.	2.4	9
6497	Whole-genome sequencing of a year-round fruiting jackfruit (<i>Artocarpus heterophyllus</i> Lam.) reveals high levels of single nucleotide variation. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	0
6498	<i>CaMYB12</i> underlies a major QTL for flavonoid content in pepper (<i>Capsicum</i>) Tj ETQq1 1,0784314,rgBT /Ove	7.3	7
6499	Integrative metagenomic and metabolomic analyses reveal the role of gut microbiota in antibody-mediated renal allograft rejection. <i>Journal of Translational Medicine</i> , 2022, 20, .	4.4	5
6501	Systematic evaluation of genome-wide metabolic landscapes in lactic acid bacteria reveals diet- and strain-specific probiotic idiosyncrasies. <i>Cell Reports</i> , 2022, 41, 111735.	6.4	8
6502	Nitrifiers Cooperate to Produce Nitrous Oxide in Plateau Wetland Sediments. <i>Environmental Science & Technology</i> , 2023, 57, 810-821.	10.0	3
6503	Metatranscriptional characterization of metabolic dynamics in anaerobic membrane bioreactor producing methane from low-strength wastewater. <i>Bioresource Technology</i> , 2023, 370, 128532.	9.6	1
6504	<i>Lactobacillus reuteri</i> improves the development and maturation of fecal microbiota in piglets through mother-to-infant microbe and metabolite vertical transmission. <i>Microbiome</i> , 2022, 10, .	11.1	14
6505	Comprehensive molecular and morphological resolution of blubber stratification in a deep-diving, fasting-adapted seal. <i>Frontiers in Physiology</i> , 0, 13, .	2.8	1
6506	DadY (PA5303) is required for fitness of <i>Pseudomonas aeruginosa</i> when growth is dependent on alanine catabolism. <i>Microbial Cell</i> , 2022, 9, 195-206.	3.2	2
6507	Characterization and Identification of a novel chromosome-encoded metallo- β -lactamase WUS-1 in <i>Myroides albus</i> P34. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	2
6508	Systematic analysis of Baobaoqu fermentation starter for Wuliangye Baijiu by the combination of metagenomics and metabolomics. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	0
6509	Compensatory Transcriptional Response of <i>Fischerella thermalis</i> to Thermal Damage of the Photosynthetic Electron Transfer Chain. <i>Molecules</i> , 2022, 27, 8515.	3.8	0

#	ARTICLE	IF	CITATIONS
6510	Identifying novel interactions of the colon-cancer related APC protein with Wnt-pathway nuclear transcription factors. <i>Cancer Cell International</i> , 2022, 22, .	4.1	1
6511	Genome-level analyses resolve an ancient lineage of symbiotic ascomycetes. <i>Current Biology</i> , 2022, 32, 5209-5218.e5.	3.9	14
6512	Cyanobacterial Blooms Are Not a Result of Positive Selection by Freshwater Eutrophication. <i>Microbiology Spectrum</i> , 2022, 10, .	3.0	2
6513	Microbial predators form a new supergroup of eukaryotes. <i>Nature</i> , 2022, 612, 714-719.	27.8	21
6514	Inflammatory Bowel Disease-Associated Gut Commensals Degrade Components of the Extracellular Matrix. <i>MBio</i> , 2022, 13, .	4.1	10
6515	Metagenomic insights into the characteristics of soil microbial communities in the decomposing biomass of Moso bamboo forests under different management practices. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	2
6516	Novel Virus Identification through Metagenomics: A Systematic Review. <i>Life</i> , 2022, 12, 2048.	2.4	7
6517	Targeted single-cell genomics reveals novel host adaptation strategies of the symbiotic bacteria <i>Endozoicomonas</i> in <i>Acropora tenuis</i> coral. <i>Microbiome</i> , 2022, 10, .	11.1	6
6518	New globally distributed bacterial phyla within the FCB superphylum. <i>Nature Communications</i> , 2022, 13, .	12.8	4
6519	Heritability of tomato rhizobacteria resistant to <i>Ralstonia solanacearum</i> . <i>Microbiome</i> , 2022, 10, .	11.1	14
6520	Transcriptome mining extends the host range of the <i>Flaviviridae</i> to non-bilaterians. <i>Virus Evolution</i> , 2023, 9, .	4.9	16
6521	Constraining the composition and quantity of organic matter used by abundant marine Thaumarchaeota. <i>Environmental Microbiology</i> , 2023, 25, 689-704.	3.8	5
6522	A chromosome-level genome assembly reveals genomic characteristics of the American mink (<i>Neogale</i>) Tj ETQq0 0 0 rgBT /Overlock 10 4.45 6	4.45	6
6523	<i>Vulcanimicrobium alpinus</i> gen. nov. sp. nov., the first cultivated representative of the candidate phylum "Eremiobacterota", is a metabolically versatile aerobic anoxygenic phototroph. <i>ISME Communications</i> , 2022, 2, .	4.2	8
6524	Integrated multi-omics analyses reveal effects of empagliflozin on intestinal homeostasis in high-fat-diet mice. <i>IScience</i> , 2023, 26, 105816.	4.1	1
6525	Mycorrhizal fungi alter root exudation to cultivate a beneficial microbiome for plant growth. <i>Functional Ecology</i> , 2023, 37, 664-675.	3.6	11
6528	Development of Simple Sequence REPEAT Markers for Genetic Diversity Analysis Based on the cDNA Sequences of Chinese Yam (<i>Dioscorea</i> spp.). <i>Horticulturae</i> , 2022, 8, 1163.	2.8	1
6530	Genome assembly and transcriptomic analyses of the repeatedly rejuvenating jellyfish <i>Turritopsis dohrnii</i> . <i>DNA Research</i> , 2023, 30, .	3.4	1

#	ARTICLE	IF	CITATIONS
6531	Population structure of an Antarctic aquatic cyanobacterium. <i>Microbiome</i> , 2022, 10, .	11.1	0
6532	Comparative Transcriptomics Sheds Light on Remodeling of Gene Expression during Diazotrophy in the Thermophilic Methanogen <i>Methanothermococcus thermolithotrophicus</i> . <i>MBio</i> , 2022, 13, .	4.1	7
6533	Metagenomics and metatranscriptomics reveal broadly distributed, active, novel methanotrophs in the Gulf of Mexico hypoxic zone and in the marine water column. <i>FEMS Microbiology Ecology</i> , 2023, 99, .	2.7	5
6534	Enhanced Arbovirus Surveillance with High-Throughput Metatranscriptomic Processing of Field-Collected Mosquitoes. <i>Viruses</i> , 2022, 14, 2759.	3.3	5
6535	Epitranscriptome changes triggered by ammonium nutrition regulate the proteome response of maritime pine roots. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	1
6537	An Insight into the Genome of Pathogenic and Non-Pathogenic <i>Acanthamoeba</i> . <i>Pathogens</i> , 2022, 11, 1558.	2.8	2
6538	Multispecies comparison of host responses to <i>Fusarium circinatum</i> challenge in tropical pines show consistency in resistance mechanisms. <i>Plant, Cell and Environment</i> , 2023, 46, 1705-1725.	5.7	1
6539	Altered vaginal eukaryotic virome is associated with different cervical disease status. <i>Virologica Sinica</i> , 2023, 38, 184-197.	3.0	2
6540	Long-Read Metagenome-Assembled Genomes Improve Identification of Novel Complete Biosynthetic Gene Clusters in a Complex Microbial Activated Sludge Ecosystem. <i>MSystems</i> , 2022, 7, .	3.8	11
6541	Virus classification for viral genomic fragments using PhaGCN2. <i>Briefings in Bioinformatics</i> , 2023, 24, .	6.5	22
6542	Integrated multi-omics of the gastrointestinal microbiome and ruminant host reveals metabolic adaptation underlying early life development. <i>Microbiome</i> , 2022, 10, .	11.1	4
6543	Impact of HIV infection and integrase strand transfer inhibitors-based treatment on the gut virome. <i>Scientific Reports</i> , 2022, 12, .	3.3	6
6544	Convergent evolution and horizontal gene transfer in Arctic Ocean microalgae. <i>Life Science Alliance</i> , 2023, 6, e202201833.	2.8	6
6545	Root Physiological Changes and Transcription Analysis of <i>Iris domestica</i> in Response to Persistent Drought. <i>Horticulturae</i> , 2022, 8, 1162.	2.8	1
6546	Metaproteomics reveals methyltransferases implicated in dichloromethane and glycine betaine fermentation by <i>Candidatus Formimonas warabiya</i> ™ strain DCMF. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	0
6547	Molecular Detection of <i>Candidatus Coxiella mudorwiae</i> in <i>Haemaphysalis concinna</i> in China. <i>Zoonoses</i> , 2022, 2, .	1.1	1
6548	Validation and Application of Long-Read Whole-Genome Sequencing for Antimicrobial Resistance Gene Detection and Antimicrobial Susceptibility Testing. <i>Antimicrobial Agents and Chemotherapy</i> , 2023, 67, .	3.2	9
6549	Evaluation of taxonomic classification and profiling methods for long-read shotgun metagenomic sequencing datasets. <i>BMC Bioinformatics</i> , 2022, 23, .	2.6	19

#	ARTICLE	IF	CITATIONS
6550	Draft genome of the medicinal tea tree <i>Melaleuca alternifolia</i> . <i>Molecular Biology Reports</i> , 2023, 50, 1545-1552.	2.3	5
6551	Independent Evolution Has Led to Distinct Genomic Signatures in Dutch Elm Disease-Causing Fungi and Other Vascular Wilts-Causing Fungal Pathogens. <i>Journal of Fungi</i> (Basel, Switzerland), 2023, 9, 2.	3.5	1
6552	Interpreting tree ensemble machine learning models with endoR. <i>PLoS Computational Biology</i> , 2022, 18, e1010714.	3.2	1
6553	Inflammatory microbes and genes as potential biomarkers of Parkinson's disease. <i>Npj Biofilms and Microbiomes</i> , 2022, 8, .	6.4	9
6555	Virus diversity and interactions with hosts in deep-sea hydrothermal vents. <i>Microbiome</i> , 2022, 10, .	11.1	12
6556	Sequencing and description of the complete mitochondrial genome of <i>Limatus durhamii</i> (Diptera: Tj ETQq1 1 0.784314 rgBT ₁ /Overlook	2.0	1
6557	Transcriptional responses indicate acclimation to prolonged deoxygenation in the coral <i>Stylophora pistillata</i> . <i>Frontiers in Marine Science</i> , 0, 9, .	2.5	0
6558	Metagenomics analysis of the effects of <i>Agaricus bisporus</i> mycelia on microbial diversity and CAZymes in compost. <i>PeerJ</i> , 0, 10, e14426.	2.0	7
6559	MetaLab-MAG: A Metaproteomic Data Analysis Platform for Genome-Level Characterization of Microbiomes from the Metagenome-Assembled Genomes Database. <i>Journal of Proteome Research</i> , 2023, 22, 387-398.	3.7	3
6560	Characterizations of the Gut Bacteriome, Mycobiome, and Virome in Patients with Osteoarthritis. <i>Microbiology Spectrum</i> , 0, , .	3.0	10
6565	Metatranscriptomes reveal the diverse responses of <i>Thaumarchaeota</i> ecotypes to environmental variations in the northern slope of the South China Sea. <i>Environmental Microbiology</i> , 0, , .	3.8	2
6567	Genome of <i>Paspalum vaginatum</i> and the role of trehalose mediated autophagy in increasing maize biomass. <i>Nature Communications</i> , 2022, 13, .	12.8	4
6568	Gene Expression Profiling of <i>Trematomus bernacchii</i> in Response to Thermal and Stabing Stress. <i>Fishes</i> , 2022, 7, 387.	1.7	1
6570	<i>Sinapis</i> genomes provide insights into whole-genome triplication and divergence patterns within tribe Brassiceae. <i>Plant Journal</i> , 2023, 113, 246-261.	5.7	5
6571	Relating biomass composition and the distribution of metabolic functions in the co-fermentation of sugarcane vinasse and glycerol. <i>International Journal of Hydrogen Energy</i> , 2023, 48, 8837-8853.	7.1	5
6572	Evolution and Phylogeny of Soybean Mosaic Virus Based on 143 Complete Genomes. <i>International Journal of Molecular Sciences</i> , 2023, 24, 22.	4.1	2
6573	The Sugar Metabolic Model of <i>Aspergillus niger</i> Can Only Be Reliably Transferred to Fungi of Its Phylum. <i>Journal of Fungi</i> (Basel, Switzerland), 2022, 8, 1315.	3.5	6
6574	Probiotic properties of <i>Lactobacillus plantarum</i> and application in prebiotic gummies. <i>LWT - Food Science and Technology</i> , 2023, 174, 114357.	5.2	2

#	ARTICLE	IF	CITATIONS
6575	Metagenomic analysis reveals novel dietary-related viruses in the gut virome of marmosets hybrids (<i>Callithrix jacchus</i> x <i>Callithrix penicillata</i>), Brazil. <i>Virus Research</i> , 2023, 325, 199017.	2.2	1
6577	A Comparative Transcriptomic with UPLC-Q-Exactive MS Reveals Differences in Gene Expression and Components of Iridoid Biosynthesis in Various Parts of <i>Gentiana macrophylla</i> . <i>Genes</i> , 2022, 13, 2372.	2.4	3
6578	A Non-Gradual Development Process of Cicada Eyes at the End of the Fifth-Instar Nymphal Stage to Obtain Visual Ability. <i>Insects</i> , 2022, 13, 1170.	2.2	0
6581	Nanopore/Illumina Hybrid Whole-genome Sequence Resource of <i>Plenodomus lindquistii</i> Strain US01 Infecting Sunflower. <i>Plant Disease</i> , 0, , .	1.4	0
6582	Draft Genome Sequences of 14 Fungal Species from <i>Alternaria</i> Section <i>Infectoriae</i> . <i>Microbiology Resource Announcements</i> , 0, , .	0.6	0
6583	A case for investment in clinical metagenomics in low-income and middle-income countries. <i>Lancet Microbe</i> , The, 2023, 4, e192-e199.	7.3	7
6584	Arable soil nitrogen dynamics reflect organic inputs via the extended composite phenotype. <i>Nature Food</i> , 2023, 4, 51-60.	14.0	3
6585	Hepeliviruses in two waterbodies in Berlin, Germany. <i>Archives of Virology</i> , 2023, 168, .	2.1	1
6586	Genome-Wide Analysis and Evolutionary History of the Necrosis- and Ethylene-Inducing Peptide 1-Like Protein (NLP) Superfamily Across the Dothideomycetes Class of Fungi. <i>Current Microbiology</i> , 2023, 80, .	2.2	2
6587	Characterization of <i>Pantoea ananatis</i> from rice planthoppers reveals a clade of rice-associated <i>P. ananatis</i> undergoing genome reduction. <i>Microbial Genomics</i> , 2022, 8, .	2.0	2
6588	Investigation of the Virome and Characterization of Issyk-Kul Virus from Swedish <i>Myotis brandtii</i> Bats. <i>Pathogens</i> , 2023, 12, 12.	2.8	1
6591	Chromosome-scale genome assembly of <i>Eustoma grandiflorum</i> , the first complete genome sequence in the genus <i>Eustoma</i> . <i>G3: Genes, Genomes, Genetics</i> , 2023, 13, .	1.8	2
6592	Genome-wide analysis of the Tritipyrum WRKY gene family and the response of TtWRKY256 in salt-tolerance. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	4
6593	Transcriptome profiling reveals the underlying mechanism of grape post-harvest pathogen <i>Penicillium olsonii</i> against the metabolites of <i>Bacillus velezensis</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	2
6594	The gut microbiota in multiple sclerosis varies with disease activity. <i>Genome Medicine</i> , 2023, 15, .	8.2	23
6595	Gut microbial community structure and function of Przewalski's horses varied across reintroduced sites in China. <i>Integrative Zoology</i> , 2023, 18, 1027-1040.	2.6	1
6597	Ecotoxicological effects of common fungicides on the eastern honeybee <i>Apis cerana cerana</i> (Hymenoptera). <i>Science of the Total Environment</i> , 2023, 868, 161637.	8.0	4
6598	The hitchhikersâ€™ guide to RNA sequencing and functional analysis. <i>Briefings in Bioinformatics</i> , 2023, 24, .	6.5	8

#	ARTICLE	IF	CITATIONS
6599	RNA-Seq and genetic diversity analysis of faba bean (<i>Vicia faba</i> L.) varieties in China. PeerJ, 0, 11, e14259.	2.0	0
6600	Studying the Association between Antibiotic Resistance Genes and Insertion Sequences in Metagenomes: Challenges and Pitfalls. Antibiotics, 2023, 12, 175.	3.7	2
6601	Novel integrative elements and genomic plasticity in ocean ecosystems. Cell, 2023, 186, 47-62.e16.	28.9	25
6603	SMRT and Illumina sequencing provide insights into mechanisms of lignin and terpenoids biosynthesis in <i>Pinus massoniana</i> Lamb. International Journal of Biological Macromolecules, 2023, 232, 123267.	7.5	3
6604	Transcriptional and Physiological Analysis Reveal New Insights into the Regulation of Fertilization (N), Tj ETQq0 0 0 rgBT /Overlock 10 Tf Journal of Molecular Sciences, 2023, 24, 1522.	4.1	3
6605	Analysis of Floral Color Differences between Different Ecological Conditions of <i>Clematis tangutica</i> (Maxim.) Korsh. Molecules, 2023, 28, 462.	3.8	2
6607	Metagenomics Shines Light on the Evolution of “Sunscreen” Pigment Metabolism in the <i>Teloschistales</i> (Lichen-Forming Ascomycota). Genome Biology and Evolution, 2023, 15, .	2.5	8
6608	Nationwide genomic surveillance reveals the prevalence and evolution of honeybee viruses in China. Microbiome, 2023, 11, .	11.1	12
6609	A widespread family of phage-inducible chromosomal islands only steals bacteriophage tails to spread in nature. Cell Host and Microbe, 2023, 31, 69-82.e5.	11.0	9
6610	The <i>in planta</i> gene expression of <i>Austropuccinia psidii</i> in resistant and susceptible <i>Eucalyptus grandis</i> . Phytopathology, 0, , .	2.2	1
6611	Gene gain facilitated endosymbiotic evolution of Chlamydiae. Nature Microbiology, 2023, 8, 40-54.	13.3	19
6612	From head to rootlet: comparative transcriptomic analysis of a rhizocephalan barnacle <i>Peltogaster reticulata</i> (Crustacea: Rhizocephala). F1000Research, 0, 11, 583.	1.6	0
6613	Discovery and Characterization of Putative Glycoprotein-Encoding Mycoviruses in the <i>Bunyavirales</i> . Journal of Virology, 0, , .	3.4	3
6614	Culturomics- and metagenomics-based insights into the microbial community and function of rhizosphere soils in Sinai desert farming systems. Environmental Microbiomes, 2023, 18, .	5.0	5
6615	Profiling the composition and metabolic functions of microbial community in pellicle-forming radish paocai. International Journal of Food Microbiology, 2023, 388, 110087.	4.7	3
6616	Plasmid-Encoded Traits Vary across Environments. MBio, 2023, 14, .	4.1	3
6617	The person-to-person transmission landscape of the gut and oral microbiomes. Nature, 2023, 614, 125-135.	27.8	111
6620	<i>Sipunculus nudus</i> genome provides insights into evolution of spiralian phyla and development. Frontiers in Marine Science, 0, 9, .	2.5	1

#	ARTICLE	IF	CITATIONS
6621	Microbiome Data Analysis and Interpretation: Correlation Inference and Dynamic Pattern Discovery. <i>Translational Bioinformatics</i> , 2023, , 119-144.	0.0	0
6622	The <i>Aphelenchoides</i> genomes reveal substantial horizontal gene transfers in the last common ancestor of free-living and major plant-parasitic nematodes. <i>Molecular Ecology Resources</i> , 2023, 23, 905-919.	4.8	2
6623	Airborne bacterial community and antibiotic resistome in the swine farming environment: Metagenomic insights into livestock relevance, pathogen hosts and public risks. <i>Environment International</i> , 2023, 172, 107751.	10.0	11
6624	Genome-wide signatures of adaptation to extreme environments in red algae. <i>Nature Communications</i> , 2023, 14, .	12.8	17
6625	Chromosome-level genome assembly of a high-altitude-adapted frog (<i>Rana kukunoris</i>) from the Tibetan plateau provides insight into amphibian genome evolution and adaptation. <i>Frontiers in Zoology</i> , 2023, 20, .	2.0	3
6626	Residue Return Effects Outweigh Tillage Effects on Soil Microbial Communities and Functional Genes in Black Soil of Northeast China. <i>Chinese Geographical Science</i> , 2023, 33, 679-692.	3.0	0
6627	The Early Microbial Colonizers of a Short-Lived Volcanic Island in the Kingdom of Tonga. <i>MBio</i> , 2023, 14, .	4.1	3
6628	Metagenomics reveals biogeochemical processes carried out by sediment microbial communities in a shallow eutrophic freshwater lake. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	3
6629	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.	2.7	1
6630	Alterations of the gut virome in patients with systemic lupus erythematosus. <i>Frontiers in Immunology</i> , 0, 13, .	4.8	10
6633	A draft <i>Diabrotica virgifera virgifera</i> genome: insights into control and host plant adaption by a major maize pest insect. <i>BMC Genomics</i> , 2023, 24, .	2.8	2
6634	Anaerobic methanotroph <i>Candidatus Methanoperedens nitroreducens</i> ™ has a pleomorphic life cycle. <i>Nature Microbiology</i> , 2023, 8, 321-331.	13.3	10
6635	CRISPR-Cas provides limited phage immunity to a prevalent gut bacterium in gnotobiotic mice. <i>ISME Journal</i> , 2023, 17, 432-442.	9.8	0
6636	Systems biology's role in leveraging microalgal biomass potential: Current status and future perspectives. <i>Algal Research</i> , 2023, 69, 102963.	4.6	1
6638	Topographically Distinguished Microbiome Taxonomy and Stress-Response Genes of Royal Belum Rainforest and Raja Muda Musa Peat Swamp Revealed through Metagenomic Inquisition. <i>International Journal of Molecular Sciences</i> , 2023, 24, 872.	4.1	0
6639	A framework for the targeted recruitment of crop-beneficial soil taxa based on network analysis of metagenomics data. <i>Microbiome</i> , 2023, 11, .	11.1	6
6640	Virome and metagenomic analysis reveal the distinct distribution of microbiota in human fetal gut during gestation. <i>Frontiers in Immunology</i> , 0, 13, .	4.8	1
6641	A microbiome-targeting fibre-enriched nutritional formula is well tolerated and improves quality of life and haemoglobin A1c in type 2 diabetes: A double-blind, randomized, placebo-controlled trial. <i>Diabetes, Obesity and Metabolism</i> , 2023, 25, 1203-1212.	4.4	7

#	ARTICLE	IF	CITATIONS
6642	Metagenomic sequencing combined with flow cytometry facilitated a novel microbial risk assessment framework for bacterial pathogens in municipal wastewater without cultivation. , 2023, 2, .		5
6643	Deterministic Effect of pH on Shaping Soil Resistome Revealed by Metagenomic Analysis. Environmental Science & Technology, 2023, 57, 985-996.	10.0	22
6645	Integrating Phylogenetics With Intron Positions Illuminates the Origin of the Complex Spliceosome. Molecular Biology and Evolution, 2023, 40, .	8.9	11
6646	Microbial survival mechanisms within serpentinizing Mariana forearc sediments. FEMS Microbiology Ecology, 2023, 99, .	2.7	0
6647	The chromosome-scale genome assembly of the yellowtail clownfish <i>Amphiprion clarkii</i> provides insights into the melanin pigmentation of anemonefish. G3: Genes, Genomes, Genetics, 2023, 13, .	1.8	4
6648	The fecal and oropharyngeal eukaryotic viromes of healthy infants during the first year of life are personal. Scientific Reports, 2023, 13, .	3.3	6
6649	Transcriptome analysis of hepatopancreas of Chinese grass shrimp, <i>Palaemonetes sinensis</i> , infected by <i>Enterocytophaga</i> <i>artemiae</i> . Fish and Shellfish Immunology, 2023, 133, 108557.	3.6	3
6650	Full-length transcriptome analysis provides insights into larval shell formation in <i>Mulinia lateralis</i> . Frontiers in Marine Science, 0, 9, .	2.5	4
6651	Functional characterization of a novel aminoglycoside phosphotransferase, APH(9)-Ic, and its variant from <i>Stenotrophomonas maltophilia</i> . Frontiers in Cellular and Infection Microbiology, 0, 12, .	3.9	0
6653	Gut bacterial species in late trimester of pregnant sows influence the occurrence of stillborn piglet through pro-inflammation response. Frontiers in Immunology, 0, 13, .	4.8	2
6656	Arsenic methylation behavior and microbial regulation mechanisms in landfill leachate saturated zones. Environmental Pollution, 2023, 320, 121064.	7.5	1
6657	Exposure to metal mixtures may decrease children's cognitive flexibility via gut microbiota. Environmental Technology and Innovation, 2023, 29, 103012.	6.1	2
6658	Discovery of novel Mamastroviruses in Bactrian camels and dromedaries reveals complex recombination history. Virus Evolution, 2023, 9, .	4.9	2
6659	Micro and macroevolution of sea anemone venom phenotype. Nature Communications, 2023, 14, .	12.8	10
6660	The META tool optimizes metagenomic analyses across sequencing platforms and classifiers. Frontiers in Bioinformatics, 0, 2, .	2.1	0
6661	Microbial communities, resistance genes, and resistome risks in urban lakes of different trophic states: Internal links and external influences. Journal of Hazardous Materials Advances, 2023, 9, 100233.	3.0	1
6662	Relative quantification of phenolic compounds in exocarp-mesocarp and endocarp of sumac (<i>Toxicodendron vernicifluum</i>) combined with transcriptome analysis provides insights into glycosylation of flavonoids and biflavonoid biosynthesis. Plant Physiology and Biochemistry, 2023, 195, 275-287.	5.8	3
6663	Day-night cycle as a key environmental factor affecting coral-Symbiodiniaceae symbiosis. Ecological Indicators, 2023, 146, 109890.	6.3	2

#	ARTICLE	IF	CITATIONS
6664	A novel gyrovirus is abundant in yellow-eyed penguin (<i>Megadyptes antipodes</i>) chicks with a fatal respiratory disease. <i>Virology</i> , 2023, 579, 75-83.	2.4	4
6665	Genetic mapping and regional association analysis revealed a CYTOKININ RESPONSE FACTOR 10 gene controlling flowering time in <i>Brassica napus</i> L.. <i>Industrial Crops and Products</i> , 2023, 193, 116239.	5.2	3
6666	Genome sequencing progenies of magic mushrooms (<i>Psilocybe subaeruginosa</i>) identifies tetrapolar mating and gene duplications in the psilocybin pathway. <i>Fungal Genetics and Biology</i> , 2023, 165, 103769.	2.1	4
6667	Exploring diversity patterns and driving mechanisms of the antibiotic resistome and microbiome in saline groundwater. <i>Journal of Hazardous Materials</i> , 2023, 446, 130734.	12.4	8
6668	Sulfide intrusion in a habitat forming seagrass can be predicted from relative abundance of sulfur cycling genes in sediments. <i>Science of the Total Environment</i> , 2023, 864, 161144.	8.0	3
6669	Potential to mitigate nitrogen emissions from paddy runoff: A microbiological perspective. <i>Science of the Total Environment</i> , 2023, 865, 161306.	8.0	3
6670	An increase in enterovirus D68 circulation and viral evolution during a period of increased influenza like illness, The Johns Hopkins Health System, USA, 2022. <i>Journal of Clinical Virology</i> , 2023, 160, 105379.	3.1	10
6671	Genome-resolved metagenomics reveals depth-related patterns of microbial community structure and functions in a highly stratified, AMD overlaying mine tailings. <i>Journal of Hazardous Materials</i> , 2023, 447, 130774.	12.4	4
6672	Easy efficient HDR-based targeted knock-in in <i>Saccharomyces cerevisiae</i> genome using CRISPR-Cas9 system. <i>Bioengineered</i> , 2022, 13, 14857-14871.	3.2	2
6673	Identification of diverse papillomaviruses in captive black-and-white ruffed lemurs (<i>Varecia variegata</i>). <i>Archives of Virology</i> , 2023, 168, .	2.1	1
6674	Protein-Protein Interaction Network Analysis Reveals Distinct Patterns of Antibiotic Resistance Genes. , 2022, , .		2
6675	Safety Evaluation and Anti-Inflammatory Efficacy of <i>Lactacisbacillus paracasei</i> PS23. <i>International Journal of Molecular Sciences</i> , 2023, 24, 724.	4.1	1
6676	Multi-Omics Analyses Identify Signatures in Patients with Liver Cirrhosis and Hepatocellular Carcinoma. <i>Cancers</i> , 2023, 15, 210.	3.7	2
6678	Metagenomic analysis reveals unexplored diversity of archaeal virome in the human gut. <i>Nature Communications</i> , 2022, 13, .	12.8	14
6679	Molecular machineries of ciliogenesis, cell survival, and vasculogenesis are differentially expressed during regeneration in explants of the demosponge <i>Halichondria panicea</i> . <i>BMC Genomics</i> , 2022, 23, .	2.8	3
6680	Metagenomic analysis of viral genes integrated in whole genome sequencing data of Thai patients with Brugada syndrome. <i>Genomics and Informatics</i> , 2022, 20, e44.	0.8	1
6681	Regulation of the Nutrient Cycle Pathway and the Microbial Loop Structure by Different Types of Dissolved Organic Matter Decomposition in Lakes. <i>Environmental Science & Technology</i> , 2023, 57, 297-309.	10.0	6
6682	Phage-Host Prediction Using a Computational Tool Coupled with 16S rRNA Gene Amplicon Sequencing. <i>Viruses</i> , 2023, 15, 76.	3.3	0

#	ARTICLE	IF	CITATIONS
6684	OpenGenomeBrowser: a versatile, dataset-independent and scalable web platform for genome data management and comparative genomics. BMC Genomics, 2022, 23, .	2.8	1
6685	Phylogenomics and systematics of Entomobryoidea (Collembola): marker design, phylogeny and classification. Cladistics, 2023, 39, 101-115.	3.3	7
6686	A chromosome-scale genome assembly of Dasypyrum villosum provides insights into its application as a broad-spectrum disease resistance resource for wheat improvement. Molecular Plant, 2023, 16, 432-451.	8.3	9
6687	To assemble or not to assemble: metagenomic profiling of microbially mediated biogeochemical pathways in complex communities. Briefings in Bioinformatics, 2023, 24, .	6.5	2
6688	Full-Length Transcriptome Characterization and Functional Analysis of Pathogenesis-Related Proteins in Lilium Oriental Hybrid “Sorbonne”™ Infected with Botrytis elliptica. International Journal of Molecular Sciences, 2023, 24, 425.	4.1	1
6689	Primary Root Excision Induces ERF071, Which Mediates the Development of Lateral Roots in Makapuno Coconut (Cocos nucifera). Plants, 2023, 12, 105.	3.5	1
6690	Resistance to white spot syndrome virus in the European shore crab is associated with suppressed virion trafficking and heightened immune responses. Frontiers in Immunology, 0, 13, .	4.8	3
6691	The gold-ringed octopus (Amphioctopus fangsiao)Âgenome and cerebral single-nucleus transcriptomes provide insights into the evolution of karyotype and neural novelties. BMC Biology, 2022, 20, .	3.8	6
6692	GCL-GO: A novel sequence-based hierarchy-aware method for protein function prediction. , 2022, , .		0
6693	Revisiting the biological pathway for methanogenesis in landfill from metagenomic perspective”A case study of county-level sanitary landfill of domestic waste in North China plain. Environmental Research, 2023, 222, 115185.	7.5	6
6695	KMCP: accurate metagenomic profiling of both prokaryotic and viral populations by pseudo-mapping. Bioinformatics, 2023, 39, .	4.1	15
6696	Postglacial adaptations enabled colonization and quasi-clonal dispersal of ammonia-oxidizing archaea in modern European large lakes. Science Advances, 2023, 9, .	10.3	12
6697	Chromosome-level genome and the identification of sex chromosomes in <i>Uloborus diversus</i>. GigaScience, 2022, 12, .	6.4	6
6698	Genome-scale metabolic reconstruction of 7,302 human microorganisms for personalized medicine. Nature Biotechnology, 2023, 41, 1320-1331.	17.5	55
6699	Genome-wide analysis reveals the crucial role of lncRNAs in regulating the expression of genes controlling pollen development. Plant Cell Reports, 0, , .	5.6	1
6701	Multifactorial Microvariability of the Italian Raw Milk Cheese Microbiota and Implication for Current Regulatory Scheme. MSystems, 2023, 8, .	3.8	5
6702	The Pathology and Splenic Transcriptome Profiling of Trionyx sinensis Challenged with Bacillus cereus. Fishes, 2023, 8, 84.	1.7	1
6703	Characterization of a Potential Probiotic Strain in Koumiss. Fermentation, 2023, 9, 87.	3.0	2

#	ARTICLE	IF	CITATIONS
6704	Diversity and Distribution Characteristics of Viruses from Soda Lakes. <i>Genes</i> , 2023, 14, 323.	2.4	7
6705	BADASS: BActeriocin-Diversity ASsessment Software. <i>BMC Bioinformatics</i> , 2023, 24, .	2.6	3
6706	The gastrointestinal microbiome in dairy cattle is constrained by the deterministic driver of the region and the modified effect of diet. <i>Microbiome</i> , 2023, 11, .	11.1	12
6708	Chromosome-scale genomics, metabolomics, and transcriptomics provide insight into the synthesis and regulation of phenols in <i>Vitis adenocladia</i> grapes. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	1
6709	Metagenomics and new enzymes for the bioeconomy to 2030. , 2023, , 165-178.		1
6710	Acute appendicitis manifests as two microbiome state types with oral pathogens influencing severity. <i>Gut Microbes</i> , 2023, 15, .	9.8	5
6711	Dysbiosis of Oral Microbiota and Metabolite Profiles Associated with Type 2 Diabetes Mellitus. <i>Microbiology Spectrum</i> , 2023, 11, .	3.0	5
6712	Selective enrichment, identification, and isolation of diclofenac, ibuprofen, and carbamazepine degrading bacteria from a groundwater biofilm. <i>Environmental Science and Pollution Research</i> , 2023, 30, 44518-44535.	5.3	6
6714	Functional metagenomics profiling of symbiotic microbiome. , 2023, , 691-713.		1
6716	Changes in the Gut Microbiome Associated with Intussusception in Patients with Peutz-Jeghers Syndrome. <i>Microbiology Spectrum</i> , 2023, 11, .	3.0	4
6718	Not out of the Mediterranean: Atlantic populations of the gorgonian <i>Paramuricea clavata</i> are a separate sister species under further lineage diversification. <i>Ecology and Evolution</i> , 2023, 13, .	1.9	5
6720	PYuARF16/33 Are Involved in the Regulation of Lignin Synthesis and Rapid Growth in <i>Populus yunnanensis</i> . <i>Genes</i> , 2023, 14, 278.	2.4	3
6722	Transcriptome analysis indicates the involvement of herbicide-responsive and plant-pathogen interaction pathways in the development of resistance to <i>ACCase</i> inhibitors in <i>Apera spica-venti</i> . <i>Pest Management Science</i> , 2023, 79, 1944-1962.	3.4	6
6723	The Nutritional Intervention Improves the Metabolic Profile of Overweight and Obese PCOS Along with the Differences in Gut Microbiota. <i>Reproductive Sciences</i> , 0, , .	2.5	0
6724	Genomic Characteristics and Phylogenetic Analyses of a Multiple Drug-Resistant <i>Klebsiella pneumoniae</i> Harboring Plasmid-Mediated MCR-1 Isolated from Tai'an City, China. <i>Pathogens</i> , 2023, 12, 221.	2.8	0
6725	Chromosome-Level Genome Assembly of <i>Herpetospermum pedunculatum</i> (Cucurbitaceae). <i>Genome Biology and Evolution</i> , 2023, 15, .	2.5	1
6728	Effects of starters with different NDF/starch ratio on rumen fermentation parameters and rumen microorganisms in lambs. <i>Frontiers in Veterinary Science</i> , 0, 10, .	2.2	2
6729	The Influence of Symbiosis on the Proteome of the <i>Exaiptasia</i> Endosymbiont <i>Brevium minutum</i> . <i>Microorganisms</i> , 2023, 11, 292.	3.6	4

#	ARTICLE	IF	CITATIONS
6730	Updated Virophage Taxonomy and Distinction from Polinton-like Viruses. <i>Biomolecules</i> , 2023, 13, 204.	4.0	11
6731	Multi-Omic Profiling, Structural Characterization, and Potent Inhibitor Screening of Evasion-Related Proteins of a Parasitic Nematode, <i>Haemonchus contortus</i> , Surviving Vaccine Treatment. <i>Biomedicines</i> , 2023, 11, 411.	3.2	1
6732	Addressing the pervasive scarcity of structural annotation in eukaryotic algae. <i>Scientific Reports</i> , 2023, 13, .	3.3	2
6733	Comparative analysis of the chrysanthemum transcriptome with DNA methylation inhibitors treatment and silencing MET1 lines. <i>BMC Plant Biology</i> , 2023, 23, .	3.6	0
6736	Genomic diversity and ecological distribution of marine <i>Pseudoalteromonas</i> phages. <i>Marine Life Science and Technology</i> , 2023, 5, 271-285.	4.6	4
6737	The genome of sheep ked (<i>Melophagus ovinus</i>) reveals potential mechanisms underlying reproduction and narrower ecological niches. <i>BMC Genomics</i> , 2023, 24, .	2.8	14
6738	First complete genome sequence of lumpy skin disease virus directly from a clinical sample in South India. <i>Virus Genes</i> , 2023, 59, 317-322.	1.6	2
6739	Glacier-Fed Stream Biofilms Harbor Diverse Resistomes and Biosynthetic Gene Clusters. <i>Microbiology Spectrum</i> , 2023, 11, .	3.0	1
6742	Structural Characteristics and Functional Genes of Biofilms in Microbial Electrolysis Cells for Chlorobenzene Abatement. <i>ACS ES&T Water</i> , 2023, 3, 500-509.	4.6	4
6743	Silent recognition of flagellins from human gut commensal bacteria by Toll-like receptor 5. <i>Science Immunology</i> , 2023, 8, .	11.9	21
6745	Longitudinal comparison of the developing gut virome in infants and their mothers. <i>Cell Host and Microbe</i> , 2023, 31, 187-198.e3.	11.0	17
6746	Revealing the mode of action of Phenylalanine application in inducing fruit resistance to fungal pathogens. <i>Postharvest Biology and Technology</i> , 2023, 199, 112298.	6.0	4
6747	Barbel regeneration and function divergence in red-tail catfish (<i>Hemibagrus wyckioides</i>) based on the chromosome-level genomes and comparative transcriptomes. <i>International Journal of Biological Macromolecules</i> , 2023, 232, 123374.	7.5	1
6748	Substance bioconversion, hydrolases activity, and metagenomic analysis to unravel the enhanced biomethanation of corn stover with urea-hydrothermal pretreatment. <i>Journal of Environmental Management</i> , 2023, 333, 117466.	7.8	1
6749	Weak environmental adaptation of rare phylotypes sustaining soil multi-element cycles in response to decades-long fertilization. <i>Science of the Total Environment</i> , 2023, 871, 162063.	8.0	4
6751	Mulching decreased the abundance of microbial functional genes in phosphorus cycling under maize. <i>Applied Soil Ecology</i> , 2023, 187, 104833.	4.3	1
6752	Extreme-Scale Many-against-Many Protein Similarity Search. , 2022, , .		0
6753	Limited cross-species virus transmission in a spatially restricted coral reef fish community. <i>Virus Evolution</i> , 2023, 9, .	4.9	4

#	ARTICLE	IF	CITATIONS
6754	<i>FLOWERING LOCUS T</i> (<i>FT</i>) gene regulates short-day flowering in low latitude Xishuangbanna cucumber (<i>Cucumis sativus</i> var.) TJ ETQq0 0 0 rgBT /Overlock 10 Tf 50 7377d (<i>xishua		
6755	Polygenic adaptation from standing genetic variation allows rapid ecotype formation. <i>ELife</i> , 0, 12, .	6.0	4
6756	Host genetic traits underlying the composition/assembly of the citrus microbiome. <i>Phytobiomes Journal</i> , 0, , .	2.7	0
6758	Nitrogen cycling activities during decreased stratification in the coastal oxygen minimum zone off Namibia. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	2
6759	PFOS Induces Lipometabolism Change, Immune Defense, and Endocrine Disorders in Black-Spotted Frogs: Application of Transcriptome Profiling. <i>Diversity</i> , 2023, 15, 196.	1.7	1
6760	The transcriptomic response of <i>Hyphantria cunea</i> (Drury) to the infection of <i>Serratia marcescens</i> Bizio based on full-length SMRT transcriptome sequencing. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 13, .	3.9	1
6761	Bile salt hydrolase in non-enterotoxigenic <i>Bacteroides</i> potentiates colorectal cancer. <i>Nature Communications</i> , 2023, 14, .	12.8	15
6763	Virome diversity of ticks feeding on domestic mammals in China. <i>Virologica Sinica</i> , 2023, 38, 208-221.	3.0	4
6765	Environmental and genealogical effects on <scp>DNA</scp> methylation in a widespread apomictic dandelion lineage. <i>Journal of Evolutionary Biology</i> , 2023, 36, 663-674.	1.7	3
6766	Latent antibiotic resistance genes are abundant, diverse, and mobile in human, animal, and environmental microbiomes. <i>Microbiome</i> , 2023, 11, .	11.1	18
6767	Panguiarchaeum symbiosum, a potential hyperthermophilic symbiont in the TACK superphylum. <i>Cell Reports</i> , 2023, 42, 112158.	6.4	3
6768	Tradeoffs of microbial life history strategies drive the turnover of microbial-derived organic carbon in coastal saline soils. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	3
6769	Variation in gene expression along an elevation gradient of <i>Rhododendron sanguineum</i> var. <i>haemaleum</i> assessed in a comparative transcriptomic analysis. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	0
6771	Genome enrichment of rare and unknown species from complicated microbiomes by nanopore selective sequencing. <i>Genome Research</i> , 2023, 33, 612-621.	5.5	3
6773	Genome mining unveils a class of ribosomal peptides with two amino termini. <i>Nature Communications</i> , 2023, 14, .	12.8	12
6774	Gut microbiota alters host bile acid metabolism to contribute to intrahepatic cholestasis of pregnancy. <i>Nature Communications</i> , 2023, 14, .	12.8	17
6775	Metagenomic and Untargeted Metabolomic Analysis of the Effect of <i>Sporisorium reilianum</i> Polysaccharide on Improving Obesity. <i>Foods</i> , 2023, 12, 1578.	4.3	4
6776	Microbial Communities of Flor Velums and the Genetic Stability of Flor Yeasts Used for a Long Time for the Industrial Production of Sherry-like Wines. <i>Fermentation</i> , 2023, 9, 367.	3.0	2

#	ARTICLE	IF	CITATIONS
6777	Transcriptome wide analyses reveal intraspecific diversity in thermal stress responses of a dominant habitat-forming species. <i>Scientific Reports</i> , 2023, 13, .	3.3	3
6779	Metatranscriptomic Sequencing Reveals Host Species as an Important Factor Shaping the Mosquito Virome. <i>Microbiology Spectrum</i> , 2023, 11, .	3.0	2
6780	Genome Sequence and Assembly of 18 <i>Fusarium</i> Isolates from Florida Citrus under High Huanglongbing Disease Pressure and California Citrus under Low Huanglongbing Disease Pressure. <i>Microbiology Resource Announcements</i> , 0, , .	0.6	0
6781	Replicated life-history patterns and subsurface origins of the bacterial sister phyla <i>Nitrospirota</i> and <i>Nitrospinota</i> . <i>ISME Journal</i> , 2023, 17, 891-902.	9.8	7
6782	Composition and Functional Capacity of Gut Microbes are Associated with Arterial Stiffness: A Prospective Study. , 2023, 3, 102-111.		1
6783	<i>Natronogracilivirga saccharolytica</i> gen. nov., sp. nov. and <i>Cyclonatronum proteinivorum</i> gen. nov., sp. nov., haloalkaliphilic organotrophic bacteroidetes from hypersaline soda lakes forming a new family <i>Cyclonatronaceae</i> fam. nov. in the order <i>Balneolales</i> . <i>Systematic and Applied Microbiology</i> , 2023, 46, 126403.	2.8	3
6784	Environmental viromes reveal global virosphere of deep-sea sediment RNA viruses. <i>Journal of Advanced Research</i> , 2024, 56, 87-102.	9.5	1
6785	Effects of the oversized microplastic pollution layer on soil aggregates and organic carbon at different soil depths. <i>Journal of Hazardous Materials</i> , 2023, 450, 131014.	12.4	9
6786	Metagenomic analyses reveal that mesophilic anaerobic digestion substantially reduces the abundance of antibiotic resistance genes and mobile genetic elements in dairy manures. <i>Environmental Technology and Innovation</i> , 2023, 30, 103128.	6.1	4
6787	Distribution and co-occurrence of antibiotic resistance genes and bacterial pathogens in the effluent of decentralized sewage treatment systems in China. <i>International Biodeterioration and Biodegradation</i> , 2023, 180, 105596.	3.9	1
6788	Soil metagenome and metabolome of peanut intercropped with sorghum reveal a prominent role of carbohydrate metabolism in salt-stress response. <i>Environmental and Experimental Botany</i> , 2023, 209, 105274.	4.2	4
6789	Functional genome annotation and transcriptome analysis of <i>Pseudozyma hubeiensis</i> BOT-O, an oleaginous yeast that utilizes glucose and xylose at equal rates. <i>Fungal Genetics and Biology</i> , 2023, 166, 103783.	2.1	1
6790	Metagenomic insights into dietary remodeling of gut microbiota and antibiotic resistome in meat rabbits. <i>Science of the Total Environment</i> , 2023, 874, 162006.	8.0	2
6791	Unraveling the effect of added microbial inoculants on ammonia emissions during co-composting of kitchen waste and sawdust: Core microorganisms and functional genes. <i>Science of the Total Environment</i> , 2023, 874, 162522.	8.0	9
6792	<i>Pseudomonas aeruginosa</i> responds to altered membrane phospholipid composition by adjusting the production of two-component systems, proteases and iron uptake proteins. <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 2023, 1868, 159317.	2.4	3
6793	Plastic leachate exposure drives antibiotic resistance and virulence in marine bacterial communities. <i>Environmental Pollution</i> , 2023, 327, 121558.	7.5	5
6794	<i>Govania unica</i> gen. nov., sp. nov., a rare biosphere bacterium that represents a novel family in the class Alphaproteobacteria. <i>Systematic and Applied Microbiology</i> , 2023, 46, 126405.	2.8	0
6795	QSP: An open sequence database for quorum sensing related gene analysis with an automatic annotation pipeline. <i>Water Research</i> , 2023, 235, 119814.	11.3	6

#	ARTICLE	IF	CITATIONS
6796	A meta-transcriptomic study of mosquito virome and blood feeding patterns at the human-animal-environment interface in Guangdong Province, China. <i>One Health</i> , 2023, 16, 100493.	3.4	2
6797	The effects of long-term hexabromocyclododecanes contamination on microbial communities in the microcosms. <i>Chemosphere</i> , 2023, 325, 138412.	8.2	3
6798	Transcriptome analysis of high mortality phenomena in polyploid fish embryos: An allotriploid embryo case study in hybrid grouper (<i>Epinephelus fuscoguttatus</i> × <i>Epinephelus lanceolatus</i>). <i>Aquaculture</i> , 2023, 571, 739446.	3.5	1
6799	A transcriptional atlas of the silk gland in <i>Antheraea pernyi</i> revealed by IsoSeq. <i>Journal of Asia-Pacific Entomology</i> , 2023, 26, 102043.	0.9	1
6800	New insights into the role of key microorganisms and wooden barrels during lambic beer fermentation and maturation. <i>International Journal of Food Microbiology</i> , 2023, 394, 110163.	4.7	4
6801	Resistome profiling reveals transmission dynamics of antimicrobial resistance genes from poultry litter to soil and plant. <i>Environmental Pollution</i> , 2023, 327, 121517.	7.5	2
6802	Cencurut virus: A novel Orthonairovirus from Asian house shrews (<i>Suncus murinus</i>) in Singapore. <i>One Health</i> , 2023, 16, 100529.	3.4	4
6803	Integrated miRNA-mRNA analysis reveals the molecular mechanism in mandarin fish (<i>Siniperca chuatsi</i>) in response to fresh baits and artificial diets feeding. <i>Aquaculture Reports</i> , 2023, 30, 101554.	1.7	2
6804	Shotgun metagenomic analysis of bacterial symbionts associated with <i>Chromodoris quadricolor</i> mantle. <i>Marine Genomics</i> , 2023, 69, 101030.	1.1	0
6805	Hot spring distribution and survival mechanisms of thermophilic comammox <i>Nitrospira</i> . <i>ISME Journal</i> , 2023, 17, 993-1003.	9.8	4
6807	Microbial community composition and metabolic potential during a succession of algal blooms from <i>Skeletonema</i> sp. to <i>Phaeocystis</i> sp.. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	2
6808	Reference genomes of channel catfish and blue catfish reveal multiple pericentric chromosome inversions. <i>BMC Biology</i> , 2023, 21, .	3.8	1
6809	Dissolved storage glycans shaped the community composition of abundant bacterioplankton clades during a North Sea spring phytoplankton bloom. <i>Microbiome</i> , 2023, 11, .	11.1	10
6810	Single-cell transcriptome reveals cell division-regulated hub genes in the unicellular eukaryote <i>Paramecium</i> . <i>European Journal of Protistology</i> , 2023, 89, 125978.	1.5	0
6811	Achievement and microbial profiles of non-aerated partial nitrification in photo sequencing batch and continuous flow reactors. <i>Journal of Water Process Engineering</i> , 2023, 53, 103600.	5.6	2
6819	The genome of a Far Eastern isolate of <i>Diaporthe caulivora</i> , a soybean fungal pathogen. <i>Applied Microbiology and Biotechnology</i> , 2023, 107, 1311-1327.	3.6	1
6820	The phylogenomics and evolutionary dynamics of the organellar genomes in carnivorous <i>Utricularia</i> and <i>Genlisea</i> species (Lentibulariaceae). <i>Molecular Phylogenetics and Evolution</i> , 2023, 181, 107711.	2.7	3
6821	A reference genome for Bluegill (Centrarchidae: <i>Lepomis macrochirus</i>). <i>G3: Genes, Genomes, Genetics</i> , 2023, 13, .	1.8	0

#	ARTICLE	IF	CITATIONS
6822	Citrus genomic resources unravel putative genetic determinants of Huanglongbing pathogenicity. IScience, 2023, 26, 106024.	4.1	6
6823	Early response of the gut microbiome and serum metabolites to Cheonggukjang intake in healthy Korean subjects. Journal of Functional Foods, 2023, 101, 105420.	3.4	1
6824	Semi-supervised and Incremental VSEARCH for Metagenomic Classification. , 2022, , .		1
6825	Function of CAZymes encoded by highly abundant genes in rhizosphere microbiome of Moringa oleifera. Saudi Journal of Biological Sciences, 2023, 30, 103578.	3.8	1
6826	The chromosome-level genome assembly of lance asiabell (Codonopsis lanceolata), a medicinal and vegetable plant of the Campanulaceae family. Frontiers in Genetics, 0, 14, .	2.3	5
6829	High-energy diet modify rumen microbial composition and microbial energy metabolism pattern in fattening sheep. BMC Veterinary Research, 2023, 19, .	1.9	2
6830	Draft genomes of Blastocystis subtypes from human samples of Colombia. Parasites and Vectors, 2023, 16, .	2.5	1
6831	Cryobacterium zhongshanensis sp. nov., an actinobacterium isolated from Antarctic soil. Archives of Microbiology, 2023, 205, .	2.2	0
6832	Mining Chromodoris quadricolor symbionts for biosynthesis of novel secondary metabolites. Marine Genomics, 2023, 68, 101017.	1.1	1
6833	Characterization of the microbiota dynamics associated with Moniliophthora roreri, causal agent of cocoa frosty pod rot disease, reveals new viral species. Frontiers in Microbiology, 0, 13, .	3.5	3
6834	Gut microbiome variations in Rhinopithecus roxellanae caused by changes in the environment. BMC Genomics, 2023, 24, .	2.8	4
6835	Rhizobiome Signature and Its Alteration Due to Watering in the Wild Plant Moringa oleifera. Sustainability, 2023, 15, 2745.	3.2	0
6841	Sequences and Genome-Wide Analysis of mRNA and microRNA Expression in Tea (<i>Camellia</i>) Tj ETQq0 0 0 rGBT /Qverlock 10 Tf 50 26	1.6	0
6842	Robust 3D modeling reveals spatiosyntenic properties of animal genomes. IScience, 2023, 26, 106136.	4.1	3
6843	Molecular hydrogen in seawater supports growth of diverse marine bacteria. Nature Microbiology, 2023, 8, 581-595.	13.3	17
6844	Comparative Genomic Analyses of Cellulolytic Machinery Reveal Two Nutritional Strategies of Marine Labyrinthulomycetes Protists. Microbiology Spectrum, 2023, 11, .	3.0	1
6845	Supergroup F Wolbachia with extremely reduced genome: transition to obligate insect symbionts. Microbiome, 2023, 11, .	11.1	5
6846	Insights into the genome of Methylobacterium sp. NMS14P, a novel bacterium for growth promotion of maize, chili, and sugarcane. PLoS ONE, 2023, 18, e0281505.	2.5	4

#	ARTICLE	IF	CITATIONS
6847	Comparative metagenomics reveals poultry and swine farming are hotspots for multidrug and tetracycline resistance. <i>Environmental Pollution</i> , 2023, 322, 121239.	7.5	6
6848	Effects of levodopa on gut bacterial antibiotic resistance in Parkinson's disease rat. <i>Frontiers in Aging Neuroscience</i> , 0, 15, .	3.4	1
6849	PanViTa: Pan Virulence and resistance analysis. <i>Frontiers in Bioinformatics</i> , 0, 3, .	2.1	3
6851	Susceptibility monitoring and comparative gene expression of susceptible and resistant strains of <i>Spodoptera frugiperda</i> to lambda-cyhalothrin and chlorpyrifos. <i>Pest Management Science</i> , 2023, 79, 2206-2219.	3.4	2
6852	Metagenomic Analysis of Anaerobic Microbial Communities Degrading Short-Chain Fatty Acids as Sole Carbon Sources. <i>Microorganisms</i> , 2023, 11, 420.	3.6	4
6853	Metagenomic insights into the effects of benzyl dodecyl dimethyl ammonium bromide (BDAB) shock on bacteria-driven nitrogen removal in a moving-bed biofilm reactor (MBBR). <i>Chemosphere</i> , 2023, 320, 138098.	8.2	6
6854	Chromosome-level Genome Assembly of <i>Euphorbia peplus</i> , a Model System for Plant Latex, Reveals that Relative Lack of Ty3 Transposons Contributed to Its Small Genome Size. <i>Genome Biology and Evolution</i> , 2023, 15, .	2.5	1
6855	Discovery of a coronavirus in the Eurasian badger (<i>Meles meles</i>) belonging to a putative new genus. <i>Infection, Genetics and Evolution</i> , 2023, 109, 105406.	2.3	3
6856	Maize protein structure resources at the maize genetics and genomics database. <i>Genetics</i> , 2023, 224, .	2.9	2
6857	Uncovering a Complex Virome Associated with the Cacao Pathogens <i>Ceratocystis cacaofunesta</i> and <i>Ceratocystis fimbriata</i> . <i>Pathogens</i> , 2023, 12, 287.	2.8	3
6858	Single-cell amplified genomes reveal most streamlined free-living marine bacteria. <i>Environmental Microbiology</i> , 2023, 25, 1136-1154.	3.8	5
6859	Genome Sequence and Analysis of <i>Nicotiana benthamiana</i> , the Model Plant for Interactions between Organisms. <i>Plant and Cell Physiology</i> , 2023, 64, 248-257.	3.1	14
6860	Responses of carbapenemase-producing and non-producing carbapenem-resistant <i>Pseudomonas aeruginosa</i> strains to meropenem revealed by quantitative tandem mass spectrometry proteomics. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	1
6861	Seasonal Changes in the Structure and Function of Gut Microbiota in the Muskrat (<i>Ondatra</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf	2.9	3
6862	Genetic mapping of microbial and host traits reveals production of immunomodulatory lipids by <i>Akkermansia muciniphila</i> in the murine gut. <i>Nature Microbiology</i> , 2023, 8, 424-440.	13.3	12
6863	The genome of <i>Magnolia hypoleuca</i> provides a new insight into cold tolerance and the evolutionary position of magnoliids. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	3
6864	The mechanism of promoting rhizosphere nutrient turnover for arbuscular mycorrhizal fungi attributes to recruited functional bacterial assembly. <i>Molecular Ecology</i> , 2023, 32, 2335-2350.	3.9	6
6865	Trait biases in microbial reference genomes. <i>Scientific Data</i> , 2023, 10, .	5.3	4

#	ARTICLE	IF	CITATIONS
6866	Shuffled ATG8 interacting motifs form an ancestral bridge between UFMylation and autophagy. EMBO Journal, 2023, 42, .	7.8	11
6867	Characterization of antibiotic resistomes by reprogrammed bacteriophage-enabled functional metagenomics in clinical strains. Nature Microbiology, 2023, 8, 410-423.	13.3	6
6868	HyperVR: a hybrid deep ensemble learning approach for simultaneously predicting virulence factors and antibiotic resistance genes. NAR Genomics and Bioinformatics, 2023, 5, .	3.2	4
6869	A Mitosome With Distinct Metabolism in the Uncultured Protist Parasite <i>Paramikrocytos cancri</i> (Rhizaria, Ascetosporea). Genome Biology and Evolution, 2023, 15, .	2.5	3
6870	Hybrid Genome Assembly of <i>Berkeleyomyces rouxiae</i> , an Emerging Cannabis Fungal Pathogen Causing Black Root-Rot in an Aeroponic Facility. Plant Disease, 0, .	1.4	0
6871	Global profiling of antibiotic resistomes in maize rhizospheres. Archives of Microbiology, 2023, 205, .	2.2	1
6873	XY sex determination in a cnidarian. BMC Biology, 2023, 21, .	3.8	2
6875	Enterovirus characterized from cerebrospinal fluid in a cohort from the Eastern United States. Journal of Clinical Virology, 2023, 161, 105401.	3.1	0
6876	è,é“ç—...æ”ç»,â† æ•°æⓂæŒ–æŽžŽâ^†æžæ–1æ³•çš„è¿žâ±•âšæŒæ˘. Scientia Sinica Vitae, 2023, , .	0.3	0
6877	<i>Wolbachia</i> and <i>Spiroplasma</i> endosymbionts in the <i>Anurida maritima</i> (Collembola) species group. , 0, , .		0
6878	A chromosome-level genome assembly of <i>Ostrea denselamellosa</i> provides initial insights into its evolution. Genomics, 2023, 115, 110582.	2.9	3
6880	Peptide microarray IgM and IgG screening of pre-SARS-CoV-2 human serum samples from Zimbabwe for reactivity with peptides from all seven human coronaviruses: a cross-sectional study. Lancet Microbe, The, 2023, 4, e215-e227.	7.3	2
6881	Recent transposable element bursts are associated with the proximity to genes in a fungal plant pathogen. PLoS Pathogens, 2023, 19, e1011130.	4.7	15
6882	Chromosome-scale genome assembly of the pink bollworm, <i>Pectinophora gossypiella</i> , a global pest of cotton. G3: Genes, Genomes, Genetics, 2023, 13, .	1.8	2
6883	The human gut microbiome of athletes: metagenomic and metabolic insights. Microbiome, 2023, 11, .	11.1	8
6884	Comprehensive Analysis of Gene Expression Profiling to Explore Predictive Markers for Eradication Therapy Efficacy against <i>Helicobacter pylori</i> -Negative Gastric MALT Lymphoma. Cancers, 2023, 15, 1206.	3.7	0
6886	Differential Expression Genes of the Head Kidney and Spleen in <i>Streptococcus iniae</i> -Infected East Asian Fourfinger Threadfin Fish (<i>Eleutheronema tetradactylum</i>). International Journal of Molecular Sciences, 2023, 24, 3832.	4.1	4
6887	Insights into the ecological generalist lifestyle of <i>Clonostachys</i> fungi through analysis of their predicted secretomes. Frontiers in Microbiology, 0, 14, .	3.5	2

#	ARTICLE	IF	CITATIONS
6888	Giant Virus Infection Signatures Are Modulated by Euphotic Zone Depth Strata and Iron Regimes of the Subantarctic Southern Ocean. <i>MSystems</i> , 0, , .	3.8	0
6889	Physiological and genomic insights into abiotic stress of halophilic archaeon <i>Natrinema altunense</i> 4.1R isolated from a saline ecosystem of Tunisian desert. <i>Genetica</i> , 2023, 151, 133-152.	1.1	2
6890	VirBot: an RNA viral contig detector for metagenomic data. <i>Bioinformatics</i> , 2023, 39, .	4.1	5
6892	Orthologs of Human-Disease-Associated Genes in Plants Are Involved in Regulating Leaf Senescence. <i>Life</i> , 2023, 13, 559.	2.4	1
6893	Phylotranscriptomics and evolution of key genes for terpene biosynthesis in Pinaceae. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	0
6894	How voles adapt to subterranean lifestyle: Insights from RNA-seq. <i>Frontiers in Ecology and Evolution</i> , 0, 11, .	2.2	3
6896	Exploring taxonomic and functional microbiome of Hawaiian stream and spring irrigation water systems using Illumina and Oxford Nanopore sequencing platforms. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	5
6897	Comparative metagenomic analysis reveals rhizosphere microbial community composition and functions help protect grapevines against salt stress. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	6
6898	Defensive Resistance of Cowpea <i>Vigna unguiculata</i> Control <i>Megalurothrips usitatus</i> Mediated by Jasmonic Acid or Insect Damage. <i>Plants</i> , 2023, 12, 942.	3.5	4
6899	The telomere-to-telomere genome of <i>Fragaria vesca</i> reveals the genomic evolution of <i>Fragaria</i> and the origin of cultivated octoploid strawberry. <i>Horticulture Research</i> , 2023, 10, .	6.3	23
6900	Genome Size Changes by Duplication, Divergence, and Insertion in <i>Caenorhabditis</i> Worms. <i>Molecular Biology and Evolution</i> , 2023, 40, .	8.9	0
6901	Whole-Genome Comparison Reveals Structural Variations behind Heading Leaf Trait in Brassica oleracea. <i>International Journal of Molecular Sciences</i> , 2023, 24, 4063.	4.1	3
6902	Metagenomes from Coastal Sediments of Kuwait: Insights into the Microbiome, Metabolic Functions and Resistome. <i>Microorganisms</i> , 2023, 11, 531.	3.6	8
6903	Species boundaries and conservation implications of <i>Cinnamomum japonicum</i> , an endangered plant in China. <i>Journal of Systematics and Evolution</i> , 2024, 62, 73-83.	3.1	1
6905	A molecular perspective on the invasibility of the southern ocean benthos: The impact of hypoxia and temperature on gene expression in South American and Antarctic <i>Aequiyoidea</i> bivalves. <i>Frontiers in Physiology</i> , 0, 14, .	2.8	1
6906	MetaGenePipe: An Automated, Portable Pipeline for Contig-based Functional and Taxonomic Analysis. <i>Journal of Open Source Software</i> , 2023, 8, 4851.	4.6	1
6907	Viral and Bacterial Communities Collaborate through Complementary Assembly Processes in Soil to Survive Organochlorine Contamination. <i>Applied and Environmental Microbiology</i> , 2023, 89, .	3.1	5
6908	A Guide to Gene-Centric Analysis Using TreeSAPP. <i>Current Protocols</i> , 2023, 3, .	2.9	0

#	ARTICLE	IF	CITATIONS
6909	Genomic, transcriptomic, and metabolomic analysis of <i>Oldenlandia corymbosa</i> reveals the biosynthesis and mode of action of anti-cancer metabolites. <i>Journal of Integrative Plant Biology</i> , 2023, 65, 1442-1466.	8.5	7
6910	Functional analysis of the apple fruit microbiome based on shotgun metagenomic sequencing of conventional and organic orchard samples. <i>Environmental Microbiology</i> , 2023, 25, 1728-1746.	3.8	4
6911	Chromosome-length genome assembly of <i>Teladorsagia circumcincta</i> – a globally important helminth parasite in livestock. <i>BMC Genomics</i> , 2023, 24, .	2.8	4
6912	Biotrickling Filtration for the Reduction of N ₂ O Emitted during Wastewater Treatment: Results from a Long-Term In Situ Pilot-Scale Testing. <i>Environmental Science & Technology</i> , 2023, 57, 3883-3892.	10.0	0
6914	Dynamics of soil microbiome throughout the cultivation life cycle of morel (<i>Morchella sextelata</i>). <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	7
6915	Field plus lab experiments help identify freezing tolerance and associated genes in subtropical evergreen broadleaf trees: A case study of <i>Camellia oleifera</i> . <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	3
6916	Meta-omics elucidates key degraders in a bacterial tris(2-butoxyethyl) phosphate (TBOEP)-degrading enrichment culture. <i>Water Research</i> , 2023, 233, 119774.	11.3	4
6917	Transcriptome Profiling Data of Tea Leaves During Infection by the Dark Brown Tea Leaf Spot Pathogen, <i>Epicoccum mackenziei</i> . <i>PhytoFrontiers</i> , 0, , .	1.6	0
6918	Carbon metabolism and biogeography of candidate phylum “Candidatus Bipolaricaulota” in geothermal environments of Biga Peninsula, Turkey. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	0
6919	Exploring the Astrovirome of Shellfish Matrices Using Nanopore Sequencing. <i>Veterinary Sciences</i> , 2023, 10, 175.	1.7	1
6920	Beyond bacteria: Reconstructing microorganism connections and deciphering the predicted mutualisms in mammalian gut metagenomes. <i>Ecology and Evolution</i> , 2023, 13, .	1.9	1
6921	Microbial methane cycling in sediments of Arctic thermokarst lagoons. <i>Global Change Biology</i> , 2023, 29, 2714-2731.	9.5	2
6922	Bipartite Genomes in Enterobacterales: Independent Origins of Chromids, Elevated Openness and Donors of Horizontally Transferred Genes. <i>International Journal of Molecular Sciences</i> , 2023, 24, 4292.	4.1	1
6923	Structure-informed microbial population genetics elucidate selective pressures that shape protein evolution. <i>Science Advances</i> , 2023, 9, .	10.3	8
6924	Gut microbial metabolism of 5-ASA diminishes its clinical efficacy in inflammatory bowel disease. <i>Nature Medicine</i> , 2023, 29, 700-709.	30.7	25
6926	A novel and diverse group of Candidatus Patescibacteria from bathypelagic Lake Baikal revealed through long-read metagenomics. <i>Environmental Microbiomes</i> , 2023, 18, .	5.0	2
6927	Genomic, metabolomic, and functional characterisation of beneficial properties of <i>Pediococcus pentosaceus</i> ST58, isolated from human oral cavity. <i>Beneficial Microbes</i> , 2023, 14, 57-72.	2.4	2
6928	Spatiotemporal Dynamics of Coastal Viral Community Structure and Potential Biogeochemical Roles Affected by an <i>Ulva prolifera</i> Green Tide. <i>MSystems</i> , 2023, 8, .	3.8	2

#	ARTICLE	IF	CITATIONS
6929	Extending and improving metagenomic taxonomic profiling with uncharacterized species using MetaPhlAn 4. <i>Nature Biotechnology</i> , 2023, 41, 1633-1644.	17.5	132
6930	Bacteriocin production enhancing mechanism of <i>Lactiplantibacillus paraplantarum</i> RX-8 response to <i>Wickerhamomyces anomalus</i> Y-5 by transcriptomic and proteomic analyses. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	3
6931	Social complexity, life-history and lineage influence the molecular basis of castes in vespid wasps. <i>Nature Communications</i> , 2023, 14, .	12.8	6
6932	The gastrointestinal antibiotic resistome in pediatric leukemia and lymphoma patients. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 13, .	3.9	2
6933	Enzyme adaptation to habitat thermal legacy shapes the thermal plasticity of marine microbiomes. <i>Nature Communications</i> , 2023, 14, .	12.8	5
6934	Gut microbiota facilitates adaptation of the plateau zokor (<i>Myospalax baileyi</i>) to the plateau living environment. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	0
6935	Genomic characterization and molecular dating of the novel bacterium <i>Permianibacter aggregans</i> HW001T, which originated from Permian ground water. <i>Marine Life Science and Technology</i> , 2023, 5, 12-27.	4.6	0
6936	MeganServer: facilitating interactive access to metagenomic data on a server. <i>Bioinformatics</i> , 2023, 39, .	4.1	6
6937	PtrVCS2 Regulates Drought Resistance by Changing Vessel Morphology and Stomatal Closure in <i>Populus trichocarpa</i> . <i>International Journal of Molecular Sciences</i> , 2023, 24, 4458.	4.1	2
6938	Transcriptomics explores the potential of flavonoid in non-medicinal parts of <i>Saposhnikovia divaricata</i> (Turcz.) Schischk. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	0
6939	Metagenomics reveal the role of microorganism and GH genes contribute to Sichuan South-road dark tea quality formation during pile fermentation. <i>LWT - Food Science and Technology</i> , 2023, 178, 114618.	5.2	6
6941	Short-Term Impact of Oxytetracycline Administration on the Fecal Microbiome, Resistome and Virulome of Grazing Cattle. <i>Antibiotics</i> , 2023, 12, 470.	3.7	0
6942	Whole-genome re-sequencing provides key genomic insights in farmed Arctic charr (<i>Salvelinus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T Applications, 0, , .	3.1	0
6943	The Colorectal Cancer Gut Environment Regulates Activity of the Microbiome and Promotes the Multidrug Resistant Phenotype of ESKAPE and Other Pathogens. <i>MSphere</i> , 2023, 8, .	2.9	4
6944	The Colorectal Cancer Microbiota Alter Their Transcriptome To Adapt to the Acidity, Reactive Oxygen Species, and Metabolite Availability of Gut Microenvironments. <i>MSphere</i> , 2023, 8, .	2.9	6
6945	Meta-omics profiling of full-scale groundwater rapid sand filters explains stratification of iron, ammonium and manganese removals. <i>Water Research</i> , 2023, 233, 119805.	11.3	6
6946	Microbial gene activity in straw residue amendments reveals carbon sequestration mechanisms in agricultural soils. <i>Soil Biology and Biochemistry</i> , 2023, 179, 108994.	8.8	2
6947	Freeze-thaw cycles alter the growth sprouting strategy of wetland plants by promoting denitrification. <i>Communications Earth & Environment</i> , 2023, 4, .	6.8	1

#	ARTICLE	IF	CITATIONS
6948	Pan-Chromosome and Comparative Analysis of <i>Agrobacterium fabrum</i> Reveal Important Traits Concerning the Genetic Diversity, Evolutionary Dynamics, and Niche Adaptation of the Species. Microbiology Spectrum, 2023, 11, .	3.0	0
6951	Recommendations for the use of metagenomics for routine monitoring of antibiotic resistance in wastewater and impacted aquatic environments. Critical Reviews in Environmental Science and Technology, 2023, 53, 1731-1756.	12.8	4
6952	Reference Genome Sequence of Flax. Compendium of Plant Genomes, 2023, , 1-17.	0.5	2
6953	Population-level impacts of antibiotic usage on the human gut microbiome. Nature Communications, 2023, 14, .	12.8	15
6955	Substantial viral and bacterial diversity at the bat-tick interface. Microbial Genomics, 2023, 9, .	2.0	2
6956	The enormous repetitive Antarctic krill genome reveals environmental adaptations and population insights. Cell, 2023, 186, 1279-1294.e19.	28.9	23
6957	From defaults to databases: parameter and database choice dramatically impact the performance of metagenomic taxonomic classification tools. Microbial Genomics, 2023, 9, .	2.0	12
6958	Exploring microbial functional biodiversity at the protein family level-From metagenomic sequence reads to annotated protein clusters. Frontiers in Bioinformatics, 0, 3, .	2.1	2
6960	Correlation of the gut microbiome and immune-related adverse events in gastrointestinal cancer patients treated with immune checkpoint inhibitors. Frontiers in Cellular and Infection Microbiology, 0, 13, .	3.9	5
6962	Surface-layer protein is a public-good matrix exopolymer for microbial community organisation in environmental anammox biofilms. ISME Journal, 2023, 17, 803-812.	9.8	7
6963	Metatranscriptomics and metabarcoding reveal spatiotemporal shifts in fungal communities and their activities in Chinese coastal waters. Molecular Ecology, 2023, 32, 2750-2765.	3.9	6
6964	Class 1 integrons and multiple mobile genetic elements in clinical isolates of the Klebsiella pneumoniae complex from a tertiary hospital in eastern China. Frontiers in Microbiology, 0, 14, .	3.5	4
6965	Effect of Dioscorea Opposite Waste Supplementation on Antioxidant Capacity, Immune Response and Rumen Microbiome in Weaned Lambs. Fermentation, 2023, 9, 256.	3.0	1
6967	Trophic level and proteobacteria abundance drive antibiotic resistance levels in fish from coastal New England. Animal Microbiome, 2023, 5, .	3.8	3
6968	Grazing disturbance increased the mobility, pathogenicity and host microbial species of antibiotic resistance genes, and multidrug resistance genes posed the highest risk in the habitats of wild animals. Frontiers in Environmental Science, 0, 11, .	3.3	1
6969	Identifying Genes Associated with Female Flower Development of Phellodendron amurense Rupr. Using a Transcriptomics Approach. Genes, 2023, 14, 661.	2.4	2
6972	Genome-wide identification, structural and evolutionary characteristics, and expression analysis of aquaporin gene family members in Mercenaria mercenaria. Frontiers in Marine Science, 0, 10, .	2.5	1
6973	Transcriptome analysis and exploration of genes involved in the biosynthesis of secoiridoids in <i>Gentiana rhodantha</i> . PeerJ, 0, 11, e14968.	2.0	0

#	ARTICLE	IF	CITATIONS
6975	Genomic Scanning and Extracellular Proteomic Analysis of <i>Dickeya dadantii</i> DCE-01 Reveal Its Excellent Performance on Ramie Degumming. <i>Fibers and Polymers</i> , 2023, 24, 1517-1525.	2.1	0
6977	Unique gene duplications and conserved microsynteny potentially associated with resistance to wood decay in the Lauraceae. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	0
6978	Genome Analysis of <i>Pseudomonas aeruginosa</i> Strains from Chronically Infected Patients with High Levels of Persister Formation. <i>Pathogens</i> , 2023, 12, 426.	2.8	3
6979	Genomics, Population Divergence, and Historical Demography of the World's Largest and Endangered Butterfly, The Queen Alexandra's Birdwing. <i>Genome Biology and Evolution</i> , 2023, 15, .	2.5	4
6980	Phenotypic and genotypic diversity of <i>Puccinia sorghi</i> in Eastern Australia: implications for maize breeding programs. <i>PhytoFrontiers</i> , 0, , .	1.6	0
6981	A hydrogenotrophic <i>Sulfurimonas</i> is globally abundant in deep-sea oxygen-saturated hydrothermal plumes. <i>Nature Microbiology</i> , 2023, 8, 651-665.	13.3	5
6988	Changes in community structures and functions of the gut microbiomes of deep-sea cold seep mussels during in situ transplantation experiment. <i>Animal Microbiome</i> , 2023, 5, .	3.8	2
6989	Transcriptome Analysis During Tetrasporogenesis of <i>Gracilariopsis lemaneiformis</i> and Preliminary Study of the Expressions of Its Meiotic Genes. <i>Journal of Ocean University of China</i> , 2023, 22, 541-554.	1.2	0
6990	Discovery of an unrecognized nidovirus associated with granulomatous hepatitis in rainbow trout. <i>IScience</i> , 2023, 26, 106370.	4.1	0
6992	Integrated <i>de novo</i> gene prediction and peptide assembly of metagenomic sequencing data. <i>NAR Genomics and Bioinformatics</i> , 2023, 5, .	3.2	0
6994	OliveAtlas: A Gene Expression Atlas Tool for <i>Olea europaea</i> . <i>Plants</i> , 2023, 12, 1274.	3.5	1
6996	Ternary Mixture of Azoxystrobin, Boscalid and Pyraclostrobin Disrupts the Gut Microbiota and Metabolic Balance of Honeybees (<i>Apis cerana cerana</i>). <i>International Journal of Molecular Sciences</i> , 2023, 24, 5354.	4.1	4
6997	Shotgun Metagenomics of Gastric Biopsies Reveals Compositional and Functional Microbiome Shifts in High- and Low-Gastric-Cancer-Risk Populations from Colombia, South America. <i>Gut Microbes</i> , 2023, 15, .	9.8	6
6998	Characterization of viral pathogens associated with symptomatic upper respiratory tract infection in adults during a low COVID-19 transmission period. <i>PeerJ</i> , 0, 11, e15008.	2.0	4
6999	MangoBase: A Genomics Portal and Gene Expression Atlas for <i>Mangifera indica</i> . <i>Plants</i> , 2023, 12, 1273.	3.5	3
7000	African army ants at the forefront of virome surveillance in a remote tropical forest. , 0, 3, .		0
7001	Seasonality of biogeochemically relevant microbial genes in a coastal ocean microbiome. <i>Environmental Microbiology</i> , 2023, 25, 1465-1483.	3.8	1
7002	<i>Aspergillus fumigatus</i> Can Display Persistence to the Fungicidal Drug Voriconazole. <i>Microbiology Spectrum</i> , 2023, 11, .	3.0	5

#	ARTICLE	IF	CITATIONS
7003	Strategy for the Adaptation to Stressful Conditions of the Novel Isolated Conditional Piezophilic Strain Halomonas titanicae ANRCS81. Applied and Environmental Microbiology, 2023, 89, .	3.1	4
7004	The tropical cookbook: Termite diet and phylogeneticsâ€”Over geographical originâ€”Drive the microbiome and functional genetic structure of nests. Frontiers in Microbiology, 0, 14, .	3.5	1
7006	AFTM: a database of transmembrane regions in the human proteome predicted by AlphaFold. Database: the Journal of Biological Databases and Curation, 2023, 2023, .	3.0	1
7007	Temporal disturbance of a model stream ecosystem by high microbial diversity from treated wastewater. MicrobiologyOpen, 2023, 12, .	3.0	2
7009	Low dissolved oxygen supply functions as a global regulator of the growth and metabolism of Aurantiochytrium sp. PKU#Mn16 in the early stages of docosahexaenoic acid fermentation. Microbial Cell Factories, 2023, 22, .	4.0	1
7010	Stoichiometric balance ratio of cellobiose and gentiobiose induces cellulase production in Talaromyces cellulolyticus. , 2023, 16, .		2
7011	A holobiont approach towards polysaccharide degradation by the highly compartmentalised gut system of the soil-feeding higher termite Labiotermes labralis. BMC Genomics, 2023, 24, .	2.8	3
7012	Diseased-induced multifaceted variations in community assembly and functions of plant-associated microbiomes. Frontiers in Microbiology, 0, 14, .	3.5	3
7013	The reciprocal changes in dominant species with complete metabolic functions explain the decoupling phenomenon of microbial taxonomic and functional composition in a grassland. Frontiers in Microbiology, 0, 14, .	3.5	1
7014	Bioinformatic and Statistical Analysis of Microbiome Data. Methods in Molecular Biology, 2023, , 183-229.	0.9	2
7015	Comparative genomics reveals the diversification of triterpenoid biosynthesis and origin of ocotillol-type triterpenes in Panax. Plant Communications, 2023, 4, 100591.	7.7	3
7016	Genomic Insights into Niche Partitioning across Sediment Depth among Anaerobic Methane-Oxidizing Archaea in Global Methane Seeps. MSystems, 2023, 8, .	3.8	4
7017	Genome assembly of the deep-sea coral Lophelia pertusa. GigaByte, 0, 2023, 1-12.	0.0	1
7018	Linking Transcriptional Dynamics of Peat Microbiomes to Methane Fluxes during a Summer Drought in Two Rewetted Fens. Environmental Science & Technology, 2023, 57, 5089-5101.	10.0	1
7019	Insights into the genomic evolution and the alkali tolerance mechanisms of Agaricus sinodeliciosus by comparative genomic and transcriptomic analyses. Microbial Genomics, 2023, 9, .	2.0	0
7020	Comparison of N2O-reducing abilities and genome features of two<i>nosZ</i>-containing denitrifying bacteria,<i>Pseudomonas veronii</i>DM15 and<i>Pseudomonas frederiksbergensis</i>DM22. Journal of Applied Microbiology, 2023, 134, .	3.1	0
7021	The <sc>NLRomes</sc> of <i>Zea mays</i>Â<sc>NAM</sc> founder lines and <i>Zea luxurians</i> display presenceâ€”absence variation, integrated domain diversity, and mobility. Molecular Plant Pathology, 2023, 24, 742-757.	4.2	3
7022	Assembly of novel microbial genomes from gut metagenomes of rhesus macaque (<i>Macaca</i> TJ ETQq1 1 0.784314.rgBT /Overlock 10	9.8	5

#	ARTICLE	IF	CITATIONS
7023	Larval transcriptomes reflect the evolutionary history of plant–insect associations. <i>Evolution; International Journal of Organic Evolution</i> , 2023, 77, 519-533.	2.3	2
7024	Evaluating coevolution in a horizontally transmitted mutualism. <i>Evolution; International Journal of Organic Evolution</i> , 2023, 77, 166-185.	2.3	2
7025	Hippocampus guttulatus diet based on DNA metabarcoding. <i>Frontiers in Marine Science</i> , 0, 10, .	2.5	2
7026	Deciphering the mechanism of fungal pathogen–induced disease–suppressive soil. <i>New Phytologist</i> , 2023, 238, 2634-2650.	7.3	13
7027	Neofunctionalization of tandem duplicate genes encoding putative Î²-D-glucanase in Arabidopsis. <i>Plant Physiology</i> , 0, .	4.8	1
7029	Transient Suppression of Bacterial Populations Associated with Gut Health is Critical in Success of Exclusive Enteral Nutrition for Children with Crohn’s Disease. <i>Journal of Crohn’s and Colitis</i> , 2023, 17, 1103-1113.	1.3	1
7030	Complete Genome Sequence of <i>Bacillus velezensis</i> strain ZY1, a Potential Biological Control Agent for Bacterial Fruit Blotch. <i>PhytoFrontiers</i> , 0, .	1.6	0
7032	Transcriptomic and Metabolomic Profiles Provide Insights into the Red-Stipe Symptom of Morel Fruiting Bodies. <i>Journal of Fungi (Basel, Switzerland)</i> , 2023, 9, 373.	3.5	5
7033	A Global Survey of the Full-Length Transcriptome of <i>Apis mellifera</i> by Single-Molecule Long-Read Sequencing. <i>International Journal of Molecular Sciences</i> , 2023, 24, 5827.	4.1	0
7034	Genome resource announcement for two isolates of <i>Phytophthora sansomeana</i> with varying levels of pathogenicity on soybean. <i>PhytoFrontiers</i> , 0, .	1.6	0
7035	Genome-centric metagenomics reveals the host-driven dynamics and ecological role of CPR bacteria in an activated sludge system. <i>Microbiome</i> , 2023, 11, .	11.1	11
7036	Gene abundance linked to climate zone: Parallel evolution of gene content along elevation gradients in lichenized fungi. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	1
7037	Floral Development Stage-Specific Transcriptomic Analysis Reveals the Formation Mechanism of Different Shapes of Ray Florets in <i>Chrysanthemum</i> . <i>Genes</i> , 2023, 14, 766.	2.4	1
7038	Hybrid De Novo Whole-Genome Assembly, Annotation, and Identification of Secondary Metabolite Gene Clusters in the Ex-Type Strain of <i>Chrysosporium keratinophilum</i> . <i>Journal of Fungi (Basel, Switzerland)</i> , 2023, 9, 389.	3.5	0
7040	Stop or Not: Genome-Wide Profiling of Reassigned Stop Codons in Ciliates. <i>Molecular Biology and Evolution</i> , 2023, 40, .	8.9	2
7041	Exploring genome gene content and morphological analysis to test recalcitrant nodes in the animal phylogeny. <i>PLoS ONE</i> , 2023, 18, e0282444.	2.5	5
7042	RNA silencing proteins and small RNAs in oomycete plant pathogens and biocontrol agents. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	2
7044	A genome sequence for <i>Biomphalaria pfeifferi</i> , the major vector snail for the human-infecting parasite <i>Schistosoma mansoni</i> . <i>PLoS Neglected Tropical Diseases</i> , 2023, 17, e0011208.	3.0	10

#	ARTICLE	IF	CITATIONS
7045	Fast and accurate protein function prediction from sequence through pretrained language model and homology-based label diffusion. <i>Briefings in Bioinformatics</i> , 2023, 24, .	6.5	12
7046	Nuclear phylogeny and insights into whole-genome duplications and reproductive development of Solanaceae plants. <i>Plant Communications</i> , 2023, 4, 100595.	7.7	8
7047	An improved reference of the grapevine genome reasserts the origin of the PN40024 highly homozygous genotype. <i>G3: Genes, Genomes, Genetics</i> , 2023, 13, .	1.8	13
7048	POSMM: an efficient alignment-free metagenomic profiler that complements alignment-based profiling. <i>Environmental Microbiomes</i> , 2023, 18, .	5.0	1
7049	Allelic diversity uncovers protein domains contributing to the emergence of antimicrobial resistance. <i>PLoS Genetics</i> , 2023, 19, e1010490.	3.5	2
7051	Comparative Transcriptome Analysis of <i>Gleditsia sinensis</i> Thorns at Different Stages of Development. <i>Plants</i> , 2023, 12, 1456.	3.5	5
7052	Metagenomic Sequencing Identified Specific Bacteriophage Signature Discriminating between Healthy and Diarrheal Neonatal Piglets. <i>Nutrients</i> , 2023, 15, 1616.	4.1	2
7053	Shotgun proteomics of quinoa seeds reveals chitinases enrichment under rainfed conditions. <i>Scientific Reports</i> , 2023, 13, .	3.3	5
7055	Identification of Tomato mottle mosaic virus in historic seed accessions originating from France, the Netherlands and Spain, indicates a wider presence before its first description. <i>European Journal of Plant Pathology</i> , 2023, 166, 485-489.	1.7	3
7056	Align-gram: Rethinking the Skip-gram Model for Protein Sequence Analysis. <i>Protein Journal</i> , 2023, 42, 135-146.	1.6	2
7057	Highly contiguous genomes of human clinical isolates of <i>Giardia duodenalis</i> reveal assemblage- and sub-assemblage-specific presence-absence variation in protein-coding genes. <i>Microbial Genomics</i> , 2023, 9, .	2.0	1
7058	Soil conditions and the plant microbiome boost the accumulation of monoterpenes in the fruit of <i>Citrus reticulata</i> ‘Chachi’™. <i>Microbiome</i> , 2023, 11, .	11.1	14
7059	The genome of <i>Lactuca saligna</i> , a wild relative of lettuce, provides insight into non-host resistance to the downy mildew <i>Bremia lactucae</i> . <i>Plant Journal</i> , 2023, 115, 108-126.	5.7	2
7061	Abundance, classification and genetic potential of Thaumarchaeota in metagenomes of European agricultural soils: a meta-analysis. <i>Environmental Microbiomes</i> , 2023, 18, .	5.0	5
7062	Chemical Pretreatments and Anaerobic Digestion Shape the Virome and Functional Microbiome in Fecal Sludge. <i>Environmental Science & Technology</i> , 2023, 57, 6008-6020.	10.0	1
7063	The link between increased <i>Desulfovibrio</i> and disease severity in Parkinson’s disease. <i>Applied Microbiology and Biotechnology</i> , 2023, 107, 3033-3045.	3.6	3
7064	Baicalein-corrected gut microbiota may underlie the amelioration of memory and cognitive deficits in APP/PS1 mice. <i>Frontiers in Pharmacology</i> , 0, 14, .	3.5	2
7065	Metagenomic analyses of a microbial assemblage in a subglacial lake beneath the Vatnajökull ice cap, Iceland. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	1

#	ARTICLE	IF	CITATIONS
7066	Chromosome-Scale Genome Assembly and Triterpenoid Saponin Biosynthesis in Korean Bellflower (<i>Platycodon grandiflorum</i>). <i>International Journal of Molecular Sciences</i> , 2023, 24, 6534.	4.1	3
7067	The effects of circularly polarized light on mating behavior and gene expression in <i>Anomala corpulenta</i> (Coleoptera: Scarabaeidae). <i>Frontiers in Physiology</i> , 0, 14, .	2.8	0
7068	A First Insight into the Microbial and Viral Communities of Comau Fjordâ€™A Unique Human-Impacted Ecosystem in Patagonia (42âˆ™ S). <i>Microorganisms</i> , 2023, 11, 904.	3.6	1
7069	Whole genome assemblies of <i>Zophobas morio</i> and <i>Tenebrio molitor</i> . <i>G3: Genes, Genomes, Genetics</i> , 2023, 13, .	1.8	8
7070	Comparative transcriptomics of aphid species that diverged >22 MYA reveals genes that are important for the maintenance of their symbiosis. <i>Scientific Reports</i> , 2023, 13, .	3.3	1
7072	Genomic investigations of unexplained acute hepatitis in children. <i>Nature</i> , 2023, 617, 564-573.	27.8	53
7073	Plant domestication shapes rhizosphere microbiome assembly and metabolic functions. <i>Microbiome</i> , 2023, 11, .	11.1	33
7075	The genetic basis of wing spots in <i>Pieris canidia</i> butterflies. <i>BMC Genomics</i> , 2023, 24, .	2.8	1
7076	Comparative transcriptome analysis of juniper branches infected by <i>Gymnosporangium</i> spp. highlights their different infection strategies associated with cytokinins. <i>BMC Genomics</i> , 2023, 24, .	2.8	0
7077	Vertically stratified methane, nitrogen and sulphur cycling and coupling mechanisms in mangrove sediment microbiomes. <i>Microbiome</i> , 2023, 11, .	11.1	7
7078	RNA Viruses Are Prevalent and Active Tenants of the Predatory Mite <i>Phytoseiulus persimilis</i> (Acari: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	2.8	1
7079	Whole-genome sequencing and comparative genomic analysis of potential biotechnological strains of <i>Trichoderma harzianum</i> , <i>Trichoderma atroviride</i> , and <i>Trichoderma reesei</i> . <i>Molecular Genetics and Genomics</i> , 2023, 298, 735-754.	2.1	4
7080	De novo full-length transcriptome analysis of two ecotypes of <i>Phragmites australis</i> (swamp reed and) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 adaptation to desert environments. <i>BMC Genomics</i> , 2023, 24, .	2.8	2
7081	Isolation and pan-genome analysis of <i>Enterobacter hormaechei</i> Z129, a ureolytic bacterium, from the rumen of dairy cow. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	2
7082	Viruses interact with hosts that span distantly related microbial domains in dense hydrothermal mats. <i>Nature Microbiology</i> , 2023, 8, 946-957.	13.3	15
7083	Potential response of dark carbon fixation to global warming in estuarine and coastal waters. <i>Global Change Biology</i> , 2023, 29, 3821-3832.	9.5	1
7084	Land use modification causes slow, but predictable, change in soil microbial community composition and functional potential. <i>Environmental Microbiomes</i> , 2023, 18, .	5.0	2
7085	Quantifying Shared and Unique Gene Content across 17 Microbial Ecosystems. <i>MSystems</i> , 0, , .	3.8	0

#	ARTICLE	IF	CITATIONS
7086	Metagenomic insights into the composition and function of the gut microbiota of mice infected with <i>Toxoplasma gondii</i> . <i>Frontiers in Immunology</i> , 0, 14, .	4.8	2
7087	Uncovering the special microbiota associated with occurrence and progression of gastric cancer by using RNA-sequencing. <i>Scientific Reports</i> , 2023, 13, .	3.3	4
7088	A survey on antimicrobial resistance genes of frequently used probiotic bacteria, 1901 to 2022. <i>Eurosurveillance</i> , 2023, 28, .	7.0	5
7090	Mesophilic and thermophilic viruses are associated with nutrient cycling during hyperthermophilic composting. <i>ISME Journal</i> , 2023, 17, 916-930.	9.8	18
7091	Protozoa as Hotspots for Potential Pathogens in the Drinking Water of a Subtropical Megacity: Diversity, Treatment, and Health Risk. <i>Environmental Science & Technology</i> , 2023, 57, 6108-6118.	10.0	3
7092	Metagenomic analysis reveals the short-term influences on conjugation of bla _{NDM-1} and microbiome in hospital wastewater by silver nanoparticles at environmental-related concentration. <i>Environmental Research</i> , 2023, 228, 115866.	7.5	1
7095	Large-scale invasion of unicellular eukaryotic genomes by integrating DNA viruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	7.1	19
7096	The GEN-ERA toolbox: unified and reproducible workflows for research in microbial genomics. <i>GigaScience</i> , 2022, 12, .	6.4	3
7097	The transcriptome of <i>Litopenaeus vannamei</i> in zoea larvae and adults infected by <i>Vibrio parahaemolyticus</i> . <i>Frontiers in Marine Science</i> , 0, 10, .	2.5	0
7098	Anaerobic thiosulfate oxidation by the <i>Roseobacter</i> group is prevalent in marine biofilms. <i>Nature Communications</i> , 2023, 14, .	12.8	13
7099	Metagenomic analysis reveals indole signaling effect on microbial community in sequencing batch reactors: Quorum sensing inhibition and antibiotic resistance enrichment. <i>Environmental Research</i> , 2023, 229, 115897.	7.5	1
7102	Complete genome sequence of zoysia mosaic virus, a novel member of the genus Poacevirus. <i>Archives of Virology</i> , 2023, 168, .	2.1	0
7103	Microbial Niche Differentiation during Nitrite-Dependent Anaerobic Methane Oxidation. <i>Environmental Science & Technology</i> , 2023, 57, 7029-7040.	10.0	4
7104	A Diverse Virome Is Identified in Parasitic Flatworms of Domestic Animals in Xinjiang, China. <i>Microbiology Spectrum</i> , 0, , .	3.0	0
7105	A2TEA: Identifying trait-specific evolutionary adaptations. <i>F1000Research</i> , 0, 11, 1137.	1.6	0
7107	Analysis of bacterioplankton genes in an impaired Great Lakes harbour reveals seasonal metabolic shifts and a previously undetected cyanobacterium. <i>Canadian Journal of Microbiology</i> , 2023, 69, 281-295.	1.7	1
7108	De novo transcriptome assembly of <i>Iphiculus spongiosus</i> Adams & White, 1849 (Decapoda); Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 2023, 62, 102960.	0.7	0
7109	African eggplant-associated virus: Characterization of a novel tobamovirus identified from <i>Solanum macrocarpon</i> and assessment of its potential impact on tomato and pepper crops. <i>PLoS ONE</i> , 2023, 18, e0277840.	2.5	1

#	ARTICLE	IF	CITATIONS
7110	Taxonomical composition and functional analysis of biofilms sampled from a nuclear storage pool. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	7
7111	Children with autism show differences in the gut DNA virome compared to non-autistic children: a case control study. <i>BMC Pediatrics</i> , 2023, 23, .	1.7	0
7112	DNA methylation signatures of duplicate gene evolution in angiosperms. <i>Plant Physiology</i> , 2023, 192, 2883-2901.	4.8	1
7113	The mechanisms of optimal nitrogen conditions to accelerate flowering of <i>Chrysanthemum vestitum</i> under short day based on transcriptome analysis. <i>Journal of Plant Physiology</i> , 2023, 285, 153982.	3.5	0
7114	Species-Level Taxonomic Characterization of Uncultured Core Gut Microbiota of Plateau Pika. <i>Microbiology Spectrum</i> , 0, , .	3.0	1
7116	The gut microbiota contributes to the pathogenesis of anorexia nervosa in humans and mice. <i>Nature Microbiology</i> , 2023, 8, 787-802.	13.3	31
7117	Unexplored diversity and ecological functions of transposable phages. <i>ISME Journal</i> , 2023, 17, 1015-1028.	9.8	2
7118	Comparative genomic analysis of <i>Halomonas campaniensis</i> wild-type and ultraviolet radiation-mutated strains reveal genomic differences associated with increased ectoine production. <i>International Microbiology</i> , 2023, 26, 1009-1020.	2.4	2
7119	Probable airborne transmission of <i>Burkholderia pseudomallei</i> causing an urban outbreak of melioidosis during typhoon season in Hong Kong, China. <i>Emerging Microbes and Infections</i> , 2023, 12, .	6.5	2
7120	Environmental viromes reveal the global distribution signatures of deep-sea DNA viruses. <i>Journal of Advanced Research</i> , 2024, 57, 107-117.	9.5	1
7122	Genome-wide transcriptional profiling provides clues to molecular mechanisms underlying cold tolerance in chickpea. <i>Scientific Reports</i> , 2023, 13, .	3.3	4
7123	Integrative Metatranscriptomic Analysis Reveals Disease-specific Microbiome–host Interactions in Oral Squamous Cell Carcinoma. <i>Cancer Research Communications</i> , 2023, 3, 807-820.	1.7	2
7124	Genomic Analysis of Infectious Bursal Disease Virus in Nigeria: Identification of Unique Mutations of Yet Unknown Biological Functions in Both Segments A and B. <i>Vaccines</i> , 2023, 11, 867.	4.4	0
7125	The whole genome of <i>Colletes collaris</i> (Hymenoptera: Colletidae): an important step in comparative genomics of cellophane bees. <i>Genome Biology and Evolution</i> , 0, , .	2.5	1
7126	Genomic insight of sulfate reducing bacterial genus <i>Desulfofabia</i> reveals their metabolic versatility in biogeochemical cycling. <i>BMC Genomics</i> , 2023, 24, .	2.8	0
7127	Genetic analysis of global faba bean diversity, agronomic traits and selection signatures. <i>Theoretical and Applied Genetics</i> , 2023, 136, .	3.6	4
7128	Metagenomic and metatranscriptomic exploration of the Egyptian Red Sea sponge <i>Theonella</i> sp. associated microbial community. <i>Marine Genomics</i> , 2023, 70, 101032.	1.1	1
7129	<i>In Situ</i> Molecular Ecological Analyses Illuminate Distinct Factors Regulating Formation and Demise of a Harmful Dinoflagellate Bloom. <i>Microbiology Spectrum</i> , 2023, 11, .	3.0	1

#	ARTICLE	IF	CITATIONS
7130	Impact of <i>in situ</i> solar irradiation on snow bacterial communities and functional potential. FEMS Microbiology Ecology, 0, , .	2.7	1
7131	Mirusviruses link herpesviruses to giant viruses. Nature, 2023, 616, 783-789.	27.8	28
7133	Swine farm groundwater is a hidden hotspot for antibiotic-resistant pathogenic <i>Acinetobacter</i> . ISME Communications, 2023, 3, .	4.2	1
7134	Metagenomics reveals elevated temperature causes nitrogen accumulation mainly by inhibiting nitrate reduction process in polluted water. Science of the Total Environment, 2023, 882, 163631.	8.0	4
7135	Exploring halophilic environments as a source of new antibiotics. Critical Reviews in Microbiology, 0, , 1-30.	6.1	2
7136	Gapless genome assembly of <i>Fusarium verticillioides</i> , a filamentous fungus threatening plant and human health. Scientific Data, 2023, 10, .	5.3	2
7137	Hybridization alters the gut microbial and metabolic profile concurrent with modifying intestinal functions in Tunchang pigs. Frontiers in Microbiology, 0, 14, .	3.5	0
7138	RAPIDprep: A Simple, Fast Protocol for RNA Metagenomic Sequencing of Clinical Samples. Viruses, 2023, 15, 1006.	3.3	1
7140	Integrated Analysis of miRNAome and Transcriptome Identify Regulators of Elm Seed Aging. Plants, 2023, 12, 1719.	3.5	2
7141	FAS: assessing the similarity between proteins using multi-layered feature architectures. Bioinformatics, 2023, 39, .	4.1	2
7142	A <i>Pseudomonas</i> Lysogenic Bacteriophage Crossing the Antarctic and Arctic, Representing a New Genus of Autographiviridae. International Journal of Molecular Sciences, 2023, 24, 7662.	4.1	3
7143	Genomic characterization of emerging invasive <i>Streptococcus agalactiae</i> serotype VIII in Alberta, Canada. European Journal of Clinical Microbiology and Infectious Diseases, 2023, 42, 747-757.	2.9	1
7144	Metapangenomics of wild and cultivated banana microbiome reveals a plethora of host-associated protective functions. Environmental Microbiomes, 2023, 18, .	5.0	3
7145	iPHoP: An integrated machine learning framework to maximize host prediction for metagenome-derived viruses of archaea and bacteria. PLoS Biology, 2023, 21, e3002083.	5.6	57
7146	Subsurface biogeochemical cycling of nitrogen in the actively serpentinizing Samail Ophiolite, Oman. Frontiers in Microbiology, 0, 14, .	3.5	3
7147	First Isolation and Genome Sequence Analysis of West Nile Virus in Mosquitoes in Brazil. Tropical Medicine and Infectious Disease, 2023, 8, 237.	2.3	2
7148	HOTSPOT: hierarchical host prediction for assembled plasmid contigs with transformer. Bioinformatics, 2023, 39, .	4.1	3
7149	Identification and biochemical characterization of a novel CH113 β -mannanase from acid mine drainage metagenome. Biochemical Engineering Journal, 2023, 192, 108837.	3.6	1

#	ARTICLE	IF	CITATIONS
7150	Holobiont Urbanism: sampling urban beehives reveals citiesâ€™ metagenomes. <i>Environmental Microbiomes</i> , 2023, 18, .	5.0	2
7151	Suppression of the gut microbiotaâ€™bile acidâ€™ <scp>FGF19</scp> axis in patients with atrial fibrillation. <i>Cell Proliferation</i> , 0, , .	5.3	1
7153	Polycyclic aromatic hydrocarbon (PAH) biodegradation capacity revealed by a genome-function relationship approach. <i>Environmental Microbiomes</i> , 2023, 18, .	5.0	2
7155	Identifying sex-differential gene expression in the antennal gland of the swimming crab by transcriptomic analysis. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2023, 46, 101087.	1.0	0
7156	Comparing genomes recovered from time-series metagenomes using long- and short-read sequencing technologies. <i>Microbiome</i> , 2023, 11, .	11.1	8
7157	Different Magmaticâ€™Hydrothermal Fluids at the Same Magma Source Support Distinct Microbial Communities: Evidence From In Situ Detection. <i>Journal of Geophysical Research: Oceans</i> , 2023, 128, .	2.6	1
7158	Plasmer: an Accurate and Sensitive Bacterial Plasmid Prediction Tool Based on Machine Learning of Shared k-mers and Genomic Features. <i>Microbiology Spectrum</i> , 2023, 11, .	3.0	1
7160	Integrated microbiome and metabolome analysis reveals the interaction between intestinal flora and serum metabolites as potential biomarkers in hepatocellular carcinoma patients. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 13, .	3.9	4
7161	Novel Gene Clusters for Natural Product Synthesis Are Abundant in the Mangrove Swamp Microbiome. <i>Applied and Environmental Microbiology</i> , 0, , .	3.1	0
7162	Characterizing sediment functional traits and ecological consequences respond to increasing antibiotic pollution. <i>Applied Microbiology and Biotechnology</i> , 0, , .	3.6	0
7163	Differences in gut microbiota and its metabolic function among different fasting plasma glucose groups in Mongolian population of China. <i>BMC Microbiology</i> , 2023, 23, .	3.3	2
7164	The hidden diversity of microbes in ballast water and sediments revealed by metagenomic sequencing. <i>Science of the Total Environment</i> , 2023, 882, 163666.	8.0	5
7165	Haplotype-resolved genome assembly of <i>Coriaria nepalensis</i> a non-legume nitrogen-fixing shrub. <i>Scientific Data</i> , 2023, 10, .	5.3	1
7167	Transfer route and driving forces of antibiotic resistance genes from reclaimed water to groundwater. <i>Environmental Pollution</i> , 2023, 330, 121800.	7.5	3
7168	A functional metagenomics study of soil carbon and nitrogen degradation networks and limiting factors on the Tibetan plateau. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	3
7169	Investigation of laboratory methods for characterization of aquatic viruses in fish infected experimentally with infectious salmon anemia virus. <i>Journal of Veterinary Diagnostic Investigation</i> , 0, , 104063872311733.	1.1	0
7171	Metagenomics of gut microbiome for migratory seagulls in Kunming city revealed the potential public risk to human health. <i>BMC Genomics</i> , 2023, 24, .	2.8	4
7172	Sulfur metabolism in subtropical marine mangrove sediments fundamentally differs from other habitats as revealed by SMDB. <i>Scientific Reports</i> , 2023, 13, .	3.3	0

#	ARTICLE	IF	CITATIONS
7174	Fertilizing-induced alterations of microbial functional profiles in soil nitrogen cycling closely associate with crop yield. <i>Environmental Research</i> , 2023, 231, 116194.	7.5	2
7175	Characterisation of the <i>E. coli</i> HMS174 and BLR host cell proteome to guide purification process development. <i>Biotechnology Journal</i> , 0, , .	3.5	1
7176	Antimicrobial resistance gene lack in tick-borne pathogenic bacteria. <i>Scientific Reports</i> , 2023, 13, .	3.3	1
7177	Metagenomic analysis of the relationship between the microorganisms and the volatiles™ development in the wines during spontaneous fermentation from the eastern foothills of the Ningxia Helan Mountains in China. <i>Journal of the Science of Food and Agriculture</i> , 0, , .	3.5	0
7178	The chromosome-level genome assembly and genes involved in biosynthesis of nervonic acid of <i>Malania oleifera</i> . <i>Scientific Data</i> , 2023, 10, .	5.3	1
7179	Genome-wide functional characterization of <i>Canavalia rosea</i> cysteine-rich trans-membrane module (CrCYSTM) genes to reveal their potential protective roles under extreme abiotic stress. <i>Plant Physiology and Biochemistry</i> , 2023, 200, 107786.	5.8	0
7180	The effects of co-culture on the expression of selected PKS genes in the lichenized fungus <i>Xanthoparmelia taractica</i> . <i>Mycological Progress</i> , 2023, 22, .	1.4	0
7181	Plasticity, Paralogy, and Pseudogenization: Rhabdoviruses of Freshwater Mussels Elucidate Mechanisms of Viral Genome Diversification and the Evolution of the Finfish-Infecting Rhabdoviral Genera. <i>Journal of Virology</i> , 2023, 97, .	3.4	5
7182	Marine phytoplankton downregulate core photosynthesis and carbon storage genes upon rapid mixed layer shallowing. <i>ISME Journal</i> , 2023, 17, 1074-1088.	9.8	1
7183	Genome Re-Annotation and Transcriptome Analyses of <i>Sanghuangporus sanghuang</i> . <i>Journal of Fungi</i> (Basel, Switzerland), 2023, 9, 505.	3.5	3
7184	Tumor-targeting engineered probiotic <i>Escherichia coli</i> Nissle 1917 inhibits colorectal tumorigenesis and modulates gut microbiota homeostasis in mice. <i>Life Sciences</i> , 2023, 324, 121709.	4.3	2
7189	Sodium butyrate promotes gastrointestinal development of preweaning bull calves via inhibiting inflammation, balancing nutrient metabolism, and optimizing microbial community functions. <i>Animal Nutrition</i> , 2023, 14, 88-100.	5.1	6
7190	Genomic capacities for Reactive Oxygen Species metabolism across marine phytoplankton. <i>PLoS ONE</i> , 2023, 18, e0284580.	2.5	1
7192	Two novel species isolated from wheat rhizospheres in Serbia: <i>Pseudomonas serbica</i> sp. nov. and <i>Pseudomonas serboccidentalis</i> sp. nov.. <i>Systematic and Applied Microbiology</i> , 2023, 46, 126425.	2.8	1
7193	Alpha-Tocopherol Significantly Improved Squalene Production Yield of <i>Aurantiochytrium</i> sp. TWZ-97 through Lowering ROS levels and Up-Regulating Key Genes of Central Carbon Metabolism Pathways. <i>Antioxidants</i> , 2023, 12, 1034.	5.1	3
7195	Analysis of the diversity of tick-borne viruses at the border areas in Liaoning Province, China. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	1
7196	Multiomics analysis reveals the molecular mechanisms underlying virulence in <i>Rhizoctonia</i> and jasmonic acid-mediated resistance in Tartary buckwheat (<i>Fagopyrum tataricum</i>). <i>Plant Cell</i> , 2023, 35, 2773-2798.	6.6	5
7198	Acetylcholine titre regulation by non-neuronal acetylcholinesterase 1 and its putative roles in honey bee physiology. <i>Insect Molecular Biology</i> , 0, , .	2.0	0

#	ARTICLE	IF	CITATIONS
7199	Effects of dietary crude protein levels in the concentrate supplement after grazing on rumen microbiota and metabolites by using metagenomics and metabolomics in Jersey-yak. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	2
7200	A novel bat coronavirus with a polybasic furin-like cleavage site. <i>Virologica Sinica</i> , 2023, 38, 344-350.	3.0	2
7201	Potential functional differentiation from microbial perspective under dryland-paddy conversion in black soils. <i>Agriculture, Ecosystems and Environment</i> , 2023, 353, 108562.	5.3	1
7202	A core of functional complementary bacteria infects oysters in Pacific Oyster Mortality Syndrome. <i>Animal Microbiome</i> , 2023, 5, .	3.8	4
7203	The association of prokaryotic antiviral systems and symbiotic phage communities in drinking water microbiomes. <i>ISME Communications</i> , 2023, 3, .	4.2	2
7204	Natural products from reconstructed bacterial genomes of the Middle and Upper Paleolithic. <i>Science</i> , 2023, 380, 619-624.	12.6	15
7206	Systematic exploration of transcriptional responses of interspecies interaction between <i>Karenia mikimotoi</i> and <i>Prorocentrum shikokuense</i> . <i>Harmful Algae</i> , 2023, 126, 102441.	4.8	0
7207	Genome-Resolved Metagenomics of Nitrogen Transformations in the Switchgrass Rhizosphere Microbiome on Marginal Lands. <i>Agronomy</i> , 2023, 13, 1294.	3.0	1
7208	Highly differentiated genomic properties underpin the different cell walls of Poaceae and eudicots. <i>Plant Physiology</i> , 2023, 194, 274-295.	4.8	2
7209	First Whole-Genome Sequence and Flow Cytometry Genome Size Data for the Lichen-Forming Fungus <i>Ramalina farinacea</i> (Ascomycota). <i>Genome Biology and Evolution</i> , 2023, 15, .	2.5	0
7210	Generation of zero-valent sulfur from dissimilatory sulfate reduction in sulfate-reducing microorganisms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	7.1	6
7211	Inactivation of the antidiabetic drug acarbose by human intestinal microbial-mediated degradation. <i>Nature Metabolism</i> , 2023, 5, 896-909.	11.9	10
7212	Endogenous biohydrogen from a rhizobium-legume association drives microbial biodegradation of polychlorinated biphenyl in contaminated soil. <i>Environment International</i> , 2023, 176, 107962.	10.0	2
7213	Plasma virome dynamics in chronic hepatitis B virus infected patients. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	5
7214	Young Adults with Major Depression Show Altered Microbiome. <i>Neuroscience</i> , 2023, 522, 23-32.	2.3	1
7215	Evolutionary pathways for deep-sea adaptation in marine planktonic Actinobacteriota. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	2
7216	Biosynthetic Potential of Hypogymnia Holobionts: Insights into Secondary Metabolite Pathways. <i>Journal of Fungi</i> (Basel, Switzerland), 2023, 9, 546.	3.5	2
7217	Genome-Wide Identification and Evolution Analysis of the CYP76 Subfamily in Rice (<i>Oryza sativa</i>). <i>International Journal of Molecular Sciences</i> , 2023, 24, 8522.	4.1	1

#	ARTICLE	IF	CITATIONS
7218	Detection and Phylogenetic Characterization of a Novel Adenovirus Found in Lesser Mouse-Eared Bat (<i>Myotis blythii</i>) in South Kazakhstan. <i>Viruses</i> , 2023, 15, 1139.	3.3	0
7219	Metagenome-derived virus-microbe ratios across ecosystems. <i>ISME Journal</i> , 2023, 17, 1552-1563.	9.8	15
7220	Administration of <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> strain BB-12 [®] in healthy children: characterization, functional composition, and metabolism of the gut microbiome. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	1
7222	A Chromosome-Level Genome Assembly and Evolution Analysis of <i>Andrena camellia</i> (Hymenoptera: Andrenidae). <i>Genome Biology and Evolution</i> , 2023, 15, .	2.5	0
7223	Insights into simultaneous nitrogen and phosphorus removal in biofilm: The overlooked comammox <i>Nitrospira</i> and the positive role of glycogen-accumulating organisms. <i>Science of the Total Environment</i> , 2023, 887, 164130.	8.0	2
7224	Identification and characterization of ABCC gene family and their roles in the response to intraperitoneal injection of microcystin-LR in liver of silver carp (<i>Hypophthalmichthys molitrix</i>). <i>Aquaculture Reports</i> , 2023, 30, 101592.	1.7	0
7225	Evidence of a divided nutritive function in rainbow Trout (<i>Oncorhynchus mykiss</i>) midgut and hindgut microbiomes by whole shotgun metagenomic approach. <i>Aquaculture Reports</i> , 2023, 30, 101601.	1.7	1
7227	Metagenomic analysis reveals specific BTEX degrading microorganisms of a bacterial consortium. <i>AMB Express</i> , 2023, 13, .	3.0	2
7228	The effect of manure-borne doxycycline combined with different types of oversized microplastic contamination layers on carbon and nitrogen metabolism in sandy loam. <i>Journal of Hazardous Materials</i> , 2023, 456, 131612.	12.4	4
7229	Distinct genomic routes underlie transitions to specialised symbiotic lifestyles in deep-sea annelid worms. <i>Nature Communications</i> , 2023, 14, .	12.8	4
7230	ODNA: identification of organellar DNA by machine learning. <i>Bioinformatics</i> , 2023, 39, .	4.1	0
7231	Conserved unique peptide patterns (CUPP) online platform 2.0: implementation of 1000 JGI fungal genomes. <i>Nucleic Acids Research</i> , 2023, 51, W108-W114.	14.5	2
7232	Chromosome-level genome assembly of an endangered plant <i>Prunus mongolica</i> using PacBio and Hi-C technologies. <i>DNA Research</i> , 2023, 30, .	3.4	1
7233	Isolation, Genomic Sequence and Physiological Characterization of <i>Parageobacillus</i> sp. G301, an Isolate Capable of Both Hydrogenogenic and Aerobic Carbon Monoxide Oxidation. <i>Applied and Environmental Microbiology</i> , 2023, 89, .	3.1	3
7234	Viromics Reveals the High Diversity of Viruses from Fishes of the Tibet Highland. <i>Microbiology Spectrum</i> , 2023, 11, .	3.0	3
7236	Combining protein sequences and structures with transformers and equivariant graph neural networks to predict protein function. <i>Bioinformatics</i> , 2023, 39, i318-i325.	4.1	2
7237	Virus Pop ² Expanding Viral Databases by Protein Sequence Simulation. <i>Viruses</i> , 2023, 15, 1227.	3.3	0
7238	Variation of Gene Expression in the Endemic Dinaric Karst Cave-Dwelling Bivalve Mollusk <i>Congeria kusceri</i> during the Summer Season. <i>Diversity</i> , 2023, 15, 707.	1.7	0

#	ARTICLE	IF	CITATIONS
7239	De novo transcriptome assembly and annotation for gene discovery in <i>Salamandra salamandra</i> at the larval stage. <i>Scientific Data</i> , 2023, 10, .	5.3	1
7240	Metagenomic insights into the response of rhizosphere microbial to precipitation changes in the alpine grasslands of northern Tibet. <i>Science of the Total Environment</i> , 2023, 892, 164212.	8.0	0
7242	Water mass age structures the auxiliary metabolic gene content of free-living and particle-attached deep ocean viral communities. <i>Microbiome</i> , 2023, 11, .	11.1	4
7243	Novel equid papillomavirus from domestic donkey. <i>Equine Veterinary Journal</i> , 2024, 56, 171-177.	1.7	0
7244	Morphological, Molecular and Genomic Identification and Characterisation of <i>Monilinia fructicola</i> in <i>Prunus persica</i> from Portugal. <i>Agronomy</i> , 2023, 13, 1493.	3.0	0
7245	Comparative genomics provides insights into the phylogeny and environmental adaptations of <i>Peritrichia</i> (Protista, Ciliophora) – A potential resource for environmental pollution control and bioremediation. <i>Molecular Phylogenetics and Evolution</i> , 2023, 186, 107835.	2.7	1
7246	High quality genome of the tree pathogen <i>Phytophthora plurivora</i> - a novel resource for epidemiological research. <i>PhytoFrontiers</i> , 0, , .	1.6	0
7247	Denitrification shifted autotroph-heterotroph interactions in <i>Microcystis</i> aggregates. <i>Environmental Research</i> , 2023, 231, 116269.	7.5	2
7248	Advances in the clinical use of metaproteomics. <i>Expert Review of Proteomics</i> , 2023, 20, 71-86.	3.0	3
7249	Gut microbiota enhance energy accumulation of black-necked crane to cope with impending migration. <i>Applied Microbiology and Biotechnology</i> , 2023, 107, 4635-4646.	3.6	1
7250	Land use change alters phosphatase enzyme activity and phosphatase-harboring microbial abundance in the subalpine ecosystem of southeastern Qinghai-Tibet Plateau, China. <i>Ecological Indicators</i> , 2023, 153, 110416.	6.3	2
7251	Strong variation in sedimental antibiotic resistomes among urban rivers, estuaries and coastal oceans: Evidence from a river-connected coastal water ecosystem in northern China. <i>Journal of Environmental Management</i> , 2023, 342, 118132.	7.8	0
7252	The gut microbiome modifies the associations of short- and long-term physical activity with body weight changes. <i>Microbiome</i> , 2023, 11, .	11.1	1
7253	Transcriptome analysis of <i>Euwallacea interjectus</i> reveals differentially expressed unigenes related to developmental stages and egg laying. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2023, 47, 101100.	1.0	0
7254	Metagenomic next generation sequencing for studying antibiotic resistance genes in the environment. <i>Advances in Applied Microbiology</i> , 2023, , .	2.4	0
7255	Influences of chronic copper exposure on intestinal histology, antioxidative and immune status, and transcriptomic response in freshwater grouper (<i>Acrossocheilus fasciatus</i>). <i>Fish and Shellfish Immunology</i> , 2023, 139, 108861.	3.6	2
7256	Metagenomic insights into genetic factors driving bacterial niche differentiation between bulk and rhizosphere soils. <i>Science of the Total Environment</i> , 2023, 891, 164221.	8.0	3
7257	Predicting yield of individual field-grown rapeseed plants from rosette-stage leaf gene expression. <i>PLoS Computational Biology</i> , 2023, 19, e1011161.	3.2	3

#	ARTICLE	IF	CITATIONS
7258	The key role of denitrification and dissimilatory nitrate reduction in nitrogen pollution along vertical landfill profiles from metagenomic perspective. <i>Journal of Environmental Management</i> , 2023, 342, 118300.	7.8	2
7259	MAIRA: Protein-based Analysis of MinION Reads on a Laptop. <i>Methods in Molecular Biology</i> , 2023, , 223-234.	0.9	0
7260	Bâ€GATA factors are required to repress highâ€light stress responses in <i>Marchantia polymorpha</i> and <i>Arabidopsis thaliana</i>. <i>Plant, Cell and Environment</i> , 2023, 46, 2376-2390.	5.7	3
7261	Recovery and Analysis of Long-Read Metagenome-Assembled Genomes. <i>Methods in Molecular Biology</i> , 2023, , 235-259.	0.9	0
7262	Disentangling hindgut metabolism in the American cockroach through single-cell genomics and metatranscriptomics. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	0
7263	DIAMOND +â€‰MEGAN Microbiome Analysis. <i>Methods in Molecular Biology</i> , 2023, , 107-131.	0.9	2
7264	Pervasive tandem duplications and convergent evolution shape coral genomes. <i>Genome Biology</i> , 2023, 24, .	8.8	11
7265	Transcriptome profiling ofÂSorghum bicolor reveals cultivar-specific molecular signatures associated with starch and phenolic compounds biosyntheses and accumulation during sorghum grain development. <i>Czech Journal of Genetics and Plant Breeding</i> , 2023, 59, 235-252.	0.8	1
7266	Chromosome-level genome assembly and annotation of the prickly nightshade <i>Solanum rostratum</i> Dunal. <i>Scientific Data</i> , 2023, 10, .	5.3	5
7268	Complete Genome Analysis of <i>Subtercola</i> sp. PAMC28395: Genomic Insights into Its Potential Role for Cold Adaptation and Biotechnological Applications. <i>Microorganisms</i> , 2023, 11, 1480.	3.6	0
7269	Eighty million years of rapid evolution of the primate Y chromosome. <i>Nature Ecology and Evolution</i> , 2023, 7, 1114-1130.	7.8	5
7270	Metagenomics insights into the functional profiles of soil carbon, nitrogen, and phosphorus cycles in a walnut orchard under various regimes of long-term fertilisation. <i>European Journal of Agronomy</i> , 2023, 148, 126887.	4.1	3
7271	Anammox bacteria adapt to long-term light irradiation in photogranules. <i>Water Research</i> , 2023, 241, 120144.	11.3	11
7272	Age-related alterations in metabolome and microbiome provide insights in dietary transition in giant pandas. <i>MSystems</i> , 2023, 8, .	3.8	1
7273	Transcriptome analysis reveals the high ribosomal inhibitory action of 1,4-naphthoquinone on <i>Meloidogyne luci</i> infective second-stage juveniles. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	0
7275	Metaproteomics reveals functional partitioning and vegetational variation among permafrost-affected Arctic soil bacterial communities. <i>MSystems</i> , 2023, 8, .	3.8	0
7277	Comprehensive analysis of gut microbiome and host transcriptome in chickens after <i>Eimeria tenella</i> infection. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 13, .	3.9	7
7278	Construction of a de novo assembly pipeline using multiple transcriptome data sets from <i>Cypripedium macranthos</i> (Orchidaceae). <i>PLoS ONE</i> , 2023, 18, e0286804.	2.5	0

#	ARTICLE	IF	CITATIONS
7279	Biotite: new tools for a versatile Python bioinformatics library. BMC Bioinformatics, 2023, 24, .	2.6	3
7280	Metagenomic and metaproteomic insights into the microbiome and the key geobiochemical potentials on the sandstone of rock-hewn Beishiku Temple in Northwest China. Science of the Total Environment, 2023, 893, 164616.	8.0	3
7281	Divergent functions of two clades of flavodoxin in diatoms mitigate oxidative stress and iron limitation. ELife, 0, 12, .	6.0	3
7282	Assessing phenotypic virulence of Salmonella enterica across serovars and sources. Frontiers in Microbiology, 0, 14, .	3.5	5
7284	Multi-omics analysis reveals changes in tryptophan and cholesterol metabolism before and after sexual maturation in captive macaques. BMC Genomics, 2023, 24, .	2.8	0
7286	A graph-based genome and pan-genome variation of the model plant Setaria. Nature Genetics, 2023, 55, 1232-1242.	21.4	28
7287	More than mcr: canonical plasmid- and transposon-encoded mobilized colistin resistance genes represent a subset of phosphoethanolamine transferases. Frontiers in Cellular and Infection Microbiology, 0, 13, .	3.9	3
7288	From genotype to phenotype: computational approaches for inferring microbial traits relevant to the food industry. FEMS Microbiology Reviews, 2023, 47, .	8.6	1
7289	Global transmission of broad-host-range plasmids derived from the human gut microbiome. Nucleic Acids Research, 0, , .	14.5	2
7290	Pan-Transcriptome Analysis of Willow Species from Diverse Geographic Distributions. Forests, 2023, 14, 1182.	2.1	0
7291	Salidroside ameliorates memory impairment following long-term ethanol intake in rats by modulating the altered intestinal microbiota content and hippocampal gene expression. Frontiers in Microbiology, 0, 14, .	3.5	2
7293	Altered fecal microbiome and metabolome profiles in rat models of short bowel syndrome. Frontiers in Microbiology, 0, 14, .	3.5	1
7294	Divergent endophytic viromes and phage genome repertoires among banana (Musa) species. Frontiers in Microbiology, 0, 14, .	3.5	0
7295	Distinctive microbial community and genome structure in coastal seawater from a human-made port and nearby offshore island in northern Taiwan facing the Northwestern Pacific Ocean. PLoS ONE, 2023, 18, e0284022.	2.5	1
7297	Reconstructor: a COBRApy compatible tool for automated genome-scale metabolic network reconstruction with parsimonious flux-based gap-filling. Bioinformatics, 2023, 39, .	4.1	2
7298	Near-Chromosomal-Level Genome Assembly of the Sea Urchin <i>Echinometra lucunter</i> , a Model for Speciation in the Sea. Genome Biology and Evolution, 2023, 15, .	2.5	2
7299	The existence of ferric hydroxide links the carbon and nitrogen cycles by promoting nitrite-coupled methane anaerobic oxidation. Water Research, 2023, 243, 120192.	11.3	2
7301	Nitrogen amendment enhances the biological methanogenic potential of bituminous coal. Fuel, 2023, 351, 128932.	6.4	3

#	ARTICLE	IF	CITATIONS
7302	Hydrostatic pressure drives microbe-mediated biodegradation of microplastics in surface sediments of deep reservoirs: Novel findings from hydrostatic pressure simulation experiments. <i>Water Research</i> , 2023, 242, 120185.	11.3	2
7305	Mycobacteriaceae Phenome Atlas (MPA): A Standardized Atlas for the Mycobacteriaceae Phenome Based on Heterogeneous Sources. <i>Phenomix</i> , 0, , .	2.9	0
7307	Exploring the Core Bacteria and Functional Traits in Pecan (<i>Carya illinoensis</i>) Rhizosphere. <i>Microbiology Spectrum</i> , 2023, 11, .	3.0	2
7308	Relation of pest insect-killing and soilborne pathogen-inhibition abilities to species diversification in environmental <i>Pseudomonas protegens</i> . <i>ISME Journal</i> , 2023, 17, 1369-1381.	9.8	3
7309	A draft genome assembly of reef-building octocoral <i>Heliopora coerulea</i> . <i>Scientific Data</i> , 2023, 10, .	5.3	2
7310	Inference and reconstruction of the heimdallarchaeal ancestry of eukaryotes. <i>Nature</i> , 2023, 618, 992-999.	27.8	40
7311	Whole Genome Sequence of <i>Lactiplantibacillus plantarum</i> HOM3204 and Its Antioxidant Effect on D-Galactose-Induced Aging in Mice. <i>Journal of Microbiology and Biotechnology</i> , 2023, , .	2.1	1
7312	Post-hybridization introgression and natural selection promoted genomic divergence of <i>Aegilops speltoides</i> and the four S-genome diploid species. <i>Plant Journal</i> , 2023, 115, 1500-1513.	5.7	2
7313	Characterization and expression of fungal defensin in <i>Escherichia coli</i> and its antifungal mechanism by RNA-seq analysis. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	0
7314	Physiological response and transcriptome analyses of leguminous <i>Indigofera bungeana</i> Walp. to drought stress. <i>PeerJ</i> , 0, 11, e15440.	2.0	0
7315	Curcumin alleviates 1-methyl- 4-phenyl- 1,2,3,6-tetrahydropyridine- induced Parkinson's disease in mice via modulating gut microbiota and short-chain fatty acids. <i>Frontiers in Pharmacology</i> , 0, 14, .	3.5	3
7316	Faecal Microbiota transplantation affects liver DNA methylation in Non-alcoholic fatty liver disease: a multi-omics approach. <i>Gut Microbes</i> , 2023, 15, .	9.8	7
7319	DETIRE: a hybrid deep learning model for identifying viral sequences from metagenomes. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	3
7320	Effects of extreme drought on soil microbial functional genes involved in carbon and nitrogen cycling in alpine peatland. <i>Frontiers in Ecology and Evolution</i> , 0, 11, .	2.2	0
7321	Shotgun metagenomics reveals a diverse mycobiome in the seawater from a High Arctic fjord (Kongsfjorden, Svalbard). <i>Environmental Research</i> , 2023, 233, 116437.	7.5	1
7322	A cytochrome P450 system initiates 4-nitroanisole degradation in <i>Rhodococcus</i> sp. strain JS3073. <i>Journal of Hazardous Materials</i> , 2023, 458, 131886.	12.4	1
7323	Towards the discovery of novel molecular clocks in Prokaryotes. <i>Critical Reviews in Microbiology</i> , 0, , 1-13.	6.1	1
7324	A chromosome-level genome assembly of tomato pinworm, <i>Tuta absoluta</i> . <i>Scientific Data</i> , 2023, 10, .	5.3	0

#	ARTICLE	IF	CITATIONS
7325	Local adaptation and demographic history of vulnerable conifer <i>Cephalotaxus oliveri</i> in southern China. <i>Journal of Systematics and Evolution</i> , 0, , .	3.1	1
7326	Comparative phylogenetic analysis and transcriptomic profiling of Dengue (DENV-3 genotype I) outbreak in 2021 in Bangladesh. <i>Virology Journal</i> , 2023, 20, .	3.4	3
7327	Enterosignatures define common bacterial guilds in the human gut microbiome. <i>Cell Host and Microbe</i> , 2023, 31, 1111-1125.e6.	11.0	14
7329	Arsenate microbial reducing behavior regulated by the temperature fields in landfills. <i>Waste Management</i> , 2023, 168, 366-375.	7.4	0
7330	Assembly of female and male hihi genomes (stitchbird; <i>Notiomystis cincta</i>) enables characterization of the W chromosome and resources for conservation genomics. <i>Molecular Ecology Resources</i> , 0, , .	4.8	1
7331	Metagenomic Sequencing to Analyze Composition and Function of Top-Gray Chalky Grain Microorganisms from Hybrid Rice Seeds. <i>Plants</i> , 2023, 12, 2358.	3.5	0
7332	The chromosome-scale genome assembly of cluster bean provides molecular insight into edible gum (galactomannan) biosynthesis family genes. <i>Scientific Reports</i> , 2023, 13, .	3.3	3
7335	PacBio single-molecule long-read sequencing provides new insights into the complexity of full-length transcripts in oriental river prawn, <i>Macrobrachium nipponense</i> . <i>BMC Genomics</i> , 2023, 24, .	2.8	2
7336	Characteristics of antibiotic resistance genes and microbial community distribution in Wanfeng Lake, upper Pearl River, China. <i>Environmental Science and Pollution Research</i> , 2023, 30, 83214-83230.	5.3	1
7337	Genome Sequence of <i>Staphylococcus aureus</i> Phage ESa2. <i>Microbiology Resource Announcements</i> , 0, , .	0.6	0
7338	Evidence of cospeciation between termites and their gut bacteria on a geological time scale. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2023, 290, .	2.6	4
7339	Soil microbe-mediated carbon and nitrogen cycling during primary succession of biological soil crusts in tailings ponds. <i>Science of the Total Environment</i> , 2023, 894, 164969.	8.0	5
7340	Prophages and plasmids can display opposite trends in the types of accessory genes they carry. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2023, 290, .	2.6	0
7342	Polymeric carbohydrates utilization separates microbiomes into niches: insights into the diversity of microbial carbohydrate-active enzymes in the inner shelf of the Pearl River Estuary, China. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	0
7343	Genomic Resequencing Unravels the Genetic Basis of Domestication, Expansion, and Trait Improvement in <i>Morus Atropurpurea</i> . <i>Advanced Science</i> , 2023, 10, .	11.2	0
7344	Phylogenomic analysis provides insights into MADS-box and TCP gene diversification and floral development of the Asteraceae, supported by de novo genome and transcriptome sequences from dandelion (<i>Taraxacum officinale</i>). <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	3
7345	Ultra-deep sequencing of Hadza hunter-gatherers recovers vanishing gut microbes. <i>Cell</i> , 2023, 186, 3111-3124.e13.	28.9	39
7346	The Importance of Entomo-Virological Investigation of Yellow Fever Virus to Strengthen Surveillance in Brazil. <i>Tropical Medicine and Infectious Disease</i> , 2023, 8, 329.	2.3	1

#	ARTICLE	IF	CITATIONS
7347	The genome of the reef-building glass sponge <i>Aphrocallistes vastus</i> provides insights into silica biomineralization. Royal Society Open Science, 2023, 10, .	2.4	3
7349	Genetic analysis of a phenotypic loss in the mechanosensory entrainment of a circalunar clock. PLoS Genetics, 2023, 19, e1010763.	3.5	0
7350	Heptamethoxyflavone Alleviates Metabolic Syndrome in High-Fat Diet-Fed Mice by Regulating the Composition, Function, and Metabolism of Gut Microbiota. Journal of Agricultural and Food Chemistry, 2023, 71, 10050-10064.	5.2	4
7352	Expansion of Armatimonadota through marine sediment sequencing describes two classes with unique ecological roles. ISME Communications, 2023, 3, .	4.2	1
7355	Current concepts, advances, and challenges in deciphering the human microbiota with metatranscriptomics. Trends in Genetics, 2023, 39, 686-702.	6.7	9
7356	Full-length transcriptome analysis provides insights into flavonoid biosynthesis in <i>Ranunculus japonicus</i> . Physiologia Plantarum, 2023, 175, .	5.2	1
7357	Intragenic Duplications in Diatoms: Search and Validation. Inland Water Biology, 2023, 16, 413-418.	0.8	0
7358	Differences of Nitrogen Transformation Pathways and Their Functional Microorganisms in Water and Sediment of a Seasonally Frozen Lake, China. Water (Switzerland), 2023, 15, 2332.	2.7	2
7359	cGLRs are a diverse family of pattern recognition receptors in innate immunity. Cell, 2023, 186, 3261-3276.e20.	28.9	20
7361	Global Antimicrobial Resistance Gene Study of <i>Helicobacter pylori</i> : Comparison of Detection Tools, ARG and Efflux Pump Gene Analysis, Worldwide Epidemiological Distribution, and Information Related to the Antimicrobial-Resistant Phenotype. Antibiotics, 2023, 12, 1118.	3.7	1
7363	An insight into the functional genomics and species classification of <i>Eudiplozoon nipponicum</i> (Monogenea, Diplozoidae), a haematophagous parasite of the common carp <i>Cyprinus carpio</i> . BMC Genomics, 2023, 24, .	2.8	0
7365	The vertically-stratified resistomes in mangrove sediments was driven by the bacterial diversity. Journal of Hazardous Materials, 2023, 458, 131974.	12.4	1
7366	Exploring environmental intra-species diversity through non-redundant pangenome assemblies. Molecular Ecology Resources, 2023, 23, 1724-1736.	4.8	2
7367	Metagenomics and metabolomics of Toddy, an Indian fermented date palm beverage. Food Research International, 2023, 172, 113205.	6.2	0
7368	Discovery of a novel bat lyssavirus in a Long-fingered bat (<i>Myotis capaccinii</i>) from Slovenia. PLoS Neglected Tropical Diseases, 2023, 17, e0011420.	3.0	3
7369	A high-quality, long-read genome assembly of the whitelined sphinx moth (Lepidoptera: Sphingidae: <i>Tj ETQq1 1 0.784314 rgBT /Over</i> Genetics, 2023, 13, .	1.8	0
7370	Mechanisms of inward transmembrane proton translocation. Nature Structural and Molecular Biology, 2023, 30, 970-979.	8.2	4
7371	<i>Oxic</i> cycling promotes coupling between complex carbon metabolism and denitrification in woodchip bioreactors. Environmental Microbiology, 2023, 25, 1696-1712.	3.8	4

#	ARTICLE	IF	CITATIONS
7372	Microbial biogeochemical cycling reveals the sustainability of the rice-crayfish co-culture model. IScience, 2023, 26, 106769.	4.1	0
7373	A Recombinant Chimeric Cedar Virus-Based Surrogate Neutralization Assay Platform for Pathogenic Henipaviruses. Viruses, 2023, 15, 1077.	3.3	2
7374	Comparative analysis reveals epigenomic evolution related to species traits and genomic imprinting in mammals. Innovation(China), 2023, 4, 100434.	9.1	2
7375	Artificial Intelligence: A Promising Tool in Exploring the Phytomicrobiome in Managing Disease and Promoting Plant Health. Plants, 2023, 12, 1852.	3.5	1
7376	Genome-Wide Identification and Expression Analysis of the Dof Transcription Factor in Annual Alfalfa Medicago polymorpha. Plants, 2023, 12, 1831.	3.5	0
7377	Prevalence of Reversed Genome Organizations for Viruses in the Family <i>Iflaviridae</i> , Order <i>Picornavirales</i>. Microbiology Spectrum, 2023, 11, .	3.0	0
7379	Whole genome sequence of Lactiplantibacillus plantarum MC5 and comparative analysis of eps gene clusters. Frontiers in Microbiology, 0, 14, .	3.5	2
7380	Sargasso Sea Vibrio bacteria: Underexplored potential pathovars in a perturbed habitat. Water Research, 2023, 242, 120033.	11.3	12
7381	Different rapid startups for high-solid anaerobic digestion treating pig manure: Metagenomic insights into antibiotic resistance genes fate and microbial metabolic pathway. Environmental Research, 2023, 231, 116038.	7.5	2
7383	Transcriptomic analysis of Chinese yam (Dioscorea polystachya Turcz.) variants indicates brassinosteroid involvement in tuber development. Frontiers in Nutrition, 0, 10, .	3.7	1
7384	Virus infection of phytoplankton increases average molar mass and reduces hygroscopicity of aerosolized organic matter. Scientific Reports, 2023, 13, .	3.3	0
7385	Transcriptomic and Metabolomic Profiling Provides Insights into Flavonoid Biosynthesis and Flower Coloring in Loropetalum chinense and Loropetalum chinense var. rubrum. Agronomy, 2023, 13, 1296.	3.0	3
7386	The spatiotemporal profile of Dendrobium huoshanense and functional identification of bHLH genes under exogenous MeJA using comparative transcriptomics and genomics. Frontiers in Plant Science, 0, 14, .	3.6	2
7387	Anastomosis Groups and Mycovirome of Rhizoctonia Isolates Causing Sugar Beet Root and Crown Rot and Their Sensitivity to Flutolanil, Thifluzamide, and Pencycuron. Journal of Fungi (Basel), Tj ETQq1 1 0.784314 rgB3.6 Overlook 10 Tf 50	3.3	0
7389	Multi-omics resources for targeted agronomic improvement of pigmented rice. Nature Food, 2023, 4, 366-371.	14.0	5
7390	Novel Rodent Arterivirus Detected in the Brazilian Amazon. Viruses, 2023, 15, 1150.	3.3	2
7392	Integrated Transcriptomic and Metabolomic Analyses Reveal Low-Temperature Tolerance Mechanism in Giant Freshwater Prawn Macrobrachium rosenbergii. Animals, 2023, 13, 1605.	2.3	1
7393	Current trends in <scp>RNA</scp> virus detection through metatranscriptome sequencing data. FEBS Open Bio, 2023, 13, 992-1000.	2.3	2

#	ARTICLE	IF	CITATIONS
7395	Short-term exposure to enrofloxacin causes hepatic metabolism disorder associated with intestinal flora dysbiosis in adult marine medaka (<i>Oryzias melastigma</i>). <i>Marine Pollution Bulletin</i> , 2023, 192, 114966.	5.0	2
7396	Sympatric <i>Pieris</i> butterfly species exhibit a high conservation of chemoreceptors. <i>Frontiers in Cellular Neuroscience</i> , 0, 17, .	3.7	1
7397	Chromosome-level genome assembly of the spotted alfalfa aphid <i>Therioaphis trifolii</i> . <i>Scientific Data</i> , 2023, 10, .	5.3	0
7398	Natural restoration of degraded karst vegetation shifts soil microbial phosphorus acquisition strategies. <i>Plant and Soil</i> , 2023, 490, 201-215.	3.7	3
7399	Operation of air conditioners affects the microbial pathogenic potential in bedrooms: A metagenomics and culture-dependent study. <i>Building and Environment</i> , 2023, 239, 110335.	6.9	0
7400	Milk protein digestion and the gut microbiome influence gastrointestinal discomfort after cow milk consumption in healthy subjects. <i>Food Research International</i> , 2023, 170, 112953.	6.2	6
7401	Centenarians have a diverse gut virome with the potential to modulate metabolism and promote healthy lifespan. <i>Nature Microbiology</i> , 2023, 8, 1064-1078.	13.3	18
7402	Independent origins and evolution of the secondary replicons of the class Gammaproteobacteria. <i>Microbial Genomics</i> , 2023, 9, .	2.0	0
7403	The Crown Pearl V2: an improved genome assembly of the European freshwater pearl mussel <i>Margaritifera margaritifera</i> (Linnaeus, 1758). <i>GigaByte</i> , 0, 2023, 1-14.	0.0	1
7404	Sulfur cycling connects microbiomes and biogeochemistry in deep-sea hydrothermal plumes. <i>ISME Journal</i> , 2023, 17, 1194-1207.	9.8	4
7405	Functional annotation of rhizospheric phageome of the wild plant species <i>Moringa oleifera</i> . <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	3
7406	Application of metagenomic next-generation sequencing in the diagnosis and resistome analysis of community-acquired pneumonia pathogens from bronchoalveolar lavage samples. <i>Journal of Applied Microbiology</i> , 2023, 134, .	3.1	0
7407	High-fat diet impairs gut barrier through intestinal microbiota-derived reactive oxygen species. <i>Science China Life Sciences</i> , 0, , .	4.9	2
7408	Distribution and transmission of β -lactamase resistance genes in meal-to-milk chain on dairy farm. <i>Environmental Pollution</i> , 2023, 331, 121831.	7.5	1
7409	In vitro simulated fecal fermentation of mixed grains on short-chain fatty acid generation and its metabolized mechanism. <i>Food Research International</i> , 2023, 170, 112949.	6.2	2
7410	The AEGEAN-169 clade of bacterioplankton is synonymous with SAR11 subclade V (HIMB59) and metabolically distinct. <i>MSystems</i> , 2023, 8, .	3.8	3
7411	Depth drives the distribution of microbial ecological functions in the coastal western Antarctic Peninsula. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	1
7412	Comparative Genomics and Physiological Investigations Supported Multifaceted Plant Growth-Promoting Activities in Two <i>Hypericum perforatum</i> L.-Associated Plant Growth-Promoting Rhizobacteria for Microbe-Assisted Cultivation. <i>Microbiology Spectrum</i> , 2023, 11, .	3.0	3

#	ARTICLE	IF	CITATIONS
7413	Abiotic and Biotic Effects on Microbial Diversity of Small Water Bodies in and around Towns. Sustainability, 2023, 15, 8151.	3.2	0
7414	Metatranscriptomic analysis uncovers prevalent viral ORFs compatible with mitochondrial translation. MSystems, 2023, 8, .	3.8	1
7415	Gut microbial signatures and their functions in Behcet's uveitis and Vogt-Koyanagi-Harada disease. Journal of Autoimmunity, 2023, 137, 103055.	6.5	7
7416	Virulent Phage vB_EfaS_WH1 Removes Enterococcus faecalis Biofilm and Inhibits Its Growth on the Surface of Chicken Meat. Viruses, 2023, 15, 1208.	3.3	1
7419	Comparative Transcriptomic Analysis Reveals Adaptive Traits in Antarctic Scallop Adamussium colbecki. Fishes, 2023, 8, 276.	1.7	2
7420	Extreme genome diversity and cryptic speciation in a harmful algal-bloom-forming eukaryote. Current Biology, 2023, 33, 2246-2259.e8.	3.9	5
7421	Disturbed microbiota-metabolites-immune interaction network is associated with olfactory dysfunction in patients with chronic rhinosinusitis. Frontiers in Immunology, 0, 14, .	4.8	1
7422	The influence of parasite load on transcriptional activity and morphology of a cestode and its ant intermediate host. Molecular Ecology, 2023, 32, 4412-4426.	3.9	0
7423	Maribacter aquimaris sp. nov., isolated from seawater adjacent to Fildes Peninsula, Antarctica. Antonie Van Leeuwenhoek, 2023, 116, 753-761.	1.7	0
7424	Chemical-microbial effects of acetic acid, oxalic acid and citric acid on arsenic transformation and migration in the rhizosphere of paddy soil. Ecotoxicology and Environmental Safety, 2023, 259, 115046.	6.0	0
7425	Flotillin-associated rhodopsin (FARhodopsin), a widespread paralog of proteorhodopsin in aquatic bacteria with streamlined genomes. MSystems, 2023, 8, .	3.8	0
7427	The Antarctic Scallop Adamussium colbecki Is Unable to Transcriptomically Respond to Captivity and Moderate Thermal Stress. Stresses, 2023, 3, 475-487.	4.8	2
7428	QTL Mapping and Transcriptome Analysis Reveal Candidate Genes Regulating Seed Color in Brassica napus. International Journal of Molecular Sciences, 2023, 24, 9262.	4.1	1
7429	Fontisphaera persica gen. nov., sp. nov., a thermophilic hydrolytic bacterium from a hot spring of Baikal lake region, and proposal of Fontisphaeraceae fam. nov., and Limisphaeraceae fam. nov. within the Limisphaerales ord. nov. (Verrucomicrobiota). Systematic and Applied Microbiology, 2023, 46, 126438.	2.8	1
7430	Effects of <i>ex situ</i> conservation on diversity and function of the gut microbiota of the Tibetan wild ass (<i>Equus kiang</i>). Integrative Zoology, 0, , .	2.6	1
7432	Endogenous viral elements reveal associations between a non-retroviral RNA virus and symbiotic dinoflagellate genomes. Communications Biology, 2023, 6, .	4.4	7
7433	PacBio Hi-Fi genome assembly of the Iberian dolphin freshwater mussel Unio delphinus Spengler, 1793. Scientific Data, 2023, 10, .	5.3	1
7434	MMSMAPlus: a multi-view multi-scale multi-attention embedding model for protein function prediction. Briefings in Bioinformatics, 2023, 24, .	6.5	0

#	ARTICLE	IF	CITATIONS
7435	Functional profile of oral plaque microbiome: Further insight into the bidirectional relationship between type 2 diabetes and periodontitis. <i>Molecular Oral Microbiology</i> , 2024, 39, 62-79.	2.7	1
7436	Epiphytic common core bacteria in the microbiomes of co-located green (<i>Ulva</i>), brown (<i>Saccharina</i>) and red (<i>Grateloupia</i> , <i>Gelidium</i>) macroalgae. <i>Microbiome</i> , 2023, 11, .	11.1	7
7438	Genomic Assessment of the Contribution of the <i>Wolbachia</i> Endosymbiont of <i>Eurosta solidaginis</i> to Gall Induction. <i>International Journal of Molecular Sciences</i> , 2023, 24, 9613.	4.1	3
7439	Metagenomics analysis reveals differences in rumen microbiota in cows with low and high milk protein percentage. <i>Applied Microbiology and Biotechnology</i> , 2023, 107, 4887-4902.	3.6	0
7441	A PacBio Hi-Fi Genome Assembly of the Painterâ€™s Mussel <i>Unio pictorum</i> (Linnaeus, 1758). <i>Genome Biology and Evolution</i> , 2023, 15, .	2.5	0
7442	<i>Thiobacillus</i> as a key player for biofilm formation in oligotrophic groundwaters of the Fennoscandian Shield. <i>Npj Biofilms and Microbiomes</i> , 2023, 9, .	6.4	1
7443	A Diet Enriched with <i>Lactocaseibacillus rhamnosus</i> HN001 and Milk Fat Globule Membrane Alters the Gut Microbiota and Decreases Amygdala GABA a Receptor Expression in Stress-Sensitive Rats. <i>International Journal of Molecular Sciences</i> , 2023, 24, 10433.	4.1	2
7444	Oil Has a Higher Methanogenic Potential than Coal in an Oil-Bearing Coal Seam. <i>ACS Omega</i> , 2023, 8, 23880-23888.	3.5	0
7445	Characterization of the Human Blood Virome in Iranian Multiple Transfused Patients. <i>Viruses</i> , 2023, 15, 1425.	3.3	2
7446	Virome Analysis Provides an Insight into the Viral Community of Chinese Mitten Crab <i>Eriocheir sinensis</i> . <i>Microbiology Spectrum</i> , 2023, 11, .	3.0	1
7447	Linking soil phosphorus fractions to associated microbial functional profiles under crop rotation on the Loess Plateau of China. <i>Soil and Tillage Research</i> , 2023, 233, 105809.	5.6	1
7448	The draft genome reveals early duplication event in <i>Pterocarpus santalinus</i> : an endemic timber species. <i>Planta</i> , 2023, 258, .	3.2	0
7449	Metagenomic Analyses Reveal the Influence of Depth Layers on Marine Biodiversity on Tropical and Subtropical Regions. <i>Microorganisms</i> , 2023, 11, 1668.	3.6	2
7450	Genome Mining and Molecular Networking Guided Isolation of Antimycin Analogs with Antifeedant Activities from the Deepâ€™Seaâ€™Derived <i>Streptomyces</i> sp. NA13. <i>Chemistry and Biodiversity</i> , 2023, 20, .	2.1	0
7451	PLASMe: a tool to identify PLASMid contigs from short-read assemblies using transformer. <i>Nucleic Acids Research</i> , 2023, 51, e83-e83.	14.5	6
7452	MetaPro: a scalable and reproducible data processing and analysis pipeline for metatranscriptomic investigation of microbial communities. <i>Microbiome</i> , 2023, 11, .	11.1	3
7453	Hierarchical graph transformer with contrastive learning for protein function prediction. <i>Bioinformatics</i> , 2023, 39, .	4.1	4
7454	Nuclear genome annotation of wheel animals and thorny-headed worms: inferences about the last common ancestor of Syndermata (<i>Rotifera</i> s.l.). <i>Hydrobiologia</i> , 0, , .	2.0	1

#	ARTICLE	IF	CITATIONS
7456	Evidence for nontraditional <i>mcr</i> -containing archaea contributing to biological methanogenesis in geothermal springs. <i>Science Advances</i> , 2023, 9, .	10.3	4
7457	Viromes of Coastal Waters of the North Caspian Sea: Initial Assessment of Diversity and Functional Potential. <i>Diversity</i> , 2023, 15, 813.	1.7	0
7458	The first homosporous lycophyte genome revealed the association between the recent dynamic accumulation of LTR-RTs and genome size variation. <i>Plant Molecular Biology</i> , 2023, 112, 325-340.	3.9	5
7459	Effect of phage therapy on survival, histopathology, and water microbiota of <i>Penaeus vannamei</i> challenged with <i>Vibrio parahaemolyticus</i> causing acute hepatopancreatic necrosis disease (AHPND). <i>Aquaculture</i> , 2023, 576, 739851.	3.5	3
7460	Zinc Oxide Quantum Dots May Provide a Novel Potential Treatment for Antibiotic-Resistant <i>Streptococcus agalactiae</i> in <i>Lama glama</i> . <i>Molecules</i> , 2023, 28, 5115.	3.8	0
7462	Short-Term Supplementation of Pectin Alters Substrate Dynamics and Modulates Microbial Carbohydrate Metabolism in the Gut of a Pig Model. <i>Journal of Agricultural and Food Chemistry</i> , 2023, 71, 10470-10482.	5.2	1
7464	Evaluating the relationship between community water and sanitation access and the global burden of antibiotic resistance: an ecological study. <i>Lancet Microbe</i> , The, 2023, 4, e591-e600.	7.3	6
7465	The long-term effect of glutaraldehyde on the bacterial community in anaerobic ammonium oxidation reactor. <i>Bioresource Technology</i> , 2023, 385, 129448.	9.6	0
7466	Transcriptome and metabolome analysis revealed the changes of Geniposide and Crocin content in <i>Gardenia jasminoides</i> fruit. <i>Molecular Biology Reports</i> , 2023, 50, 6851-6861.	2.3	2
7467	A Metagenomic Time-Series Approach to Assess the Ecological Stability of Microbial Mats in a Seasonally Fluctuating Environment. <i>Microbial Ecology</i> , 0, , .	2.8	2
7468	Transcriptomic profile of lettuce seedlings (<i>Lactuca sativa</i>) response to microalgae extracts used as biostimulant agents. <i>AoB PLANTS</i> , 2023, 15, .	2.3	1
7469	CACO: A Core-Attachment Method With Cross-Species Functional Ortholog Information to Detect Human Protein Complexes. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2023, 27, 4569-4578.	6.3	2
7470	Hybridization altered the gut microbiota of pigs. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	0
7471	Characteristics of the spiny dogfish (<i>Squalus acanthias</i>) nuclear genome. <i>G3: Genes, Genomes, Genetics</i> , 2023, 13, .	1.8	1
7473	Molecular characterization of a novel ambiguvirus isolated from the phytopathogenic fungus <i>Setosphaeria turcica</i> . <i>Archives of Virology</i> , 2023, 168, .	2.1	0
7474	Different techniques reveal the difference of community structure and function of fungi from root and rhizosphere of <i>Salvia miltiorrhiza</i> Bunge. <i>Plant Biology</i> , 2023, 25, 848-859.	3.8	2
7475	Chromosome-Level Analysis of the <i>Pelochelys cantorii</i> Genome Provides Insights to Its Immunity, Growth and Longevity. <i>Biology</i> , 2023, 12, 939.	2.8	1
7476	Mitochondrial genome annotation with MFannot: a critical analysis of gene identification and gene model prediction. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	19

#	ARTICLE	IF	CITATIONS
7478	Metagenomic Insights Reveal the Microbial Diversity and Associated Algal-Polysaccharide-Degrading Enzymes on the Surface of Red Algae among Remote Regions. <i>International Journal of Molecular Sciences</i> , 2023, 24, 11019.	4.1	1
7480	Metagenomic insights into the alteration of soil Nâ€œcyclingâ€œrelated microbiome and functions under longâ€œterm conversion of cropland to <i>Miscanthus</i>. <i>GCB Bioenergy</i> , 0, , .	5.6	1
7481	A microbial consortium alters intestinal <i>Pseudomonadota</i> and antimicrobial resistance genes in individuals with recurrent <i>Clostridioides difficile</i> infection. <i>MBio</i> , 0, , .	4.1	1
7482	<scp>TransMCL</scp> enables the assembly of fullâ€œlength coding genes for collecting complete hierarchical orthogroups. <i>Methods in Ecology and Evolution</i> , 2023, 14, 2137-2149.	5.2	1
7484	The RNA Viruses in Samples of Endemic Lake Baikal Sponges. <i>Diversity</i> , 2023, 15, 835.	1.7	1
7485	Taxonomic and carbon metabolic diversification of Bathyarchaea during its coevolution history with early Earth surface environment. <i>Science Advances</i> , 2023, 9, .	10.3	11
7486	Comparative Genomic Analysis of Biofilm-Forming Polar Microbacterium sp. Strains PAMC22086 and PAMC21962 Isolated from Extreme Habitats. <i>Microorganisms</i> , 2023, 11, 1757.	3.6	0
7487	Plant myo-inositol transport influences bacterial colonization phenotypes. <i>Current Biology</i> , 2023, 33, 3111-3124.e5.	3.9	4
7488	Transcriptome analysis of flower colour reveals the correlation between SNP and differential expression genes in <i>Phalaenopsis</i> . <i>Genes and Genomics</i> , 0, , .	1.4	0
7489	Long-Read Metagenomics of Marine Microbes Reveals Diversely Expressed Secondary Metabolites. <i>Microbiology Spectrum</i> , 0, , .	3.0	0
7491	PearMODB: a multiomics database forÂpear (<i>Pyrus</i>) genomics, genetics andÂbreeding study. <i>Database: the Journal of Biological Databases and Curation</i> , 2023, 2023, .	3.0	2
7492	Enhanced nitrogen removal in low-carbon saline wastewater by adding functional bacteria into <i>Sesuvium portulacastrum</i> constructed wetlands. <i>Ecotoxicology and Environmental Safety</i> , 2023, 263, 115234.	6.0	2
7493	First metagenomic analysis of the Andean condor (<i>Vultur gryphus</i>) gut microbiome reveals microbial diversity and wide resistome. <i>PeerJ</i> , 0, 11, e15235.	2.0	2
7494	Novel diversity of polar Cyanobacteria revealed by genome-resolved metagenomics. <i>Microbial Genomics</i> , 2023, 9, .	2.0	2
7495	Genome analysis of Parmales, the sister group of diatoms, reveals the evolutionary specialization of diatoms from phago-mixotrophs to photoautotrophs. <i>Communications Biology</i> , 2023, 6, .	4.4	3
7496	Monitoring terrestrial wildlife by combining hybridization capture and metabarcoding data from waterhole environmental DNA. <i>Biological Conservation</i> , 2023, 284, 110168.	4.1	1
7497	Unraveling the roles of coastal bacterial consortia in degradation of various lignocellulosic substrates. <i>MSystems</i> , 0, , .	3.8	1
7498	Functional and sequence-based metagenomics to uncover carbohydrate-degrading enzymes from composting samples. <i>Applied Microbiology and Biotechnology</i> , 2023, 107, 5379-5401.	3.6	2

#	ARTICLE	IF	CITATIONS
7499	Atlantic water influx and sea-ice cover drive taxonomic and functional shifts in Arctic marine bacterial communities. ISME Journal, 2023, 17, 1612-1625.	9.8	4
7500	A chromosome-scale genome and proteome draft of <i>Tremella fuciformis</i> . International Journal of Biological Macromolecules, 2023, 247, 125749.	7.5	1
7501	Phylogenomics reveals extreme gene tree discordance in a lineage of dominant trees: hybridization, introgression, and incomplete lineage sorting blur deep evolutionary relationships despite clear species groupings in <i>Eucalyptus</i> subgenus <i>Eudesmia</i> . Molecular Phylogenetics and Evolution, 2023, 187, 107869.	2.7	3
7505	The genome of the glasshouse plant noble rhubarb (<i>Rheum nobile</i>) provides a window into alpine adaptation. Communications Biology, 2023, 6, .	4.4	3
7506	Roving methyltransferases generate a mosaic epigenetic landscape and influence evolution in <i>Bacteroides fragilis</i> group. Nature Communications, 2023, 14, .	12.8	1
7509	Integrative Metabolic and Transcriptomic Profiling in <i>Camellia oleifera</i> and <i>Camellia meiocarpa</i> Uncover Potential Mechanisms That Govern Triacylglycerol Degradation during Seed Desiccation. Plants, 2023, 12, 2591.	3.5	0
7510	Physiology, Transcriptome and Root Exudates Analysis of Response to Aluminum Stress in <i>Pinus massoniana</i> . Forests, 2023, 14, 1410.	2.1	4
7511	Effects of straw and plastic film mulching on microbial functional genes involved in soil nitrogen cycling. Frontiers in Microbiology, 0, 14, .	3.5	2
7512	Decoding the <scp>DNA</scp> and <scp>RNA</scp> viromes of a tropical urban lagoon. Environmental Microbiology, 2023, 25, 2368-2387.	3.8	1
7513	Metagenomics combined with metabolomics reveals the effect of <i>Enterobacter</i> sp. inoculation on the rhizosphere microenvironment of <i>Bidens pilosa</i> L. in heavy metal contaminated soil. Journal of Hazardous Materials, 2023, 458, 132033.	12.4	1
7514	Antifungal Mechanism of Phenazine-1-Carboxylic Acid against <i>Pestalotiopsis kenyana</i> . International Journal of Molecular Sciences, 2023, 24, 11274.	4.1	3
7515	Comparison of the Strengths and Weaknesses of Machine Learning Algorithms and Feature Selection on KEGG Database Microbial Gene Pathway Annotation and Its Effects on Reconstructed Network Topology. Journal of Computational Biology, 2023, 30, 766-782.	1.6	0
7517	A haplotype-resolved genome assembly of <i>Rhododendron vialii</i> based on PacBio HiFi reads and Hi-C data. Scientific Data, 2023, 10, .	5.3	3
7518	Carbon source shaped microbial ecology, metabolism and performance in denitrification systems. Water Research, 2023, 243, 120330.	11.3	7
7519	Midgut transcriptomic responses to dengue and chikungunya viruses in the vectors <i>Aedes albopictus</i> and <i>Aedes malayensis</i> . Scientific Reports, 2023, 13, .	3.3	2
7520	In host evolution of <i>Exophiala dermatitidis</i> in cystic fibrosis lung micro-environment. G3: Genes, Genomes, Genetics, 2023, 13, .	1.8	0
7521	Longitudinal anellome dynamics in the upper respiratory tract of children with acute respiratory tract infections. Virus Evolution, 0, , .	4.9	0
7522	Short-Term Dietary Intervention with Whole Oats Protects from Antibiotic-Induced Dysbiosis. Microbiology Spectrum, 0, , .	3.0	1

#	ARTICLE	IF	CITATIONS
7523	Hybridisation has shaped a recent radiation of grass-feeding aphids. <i>BMC Biology</i> , 2023, 21, .	3.8	0
7524	Chromosome-level genome assembly of the sea cucumber <i>Apostichopus japonicus</i> . <i>Scientific Data</i> , 2023, 10, .	5.3	2
7525	Effects of environmental disinfection on microbial population and resistance genes: A case study of the microecology within a panda enclosure. <i>Environmental Research</i> , 2023, 235, 116662.	7.5	3
7526	A newly isolated <i>Bacillus megaterium</i> QO560352 promotes maize growth in saline soils by altering rhizosphere microbial communities and organic phosphorus utilization. <i>Rhizosphere</i> , 2023, 27, 100746.	3.0	2
7527	Comparative Genomic Analysis of Warthog and Sus Scrofa Identifies Adaptive Genes Associated with African Swine Fever. <i>Biology</i> , 2023, 12, 1001.	2.8	2
7528	Crosstalk between Breast Milk N-Acetylneuraminic Acid and Infant Growth in a Gut Microbiota-Dependent Manner. <i>Metabolites</i> , 2023, 13, 846.	2.9	4
7529	Phylogenomic and syntenic data demonstrate complex evolutionary processes in early radiation of the rosids. <i>Molecular Ecology Resources</i> , 2023, 23, 1673-1688.	4.8	2
7530	Shotgun Metagenomic Sequencing Reveals Virome Composition of Mosquitoes from a Transition Ecosystem of North-Northeast Brazil. <i>Genes</i> , 2023, 14, 1443.	2.4	2
7531	Distribution and Activity of Sulfur-Metabolizing Bacteria along the Temperature Gradient in Phototrophic Mats of the Chilean Hot Spring Porcelana. <i>Microorganisms</i> , 2023, 11, 1803.	3.6	1
7532	Microbial communities in aerosol generated from cyanobacterial bloom-affected freshwater bodies: an exploratory study in Nakdong River, South Korea. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	1
7533	Phosphorus-mediated succession of microbial nitrogen, carbon, and sulfur functions in rice-driven saline-alkali soil remediation. <i>Soil Biology and Biochemistry</i> , 2023, 184, 109125.	8.8	2
7534	Functional genomic characterization unveils probiotic features of G1-11 isolated from the gut of the hybrid grouper (<i>Epinephelus fuscoguttatus</i> ™ × <i>E. lanceolatus</i> ™). <i>LWT - Food Science and Technology</i> , 2023, 184, 115088.	5.2	3
7535	Macrofungi promote SOC decomposition and weaken sequestration by modulating soil microbial function in temperate steppe. <i>Science of the Total Environment</i> , 2023, 899, 165556.	8.0	2
7536	Improving Taxonomic Classification with Feature Space Balancing. <i>Bioinformatics Advances</i> , 0, , .	2.4	0
7537	hybpiperâ€” and paragoneâ€”: Containerization and additional options for target capture assembly and paralog resolution. <i>Applications in Plant Sciences</i> , 2023, 11, .	2.1	7
7539	Functional response of microbial communities in lab-controlled oil-contaminated marine sediment. <i>Molecular Omics</i> , 0, , .	2.8	1
7540	Lampshade web spider <i>Ectatosticta davidi</i> chromosome-level genome assembly provides evidence for its phylogenetic position. <i>Communications Biology</i> , 2023, 6, .	4.4	1
7541	Inferring and comparing metabolism across heterogeneous sets of annotated genomes using AuCoMe. <i>Genome Research</i> , 2023, 33, 972-987.	5.5	4

#	ARTICLE	IF	CITATIONS
7542	Gastrointestinal microbiome, resistance genes, and risk assessment of heavy metals in wild giant pandas. <i>Science of the Total Environment</i> , 2023, 899, 165671.	8.0	2
7543	Simultaneous partial nitrification, denitrification, and phosphorus removal in sequencing batch reactors via controlled reduced aeration and short-term sludge retention time decrease. <i>Journal of Environmental Management</i> , 2023, 344, 118598.	7.8	4
7544	Genus-wide genomic characterization of <i>Macrococcus</i> : insights into evolution, population structure, and functional potential. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	2
7545	Protein family neighborhood analyzer—ProFaNA. <i>PeerJ</i> , 0, 11, e15715.	2.0	0
7546	Effects of <i>Candidatus Liberibacter asiaticus</i> infection on metagenome of <i>Diaphorina citri</i> gut endosymbiont. <i>Scientific Data</i> , 2023, 10, .	5.3	2
7547	Comparative transcriptome and metabolome analyses of wild and mutant Oujiang color common carp through editing <i>SCARB1</i> gene by CRISPR/Cas technology. <i>Aquaculture</i> , 2023, 577, 739901.	3.5	2
7549	The Rhodoexplorer Platform for Red Algal Genomics and Whole-Genome Assemblies for Several <i>Gracilaria</i> Species. <i>Genome Biology and Evolution</i> , 2023, 15, .	2.5	2
7550	Flavonoid Synthesis by <i>Deinococcus</i> sp. 43 Isolated from the Ginkgo Rhizosphere. <i>Microorganisms</i> , 2023, 11, 1848.	3.6	1
7551	The gut microbiome as a potential source of non-invasive biomarkers of chronic obstructive pulmonary disease. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	3
7553	Evidence that an Unnamed Isometric Virus Associated with Potato Rugose Disease in Peru Is a New Species of Genus <i>Torradovirus</i> . <i>Phytopathology</i> , 2023, 113, 1716-1728.	2.2	4
7554	Effect of a multichannel oral irrigator on periodontal health and the oral microbiome. <i>Scientific Reports</i> , 2023, 13, .	3.3	1
7555	Microbial Communities in Ferromanganese Sediments from the Northern Basin of Lake Baikal (Russia). <i>Microorganisms</i> , 2023, 11, 1865.	3.6	1
7556	Near-chromosome level genome assembly of devil firefish, <i>Apterois miles</i> . , 0, 3, .		0
7557	Multiple infections of zoonotic pathogens in wild Brandt's voles (<i>Lasiopodomys brandtii</i>). <i>Veterinary Medicine and Science</i> , 2023, 9, 2201-2211.	1.6	0
7558	Comparative Transcriptomic Analysis of the Metabolism of Betalains and Flavonoids in Red Amaranth Hypocotyl under Blue Light and Dark Conditions. <i>Molecules</i> , 2023, 28, 5627.	3.8	0
7559	Genomes and transcriptomes help unravel the complex life cycle of the blastoclad fungus, <i>Coelomomyces lativittatus</i> , an obligate parasite of mosquitoes and microcrustaceans. <i>Mycologia</i> , 2023, 115, 630-647.	1.9	1
7561	Alterations in the gut microbiome implicate key taxa and metabolic pathways across inflammatory arthritis phenotypes. <i>Science Translational Medicine</i> , 2023, 15, .	12.4	4
7562	Metabolites and metagenomic analysis reveals the quality of Pu-erh tea head. <i>Food Chemistry</i> , 2023, 429, 136992.	8.2	1

#	ARTICLE	IF	CITATIONS
7563	A predicted CRISPR-mediated symbiosis between uncultivated archaea. <i>Nature Microbiology</i> , 2023, 8, 1619-1633.	13.3	4
7564	Garlic essential oil supplementation modulates colonic microbiota compositions and regulates immune response in weaned piglets. <i>Heliyon</i> , 2023, 9, e18729.	3.2	1
7565	Comparative genomics of flowering behavior in <i>Cannabis sativa</i> . <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	1
7567	Circulation of influenza C virus of C/Sao Paulo/378/82 lineage among pediatric acute respiratory cases, Shandong, China. <i>Virology</i> , 2023, 587, 109855.	2.4	0
7568	Metagenomic analysis insights into the influence of 3,4-dimethylpyrazole phosphate application on nitrous oxide mitigation efficiency across different climate zones in Eastern China. <i>Environmental Research</i> , 2023, , 116761.	7.5	1
7569	Insights into the Ecological Diversification of the Hymenochaetales based on Comparative Genomics and Phylogenomics With an Emphasis on <i>Coltricia</i> . <i>Genome Biology and Evolution</i> , 2023, 15, .	2.5	3
7570	Bioinformatics on the Road: Taking Training to Students and Researchers Beyond State Capitals. <i>Frontiers in Education</i> , 0, 6, .	2.1	1
7571	Genome analyses ofÂspecies A rotavirus isolated from various mammalian hosts inÂNorthern Ireland during 2013â2016. <i>Virus Evolution</i> , 2023, 9, .	4.9	0
7572	Rampant loss of universal metazoan genes revealed by a chromosome-level genome assembly of the parasitic Nematomorpha. <i>Current Biology</i> , 2023, 33, 3514-3521.e4.	3.9	8
7573	The combination of metagenome and metabolome to compare the differential effects and mechanisms of fructose and sucrose on the metabolic disorders and gut microbiota <i>in vitro</i> and <i>in vivo</i> . <i>Food and Function</i> , 2023, 14, 7284-7298.	4.6	2
7574	Metagenomic analysis reveals the dissemination mechanisms and risks of resistance genes in plateau lakes. <i>IScience</i> , 2023, 26, 107508.	4.1	1
7575	The role and risks of selective adaptation in extreme coral habitats. <i>Nature Communications</i> , 2023, 14, .	12.8	2
7576	RNA-Seq Virus Fraction in Lake Baikal and Treated Wastewaters. <i>International Journal of Molecular Sciences</i> , 2023, 24, 12049.	4.1	1
7577	Continuous presence of genetically diverse rustrela virus lineages in yellow-necked field mouse reservoir populations in northeastern Germany. <i>Virus Evolution</i> , 0, , .	4.9	0
7578	Denitrification fractionates N and O isotopes of nitrate following a ratio independent of carbon sources in freshwaters. <i>Environmental Microbiology</i> , 2023, 25, 2404-2415.	3.8	1
7580	Abundance of microbial community genes encoding terminal proteins of the aerobic and denitrification respiratory chains as indicators of ecohydrologic gradients in a coastal temperate rainforest. <i>Ecological Indicators</i> , 2023, 154, 110702.	6.3	0
7581	Bioinformatic Surveillance Leads to Discovery of Two Novel Putative Bunyaviruses Associated with Black Soldier Fly. <i>Viruses</i> , 2023, 15, 1654.	3.3	2
7583	Habitat-specific environmental factors regulate the spatial variability of biological soil crust microbial communities on the Qinghai-Tibet Plateau. <i>Science of the Total Environment</i> , 2023, 901, 165937.	8.0	4

#	ARTICLE	IF	CITATIONS
7584	Influence of nitrate starvation on transcript levels of nitrate transporter (Nrt2) and β -subunit of phycoerythrin (Cpeb) genes in <i>Rhodomonas</i> sp.. <i>Algal Research</i> , 2023, 74, 103217.	4.6	0
7585	Impact of the fungal pathogen <i>Fusarium oxysporum</i> on the taxonomic and functional diversity of the common bean root microbiome. <i>Environmental Microbiomes</i> , 2023, 18, .	5.0	4
7586	Nitrate removal in iron sulfide-driven autotrophic denitrification biofilter: Biochemical and chemical transformation pathways and its underlying microbial mechanism. <i>Science of the Total Environment</i> , 2023, 901, 165908.	8.0	2
7587	Functional divergence of CYP76AKs shapes the chemodiversity of abietane-type diterpenoids in genus <i>Salvia</i> . <i>Nature Communications</i> , 2023, 14, .	12.8	2
7589	Presence and role of viruses in anaerobic digestion of food waste under environmental variability. <i>Microbiome</i> , 2023, 11, .	11.1	2
7590	Metagenomics revealed a correlation of gut phageome with autism spectrum disorder. <i>Gut Pathogens</i> , 2023, 15, .	3.4	2
7591	A chromosome-level genome assembly of <i>Stenchaetothrips biformis</i> and comparative genomic analysis highlights distinct host adaptations among thrips. <i>Communications Biology</i> , 2023, 6, .	4.4	2
7592	Dengue virus serotype 2 genotype III evolution during the 2019 outbreak in Mato Grosso, Midwestern Brazil. <i>Infection, Genetics and Evolution</i> , 2023, 113, 105487.	2.3	1
7594	metaSpectraST: an unsupervised and database-independent analysis workflow for metaproteomic MS/MS data using spectrum clustering. <i>Microbiome</i> , 2023, 11, .	11.1	0
7595	Lower viral evolutionary pressure under stable versus fluctuating conditions in subzero Arctic brines. <i>Microbiome</i> , 2023, 11, .	11.1	3
7596	Transcriptome analyses of leaf architecture in <i>Sansevieria</i> support a common genetic toolkit in the parallel evolution of unifacial leaves in monocots. <i>Plant Direct</i> , 2023, 7, .	1.9	1
7599	Comparative virome analysis of individual shedding routes of <i>Miniopterus phillipsi</i> bats inhabiting the Wavul Galge cave, Sri Lanka. <i>Scientific Reports</i> , 2023, 13, .	3.3	0
7600	The Diversity and Metabolism of Culturable Nitrate-Reducing Bacteria from the Photic Zone of the Western North Pacific Ocean. <i>Microbial Ecology</i> , 2023, 86, 2781-2789.	2.8	0
7602	Patters of reactive nitrogen removal at the waters in the semi-constructed wetland. <i>Journal of Environmental Management</i> , 2023, 344, 118733.	7.8	2
7603	Physiological and evolutionary contexts of a new symbiotic species from the nitrogen-recycling gut community of turtle ants. <i>ISME Journal</i> , 2023, 17, 1751-1764.	9.8	0
7604	Dietary protein levels modulate the gut microbiome composition through fecal samples derived from lactating ewes. <i>Frontiers in Endocrinology</i> , 0, 14, .	3.5	1
7605	Making sense of complexity: Advances in bioinformatics for plant biology. <i>Applications in Plant Sciences</i> , 2023, 11, .	2.1	0
7606	Characterization of a novel psyllid-transmitted waikavirus in carrots. <i>Virus Research</i> , 2023, 335, 199192.	2.2	0

#	ARTICLE	IF	CITATIONS
7607	Viruses of Freshwater Mussels during Mass Mortality Events in Oregon and Washington, USA. <i>Viruses</i> , 2023, 15, 1719.	3.3	2
7608	Characterization of the pig lower respiratory tract antibiotic resistome. <i>Nature Communications</i> , 2023, 14, .	12.8	3
7609	Elemental sulfur autotrophic partial denitrification (SO-PDN) with high pH and free ammonia control strategy for low-carbon wastewater: From performance to microbial mechanism. <i>Chemical Engineering Journal</i> , 2023, 474, 145419.	12.7	1
7610	<scp>DNA</scp> isolation and genome sequence of the 134â€yearâ€old holotype specimen of <i>Boletus subvelutipes</i> Peck. <i>Ecology and Evolution</i> , 2023, 13, .	1.9	0
7614	Metagenomics reveals taxon-specific responses of soil nitrogen cycling under different fertilization regimes in heavy metal contaminated soil. <i>Journal of Environmental Management</i> , 2023, 345, 118766.	7.8	2
7615	Biotransformation of Rutin in In Vitro Porcine Ileal and Colonic Fermentation Models. <i>Journal of Agricultural and Food Chemistry</i> , 2023, 71, 12487-12496.	5.2	0
7619	Distribution and prevalence of viral genomes in Italian populations of the invasive brown marmorated stink bug <i>Halyomorpha halys</i> . <i>Journal of Invertebrate Pathology</i> , 2023, 200, 107977.	3.2	0
7620	The first chromosome-level genome assembly of <i>Entomobrya proxima</i> Folsom, 1924 (Collembola: Tj ETQq1 1 0.784314 rgBT ₁ /Overload	3.3	0
7621	Effect of endophytic diazotroph <i>Enterobacter roggenkampii</i> ED5 on nitrogen-metabolism-related microecology in the sugarcane rhizosphere at different nitrogen levels. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	0
7623	HiFun: homology independent protein function prediction by a novel protein-language self-attention model. <i>Briefings in Bioinformatics</i> , 2023, 24, .	6.5	1
7625	CCNB1 is a novel prognostic biomarker and promotes proliferation, migration and invasion in Wilms tumor. <i>BMC Medical Genomics</i> , 2023, 16, .	1.5	2
7626	Genetic diversity, recombination and cross-species transmission of a waterbird gammacoronavirus in the wild. <i>Journal of General Virology</i> , 2023, 104, .	2.9	0
7627	Adapting antibacterial display to identify serum-active macrocyclic peptide antibiotics. , 2023, 2, .		0
7628	Chromosome-level genome of butterflyfish unveils genomic features of unique colour patterns and morphological traits. <i>DNA Research</i> , 2023, 30, .	3.4	0
7629	Distribution of Genes and Microbial Taxa Related to Soil Phosphorus Cycling across Soil Depths in Subtropical Forests. <i>Forests</i> , 2023, 14, 1665.	2.1	2
7630	Diversity of virulence and antibiotic resistance genes expressed in Class A biosolids and biosolids-amended soil as revealed by metatranscriptomic analysis. <i>Letters in Applied Microbiology</i> , 2023, 76, .	2.2	2
7631	A moderately thermophilic origin of a novel family of marine group II euryarchaeota from deep ocean. <i>IScience</i> , 2023, 26, 107664.	4.1	0
7632	Widely Targeted Metabolomic Profiling Combined with Transcriptome Analysis Provides New Insights into Lipid Biosynthesis in Seed Kernels of <i>Pinus koraiensis</i> . <i>International Journal of Molecular Sciences</i> , 2023, 24, 12887.	4.1	0

#	ARTICLE	IF	CITATIONS
7633	Investigation of sex expression profiles and the cantharidin biosynthesis genes in two blister beetles. PLoS ONE, 2023, 18, e0290245.	2.5	1
7634	A comparative study reveals the relative importance of prokaryotic and eukaryotic proton pump rhodopsins in a subtropical marginal sea. ISME Communications, 2023, 3, .	4.2	1
7636	Well-hidden methanogenesis in deep, organic-rich sediments of Guaymas Basin. ISME Journal, 2023, 17, 1828-1838.	9.8	5
7637	Expanding the genetic toolbox of <i>Rhodotorula toruloides</i> by identification and validation of six novel promoters induced or repressed under nitrogen starvation. Microbial Cell Factories, 2023, 22, .	4.0	0
7638	Human oral mucosa and oral microbiome interactions following supragingival plaque reconstitution in healthy volunteers: a diet-controlled balanced design proof-of-concept model to investigate oral pathologies. Journal of Oral Microbiology, 2023, 15, .	2.7	0
7639	mTORC1 regulates phagosome digestion of symbiotic bacteria for intracellular nutritional symbiosis in a deep-sea mussel. Science Advances, 2023, 9, .	10.3	1
7640	Epigenomic divergence correlates with sequence polymorphism in Arabidopsis paralogs. New Phytologist, 2023, 240, 1292-1304.	7.3	2
7641	Fiber supplementation protects from antibiotic-induced gut microbiome dysbiosis by modulating gut redox potential. Nature Communications, 2023, 14, .	12.8	5
7643	Spatial scale influences the distribution of viral diversity in the eukaryotic virome of the mosquito <i>Culex pipiens</i> . Virus Evolution, 2023, 9, .	4.9	2
7645	Accurate and fast graph-based pangenome annotation and clustering with ggCaller. Genome Research, 2023, 33, 1622-1637.	5.5	4
7646	Transcriptomic investigation of the molecular mechanisms underlying resistance to the neonicotinoid thiamethoxam and the pyrethroid lambda-cyhalothrin in <i>Euschistus heros</i> (Hemiptera: Pentatomidae). Pest Management Science, 2023, 79, 5349-5361.	3.4	1
7647	Chemoautotrophic sulphur oxidizers dominate microbial necromass carbon formation in coastal blue carbon ecosystems. Functional Ecology, 2023, 37, 2634-2651.	3.6	1
7650	Intestinal acetic acid regulates the synthesis of sex pheromones in captive giant pandas. Frontiers in Microbiology, 2023, 14, .	3.5	0
7651	Stratified microbial communities in Australia's only anchialine cave are taxonomically novel and drive chemotrophic energy production via coupled nitrogen-sulphur cycling. Microbiome, 2023, 11, .	11.1	1
7652	Transcriptomic analysis reveals the role of Glycolysis pathway in <i>Litopenaeus vannamei</i> during DIV1 infection. Fish and Shellfish Immunology, 2023, 141, 109036.	3.6	2
7653	Characterization of Diverse Anelloviruses, Cressdnaviruses, and Bacteriophages in the Human Oral DNA Virome from North Carolina (USA). Viruses, 2023, 15, 1821.	3.3	0
7654	Identifying and tracking mobile elements in evolving compost communities yields insights into the nanobiome. ISME Communications, 2023, 3, .	4.2	1
7655	Environmental gradients reveal stress hubs pre-dating plant terrestrialization. Nature Plants, 2023, 9, 1419-1438.	9.3	13

#	ARTICLE	IF	CITATIONS
7660	Isolation and genome sequencing of cytomegaloviruses from Natal multimammate mice (<i>Mastomys</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	2.9	1
7661	Responses of the microbial community and the production of extracellular polymeric substances to sulfamethazine shocks in a novel two-stage biological contact oxidation system. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	0
7663	Signatures of Extreme Longevity: A Perspective from Bivalve Molecular Evolution. <i>Genome Biology and Evolution</i> , 2023, 15, .	2.5	1
7664	Acetate supplementation rescues social deficits and alters transcriptional regulation in prefrontal cortex of Shank3 deficient mice. <i>Brain, Behavior, and Immunity</i> , 2023, 114, 311-324.	4.1	3
7665	mRNA-Seq and miRNA-Seq Analyses Provide Insights into the Mechanism of <i>Pinellia ternata</i> Bulbil Initiation Induced by Phytohormones. <i>Genes</i> , 2023, 14, 1727.	2.4	1
7666	OntoPred: An Efficient Attention-Based Approach for Protein Function Prediction Using Skip-Gram Features. <i>SN Computer Science</i> , 2023, 4, .	3.6	0
7667	Carbohydrate dynamics in <i>Populus</i> trees under drought: An expression atlas of genes related to sensing, translocation, and metabolism across organs. <i>Physiologia Plantarum</i> , 2023, 175, .	5.2	2
7668	Origin and functional diversification of PAS domain, a ubiquitous intracellular sensor. <i>Science Advances</i> , 2023, 9, .	10.3	6
7670	Viruses in Laboratory <i>Drosophila</i> and Their Impact on Host Gene Expression. <i>Viruses</i> , 2023, 15, 1849.	3.3	1
7671	De novo transcriptome sequencing and gene expression profiling of sweetpotato leaves during low temperature stress. <i>Plant Biotechnology Reports</i> , 0, , .	1.5	2
7672	<i>Vitis labrusca</i> genome assembly reveals diversification between wild and cultivated grapevine genomes. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	0
7673	Mining Public Data to Investigate the Virome of Neglected Pollinators and Other Floral Visitors. <i>Viruses</i> , 2023, 15, 1850.	3.3	0
7674	Human milk oligosaccharides modulate the intestinal microbiome of healthy adults. <i>Scientific Reports</i> , 2023, 13, .	3.3	3
7675	An exhaustive review of computational prediction techniques for PPI sites, protein locations, and protein functions. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2023, 12, .	2.1	1
7676	Metagenomics uncovers dietary adaptations for chitin digestion in the gut microbiota of convergent myrmecophagous mammals. <i>MSystems</i> , 0, , .	3.8	0
7677	Integrated metabolome, full-length sequencing, and transcriptome analyses unveil the molecular mechanisms of color formation of the canary yellow and red bracts of <i>Bougainvillea</i> — <i>buttiana</i> â€”Chitraâ€™™. <i>Plant Journal</i> , 2023, 116, 1441-1461.	5.7	1
7678	Biochar Enhances Soil Resource Availability and Suppresses Microbial Metabolism Genes in the Rhizosphere of Wheat. <i>Life</i> , 2023, 13, 1843.	2.4	0
7679	Galba: genome annotation with miniprot and AUGUSTUS. <i>BMC Bioinformatics</i> , 2023, 24, .	2.6	4

#	ARTICLE	IF	CITATIONS
7680	Removal of false positives in metagenomics-based taxonomy profiling via targeting Type IIB restriction sites. <i>Nature Communications</i> , 2023, 14, .	12.8	3
7681	Heat shock factor binding protein BrHSBP1 regulates seed and pod development in <i>Brassica rapa</i> . <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	0
7682	Intestinal microbiota links to allograft stability after lung transplantation: a prospective cohort study. <i>Signal Transduction and Targeted Therapy</i> , 2023, 8, .	17.1	4
7685	Ectomycorrhizal symbiosis prepares its host locally and systemically for abiotic cue signaling. <i>Plant Journal</i> , 2023, 116, 1784-1803.	5.7	0
7686	Integrated meta-omics approaches reveal <i>Saccharopolyspora</i> as the core functional genus in huangjiu fermentations. <i>Npj Biofilms and Microbiomes</i> , 2023, 9, .	6.4	2
7687	Comparison of the Structure of Soil Microbial Communities of Different Ecosystems Using the Microbiome Sequencing Approach. <i>Soil Systems</i> , 2023, 7, 70.	2.6	1
7688	FunTaxIS-lite: a simple and light solution to investigate protein functions in all living organisms. <i>Bioinformatics</i> , 2023, 39, .	4.1	0
7689	Viral community composition of hypersaline lakes. <i>Virus Evolution</i> , 2023, 9, .	4.9	3
7690	Identification of hidden N4-like viruses and their interactions with hosts. <i>MSystems</i> , 2023, 8, .	3.8	1
7691	Metaphorâ€”A workflow for streamlined assembly and binning of metagenomes. <i>GigaScience</i> , 2022, 12, .	6.4	3
7692	Complete genome sequence of the broad host range <i>Acinetobacter baumannii</i> phage EAb13. <i>Microbiology Resource Announcements</i> , 2023, 12, .	0.6	0
7693	Genetic diversity and characterization of rhinoviruses from Chinese clinical samples with a global perspective. <i>Microbiology Spectrum</i> , 2023, 11, .	3.0	1
7694	Unfolding the secrets of microbiome (Symbiodiniaceae and bacteria) in cold-water coral. <i>Microbiology Spectrum</i> , 2023, 11, .	3.0	0
7695	Identification and genomic analysis of temperate <i>Halomonas</i> bacteriophage vB_HmeY_H4907 from the surface sediment of the Mariana Trench at a depth of 8,900 m. <i>Microbiology Spectrum</i> , 2023, 11, .	3.0	0
7696	Highly divergent CRESS DNA and picorna-like viruses associated with bleached thalli of the green seaweed <i>Ulva</i> . <i>Microbiology Spectrum</i> , 2023, 11, .	3.0	0
7697	Antimicrobial resistance, pathogenic potential, and genomic features of carbapenem-resistant <i>Klebsiella pneumoniae</i> isolated in Chile: high-risk ST25 clones and novel mobile elements. <i>Microbiology Spectrum</i> , 2023, 11, .	3.0	2
7698	Identification and characterization of novel alphacoronaviruses in <i>Tadarida brasiliensis</i> (Chiroptera, Molossidae) from Argentina: insights into recombination as a mechanism favoring bat coronavirus cross-species transmission. <i>Microbiology Spectrum</i> , 2023, 11, .	3.0	0
7699	Microbial communities related to the sulfur cycle in the Sansha Yongle Blue Hole. <i>Microbiology Spectrum</i> , 2023, 11, .	3.0	1

#	ARTICLE	IF	CITATIONS
7700	A scaffolded and annotated reference genome of giant kelp (<i>Macrocystis pyrifera</i>). <i>BMC Genomics</i> , 2023, 24, .	2.8	5
7701	Antibiotic resistance gene profiles and evolutions in composting regulated by reactive oxygen species generated via nano ZVI loaded on biochar. <i>Science of the Total Environment</i> , 2023, 902, 166487.	8.0	1
7702	Metabolomic and transcriptomic profiling reveals the effect of dietary protein and lipid levels on growth performance in loach (<i>Paramisgurnus dabryanus</i>). <i>Frontiers in Immunology</i> , 0, 14, .	4.8	0
7703	Quantifying health risks of plastisphere antibiotic resistome and deciphering driving mechanisms in an urbanizing watershed. <i>Water Research</i> , 2023, 245, 120574.	11.3	4
7704	A near-complete assembly of asparagus bean provides insights into anthocyanin accumulation in pods. <i>Plant Biotechnology Journal</i> , 0, , .	8.3	3
7705	Virome of high-altitude canine digestive tract and genetic characterization of novel viruses potentially threatening human health. <i>MSphere</i> , 2023, 8, .	2.9	0
7706	Stepwise pathway for early evolutionary assembly of dissimilatory sulfite and sulfate reduction. <i>ISME Journal</i> , 2023, 17, 1680-1692.	9.8	5
7707	Metagenome meta-analysis reveals an increase in the abundance of some multidrug efflux pumps and mobile genetic elements in chemically polluted environments. <i>Applied and Environmental Microbiology</i> , 0, , .	3.1	1
7708	Risks of Antibiotic Resistance Dissemination by Leachates from Municipal Landfills of Different Ages. <i>Water (Switzerland)</i> , 2023, 15, 3349.	2.7	0
7709	Population and Transcriptomic Changes of the Tropical Fish Parasite <i>Caligus confusus</i> (Copepoda: Tj ETQq1 1 0.784314 rgBT ₀ /Overlock	1.7	0
7710	Transcriptomic Analysis of Light-Induced Genes in <i>Nasonia vitripennis</i> : Possible Implications for Circadian Light Entrainment Pathways. <i>Biology</i> , 2023, 12, 1215.	2.8	0
7711	Integrated Analysis of Transcriptome and Metabolome Reveals Molecular Mechanisms of Rice with Different Salinity Tolerances. <i>Plants</i> , 2023, 12, 3359.	3.5	0
7712	Metagenomic Analysis Reveals Variations in Gut Microbiomes of the <i>Schistosoma mansoni</i> -Transmitting Snails <i>Biomphalaria straminea</i> and <i>Biomphalaria glabrata</i> . <i>Microorganisms</i> , 2023, 11, 2419.	3.6	2
7713	Plastics shape the black soldier fly larvae gut microbiome and select for biodegrading functions. <i>Microbiome</i> , 2023, 11, .	11.1	0
7714	Long-read assembled metagenomic approaches improve our understanding on metabolic potentials of microbial community in mangrove sediments. <i>Microbiome</i> , 2023, 11, .	11.1	2
7715	Integrated omic profiling of the medicinal mushroom <i>Inonotus obliquus</i> under submerged conditions. <i>BMC Genomics</i> , 2023, 24, .	2.8	1
7716	Correlation between the gut microbiome and neurodegenerative diseases: a review of metagenomics evidence. <i>Neural Regeneration Research</i> , 2024, 19, 833-845.	3.0	4
7718	The genome of <i>Anoplarchus purpureus</i> (Stichaeidae) reflects its carnivorous diet. <i>Molecular Genetics and Genomics</i> , 2023, 298, 1419-1434.	2.1	1

#	ARTICLE	IF	CITATIONS
7719	Transcriptomic analyses during development reveal mechanisms of integument structuring and color production. <i>Evolutionary Ecology</i> , 0, , .	1.2	0
7720	Einkorn genomics sheds light on history of the oldest domesticated wheat. <i>Nature</i> , 2023, 620, 830-838.	27.8	18
7721	Genome sequencing reveals the genetic architecture of heterostyly and domestication history of common buckwheat. <i>Nature Plants</i> , 2023, 9, 1236-1251.	9.3	5
7722	Holistic view of the seascape dynamics and environment impact on macro-scale genetic connectivity of marine plankton populations. <i>Bmc Ecology and Evolution</i> , 2023, 23, .	1.6	0
7723	A systematic analysis of marine lysogens and proviruses. <i>Nature Communications</i> , 2023, 14, .	12.8	4
7724	Synergistic benefits of lime and 3,4-dimethylpyrazole phosphate application to mitigate the nitrous oxide emissions from acidic soils. <i>Ecotoxicology and Environmental Safety</i> , 2023, 263, 115387.	6.0	0
7725	Dynamics of Benthic Nitrate Reduction Pathways and Associated Microbial Communities Responding to the Development of Seasonal Deoxygenation in a Coastal Mariculture Zone. <i>Environmental Science & Technology</i> , 2023, 57, 15014-15025.	10.0	4
7726	Identification and characterization of a polyomavirus in the thornback skate (<i>Raja clavata</i>). <i>Virology Journal</i> , 2023, 20, .	3.4	1
7727	The effect of hyperthyroidism on cognitive function, neuroinflammation, and necroptosis in APP/PS1 mice. <i>Journal of Translational Medicine</i> , 2023, 21, .	4.4	3
7728	Strengthen high-loading operation of wastewater treatment plants by composite micron powder carrier: Microscale control of carbon, nitrogen, and sulfur metabolic pathways. <i>Science of the Total Environment</i> , 2023, 904, 166593.	8.0	0
7729	<scp><i>Prevotella copri</i></scp> alleviates sarcopenia via attenuating muscle mass loss and function decline. <i>Journal of Cachexia, Sarcopenia and Muscle</i> , 2023, 14, 2275-2288.	7.3	1
7730	A single-cell atlas of West African lungfish respiratory system reveals evolutionary adaptations to terrestrialization. <i>Nature Communications</i> , 2023, 14, .	12.8	0
7731	Auxin-producing bacteria promote barley rhizosheath formation. <i>Nature Communications</i> , 2023, 14, .	12.8	3
7732	Identification of Intestinal Microbial Community in Gallstone Patients with Metagenomic Next-Generation Sequencing. <i>Diagnostics</i> , 2023, 13, 2712.	2.6	1
7733	Viral but not bacterial community successional patterns reflect extreme turnover shortly after rewetting dry soils. <i>Nature Ecology and Evolution</i> , 2023, 7, 1809-1822.	7.8	6
7734	Gene losses, parallel evolution and heightened expression confer adaptations to dedicated cleaning behaviour. <i>BMC Biology</i> , 2023, 21, .	3.8	2
7735	Comparative genomics of Mollicutes-related endobacteria supports a late invasion into Mucoromycota fungi. <i>Communications Biology</i> , 2023, 6, .	4.4	0
7736	Evidence that the domesticated fungus <i>Leucoagaricus gongylophorus</i> recycles its cytoplasmic contents as nutritional rewards to feed its leafcutter ant farmers. <i>IMA Fungus</i> , 2023, 14, .	3.8	0

#	ARTICLE	IF	CITATIONS
7737	Validation of key sponge symbiont pathways using genome‐centric metatranscriptomics. Environmental Microbiology, 2023, 25, 3207-3224.	3.8	0
7738	Genome-wide analysis of the AP2/ERF gene family in Tritipyrum and the response of TtERF_B2-50 in salt-tolerance. BMC Genomics, 2023, 24, .	2.8	1
7739	Abundance and prevalence of ESBL coding genes in patients undergoing first line eradication therapy for Helicobacter pylori. PLoS ONE, 2023, 18, e0289879.	2.5	0
7740	Genome-scale metabolic modeling of Aspergillus fumigatus strains reveals growth dependencies on the lung microbiome. Nature Communications, 2023, 14, .	12.8	3
7741	Analysis of gut microbiota in chinese donkey in different regions using metagenomic sequencing. BMC Genomics, 2023, 24, .	2.8	0
7742	Multi-omics analysis reveals substantial linkages between the oral-gut microbiomes and inflamm-aging molecules in elderly pigs. Frontiers in Microbiology, 0, 14, .	3.5	0
7743	I am better than I look: genome based safety assessment of the probiotic Lactiplantibacillus plantarum IS-10506. BMC Genomics, 2023, 24, .	2.8	3
7744	Genome analysis of clinical genotype <i>Vibrio vulnificus</i> isolated from seafood in Mangaluru Coast, India provides insights into its pathogenicity. Veterinary Quarterly, 2023, 43, 1-17.	6.7	0
7745	Metagenomic analysis reveals the relationship between intestinal protozoan parasites and the intestinal microecological balance in calves. Parasites and Vectors, 2023, 16, .	2.5	2
7746	New Representatives of the Class Ignabacteria Inhabiting Subsurface Aquifers of Yessentuki Mineral Water Deposit. Water (Switzerland), 2023, 15, 3451.	2.7	2
7747	Gastrointestinal symptoms of long COVID-19 related to the ectopic colonization of specific bacteria that move between the upper and lower alimentary tract and alterations in serum metabolites. BMC Medicine, 2023, 21, .	5.5	6
7748	Integrated Transcriptome and Biochemical Analysis Provides New Insights into the Leaf Color Change in Acer fabri. Forests, 2023, 14, 1638.	2.1	2
7749	<i>Synechococcus</i> nitrogen gene loss in iron-limited ocean regions. ISME Communications, 2023, 3, .	4.2	1
7750	Isolation and Identification of Endophytic Bacteria Bacillus sp. ME9 That Exhibits Biocontrol Activity against Xanthomonas phaseoli pv. manihotis. Biology, 2023, 12, 1231.	2.8	1
7751	Innovative strategy for the conservation of a millennial mausoleum from biodeterioration through artificial light management. Npj Biofilms and Microbiomes, 2023, 9, .	6.4	3
7752	Bridging the Gap: Combining Genomics and Transcriptomics Approaches to Understand Stylosanthes scabra, an Orphan Legume from the Brazilian Caatinga. Plants, 2023, 12, 3246.	3.5	0
7754	ä,ä>1/2ä11/4ä1'æž—é²(Moschus berezovskii Flerov, 1929)é ™è...²ä'CEçš®è,ä^tæ³CEä;æ•ç'çš,,é—ä1/4ä'CEç»,ç»#ä ä...³ä³. Journal of Zhejiang	2.3	0
7755	Effect of salinity on genes involved in the stress response in mangrove soils. Antonie Van Leeuwenhoek, 2023, 116, 1171-1184.	1.7	0

#	ARTICLE	IF	CITATIONS
7756	Genome-Wide Survey Reveals the Microsatellite Characteristics and Phylogenomic Relationships of <i>Dictyosoma burgeri</i> (Zoarcales, Perciformes). <i>Thalassas</i> , 2023, 39, 609-619.	0.5	0
7757	Recovery of the gut microbiome following enteric infection and persistence of antimicrobial resistance genes in specific microbial hosts. <i>Scientific Reports</i> , 2023, 13, .	3.3	0
7758	Genome-centric investigation of the potential succession pattern in gut microbiota and altered functions under high-protein diet. <i>Current Research in Food Science</i> , 2023, 7, 100600.	5.8	1
7759	Prebiotic inulin enhances gut microbial metabolism and anti-inflammation in apolipoprotein E4 mice with sex-specific implications. <i>Scientific Reports</i> , 2023, 13, .	3.3	1
7760	Comparative analysis of gut DNA viromes in wild and captive Himalayan vultures. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	0
7761	Asymmetric responses of abundance and diversity of N-cycling genes to altered precipitation in arid grasslands. <i>Functional Ecology</i> , 2023, 37, 2953-2966.	3.6	3
7762	Metagenomics reveals the self-recovery and risk of antibiotic resistomes during carcass decomposition of wild mammals. <i>Environmental Research</i> , 2023, 238, 117222.	7.5	1
7763	Jellyfish detritus supports niche partitioning and metabolic interactions among pelagic marine bacteria. <i>Microbiome</i> , 2023, 11, .	11.1	4
7764	Archaeome structure and function of the intestinal tract in healthy and H1N1 infected swine. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	0
7765	Microbes from mature compost to promote bacterial chemotactic motility via tricarboxylic acid cycle-regulated biochemical metabolisms for enhanced composting performance. <i>Bioresource Technology</i> , 2023, 387, 129633.	9.6	2
7766	CTGF promotes the repair and regeneration of alveoli after acute lung injury by promoting the proliferation of subpopulation of AEC2s. <i>Respiratory Research</i> , 2023, 24, .	3.6	1
7767	Fecal Metagenomics Study Reveals That a Low-Fiber Diet Drives the Migration of Wild Asian Elephants in Xishuangbanna, China. <i>Animals</i> , 2023, 13, 3193.	2.3	0
7768	Specific biomarker mining and rapid detection of <i>Burkholderia cepacia</i> complex by recombinase polymerase amplification. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	0
7769	Phylogenetic diversity and functional potential of the microbial communities along the Bay of Bengal coast. <i>Scientific Reports</i> , 2023, 13, .	3.3	0
7770	Functional analysis of bacterial genes accidentally packaged in rhizospheric phageome of the wild plant species <i>Abutilon fruticosum</i> . <i>Saudi Journal of Biological Sciences</i> , 2023, 30, 103789.	3.8	0
7771	Whole genome sequence of the deep-sea sponge <i>Geodia barretti</i> (Metazoa, Porifera). <i>Tj ETQq1 1 0.784314</i> <i>rgBT /Overlock 10 TF</i>	1.8	0
7772	Metagenomic survey reveals global distribution and evolution of microbial sialic acid catabolism. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	0
7773	Abundances and key driving factors of combined contaminations of antibiotic resistome and metal resistome in tilapia aquaculture. <i>Chemical Engineering Research and Design</i> , 2023, 179, 513-524.	5.6	0

#	ARTICLE	IF	CITATIONS
7774	PandaGUT provides new insights into bacterial diversity, function, and resistome landscapes with implications for conservation. <i>Microbiome</i> , 2023, 11, .	11.1	2
7775	Mabs, a suite of tools for gene-informed genome assembly. <i>BMC Bioinformatics</i> , 2023, 24, .	2.6	2
7776	A glimpse of the paleome in endolithic microbial communities. <i>Microbiome</i> , 2023, 11, .	11.1	1
7777	Genome assembly and analysis of <i>Lactuca virosa</i> : implications for lettuce breeding. <i>G3: Genes, Genomes, Genetics</i> , 2023, 13, .	1.8	0
7778	<i>Serratia marcescens</i> Outbreak at a Correctional Facility: Environmental Sampling, Laboratory Analyses and Genomic Characterization to Assess Sources and Persistence. <i>International Journal of Environmental Research and Public Health</i> , 2023, 20, 6709.	2.6	0
7779	Genome-wide identification, comparative analysis and functional roles in flavonoid biosynthesis of cytochrome P450 superfamily in pear (<i>Pyrus</i> spp.). <i>BMC Genomic Data</i> , 2023, 24, .	1.7	1
7780	Insights into early evolutionary adaptations of the <i>Akkermansia</i> genus to the vertebrate gut. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	0
7781	De novo transcriptome assembly of an Antarctic nematode for the study of thermal adaptation in marine parasites. <i>Scientific Data</i> , 2023, 10, .	5.3	1
7782	Transcriptome analysis of anuran breeding glands reveals a surprisingly high expression and diversity of NNMT-like genes. <i>Biological Journal of the Linnean Society</i> , 0, , .	1.6	0
7783	A chromosome-level assembly supports genome-wide investigation of the DMRT gene family in the golden mussel (<i>Limnoperna fortunei</i>). <i>GigaScience</i> , 2022, 12, .	6.4	0
7784	Changes of gut microbiota under different nutritional methods in elderly patients with severe COVID-19 and their relationship with prognosis. <i>Frontiers in Immunology</i> , 0, 14, .	4.8	2
7785	Globally distributed <i>Myxococcota</i> with photosynthesis gene clusters illuminate the origin and evolution of a potentially chimeric lifestyle. <i>Nature Communications</i> , 2023, 14, .	12.8	5
7786	Pangenome-level analysis of nucleoid-associated proteins in the <i>Acidithiobacillia</i> class: insights into their functional roles in mobile genetic elements biology. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	0
7787	Population genomic analyses suggest recent dispersal events of the pathogen <i>Cercospora zeina</i> into East and Southern African maize cropping systems. <i>G3: Genes, Genomes, Genetics</i> , 2023, 13, .	1.8	0
7788	Genome sequencing-based transcriptomic analysis reveals novel genes in <i>Peucedanum praeruptorum</i> . <i>BMC Genomic Data</i> , 2023, 24, .	1.7	2
7789	The mechanism of polysaccharide synthesis of <i>Sanghuangporus sanghuang</i> based on multi-omic analyses and feedback inhibition. <i>Carbohydrate Polymers</i> , 2023, 321, 121288.	10.2	1
7790	Resources and tools for studying convergent evolution in different lineages of smut fungi. <i>Mycological Progress</i> , 2023, 22, .	1.4	0
7791	The pederin-producing bacteria density dynamics in <i>Paederus fuscipes</i> at different developmental stages. <i>Medical and Veterinary Entomology</i> , 2024, 38, 59-72.	1.5	0

#	ARTICLE	IF	CITATIONS
7792	A mysterious cloak: the peptidoglycan layer of algal and plant plastids. <i>Protoplasma</i> , 2024, 261, 173-178.	2.1	2
7793	A reference genome for the long-term kleptoplast-retaining sea slug <i>Elysia crispata</i> morphotype clarki. <i>G3: Genes, Genomes, Genetics</i> , 0, , .	1.8	0
7794	Homologous Pairs of Low and High Temperature Originating Proteins Spanning the Known Prokaryotic Universe. <i>Scientific Data</i> , 2023, 10, .	5.3	1
7795	A glossy mutant in onion (<i>Allium cepa</i> L.) shows decreased expression of wax biosynthesis genes. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	0
7796	Global diversity and biogeography of DNA viral communities in activated sludge systems. <i>Microbiome</i> , 2023, 11, .	11.1	1
7797	MetaSVs: A pipeline combining long and short reads for analysis and visualization of structural variants in metagenomes. , 2023, 2, .		1
7798	Chromosome-level genome of the venomous snail <i>Kalloconus canariensis</i> : a valuable model for venomics and comparative genomics. <i>GigaScience</i> , 2022, 12, .	6.4	0
7799	Anthropogenic activities mediate stratification and stability of microbial communities in freshwater sediments. <i>Microbiome</i> , 2023, 11, .	11.1	2
7800	Transcriptomic analysis of colour dimorphism of <i>Opsariichthys bidens</i> provides insights into the mechanism of male colour. <i>Aquaculture Reports</i> , 2023, 33, 101756.	1.7	0
7801	VAPEx: an interactive web server for the deep exploration of natural virus and phage genomes. <i>Bioinformatics</i> , 2023, 39, .	4.1	0
7802	Marine viruses disperse bidirectionally along the natural water cycle. <i>Nature Communications</i> , 2023, 14, .	12.8	2
7803	Comparison of Oral Microbial Composition and Determinants Encoding Antimicrobial Resistance in Dogs and Their Owners. <i>Antibiotics</i> , 2023, 12, 1554.	3.7	2
7804	Microbial community dynamics and metagenomics reveal the potential role of unconventional functional microorganisms in nitrogen and phosphorus removal biofilm system. <i>Science of the Total Environment</i> , 2023, 905, 167194.	8.0	0
7805	The Roles of Hormone Signals Involved in Rhizosphere Pressure Response Induce Corm Expansion in <i>Sagittaria trifolia</i> . <i>International Journal of Molecular Sciences</i> , 2023, 24, 12345.	4.1	0
7806	De novo transcriptome profiling and development of novel secondary metabolites based genic SSRs in medicinal plant <i>Phyllanthus emblica</i> L. (Aonla). <i>Scientific Reports</i> , 2023, 13, .	3.3	1
7807	Microbial composition, rumen fermentation parameters, enteric methane emissions, and lactational performance of phenotypically high and low methane-emitting dairy cows. <i>Journal of Dairy Science</i> , 2023, 106, 6146-6170.	3.4	5
7808	Metagenome-wide analysis uncovers gut microbial signatures and implicates taxon-specific functions in end-stage renal disease. <i>Genome Biology</i> , 2023, 24, .	8.8	3
7810	Nasopharyngeal fungal subtypes of infant bronchiolitis and disease severity risk. <i>EBioMedicine</i> , 2023, 95, 104742.	6.1	0

#	ARTICLE	IF	CITATIONS
7811	Designing Efficient SIMD Kernels for High Performance Sequence Alignment. , 2023, , .		0
7813	Metagenomics and metatranscriptomics suggest pathways of 3-chloroaniline degradation in wastewater reactors. Science of the Total Environment, 2023, 903, 166066.	8.0	0
7814	Transcriptome analysis reveals insights into adaptive responses of two marine microalgae species to Nordic seasons. Algal Research, 2023, 74, 103222.	4.6	0
7818	GOgetter: A pipeline for summarizing and visualizing GO slim annotations for plant genetic data. Applications in Plant Sciences, 2023, 11, .	2.1	1
7820	Data of de novo assembly and functional annotation of transcriptome of Peninsular Malaysian Amomum Roxb. species. Data in Brief, 2023, 50, 109507.	1.0	0
7822	Comparative genomics of bacteria from amphibian skin associated with inhibition of an amphibian fungal pathogen, <i>Batrachochytrium dendrobatidis</i> . PeerJ, 0, 11, e15714.	2.0	1
7823	Deionococcus proteotlycius Genomic Library Exploration Enhances Oxidative Stress Resistance and Poly-3-hydroxybutyrate Production in Recombinant Escherichia coli. Microorganisms, 2023, 11, 2135.	3.6	1
7824	Chromosome-level reference genome assembly provides insights into the evolution of Pennisetum alopecuroides. Frontiers in Plant Science, 0, 14, .	3.6	0
7830	Metabolome and transcriptome analyses identify the characteristics and expression of related saponins of the three genealogical plants of bead ginseng. PeerJ, 0, 11, e16034.	2.0	0
7831	Dominant influence of plants on soil microbial carbon cycling functions during natural restoration of degraded karst vegetation. Journal of Environmental Management, 2023, 345, 118889.	7.8	1
7832	Transcriptome analysis of tomato plants following salicylic acid-induced immunity against <i>Clavibacter michiganensis</i> ssp. <i>michiganensis</i> . Plant Biotechnology, 2023, 40, 273-282.	1.0	0
7833	Environmental selection and evolutionary process jointly shape genomic and functional profiles of mangrove rhizosphere microbiomes. , 2023, 2, 253-266.		1
7840	Host phylogeny shapes viral transmission networks in an island ecosystem. Nature Ecology and Evolution, 2023, 7, 1834-1843.	7.8	4
7841	Chromosome level genome assembly of oriental armyworm <i>Mythimna separata</i> . Scientific Data, 2023, 10, .	5.3	2
7842	<i>Alkalimarinus alittae</i> sp. nov., isolated from gut of marine sandworm (<i>Alitta virens</i>) and emended description of the genus <i>Alkalimarinus</i> . International Journal of Systematic and Evolutionary Microbiology, 2023, 73, .	1.7	0
7844	Metagenomic analysis unveils the underexplored roles of prokaryotic viruses in a full-scale landfill leachate treatment plant. Water Research, 2023, 245, 120611.	11.3	2
7846	Unraveling the importance of top-down predation on bacterial diversity at the soil aggregate level. Geoderma, 2023, 439, 116658.	5.1	1
7847	Simplification of soil biota communities impairs nutrient recycling and enhances above- and belowground nitrogen losses. New Phytologist, 2023, 240, 2020-2034.	7.3	2

#	ARTICLE	IF	CITATIONS
7848	Effects of tissue type and season on the detection of regulated sugarcane viruses by high throughput sequencing. CABI Agriculture and Bioscience, 2023, 4, .	2.4	0
7850	Transcriptome analysis revealed the existence of family-specific regulation of growth traits in grass carp. Genomics, 2023, 115, 110706.	2.9	0
7851	Investigating Variability in Viral Presence and Abundance across Soybean Seed Development Stages Using Transcriptome Analysis. Plants, 2023, 12, 3257.	3.5	1
7854	ARGem: a new metagenomics pipeline for antibiotic resistance genes: metadata, analysis, and visualization. Frontiers in Genetics, 0, 14, .	2.3	1
7856	The low-temperature germinating spores of the thermophilic Desulfofundulus contribute to an extremely high sulfate reduction in burning coal seams. Frontiers in Microbiology, 0, 14, .	3.5	0
7858	Comparative genomics and transcriptome analysis reveals potential pathogenic mechanisms of Microdochium paspali on seashore paspalum. Frontiers in Microbiology, 0, 14, .	3.5	0
7859	Deciphering m6A dynamics at a single-base level during planarian anterior-posterior axis specification. Computational and Structural Biotechnology Journal, 2023, 21, 4567-4579.	4.1	0
7860	Metagenomic insights into the energy metabolism and immune variation of sea cucumber Apostichopus japonicus during reproduction. Aquaculture, 2024, 579, 740125.	3.5	1
7861	Model of shrimp pond-mediated spatiotemporal dynamic distribution of antibiotic resistance genes in the mangrove habitat of a subtropical gulf. Science of the Total Environment, 2023, 905, 167199.	8.0	1
7862	Pseudomonas benzopyrenica sp. nov., isolated from soil, exhibiting high-efficiency degradation of benzo(a)pyrene. International Journal of Systematic and Evolutionary Microbiology, 2023, 73, .	1.7	1
7864	Uncovering the potential of landfill leachate for biodegradation of cassava-derived plastics. Bioresource Technology Reports, 2023, 24, 101628.	2.7	0
7865	Deciphering the Î²-carotene hyperaccumulation in <i>Dunaliella</i> by the comprehensive analysis of <i>Dunaliella salina</i> and <i>Dunaliella tertiolecta</i> under high light conditions. Plant, Cell and Environment, 2024, 47, 213-229.	5.7	2
7866	Organic management increases beneficial microorganisms and promotes the stability of microecological networks in tea plantation soil. Frontiers in Microbiology, 0, 14, .	3.5	0
7867	Host traits shape virome composition and virus transmission in wild small mammals. Cell, 2023, 186, 4662-4675.e12.	28.9	6
7868	Fumigant activity and transcriptomic analysis of two plant essential oils against the tea green leafhopper, Empoasca onukii Matsuda. Frontiers in Physiology, 0, 14, .	2.8	0
7869	Chromosome-level genome assembly and population genetic analysis of a near-threatened rosewood species (Dalbergia cultrata Pierre Graham ex Benth) provide insights into its evolutionary and cold stress responses. Frontiers in Plant Science, 0, 14, .	3.6	0
7870	Widespread Distribution of the <i>arsO</i> Gene Confers Bacterial Resistance to Environmental Antimony. Environmental Science & Technology, 2023, 57, 14579-14588.	10.0	1
7871	Chromosome-level genome assembly of Quercus variabilis provides insights into the molecular mechanism of cork thickness. Plant Science, 2023, 337, 111874.	3.6	0

#	ARTICLE	IF	CITATIONS
7876	Microbiome and metabolome in home-made fermented soybean foods of India revealed by metagenome-assembled genomes and metabolomics. <i>International Journal of Food Microbiology</i> , 2023, 407, 110417.	4.7	1
7877	The putatively high-altitude adaptation of macaque monkeys: Evidence from the fecal metabolome and gut microbiome. <i>Evolutionary Applications</i> , 2023, 16, 1708-1720.	3.1	0
7878	Copper in different forms and tetracycline affect behavior and risk of antibiotic resistance in thermophilic anaerobic digestion of cattle manure. <i>Environmental Science and Pollution Research</i> , 0, , .	5.3	0
7879	Coding-complete genome of human alphaherpesvirus 1 isolated from a case of fulminant hepatitis. <i>Microbiology Resource Announcements</i> , 2023, 12, .	0.6	0
7882	Uncovering Microbiome Adaptations in a Full-Scale Biogas Plant: Insights from MAG-Centric Metagenomics and Metaproteomics. <i>Microorganisms</i> , 2023, 11, 2412.	3.6	0
7885	Artificial switches induce the bespoke production of functional compounds in marine microalgae <i>Chlorella</i> by neutralizing CO ₂ . , 2023, 16, .		2
7886	Infants exposed <i>in utero</i> to Hurricane Maria have gut microbiomes with reduced diversity and altered metabolic capacity. <i>MSphere</i> , 2023, 8, .	2.9	0
7887	High potential for biomass-degrading CAZymes revealed by pine forest soil metagenomics. <i>Journal of Biomolecular Structure and Dynamics</i> , 0, , 1-12.	3.5	0
7888	A Preliminary Study of the Potential Molecular Mechanisms of Individual Growth and Rumen Development in Calves with Different Feeding Patterns. <i>Microorganisms</i> , 2023, 11, 2423.	3.6	1
7890	Unraveling the antibiotic resistance in backwater zones of large cascade reservoirs: Co-occurrence patterns, horizontal transfer directions and health risks. <i>Journal of Environmental Management</i> , 2023, 347, 119144.	7.8	0
7891	Interactions between quorum sensing/quorum quenching and virulence genes may affect coral health by regulating symbiotic bacterial community. <i>Environmental Research</i> , 2023, 238, 117221.	7.5	1
7892	A chromosome-level genome assembly provides insights into <i>Cornus wilsoniana</i> evolution, oil biosynthesis, and floral bud development. <i>Horticulture Research</i> , 2023, 10, .	6.3	1
7893	Efficient gene orthology inference via large-scale rearrangements. <i>Algorithms for Molecular Biology</i> , 2023, 18, .	1.2	0
7894	Discovery of long non-coding RNAs in the liver fluke, <i>Fasciola hepatica</i> . <i>PLoS Neglected Tropical Diseases</i> , 2023, 17, e0011663.	3.0	0
7895	The resistome and microbiome of wastewater treatment plant workers – The AWARE study. <i>Environment International</i> , 2023, 180, 108242.	10.0	1
7896	Multi-omics revealed the long-term effect of ruminal keystone bacteria and the microbial metabolome on lactation performance in adult dairy goats. <i>Microbiome</i> , 2023, 11, .	11.1	5
7899	Metagenomic characterization of the cecal microbiota community and functions in finishing pigs fed fermented <i>Boehmeria nivea</i> . <i>Frontiers in Veterinary Science</i> , 0, 10, .	2.2	0
7900	Phylogenetic analysis of rabies surveillance samples from north and northeast Brazil. <i>Frontiers in Veterinary Science</i> , 0, 10, .	2.2	0

#	ARTICLE	IF	CITATIONS
7901	Biochemical characterization and key catalytic residue identification of a novel alpha-agarase with CBM2 domain. <i>Food Chemistry</i> , X, 2023, 20, 100915.	4.3	0
7902	Genomic Analysis and Taxonomic Characterization of Seven Bacteriophage Genomes Metagenomic-Assembled from the Dishui Lake. <i>Viruses</i> , 2023, 15, 2038.	3.3	1
7903	Resolving Deep Relationships and Revealing Ancient Whole-Genome Duplications in Pteridaceae using Transcriptomic Data. <i>American Fern Journal</i> , 2023, 113, .	0.3	0
7904	Lake plastisphere as a new biotope in the Anthropocene: Potential pathogen colonization and distinct microbial functionality. <i>Journal of Hazardous Materials</i> , 2024, 461, 132693.	12.4	1
7905	Benchmarking Metagenomic Classifiers on Simulated Ancient and Modern Metagenomic Data. <i>Microorganisms</i> , 2023, 11, 2478.	3.6	0
7906	Dynamics and ecological reassembly of the human gut microbiome and the host metabolome in response to prolonged fasting. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	1
7910	Environmental transcriptomics under heat stress: Can environmental <scp>RNA</scp> reveal changes in gene expression of aquatic organisms?. <i>Molecular Ecology</i> , 0, , .	3.9	3
7911	Daqu and environmental microbiota regulate fatty acid biosynthesis via driving the core microbiota in soy sauce aroma type liquor fermentation. <i>International Journal of Food Microbiology</i> , 2024, 408, 110423.	4.7	6
7912	Anatomical and Transcriptome Analyses of Moso Bamboo Culm Neck Growth: Unveiling Key Insights. <i>Plants</i> , 2023, 12, 3478.	3.5	0
7913	Multi-omics analysis reveals the molecular basis of flavonoid accumulation in fructus of <i>Gardenia</i> (<i>Gardenia jasminoides</i> Ellis). <i>BMC Genomics</i> , 2023, 24, .	2.8	0
7914	Metagenomic investigations on antibiotic resistance and microbial virulence in oil-polluted soils from China. <i>Environmental Science and Pollution Research</i> , 2023, 30, 110590-110599.	5.3	1
7915	Colorectal cancer-associated T cell receptor repertoire abnormalities are linked to gut microbiome shifts and somatic cell mutations. <i>Gut Microbes</i> , 2023, 15, .	9.8	2
7916	Comparative genomic analysis of <i>Chryseobacterium</i> species: deep insights into plant-growth-promoting and halotolerant capacities. <i>Microbial Genomics</i> , 2023, 9, .	2.0	0
7917	Symmetric expression of ohnologs encoding conserved antiviral responses in tetraploid common carp suggest absence of subgenome dominance after whole genome duplication. <i>Genomics</i> , 2023, 115, 110723.	2.9	1
7918	The transcriptome profile of the marine Calanoid copepod <i>Parvocalanus crassirostris</i> isolated from Kuwait territorial waters and generations cultured under different ocean acidification scenarios. <i>Regional Studies in Marine Science</i> , 2023, 67, 103231.	0.7	0
7919	Investigating microbiome and transcriptome data to uncover the key microbial community involved in lignocellulose degradation within the Deulajhari hot spring consortium. <i>Data in Brief</i> , 2023, 51, 109648.	1.0	0
7920	NCRD: A non-redundant comprehensive database for detecting antibiotic resistance genes. <i>IScience</i> , 2023, 26, 108141.	4.1	2
7921	Metabolically Active Microbial Communities in Oilfields: A Systematic Review and Synthesis of RNA Preservation, Extraction, and Sequencing Methods. <i>Applied Microbiology</i> , 2023, 3, 1144-1163.	1.6	0

#	ARTICLE	IF	CITATIONS
7922	Effects of artificial sweetener acesulfame on soil-dwelling earthworms (<i>Eisenia fetida</i>) and its gut microbiota. <i>Science of the Total Environment</i> , 2024, 907, 167641.	8.0	1
7923	Metatranscriptomic sequencing reveals there were abundant and diverse viruses in the midgut of diseased silkworm (<i>Bombyx mori</i>) with soft rot symptoms. <i>Journal of Asia-Pacific Entomology</i> , 2023, 26, 102159.	0.9	0
7925	Metaproteomics, metagenomics and 16S rRNA sequencing provide different perspectives on the aerobic granular sludge microbiome. <i>Water Research</i> , 2023, 246, 120700.	11.3	3
7926	The leaf idioblastome of the medicinal plant <i>Catharanthus roseus</i> reveals commitment with stress resistance and alkaloid metabolism. <i>Journal of Experimental Botany</i> , 0, , .	4.8	0
7927	Molecular and evolutionary basis of O-antigenic polysaccharide-driven phage sensitivity in environmental pseudomonads. <i>Microbiology Spectrum</i> , 0, , .	3.0	0
7928	Comparative analysis of Presence-Absence gene Variations in five hard tick species: impact and functional considerations. <i>International Journal for Parasitology</i> , 2023, , .	3.1	0
7929	Chromosome-scale assemblies of <i>S. malaccense</i> , <i>S. aqueum</i> , <i>S. jambos</i> , and <i>S. syzygioides</i> provide insights into the evolution of <i>Syzygium</i> genomes. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	0
7930	The chromosome-level genome of Chinese praying mantis <i>Tenodera sinensis</i> (Mantodea: Tj ETQq1 1 0.784314 rgBT /Qoverlock 6.4	6.4	0
7931	<i>Halapricum hydrolyticum</i> sp. nov., a beta-1,3-glucan utilizing haloarchaeon from hypersaline lakes. <i>Systematic and Applied Microbiology</i> , 2023, 46, 126471.	2.8	1
7932	The regulatory mechanisms of delayed senescence of nitric oxide treatment of hyacinth beans. <i>Postharvest Biology and Technology</i> , 2024, 207, 112592.	6.0	0
7933	The highly improved genome of <i>Ixodes scapularis</i> with X and Y pseudochromosomes. <i>Life Science Alliance</i> , 2023, 6, e202302109.	2.8	2
7935	Genome sequence of parvovirus from budgerigar (<i>Melopsittacus undulatus</i>). <i>Microbiology Resource Announcements</i> , 0, , .	0.6	0
7937	Mechanisms of lead-containing pigment discoloration caused by <i>Naumannella cuiyingiana</i> AFT2T isolated from 1500 years tomb wall painting of China. <i>International Biodeterioration and Biodegradation</i> , 2023, 185, 105689.	3.9	0
7938	Systematic dissection of genomic features determining the vast diversity of conotoxins. <i>BMC Genomics</i> , 2023, 24, .	2.8	0
7939	Unraveling the microbiotas and key genetic contexts identified on stone heritage using illumina and nanopore sequencing platforms. <i>International Biodeterioration and Biodegradation</i> , 2023, 185, 105688.	3.9	0
7940	Virome analysis of irrigation water sources provides extensive insights into the diversity and distribution of plant viruses in agroecosystems. <i>Water Research</i> , 2024, 249, 120712.	11.3	0
7941	Comparative Population Transcriptomics Provide New Insight into the Evolutionary History and Adaptive Potential of World Ocean Krill. <i>Molecular Biology and Evolution</i> , 2023, 40, .	8.9	1
7942	Unlocking the Viral Universe: Metagenomic Analysis of Bat Samples Using Next-Generation Sequencing. <i>Microorganisms</i> , 2023, 11, 2532.	3.6	1

#	ARTICLE	IF	CITATIONS
7944	The Inhibiting Effects of High-Dose Biochar Application on Soil Microbial Metagenomics and Rice (<i>Oryza sativa</i> L.) Production. <i>International Journal of Molecular Sciences</i> , 2023, 24, 15043.	4.1	0
7945	FicD genes in invertebrates: A tale of transposons, pathogenic and integrated viruses. <i>Gene</i> , 2024, 893, 147895.	2.2	0
7947	Morphological and genetic mechanisms underlying the plasticity of the coral <i>Porites astreoides</i> across depths in Bermuda. <i>Journal of Structural Biology</i> , 2023, 215, 108036.	2.8	0
7948	Flexible catabolism of monoaromatic hydrocarbons by anaerobic microbiota adapting to oxygen exposure. <i>Journal of Hazardous Materials</i> , 2024, 462, 132762.	12.4	0
7949	Unraveling the evolutionary dynamics of the TPS gene family in land plants. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	0
7950	Morphological, phylogenetic, and genomic evidence reveals the causal agent of thread blight disease of cacao in Peru is a new species of <i>Marasmius</i> in the section <i>Neosessiles</i> , <i>Marasmius infestans</i> sp. nov.. <i>F1000Research</i> , 0, 12, 1327.	1.6	0
7951	Whole genome sequence and annotation dataset of rare actinobacteria, <i>Barrientosiiimonas humi</i> gen. nov., sp. nov. 39T from Antarctica. <i>Data in Brief</i> , 2023, 51, 109657.	1.0	0
7952	Do chromosome rearrangements fix by genetic drift or natural selection? Insights from <i>Brenthis</i> butterflies. <i>Molecular Ecology</i> , 0, , .	3.9	3
7953	Molecular insights into nitrogen constraint for niche partitioning and physiological adaptation of coastal <i>Synechococcus</i> assemblages. <i>Environmental Research</i> , 2023, 239, 117383.	7.5	0
7954	The genomic and epidemiological investigations of enteric viruses of domestic caprine (<i>Capra</i>) Tj ETQq1 1 0.784314 rgBT /Overlooked ruminant livestock species. <i>Microbiology Spectrum</i> , 2023, 11, .	3.0	1
7955	MGS2AMR: a gene-centric mining of metagenomic sequencing data for pathogens and their antimicrobial resistance profile. <i>Microbiome</i> , 2023, 11, .	11.1	0
7956	Metagenomic analysis reveals a dynamic microbiome with diversified adaptive functions that respond to ovulation regulation in the mouse endometrium. <i>BMC Genomics</i> , 2023, 24, .	2.8	0
7957	Cooperation of an external carbonic anhydrase and HCO ₃ [−] transporter supports underwater photosynthesis in submerged leaves of the amphibious plant <i>Hydrophila difformis</i> . <i>Annals of Botany</i> , 0, , .	2.9	0
7958	Pangenome of water caltrop reveals structural variations and asymmetric subgenome divergence after allopolyploidization. <i>Horticulture Research</i> , 0, , .	6.3	0
7959	Livestock grazing is associated with the gut microbiota and antibiotic resistance genes in sympatric plateau pika (<i>Ochotona curzoniae</i>). <i>Integrative Zoology</i> , 0, , .	2.6	0
7963	Coexistence of specialist and generalist species within mixed plastic derivative-utilizing microbial communities. <i>Microbiome</i> , 2023, 11, .	11.1	0
7964	Temporal and spatial variations in body mass and thermogenic capacity associated with alterations in the gut microbiota and host transcriptome in mammalian herbivores. <i>Science of the Total Environment</i> , 2024, 907, 167776.	8.0	0
7965	Distantly related <i>Alteromonas</i> bacteriophages share tail fibers exhibiting properties of transient chaperone caps. <i>Nature Communications</i> , 2023, 14, .	12.8	2

#	ARTICLE	IF	CITATIONS
7966	Genomic Characteristics and Comparative Genomics Analysis of the Endophytic Fungus <i>Paraphoma chrysanthemicola</i> DS-84 Isolated from <i>Codonopsis pilosula</i> Root. <i>Journal of Fungi</i> (Basel,) Tj ETQq0 0 0 rgBT /Overlck 10 Tf 50 737 Td (
7967	Metatranscriptomics reveals diversity of symbiotic interaction and mechanisms of carbon exchange in the marine cyanolichen <i>Lichina pygmaea</i> . <i>New Phytologist</i> , 2024, 241, 2243-2257.	7.3	3
7968	<i>Pyrofoliis japonicus</i> gen. nov. sp. nov., a novel member of the family Pyrodictiaceae isolated from the Iheya North hydrothermal field. <i>Extremophiles</i> , 2023, 27, .	2.3	0
7969	Struct2GO: protein function prediction based on Graph pooling algorithm and AlphaFold2 structure information. <i>Bioinformatics</i> , 0, , .	4.1	1
7970	The genome of <i>Salmacisia buchloana</i> , the parasitic puppet master pulling strings of sexual phenotypic monstrosities in buffalograss. <i>G3: Genes, Genomes, Genetics</i> , 2024, 14, .	1.8	0
7971	Multidrug-resistant <i>E. coli</i> encoding high genetic diversity in carbohydrate metabolism genes displace commensal <i>E. coli</i> from the intestinal tract. <i>PLoS Biology</i> , 2023, 21, e3002329.	5.6	3
7972	Vertical niche occupation and potential metabolic interplay of microbial consortia in a deeply stratified meromictic model lake. <i>Limnology and Oceanography</i> , 0, , .	3.1	1
7973	Clinical metagenomics in a resource-limited setting. <i>Journal of Infection</i> , 2023, 87, 604-606.	3.3	0
7974	Transcriptomic analysis revealing the molecular response to arsenic stress in desert <i>Eremostachys moluccelloides</i> Bunge. <i>Ecotoxicology and Environmental Safety</i> , 2023, 266, 115608.	6.0	0
7975	Genomic insights into the phage-defense systems of <i>Stenotrophomonas maltophilia</i> clinical isolates. <i>Microbiological Research</i> , 2024, 278, 127528.	5.3	1
7976	Integrated transcriptomic, proteomic and metabolomic analysis provides new insights into tetracycline stress tolerance in pumpkin. <i>Environmental Pollution</i> , 2023, , 122777.	7.5	0
7977	Chromosome-level genome assembly of <i>Niphotrichum japonicum</i> provides new insights into heat stress responses in mosses. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	0
7978	Biosynthetic gene cluster synteny: Orthologous polyketide synthases in <i>Hypogymnia physodes</i> , <i>Hypogymnia tubulosa</i> , and <i>Parmelia sulcata</i> . <i>MicrobiologyOpen</i> , 2023, 12, .	3.0	0
7979	gcPathogen: a comprehensive genomic resource of human pathogens for public health. <i>Nucleic Acids Research</i> , 0, , .	14.5	0
7980	Linking coral fluorescence phenotypes to thermal bleaching in the reef-building <i>Galaxea fascicularis</i> from the northern South China Sea. <i>Marine Life Science and Technology</i> , 2024, 6, 155-167.	4.6	0
7981	Phylogeny and Functional Diversity of Halophilic Microbial Communities from an Thalasso Environment. <i>Saudi Journal of Biological Sciences</i> , 2023, , 103841.	3.8	0
7984	Rotenone impairs brain glial energetics and locomotor behavior in bumblebees. <i>Science of the Total Environment</i> , 2024, 907, 167870.	8.0	0
7985	Tumor-resident <i>Lactobacillus iners</i> confer chemoradiation resistance through lactate-induced metabolic rewiring. <i>Cancer Cell</i> , 2023, 41, 1945-1962.e11.	16.8	9

#	ARTICLE	IF	CITATIONS
7986	Exploring the biosynthetic gene clusters in <i>Brevibacterium</i> : a comparative genomic analysis of diversity and distribution. BMC Genomics, 2023, 24, .	2.8	1
7987	Genome-wide analysis of horizontal transfer in non-model wild species from a natural ecosystem reveals new insights into genetic exchange in plants. PLoS Genetics, 2023, 19, e1010964.	3.5	0
7988	<i>Bacillus subtilis</i> and <i>Macleaya cordata</i> extract regulate the rumen microbiota associated with enteric methane emission in dairy cows. Microbiome, 2023, 11, .	11.1	1
7989	The Time-Resolved Salt Stress Response of <i>Dunaliella tertiolecta</i> —A Comprehensive System Biology Perspective. International Journal of Molecular Sciences, 2023, 24, 15374.	4.1	1
7990	Salinity causes differences in stratigraphic methane sources and sinks. Environmental Science and Ecotechnology, 2023, , 100334.	13.5	0
7991	Exercise and microbiome: From big data to therapy. Computational and Structural Biotechnology Journal, 2023, 21, 5434-5445.	4.1	0
7992	imMeta: An Incremental Sub-graph Merging for Feature Extraction in Metagenomic Binning. Lecture Notes on Data Engineering and Communications Technologies, 2023, , 214-223.	0.7	0
7993	Total infectome investigation of diphtheritic stomatitis in yellow-eyed penguins (<i>Megadyptes</i>) Tj ETQq1 1 0.784314 1.9 BT /Overlock 10 T	1.9	0
7995	Genome haplotype phasing and comparison of eastern filbert blight resistance sources in European hazelnut (<i>Corylus avellana</i>). Acta Horticulturae, 2023, , 97-104.	0.2	0
7996	Four functional profiles for fibre and mucin metabolism in the human gut microbiome. Microbiome, 2023, 11, .	11.1	1
7998	Sanwei sandalwood decoction improves function of the gut microbiota in heart failure. Frontiers in Microbiology, 0, 14, .	3.5	1
7999	Complete genome sequence of the carrot black rot pathogen <i>Alternaria radicina</i> isolate CBR2. Microbial Pathogenesis, 2023, 185, 106421.	2.9	0
8001	Quinone-mediated extracellular electron transfer processes in ex situ biomethanation reactors. Bioresource Technology Reports, 2023, , 101671.	2.7	0
8002	Pet cats may shape the antibiotic resistome of their owner's gut and living environment. Microbiome, 2023, 11, .	11.1	3
8003	Yeast metagenomics: analytical challenges in the analysis of the eukaryotic microbiome. , 0, 3, .		1
8004	<i>De-novo</i> whole genome assembly of the orange jewelweed, <i>Impatiens capensis</i> Meerb. (Balsaminaceae) using nanopore long-read sequencing. PeerJ, 0, 11, e16328.	2.0	0
8005	Chlorothalonil drives the antibiotic resistome in earthworm guts. Journal of Hazardous Materials, 2024, 463, 132831.	12.4	0
8006	The Impact of Bamboo Consumption on the Spread of Antibiotic Resistance Genes in Giant Pandas. Veterinary Sciences, 2023, 10, 630.	1.7	0

#	ARTICLE	IF	CITATIONS
8008	Genomic and transcriptomic insights into complex virus–prokaryote interactions in marine biofilms. ISME Journal, 2023, 17, 2303-2312.	9.8	0
8009	PerFSeeB: designing long high-weight single spaced seeds for full sensitivity alignment with a given number of mismatches. BMC Bioinformatics, 2023, 24, .	2.6	0
8010	MACI: A machine learning-based approach to identify drug classes of antibiotic resistance genes from metagenomic data. Computers in Biology and Medicine, 2023, 167, 107629.	7.0	0
8011	Metagenomic analysis of gut microbiome and resistome of Whooper and Black Swans: a one health perspective. BMC Genomics, 2023, 24, .	2.8	0
8012	Functional enrichment of integrons: Facilitators of antimicrobial resistance and niche adaptation. IScience, 2023, 26, 108301.	4.1	0
8013	TMPRSS2 is a functional receptor for human coronavirus HKU1. Nature, 2023, 624, 207-214.	27.8	8
8014	Microbial drivers of DMSO reduction and DMS-dependent methanogenesis in saltmarsh sediments. ISME Journal, 2023, 17, 2340-2351.	9.8	0
8015	Extension of the Segatella copri complex to 13 species with distinct large extrachromosomal elements and associations with host conditions. Cell Host and Microbe, 2023, 31, 1804-1819.e9.	11.0	3
8016	Chromosome-scale assembly of the wild wheat relative Aegilops umbellulata. Scientific Data, 2023, 10, .	5.3	2
8017	ORFanID: A web-based search engine for the discovery and identification of orphan and taxonomically restricted genes. PLoS ONE, 2023, 18, e0291260.	2.5	0
8018	Virus diversity and activity is driven by snowmelt and host dynamics in a high-altitude watershed soil ecosystem. Microbiome, 2023, 11, .	11.1	2
8019	Arbuscular mycorrhizal fungi heterokaryons have two nuclear populations with distinct roles in host–plant interactions. Nature Microbiology, 2023, 8, 2142-2153.	13.3	4
8020	Single-cell transcriptomics reveals the brain evolution of web-building spiders. Nature Ecology and Evolution, 2023, 7, 2125-2142.	7.8	1
8021	A pilot study of the use of the oral and faecal microbiota for the diagnosis of ulcerative colitis and Crohn's disease in a paediatric population. Frontiers in Pediatrics, 0, 11, .	1.9	0
8022	Revealing the developmental characterization of rumen microbiome and its host in newly received cattle during receiving period contributes to formulating precise nutritional strategies. Microbiome, 2023, 11, .	11.1	0
8023	Integrated metagenomic and metaproteomic analyses reveal bacterial micro-ecological mechanisms in coral bleaching. MSystems, 2023, 8, .	3.8	0
8024	Transcriptome analysis of Corvus splendens reveals a repertoire of antimicrobial peptides. Scientific Reports, 2023, 13, .	3.3	0
8025	What can be lost? Genomic perspective on the lipid metabolism of Mucoromycota. IMA Fungus, 2023, 14, .	3.8	0

#	ARTICLE	IF	CITATIONS
8026	A High-Quality Reference Genome Assembly of <i>Prinsepia uniflora</i> (Rosaceae). <i>Genes</i> , 2023, 14, 2035.	2.4	0
8027	Multimomics analysis reveals the genetic and metabolic characteristics associated with the low prevalence of dental caries. <i>Journal of Oral Microbiology</i> , 2023, 15, .	2.7	0
8028	Short-term acidification promotes diverse iron acquisition and conservation mechanisms in upwelling-associated phytoplankton. <i>Nature Communications</i> , 2023, 14, .	12.8	0
8029	Domain-PFP allows protein function prediction using function-aware domain embedding representations. <i>Communications Biology</i> , 2023, 6, .	4.4	0
8030	The novel nematocide chiricanine A suppresses <i>Bursaphelenchus xylophilus</i> pathogenicity in <i>Pinus massoniana</i> by inhibiting <i>Aspergillus</i> and its secondary metabolite, sterigmatocystin. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	1
8031	Genomics of soil depth niche partitioning in the Thaumarchaeota family <i>Gagatemarkaeaceae</i> . <i>Nature Communications</i> , 2023, 14, .	12.8	2
8032	First shotgun metagenomics study of Juan de Fuca deep-sea sediments reveals distinct microbial communities above, within, between, and below sulfate methane transition zones. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	0
8033	Metatranscriptomic responses and microbial degradation of background polycyclic aromatic hydrocarbons in the coastal Mediterranean and Antarctica. <i>Environmental Science and Pollution Research</i> , 2023, 30, 119988-119999.	5.3	0
8034	A chromosome-level genome assembly of the <i>Knoxia roxburghii</i> (Rubiaceae). <i>Scientific Data</i> , 2023, 10, .	5.3	0
8035	Hub genes and pathways related to caries-free dental biofilm: clinical metatranscriptomic study. <i>Clinical Oral Investigations</i> , 2023, 27, 7725-7735.	3.0	0
8036	Interplay between autotrophic and heterotrophic prokaryotic metabolism in the bathypelagic realm revealed by metatranscriptomic analyses. <i>Microbiome</i> , 2023, 11, .	11.1	0
8037	Genomic signals of local adaptation in <i>Picea crassifolia</i> . <i>BMC Plant Biology</i> , 2023, 23, .	3.6	0
8038	Cross-Feeding between Filamentous Cyanobacteria and Symbiotic Bacteria Favors Rapid Photogranulation. <i>Environmental Science & Technology</i> , 2023, 57, 16953-16963.	10.0	2
8039	Gut butyrate-producers confer post-infarction cardiac protection. <i>Nature Communications</i> , 2023, 14, .	12.8	6
8040	<i>Psychrobacter</i> species enrichment as potential microplastic degrader and the putative biodegradation mechanism in Shenzhen Bay sediment, China. <i>Journal of Hazardous Materials</i> , 2024, 464, 132971.	12.4	1
8041	A genomic catalogue of soil microbiomes boosts mining of biodiversity and genetic resources. <i>Nature Communications</i> , 2023, 14, .	12.8	4
8042	Intestinal flora altered and correlated with interleukin-2/4 in patients with primary immune thrombocytopenia. <i>Hematology</i> , 2023, 28, .	1.5	0
8043	Alterations in Redox Homeostasis and Profound Developmental Consequences Are at the Core of Sudden Gravity Change Responses of Sugarcane Plants. <i>Journal of Plant Growth Regulation</i> , 0, , .	5.1	0

#	ARTICLE	IF	CITATIONS
8044	Identification of Fatty Acid Components and Key Genes for Synthesis during the Development of Pecan Fruit. Horticulturae, 2023, 9, 1199.	2.8	0
8045	Molecular characteristics and hypovirulence of different RNA viruses in Alternaria spp. strains, the pathogenic agent of pear black spot disease in China. Scientia Horticulturae, 2024, 325, 112622.	3.6	0
8046	Remediation and regulatory factors of petroleum hydrocarbon contaminated soil on site through Fe2+/Na2S2O8-Enterobacter himalayensis GZ6. Journal of Environmental Chemical Engineering, 2023, 11, 111366.	6.7	1
8047	Comparative spatial proteomics of Plasmodium-infected erythrocytes. Cell Reports, 2023, 42, 113419.	6.4	1
8048	A 1.5-Mb continuous endogenous viral region in the arbuscular mycorrhizal fungus <i>Rhizophagus irregularis</i> . Virus Evolution, 2023, 9, .	4.9	3
8049	Impacts of substrate properties and aquatic nutrient concentrations on the relative abundance of nitrifying/denitrifying genes and the associated microbes in epilithic biofilms. Environmental Science and Pollution Research, 2023, 30, 120930-120944.	5.3	0
8050	Co-option of a non-retroviral endogenous viral element in planthoppers. Nature Communications, 2023, 14, .	12.8	0
8051	Integrative metabolomic and transcriptomic reveals potential mechanism for promotion of ginsenoside synthesis in Panax ginseng leaves under different light intensities. Frontiers in Bioengineering and Biotechnology, 0, 11, .	4.1	0
8052	Functional players involved in the distinct nitrogen metabolism in two geographically different paddy soils. Biology and Fertility of Soils, 0, , .	4.3	1
8053	ATP synthase evolution on a cross-braced dated tree of life. Nature Communications, 2023, 14, .	12.8	3
8054	Light-dark fluctuated metabolic features of diazotrophic and non-diazotrophic cyanobacteria and their coexisting bacteria. Science of the Total Environment, 2024, 910, 168702.	8.0	0
8055	Toxic effects on ciliates under nano-/micro-plastics coexist with silver nanoparticles. Journal of Hazardous Materials, 2024, 465, 133058.	12.4	1
8056	Concentration of total microcystins associates with nitrate and nitrite, and may disrupt the nitrogen cycle, in warm-monomictic lakes of the southcentral United States. Harmful Algae, 2023, 130, 102542.	4.8	1
8057	Differences in Physiological Performance and Gut Microbiota between Deep-Sea and Coastal Aquaculture of Thachinotus Ovatus: A Metagenomic Approach. Animals, 2023, 13, 3365.	2.3	0
8058	Microbial iron acquisition is influenced by spatial and temporal conditions in a glacial influenced river and estuary system. Environmental Microbiology, 2023, 25, 3450-3465.	3.8	0
8059	Characterization and biocontrol mechanism of Streptomyces olivoreticuli as a potential biocontrol agent against Rhizoctonia solani. Pesticide Biochemistry and Physiology, 2023, 197, 105681.	3.6	0
8060	Phosphonate consumers potentially contributing to methane production in Brazilian soda lakes. Extremophiles, 2024, 28, .	2.3	0
8061	Unraveling the complex evolutionary history of lepidopteran chromosomes through ancestral chromosome reconstruction and novel chromosome nomenclature. BMC Biology, 2023, 21, .	3.8	0

#	ARTICLE	IF	CITATIONS
8062	Cold stress induces differential gene expression of retained homeologs in <i>Camelina sativa</i> cv Suneson. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	1
8063	Known phyla dominate the Tara Oceans RNA virome. <i>Virus Evolution</i> , 2023, 9, .	4.9	0
8064	Exploring clonality and virulence gene associations in bloodstream infections using whole-genome sequencing and clinical data. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 13, .	3.9	0
8065	Comparative Physiological and Transcriptome Analysis of <i>Crossostephium chinense</i> Reveals Its Molecular Mechanisms of Salt Tolerance. <i>International Journal of Molecular Sciences</i> , 2023, 24, 16812.	4.1	0
8066	Analysis of gut microbiome, host genetics, and plasma metabolites reveals gut microbiome-host interactions in the Japanese population. <i>Cell Reports</i> , 2023, 42, 113324.	6.4	0
8067	Distinct taxonomic and ecological functions of microbiome in sediments of different depth in Bohai Sea and Yellow Sea. <i>Journal of Oceanology and Limnology</i> , 2023, 41, 1765-1780.	1.3	0
8068	Oligoagars and microbial agents show potential for <i>Porphyra</i> disease prevention. <i>AMB Express</i> , 2023, 13, .	3.0	0
8069	Viral Diversity in Benthic Abyssal Ecosystems: Ecological and Methodological Considerations. <i>Viruses</i> , 2023, 15, 2282.	3.3	0
8070	Differences in microbial communities and potato growth in two soil types under organic cultivation. <i>3 Biotech</i> , 2023, 13, .	2.2	0
8071	Transcription factor network analysis of the Cf-19-mediated resistance response in tomato infected by <i>Cladosporium fulvum</i> . <i>Scientia Horticulturae</i> , 2024, 325, 112681.	3.6	0
8072	Altered microbiota, antimicrobial resistance genes, and functional enzyme profiles in the rumen of yak calves fed with milk replacer. <i>Microbiology Spectrum</i> , 0, , .	3.0	0
8073	Comparative transcriptome analysis reveals candidate genes related to the sex differentiation of <i>Schisandra chinensis</i> . <i>Functional and Integrative Genomics</i> , 2023, 23, .	3.5	0
8074	PhaGenus: genus-level classification of bacteriophages using a Transformer model. <i>Briefings in Bioinformatics</i> , 2023, 24, .	6.5	0
8075	Comparative transcriptomes of four Elm species provide insights into the genetic features and adaptive evolution of <i>Ulmus</i> spp.. <i>Forest Ecology and Management</i> , 2024, 553, 121560.	3.2	0
8076	Metagenomics and metagenome-assembled genomes analysis of sieng, an ethnic fermented soybean food of Cambodia. <i>Food Bioscience</i> , 2023, 56, 103277.	4.4	0
8077	Comparative transcriptome analysis reveals deep molecular landscapes in stony coral <i>Montipora</i> clade. <i>Frontiers in Genetics</i> , 0, 14, .	2.3	0
8078	De novo transcriptome assembly of <i>Dalbergia sissoo</i> Roxb. (Fabaceae) under <i>Botryodiplodia theobromae</i> -induced dieback disease. <i>Scientific Reports</i> , 2023, 13, .	3.3	0
8079	Effect of castration timing and weaning strategy on the taxonomic and functional profile of ruminal bacteria and archaea of beef calves. <i>Animal Microbiome</i> , 2023, 5, .	3.8	0

#	ARTICLE	IF	CITATIONS
8080	Diversity, Taxonomic Novelty, and Encoded Functions of Salar de Ascot�n Microbiota, as Revealed by Metagenome-Assembled Genomes. Microorganisms, 2023, 11, 2819.	3.6	0
8081	Impact of biochar on the antibiotic resistome and associated microbial functions in rhizosphere and bulk soil in water-saving and flooding irrigated paddy fields. Environmental Pollution, 2024, 342, 123026.	7.5	0
8082	Core genes of biomineralization and cis-regulatory long non-coding RNA regulate shell growth in bivalves. Journal of Advanced Research, 2023, , .	9.5	0
8083	Functional analysis of the AUG initiator codon context reveals novel conserved sequences that disfavor mRNA translation in eukaryotes. Nucleic Acids Research, 2024, 52, 1064-1079.	14.5	0
8084	Engraftment of essential functions through multiple fecal microbiota transplants in chronic antibiotic-resistant pouchitis��a case study using metatranscriptomics. Microbiome, 2023, 11, .	11.1	0
8085	Simultaneously enhanced autotrophic��heterotrophic denitrification in iron-based ecological floating bed by plant biomass: Metagenomics insights into microbial communities, functional genes and nitrogen metabolic pathways. Water Research, 2024, 248, 120868.	11.3	1
8086	Microbial Community Shifts with Soil Properties and Enzyme Activities in Inter-/Mono-Cropping Systems in Response to Tillage. Agronomy, 2023, 13, 2707.	3.0	0
8087	Dancing the Nanopore limbo �� Nanopore metagenomics from small DNA quantities for bacterial genome reconstruction. BMC Genomics, 2023, 24, .	2.8	0
8088	Chicken manure application alters microbial community structure and the distribution of antibiotic-resistance genes in rhizosphere soil of <i>Cinnamomum camphora</i> forests. FEMS Microbiology Ecology, 2023, 99, .	2.7	0
8089	Comparative genomic analysis of strong biofilm-forming <i>Klebsiella pneumoniae</i> isolates uncovers novel IS <i>Ecp</i> 1-mediated chromosomal integration of a full plasmid-like sequence. Infectious Diseases, 2024, 56, 91-109.	2.8	0
8090	Natural product biosynthetic potential reflects macroevolutionary diversification within a widely distributed bacterial taxon. MSystems, 2023, 8, .	3.8	1
8091	Soil-specific responses in the antibiotic resistome of culturable <i>Acinetobacter</i> spp. and other non-fermentative Gram-negative bacteria following experimental manure application. FEMS Microbiology Ecology, 2023, 99, .	2.7	0
8092	The <i>de novo</i> genome of the Black-necked Snakefly (<i>Venustoraphidia nigricollis</i> Albarda,) Tj ETQq0 0 0,rgBT /Overlock 10 Tf	2.4	0
8093	Contraction of Heat Shock Protein 70 Genes Uncovers Heat Adaptability of Ostrea denselamellosa. Journal of Ocean University of China, 2023, 22, 1669-1676.	1.2	1
8094	Dried tea residue can alter the blood metabolism and the composition and functionality of the intestinal microbiota in Hu sheep. Frontiers in Microbiology, 0, 14, .	3.5	0
8095	Precision Metagenomics in a Low-End Computation Infrastructure: A Tool to Augment Research on Bioremediation of Plastic and Microplastic Contamination. ACS Symposium Series, 0, , 125-140.	0.5	0
8096	Metatranscriptomic characterization of six types of forensic samples and its potential application to body fluid/tissue identification: A pilot study. Forensic Science International: Genetics, 2024, 68, 102978.	3.1	0
8097	Genomic insights into the adaptation of Synechococcus to the coastal environment on Xiamen. Frontiers in Microbiology, 0, 14, .	3.5	1

#	ARTICLE	IF	CITATIONS
8098	Transcriptome analysis and identification of genes related to environmental adaptation of <i>Grylloprimevala jilina</i> Zhou & Ren 2023. Ecology and Evolution, 2023, 13, .	1.9	0
8099	Landscape of gut microbiota and metabolites and their interaction in comorbid heart failure and depressive symptoms: a random forest analysis study. MSystems, 2023, 8, .	3.8	0
8100	Changes in community structure and microbiological risks in a small stream after receiving treated shale gas wastewater for two years. Environmental Pollution, 2024, 340, 122799.	7.5	0
8101	StORF-Reporter: finding genes between genes. Nucleic Acids Research, 2023, 51, 11504-11517.	14.5	0
8102	Coastal upwelling systems as dynamic mosaics of bacterioplankton functional specialization. Frontiers in Marine Science, 0, 10, .	2.5	0
8103	Metagenomic analysis reveals the microbial response to petroleum contamination in oilfield soils. Science of the Total Environment, 2024, 912, 168972.	8.0	0
8104	Molecular characterization and in-depth genomic analysis to unravel the pathogenic features of an environmental isolate Enterobacter sp. S-33. International Microbiology, 0, , .	2.4	0
8105	Metagenomic binning of PacBio HiFi data prior to assembly reveals a complete genome of <i>Cosmopolites sordidus</i> (Germar) (Coleoptera: Curculionidae, Dryophthorinae) the most damaging arthropod pest of bananas and plantains. PeerJ, 0, 11, e16276.	2.0	0
8106	Improved high-quality reference genome of red drum facilitates the processes of resistance-related gene exploration. Scientific Data, 2023, 10, .	5.3	0
8107	CGG toolkit: Software components for computational genomics. PLoS Computational Biology, 2023, 19, e1011498.	3.2	0
8108	The draft genome of the Temminck's tragopan (<i>Tragopan temminckii</i>) with evolutionary implications. BMC Genomics, 2023, 24, .	2.8	0
8109	Genome-wide characterization of the tomato UDP-glycosyltransferase gene family and functional identification of SIUDPGT52 in drought tolerance. , 2023, 1, .		0
8113	The pig pang genome provides insights into the roles of coding structural variations in genetic diversity and adaptation. Genome Research, 2023, 33, 1833-1847.	5.5	2
8114	Telomeric repeat evolution in the phylum Nematoda revealed by high-quality genome assemblies and subtelomere structures. Genome Research, 2023, 33, 1947-1957.	5.5	1
8115	Blue carbon sink capacity of mangroves determined by leaves and their associated microbiome. Global Change Biology, 2024, 30, .	9.5	0
8117	Comparative analysis of shotgun metagenomics and 16S rDNA sequencing of gut microbiota in migratory seagulls. PeerJ, 0, 11, e16394.	2.0	0
8118	Functional genomic analysis of nutrient cycling of plant-soil continuum in the mossy biocrust in the Tengger Desert. Rhizosphere, 2023, 28, 100806.	3.0	0
8121	RNA virus diversity in three parasitoid wasps of tephritid flies: insights from novel and known species. Microbiology Spectrum, 2023, 11, .	3.0	0

#	ARTICLE	IF	CITATIONS
8123	Unraveling the dataset transcriptomic response of <i>Hydrangea macrophylla</i> stem to mechanical stimulation: De novo assembly and functional annotation. <i>Data in Brief</i> , 2023, 51, 109784.	1.0	0
8124	Comparative Pangenomic Insights into the Distinct Evolution of Virulence Factors Among Grapevine Trunk Pathogens. <i>Molecular Plant-Microbe Interactions</i> , 2024, 37, 127-142.	2.6	0
8126	Fecal Metagenomics to Identify Biomarkers of Food Intake in Healthy Adults: Findings from Randomized, Controlled, Nutrition Trials. <i>Journal of Nutrition</i> , 2024, 154, 271-283.	2.9	0
8128	Genomic analysis and characterization of new loci associated with seed protein and oil content in soybeans. <i>Plant Genome</i> , 2023, 16, .	2.8	0
8130	A chromosome-level genome assembly of Korean mint (<i>Agastache rugosa</i>). <i>Scientific Data</i> , 2023, 10, .	5.3	0
8133	Pithoviruses Are Invaded by Repeats That Contribute to Their Evolution and Divergence from Cedratviruses. <i>Molecular Biology and Evolution</i> , 2023, 40, .	8.9	0
8134	GlcNac produced by the gut microbiome enhances host influenza resistance by modulating NK cells. <i>Gut Microbes</i> , 2023, 15, .	9.8	0
8135	Ready Reckoner for Using Bioinformatics Tools in Fish and Shellfish Microbiome Analysis. , 2023, , 93-120.		0
8136	A reference assembly for the legume cover crop hairy vetch (<i>Vicia villosa</i>). <i>GigaByte</i> , 0, 2023, 1-20.	0.0	1
8137	Biofilm dysbiosis and caries activity: a surface or an individual issue?. <i>Journal of Applied Oral Science</i> , 0, 31, .	1.8	1
8138	Role of Relebactam in the Antibiotic Resistance Acquisition in <i>Pseudomonas aeruginosa</i> : In Vitro Study. <i>Antibiotics</i> , 2023, 12, 1619.	3.7	0
8139	Time-series transcriptomic profiling of larval exsheathment in a model parasitic nematode of veterinary importance. <i>Frontiers in Cell and Developmental Biology</i> , 0, 11, .	3.7	0
8140	VIGA: a one-stop tool for eukaryotic virus identification and genome assembly from next-generation-sequencing data. <i>Briefings in Bioinformatics</i> , 2023, 25, .	6.5	0
8141	Fiber-deficient diet inhibits colitis through the regulation of the niche and metabolism of a gut pathobiont. <i>Cell Host and Microbe</i> , 2023, 31, 2007-2022.e12.	11.0	3
8142	Sign of APOBEC editing, purifying selection, frameshift, and in-frame nonsense mutations in the microevolution of lumpy skin disease virus. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	0
8143	Metagenomic analysis of oral and intestinal microbiome of patients during the initial stage of orthodontic treatment. <i>American Journal of Orthodontics and Dentofacial Orthopedics</i> , 2024, 165, 161-172.e3.	1.7	0
8144	Is Carbapenem Therapy Necessary for the Treatment of Non-CTX-M Extended-Spectrum β -Lactamase-Producing Enterobacterales Bloodstream Infections?. <i>Clinical Infectious Diseases</i> , 0, , .	5.8	0
8145	Biosolids amendment effects on nitrogen cycling gene expression by the soil prokaryotic community as revealed by metatranscriptomic analysis. <i>Soil Research</i> , 2023, , .	1.1	0

#	ARTICLE	IF	CITATIONS
8146	De novo transcriptional analysis of the response to starvation stress in the white ridgetail prawn, <i>Exopalaemon carinicauda</i> . <i>Genomics</i> , 2023, 115, 110746.	2.9	0
8151	Haplotype-resolved chromosome-level genome of hexaploid Jerusalem artichoke provides insights into its origin, evolution, and inulin metabolism. <i>Plant Communications</i> , 2023, , 100767.	7.7	0
8153	Temporal dynamics of microbial composition and antibiotic resistome in fermentation bed culture pig farms across various ages. <i>Science of the Total Environment</i> , 2024, 912, 168728.	8.0	1
8157	Transcriptomic insights into the acclimatization response of the cold-water Ophiuroid <i>Ophiopholis mirabilis</i> to elevated temperatures. <i>Marine Biology</i> , 2024, 171, .	1.5	0
8158	Advanced Metatranscriptomic Approaches for Exploring the Taxonomic and Functional Features Relevant to the Aquaculture Industry. , 2023, , 175-195.		0
8159	Identifying Novel Antibiotic Resistance Genes (ARGs): Important Aspect of Metagenomic Research. , 2023, , 231-246.		0
8161	PanDelos-frags: A methodology for discovering pangenomic content of incomplete microbial assemblies. <i>Journal of Biomedical Informatics</i> , 2023, 148, 104552.	4.3	1
8162	Seven-year N and P inputs regulate soil microbial communities via bottom-up effects on carbon and nutrient supply and top-down effects on protist relative abundance. <i>Forest Ecology and Management</i> , 2024, 552, 121582.	3.2	1
8163	IPOP: An Integrative Plant Multi-omics Platform for Cross-species Comparison and Evolutionary Study. <i>Molecular Biology and Evolution</i> , 2023, 40, .	8.9	0
8164	PLM-ARG: antibiotic resistance gene identification using a pretrained protein language model. <i>Bioinformatics</i> , 2023, 39, .	4.1	0
8165	Cereals rhizosphere microbiome undergoes host selection of nitrogen cycle guilds correlated to crop productivity. <i>Science of the Total Environment</i> , 2024, 911, 168794.	8.0	1
8166	Ancestors in the Extreme: A Genomics View of Microbial Diversity in Hypersaline Aquatic Environments. <i>Results and Problems in Cell Differentiation</i> , 2024, , 185-212.	0.7	0
8167	Comparative analysis of mitochondrion-related organelles in anaerobic amoebozoans. <i>Microbial Genomics</i> , 2023, 9, .	2.0	0
8168	Discordant patterns between nitrogen-cycling functional traits and taxa in distant coastal sediments reveal important community assembly mechanisms. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	0
8169	Metagenomic insights into the diversity of 2,4-dichlorophenol degraders and the cooperation patterns in a bacterial consortium. <i>Science of the Total Environment</i> , 2024, 912, 168723.	8.0	2
8170	A chromosome-scale genome sequence of <i>Aeonium</i> (<i>Aeonium arboreum</i> 'Velour') provides novel insights into the evolution of anthocyanin synthesis. <i>Gene</i> , 2024, 896, 148031.	2.2	0
8171	Elucidation of the complete degradation mechanism of N,N-dimethylformamide (DMF) and substrate preference within a synthetic bacterial consortium (DMFsyn) formed via a "top-down" strategy. <i>Chemical Engineering Journal</i> , 2024, 479, 147658.	12.7	1
8172	Detection and Analysis of <i>Wolbachia</i> in Plant-Parasitic Nematodes and Insights into <i>Wolbachia</i> Evolution. <i>Methods in Molecular Biology</i> , 2024, , 115-134.	0.9	0

#	ARTICLE	IF	CITATIONS
8173	Chromosome-level genome assembly of navel orange cv. Gannanzao (<i>Citrus sinensis</i> Osbeck cv.) Tj ETQq0 0.0rgBT /Overlock 10	1.8	0
8174	Horizontal gene transfer in activated sludge enhances microbial antimicrobial resistance and virulence. Science of the Total Environment, 2024, 912, 168908.	8.0	0
8175	Transcriptome and metabolome comprehensive analysis reveal the molecular basis of slow-action and non-repellency of cyclozaprid against an eusocial pest, Solenopsis invicta. Frontiers in Physiology, 0, 14, .	2.8	0
8176	RNA is a key component of extracellular DNA networks in Pseudomonas aeruginosa biofilms. Nature Communications, 2023, 14, .	12.8	3
8177	iCAZyGFADB: an insect CAZyme andÂgene function annotation database. Database: the Journal of Biological Databases and Curation, 2023, 2023, .	3.0	0
8178	Phenotypic and genomic insights into the pathogenicity and antimicrobial resistance of an <i>Enterobacter roggenkampii</i> strain isolated from diseased silver arowana (<i>Osteoglossum</i>) Tj ETQq1 1 0.7849 14 rgBT /Overlock	0.7849	14
8179	Genomic analysis of Streptococcus pneumoniae serogroup 20 isolates in Alberta, Canada from 1993â€“2019. Microbial Genomics, 2023, 9, .	2.0	0
8181	Physiology governing diatom vs. dinoflagellate bloom and decline in coastal Santa Monica Bay. Frontiers in Microbiology, 0, 14, .	3.5	0
8182	Comparative Transcriptome Sequencing and Endogenous Phytohormone Content of Annual Grafted Branches of Zelkova schneideriana and Its Dwarf Variety HenTianGao. International Journal of Molecular Sciences, 2023, 24, 16902.	4.1	0
8183	Rhizocompartmental microbiomes of arrow bamboo (<i>Fargesia nitida</i>) and their relation to soil properties in Subalpine Coniferous Forests. PeerJ, 0, 11, e16488.	2.0	0
8184	Novel tiny textural motif pattern-based RNA virus protein sequence classification model. Expert Systems With Applications, 2024, 242, 122781.	7.6	2
8185	A targeted approach to enrich host-associated bacteria for metagenomic sequencing. FEMS Microbes, 0, , .	2.1	1
8186	Identification of Bioactive Phytocytokines Using Transcriptomic Data and Plant Bioassays. Methods in Molecular Biology, 2024, , 23-35.	0.9	0
8187	Transcriptomic response to salinity variation in native and introduced mud-tidal gastropod Batillaria attramentaria. Frontiers in Marine Science, 0, 10, .	2.5	0
8188	Gut-immunity modulation in Lepidocephalichthys guntea during Aeromonas hydrophila-infection and recovery assessed with transcriptome data. Heliyon, 2023, 9, e22936.	3.2	0
8190	The diversity of the antimicrobial resistome of lake Tanganyika increases with the water depth. Environmental Pollution, 2024, 342, 123065.	7.5	0
8191	Draft genome sequence of <i>Sphingomonas paucimobilis</i> strain Sph5, isolated from tap water filtration membrane. Microbiology Resource Announcements, 0, , .	0.6	0
8192	Integrative multiomics profiling of passion fruit reveals the genetic basis for fruit color and aroma. Plant Physiology, 2024, 194, 2491-2510.	4.8	0

#	ARTICLE	IF	CITATIONS
8194	Temporal and spatial differences in the vaginal microbiome of Chinese healthy women. <i>PeerJ</i> , 0, 11, e16438.	2.0	0
8195	Shotgun Metagenomics-Guided Prediction Reveals the Metal Tolerance and Antibiotic Resistance of Microbes in Poly-Extreme Environments in the Danakil Depression, Afar Region. <i>Antibiotics</i> , 2023, 12, 1697.	3.7	0
8197	Influence of three different manure treatments on antimicrobial resistance genes and mobile genetic elements. , 0, 1, .		0
8198	Genomic characterization of <i>Mycobacterium lepromatosis</i> from ENL patients from India. <i>Infection, Genetics and Evolution</i> , 2023, 116, 105537.	2.3	0
8199	Domestication through clandestine cultivation constrained genetic diversity in magic mushrooms relative to naturalized populations. <i>Current Biology</i> , 2023, 33, 5147-5159.e7.	3.9	0
8200	Viral diversity in wild and urban rodents of Yunnan Province, China. <i>Emerging Microbes and Infections</i> , 2024, 13, .	6.5	1
8201	Metagenomics coupled with thermodynamic analysis revealed a potential way to improve the nitrogen removal efficiency of the aerobic methane oxidation coupled to denitrification process under the hypoxic condition. <i>Science of the Total Environment</i> , 2024, 912, 168953.	8.0	0
8202	A large-scale genomically predicted protein mass database enables rapid and broad-spectrum identification of bacterial and archaeal isolates by mass spectrometry. <i>Genome Biology</i> , 2023, 24, .	8.8	0
8203	Strategies of chemolithoautotrophs adapting to high temperature and extremely acidic conditions in a shallow hydrothermal ecosystem. <i>Microbiome</i> , 2023, 11, .	11.1	0
8204	<scp>PEO</scp>: Plant Expression Omnibus “ a comparative transcriptomic database for 103 Archaeplastida. <i>Plant Journal</i> , 2024, 117, 1592-1603.	5.7	0
8205	Faster cycling but lower efficiency: A microbial metabolic perspective on carbon loss after wetland conversion to cropland. <i>Soil Biology and Biochemistry</i> , 2024, 189, 109260.	8.8	0
8206	Structural changes in the gut virome of patients with atherosclerotic cardiovascular disease. <i>Microbiology Spectrum</i> , 2024, 12, .	3.0	2
8207	<i>De Novo</i> Synthesis of a Conjugative System from Human Gut Metagenomic Data for Targeted Delivery of Cas9 Antimicrobials. <i>ACS Synthetic Biology</i> , 2023, 12, 3578-3590.	3.8	1
8208	Phylogenetic Inference of Homologous/Orthologous Genes among Distantly Related Plants. <i>Bio-protocol</i> , 2023, 13, .	0.4	0
8210	Host DNA depletion methods and genome-centric metagenomics of bovine hindmilk microbiome. <i>MSphere</i> , 0, , .	2.9	0
8211	Comparative analysis of functional diversity of rumen microbiome in bison and beef heifers. <i>Applied and Environmental Microbiology</i> , 0, , .	3.1	0
8212	Metagenomics-based exploration of key soil microorganisms contributing to continuously planted <i>Casuarina equisetifolia</i> growth inhibition and their interactions with soil nutrient transformation. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	0
8214	Phosphate-related genomic islands as drivers of environmental adaptation in the streamlined marine alphaproteobacterial HIMB59. <i>MSystems</i> , 0, , .	3.8	0

#	ARTICLE	IF	CITATIONS
8215	Characterization of microbial contamination in agricultural soil: A public health perspective. <i>Science of the Total Environment</i> , 2024, 912, 169139.	8.0	1
8217	Mining salt stress-related genes in <i>Spartina alterniflora</i> via analyzing co-evolution signal across 365 plant species using phylogenetic profiling. <i>ABIOTECH</i> , 2023, 4, 291-302.	3.9	1
8218	Anammox activity improved significantly by the cross-fed NO from ammonia-oxidizing bacteria and denitrifying bacteria to anammox bacteria. <i>Water Research</i> , 2024, 249, 120986.	11.3	3
8219	The connection between the antibiotic resistome and nitrogen-cycling microorganisms in paddy soil is enhanced by application of chemical and plant-derived organic fertilizers. <i>Environmental Research</i> , 2024, 243, 117880.	7.5	0
8220	Freshwater Viral Metagenome Analyses Targeting dsDNA Viruses. <i>Methods in Molecular Biology</i> , 2024, , 29-44.	0.9	0
8221	TADA: Taxonomy-Aware Dataset Aggregator. <i>Bioinformatics</i> , 0, , .	4.1	0
8224	The MetalInvert soil invertebrate genome resource provides insights into below-ground biodiversity and evolution. <i>Communications Biology</i> , 2023, 6, .	4.4	0
8225	Genome-wide expansion and reorganization during grass evolution: from 30ÂMb chromosomes in rice and <i>Brachypodium</i> to 550ÂMb in <i>Avena</i> . <i>BMC Plant Biology</i> , 2023, 23, .	3.6	0
8226	In situ metagenomics: A platform for rapid sequencing and analysis of metagenomes in less than oneâ€day. <i>Molecular Ecology Resources</i> , 0, , .	4.8	0
8228	Metagenomic analysis for exploring the potential of <i>Lactobacillus yoelii</i> FYL1 to mitigate bacterial diarrhea and changes in the gut microbiota of juvenile yaks. <i>Microbial Pathogenesis</i> , 2024, 186, 106496.	2.9	0
8229	A draft genome of the neritid snail <i>Theodoxus fluviatilis</i>. <i>G3: Genes, Genomes, Genetics</i> , 2024, 14, .	1.8	0
8230	Unravelling biosynthesis and biodegradation potentials of microbial dark matters in hypersaline lakes. <i>Environmental Science and Ecotechnology</i> , 2024, 20, 100359.	13.5	0
8231	Carbohydrates and carbohydrate degradation gene abundance and transcription in Atlantic waters of the Arctic. <i>ISME Communications</i> , 2023, 3, .	4.2	3
8232	Metatranscriptome analysis reveals the putative venom toxin repertoire of the biofouling hydroid <i>Ectopleura larynx</i> . <i>Toxicon</i> , 2024, 237, 107556.	1.6	0
8233	Andean soil-derived lignocellulolytic bacterial consortium as a source of novel taxa and putative plastic-active enzymes. <i>Systematic and Applied Microbiology</i> , 2024, 47, 126485.	2.8	0
8234	Physiological and transcriptomic analysis reveals the toxic and protective mechanisms of marine microalga <i>Chlorella pyrenoidosa</i> in response to TiO2 nanoparticles and UV-B radiation. <i>Science of the Total Environment</i> , 2024, 912, 169174.	8.0	0
8236	Pathogen Eradication in Garlic in the Phytobiome Context: Should We Aim for Complete Cleaning?. <i>Plants</i> , 2023, 12, 4125.	3.5	0
8237	Sequencing and Analysis of the Mitochondrial Genome of <i>Aedes aegypti</i> (Diptera: Culicidae) from the Brazilian Amazon Region. <i>Insects</i> , 2023, 14, 938.	2.2	0

			CITATION REPORT	
#	ARTICLE	IF	CITATIONS	
8239	Effects of polystyrene microplastics on <i>Euglena gracilis</i> : Intracellular distribution and the protozoan transcriptional responses. <i>Aquatic Toxicology</i> , 2024, 266, 106802.	4.0	0	
8240	Unravelling the postharvest quality diversities of different sweet corn varieties. <i>Postharvest Biology and Technology</i> , 2024, 209, 112718.	6.0	0	
8241	Resolving the phylogeny of <i>Thladiantha</i> (Cucurbitaceae) with three different target capture pipelines. <i>Bmc Ecology and Evolution</i> , 2023, 23, .	1.6	0	
8242	Metabolic improvements of novel microbial fermentation on black tea by <i>Eurotium cristatum</i> . <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	0	
8243	Gut microbiota-related metabolite alpha-linolenic acid mitigates intestinal inflammation induced by oral infection with <i>Toxoplasma gondii</i> . <i>Microbiome</i> , 2023, 11, .	11.1	0	
8244	Single-cell transcriptome and metagenome profiling reveals the genetic basis of rumen functions and convergent developmental patterns in ruminants. <i>Genome Research</i> , 2023, 33, 1690-1707.	5.5	0	
8245	Identification and characterization of two closely related virga-like viruses latently infecting rubber trees (<i>Hevea brasiliensis</i>). <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	0	
8246	Evidential deep learning for trustworthy prediction of enzyme commission number. <i>Briefings in Bioinformatics</i> , 2023, 25, .	6.5	0	
8247	Microbial organic fertilizer prepared by co-composting of <i>Trichoderma dregs</i> mitigates dissemination of resistance, virulence genes, and bacterial pathogens in soil and rhizosphere. <i>Environmental Research</i> , 2024, 241, 117718.	7.5	0	
8248	Duck panâ€šgenome reveals two transposon insertions caused bodyweight enlarging and white plumage phenotype formation during evolution. , 2024, 3, .		0	
8249	A super-pangenome of the North American wild grape species. <i>Genome Biology</i> , 2023, 24, .	8.8	3	
8250	Biosynthesis mechanisms of medium-chain carboxylic acids and alcohols in anaerobic microalgae fermentation regulated by pH conditions. <i>Applied and Environmental Microbiology</i> , 0, , .	3.1	0	
8251	MarFERReT, an open-source, version-controlled reference library of marine microbial eukaryote functional genes. <i>Scientific Data</i> , 2023, 10, .	5.3	1	
8252	Molecular tuning of sea anemone stinging. <i>ELife</i> , 0, 12, .	6.0	1	
8253	Performance Analysis of Cross-Assembly of Metatranscriptomic Datasets in Viral Community Studies. <i>Mathematical Biology and Bioinformatics</i> , 2023, 18, 418-433.	0.6	0	
8255	Molecular analysis of adenovirus strains responsible for gastroenteritis in children, under five, in Tunisia. <i>Heliyon</i> , 2024, 10, e22969.	3.2	0	
8258	Viral Diversity in Samples of Freshwater Gastropods <i>Benedictia baicalensis</i> (Caenogastropoda:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 10 24, 17022.	4.1	0	
8259	Pathogen invasion increases the abundance of predatory protists and their prey associations in the plant microbiome. <i>Molecular Ecology</i> , 2024, 33, .	3.9	1	

#	ARTICLE	IF	CITATIONS
8261	Effect of reactor operation modes on mitigating antibiotic resistance genes (ARGs) and methane production from hydrothermally-pretreated pig manure. <i>Environmental Research</i> , 2024, 244, 117894.	7.5	0
8262	Gut microbiota changes in <i>Hexagrammos otakii</i> during development and association with diets based on metagenomics sequencing. <i>Aquaculture Reports</i> , 2023, 33, 101881.	1.7	0
8263	Outbreak of piglet diarrhea associated with a new reassortant porcine rotavirus B. <i>Veterinary Microbiology</i> , 2024, 288, 109947.	1.9	0
8264	Functional guilds and drivers of diversity in seaweed-associated bacteria. <i>FEMS Microbes</i> , 0, , .	2.1	0
8266	Associated bacterial communities, confrontation studies, and comparative genomics reveal important interactions between <i>Morchella</i> with <i>Pseudomonas</i> spp.. <i>Frontiers in Fungal Biology</i> , 0, 4, .	2.0	0
8267	Phylogeography of Two Enigmatic Sulphur Butterflies, <i>Colias mongola</i> Alphärsky, 1897 and <i>Colias tamerlana</i> Staudinger, 1897 (Lepidoptera, Pieridae), with Relations to Wolbachia Infection. <i>Insects</i> , 2023, 14, 943.	2.2	0
8268	The potential mechanism of response to light intensity in energy metabolism mediated by miRNA in <i>Isatis indigotica</i> . <i>Gene</i> , 2024, 897, 148083.	2.2	0
8269	Proteinortho6: pseudo-reciprocal best alignment heuristic for graph-based detection of (co-)orthologs. <i>Frontiers in Bioinformatics</i> , 0, 3, .	2.1	0
8271	Role of plant metabolites in the formation of bacterial communities in the rhizosphere of <i>Tetrastigma hemsleyanum</i> . <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	0
8274	Integrated metabolome and transcriptome analyses of anthocyanin biosynthesis reveal key candidate genes involved in colour variation of <i>Scutellaria baicalensis</i> flowers. <i>BMC Plant Biology</i> , 2023, 23, .	3.6	0
8275	Exploring the Diversity of Plant-Associated Viruses and Related Viruses in Riverine Freshwater Samples Collected in Berlin, Germany. <i>Pathogens</i> , 2023, 12, 1458.	2.8	0
8276	Chromosome-level genome assembly of the Stoliczka©TM's Asian trident bat (<i>Aselliscus stoliczkanus</i>). <i>Scientific Data</i> , 2023, 10, .	5.3	0
8277	Haplotype-resolved chromosomal-level genome assembly of <i>Buzhayia</i> (<i>Microcos paniculata</i>). <i>Scientific Data</i> , 2023, 10, .	5.3	0
8279	Breakdown of hardly degradable carbohydrates (lignocellulose) in a two-stage anaerobic digestion plant is favored in the main fermenter. <i>Water Research</i> , 2024, 250, 121020.	11.3	0
8281	PEPMatch: a tool to identify short peptide sequence matches in large sets of proteins. <i>BMC Bioinformatics</i> , 2023, 24, .	2.6	1
8282	The olfactory system of <i>Pieris brassicae</i> caterpillars: from receptors to glomeruli. <i>Insect Science</i> , 0, , .	3.0	0
8283	Evolution and ecology of Jeilongvirus among wild rodents and shrews in Singapore. <i>One Health Outlook</i> , 2023, 5, .	3.4	0
8284	<i>Ceratobasidium</i> sp. is associated with cassava witches©TM broom disease, a re-emerging threat to cassava cultivation in Southeast Asia. <i>Scientific Reports</i> , 2023, 13, .	3.3	0

#	ARTICLE	IF	CITATIONS
8285	<i>Bifidobacterium animalis</i> subsp. <i>lactis</i> Probio-M8 alleviates abnormal behavior and regulates gut microbiota in a mouse model suffering from autism. <i>MSystems</i> , 0, , .	3.8	0
8286	A transcriptional program underlying the circannual rhythms of gonadal development in medaka. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	7.1	0
8287	Functional and evolutionary significance of unknown genes from uncultivated taxa. <i>Nature</i> , 2024, 626, 377-384.	27.8	5
8288	The Viromes of Six Ecosystem Service Provider Parasitoid Wasps. <i>Viruses</i> , 2023, 15, 2448.	3.3	1
8289	Unveiling bacterial consortium for xenobiotic biodegradation from Pichavaram mangrove forest soil: a metagenomic approach. <i>Archives of Microbiology</i> , 2024, 206, .	2.2	1
8290	Identification of Incomplete Annotations of Biosynthesis Pathways in Rhodophytes Using a Multi-Omics Approach. <i>Marine Drugs</i> , 2024, 22, 3.	4.6	0
8291	Chromosome-level genome of putative autohexaploid <i>Actinidia deliciosa</i> provides insights into polyploidisation and evolution. <i>Plant Journal</i> , 0, , .	5.7	0
8292	Tools and Techniques for Exploring Hidden Microorganisms: A Potential Future of Human Health Diagnosis. , 2023, , 251-279.		0
8294	C4-HSL-mediated quorum sensing regulates nitrogen removal in activated sludge process at Low temperatures. <i>Environmental Research</i> , 2024, 244, 117928.	7.5	0
8295	Gut microbiota affects the estrus return of sows by regulating the metabolism of sex steroid hormones. <i>Journal of Animal Science and Biotechnology</i> , 2023, 14, .	5.3	0
8296	Prenatal exposure to hexafluoropropylene oxide trimer acid (HFPO-TA) disrupts the maternal gut microbiome and fecal metabolome homeostasis. <i>Science of the Total Environment</i> , 2023, , 169330.	8.0	0
8297	Microbial ecology and activity of snow algae within a Pacific Northwest snowpack. <i>Arctic, Antarctic, and Alpine Research</i> , 2023, 55, .	1.1	0
8298	Identification of key microbial communities and intracellular metabolic pathways to response micro-aerobic environment for enhancing degradation of N, N-dimethylformamide in refractory membrane-making wastewater. <i>Chemical Engineering Journal</i> , 2024, 480, 148179.	12.7	0
8299	Toxinome—the bacterial protein toxin database. <i>MBio</i> , 0, , .	4.1	0
8300	Metagenomic and genomic analysis of heavy metal-tolerant and -resistant bacteria in resource islands in a semi-arid zone of the Colombian Caribbean. <i>Environmental Science and Pollution Research</i> , 0, , .	5.3	0
8302	Comparative analysis of microbial succession and proteolysis focusing on amino acid pathways in Asiago-PDO cheese from two dairies. <i>International Journal of Food Microbiology</i> , 2024, 411, 110548.	4.7	0
8303	Microflora structure and functional capacity in Tibetan kefir grains and selenium-enriched Tibetan kefir grains: A metagenomic analysis. <i>Food Microbiology</i> , 2023, , 104454.	4.2	0
8305	The nematicide emamectin benzoate increases ROS accumulation in <i>Pinus massoniana</i> and poison <i>Monochamus alternatus</i> . <i>PLoS ONE</i> , 2023, 18, e0295945.	2.5	1

#	ARTICLE	IF	CITATIONS
8306	Pan-metagenome reveals the abiotic stress resistome of cigar tobacco phyllosphere microbiome. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	0
8309	Metagenomic and metabolomic analysis of the effect of bleaching on unsaturated fatty acid synthesis pathways in coral symbionts. <i>Science of the Total Environment</i> , 2023, , 169487.	8.0	0
8310	Nitrate removal by anammox bacteria utilizing photoexcited electrons via inward extracellular electron transfer channel. <i>Water Research</i> , 2024, 250, 121059.	11.3	0
8311	Draft genome sequence and comparative genomic analysis of <i>Penicillium pancosmium</i> MUM 23.27 isolated from raw honey. <i>Archives of Microbiology</i> , 2024, 206, .	2.2	0
8315	Comparative Physiological and Transcriptome Analyses of Tolerant and Susceptible Cultivars Reveal the Molecular Mechanism of Cold Tolerance in <i>Anthurium andraeanum</i> . <i>International Journal of Molecular Sciences</i> , 2024, 25, 250.	4.1	0
8316	Cytokinin biosynthesis in Hexapoda and Insecta: a bioinformatic analysis. <i>Arthropod-Plant Interactions</i> , 0, , .	1.1	1
8317	Eyeless cave-dwelling <i>Leptonetela</i> spiders still rely on light. <i>Science Advances</i> , 2023, 9, .	10.3	0
8318	Metallic micronutrients are associated with the structure and function of the soil microbiome. <i>Nature Communications</i> , 2023, 14, .	12.8	5
8319	Polyploid Genome Assembly Provides Insights into Morphological Development and Ascorbic Acid Accumulation of <i>Sauropus androgynus</i> . <i>International Journal of Molecular Sciences</i> , 2024, 25, 300.	4.1	0
8320	Chromosome-level genome assembly and demographic history of <i>Euryodendron excelsum</i> , in monotypic genus endemic to China. <i>DNA Research</i> , 0, , .	3.4	0
8321	Seascapes Shaped the Local Adaptation and Population Structure of South China Coast Yellowfin Seabream (<i>Acanthopagrus latus</i>). <i>Marine Biotechnology</i> , 2024, 26, 60-73.	2.4	0
8322	The diversity and ecological significance of microbial traits potentially involved in B ₁₂ biosynthesis in the global ocean. , 2023, 2, 416-427.		2
8323	<i>Lactococcus lactis</i> in Dairy Fermentation—Health-Promoting and Probiotic Properties. <i>Fermentation</i> , 2024, 10, 16.	3.0	0
8324	Interspecies Papillomavirus Type Infection and a Novel Papillomavirus Type in Red Ruffed Lemurs (<i>Varecia rubra</i>). <i>Viruses</i> , 2024, 16, 37.	3.3	1
8325	Relationships between diet and gut microbiome in an Italian and Dutch cohort: does the dietary protein to fiber ratio play a role?. <i>European Journal of Nutrition</i> , 2024, 63, 741-750.	3.9	0
8326	Comparative Rumen Metagenome and CAZyme Profiles in Cattle and Buffaloes: Implications for Methane Yield and Rumen Fermentation on a Common Diet. <i>Microorganisms</i> , 2024, 12, 47.	3.6	0
8327	<i>fosA11</i> , a novel chromosomal-encoded fosfomycin resistance gene identified in <i>Providencia rettgeri</i> . <i>Microbiology Spectrum</i> , 2024, 12, .	3.0	0
8328	Metatranscriptomic insights into the microbial metabolic activities during an <i>Ulva prolifera</i> green tide in coastal Qingdao areas. <i>Environmental Pollution</i> , 2024, 343, 123217.	7.5	0

#	ARTICLE	IF	CITATIONS
8329	Insights into antibiotic and heavy metal resistance interactions in <i>Escherichia coli</i> isolated from livestock manure and fertilized soil. <i>Journal of Environmental Management</i> , 2024, 351, 119935.	7.8	1
8330	Metatranscriptomics sheds light on the links between the functional traits of fungal guilds and ecological processes in forest soil ecosystems. <i>New Phytologist</i> , 0, , .	7.3	1
8331	Soil microbial ecology through the lens of metatranscriptomics. <i>Soil Ecology Letters</i> , 2024, 6, .	4.5	0
8332	Microbiome assembly and stability during start-up of a full-scale, two-phase anaerobic digester fed cow manure and mixed organic feedstocks. <i>Bioresource Technology</i> , 2024, 394, 130247.	9.6	0
8333	Revealing viral diversity in the Napahai plateau wetland based on metagenomics. <i>Antonie Van Leeuwenhoek</i> , 2024, 117, .	1.7	0
8334	Diversified molecular adaptations of inorganic nitrogen assimilation and signaling machineries in plants. <i>New Phytologist</i> , 2024, 241, 2108-2123.	7.3	0
8335	Water Level Fluctuations Modulate the Microbiomes Involved in Biogeochemical Cycling in Floodplains. <i>Microbial Ecology</i> , 2024, 87, .	2.8	0
8336	A centromere map based on super pan-€genome highlights the structure and function of rice centromeres. <i>Journal of Integrative Plant Biology</i> , 2024, 66, 196-207.	8.5	0
8337	Functional traits and health implications of the global household drinking-water microbiome retrieved using an integrative genome-centric approach. <i>Water Research</i> , 2024, 250, 121094.	11.3	1
8338	Reference gene catalog and metagenome-assembled genomes from the gut microbiome reveal the microbial composition, antibiotic resistome, and adaptability of a lignocellulose diet in the giant panda. <i>Environmental Research</i> , 2024, 245, 118090.	7.5	0
8339	First Contiguous Genome Assembly of Japanese Lady Bell (<i>Adenophora triphylla</i>) and Insights into Development of Different Leaf Types. <i>Genes</i> , 2024, 15, 58.	2.4	0
8340	Red Cabbage Juice-Mediated Gut Microbiota Modulation Improves Intestinal Epithelial Homeostasis and Ameliorates Colitis. <i>International Journal of Molecular Sciences</i> , 2024, 25, 539.	4.1	0
8341	Functional annotation of a divergent genome using sequence and structure-based similarity. <i>BMC Genomics</i> , 2024, 25, .	2.8	0
8342	First genome assembly and annotation of <i>Sanguangporus weigela</i> uncovers its medicinal functions, metabolic pathways, and evolution. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 13, .	3.9	0
8343	Prophage enhances the ability of deep-sea bacterium <i>Shewanella psychrophila</i> WP2 to utilize D-amino acid. <i>Microbiology Spectrum</i> , 2024, 12, .	3.0	0
8344	Precision enzyme discovery through targeted mining of metagenomic data. <i>Natural Products and Bioprospecting</i> , 2024, 14, .	4.3	0
8345	Subgenome phasing for complex allopolyploidy: case-based benchmarking and recommendations. <i>Briefings in Bioinformatics</i> , 2023, 25, .	6.5	0
8346	Interactive dynamics between rhizosphere bacterial and viral communities facilitate soybean fitness to cadmium stress revealed by time-series metagenomics. <i>Soil Biology and Biochemistry</i> , 2024, 190, 109313.	8.8	0

#	ARTICLE	IF	CITATIONS
8347	Evolutionary genomics of three agricultural pest moths reveals rapid evolution of host adaptation and immune-related genes. <i>GigaScience</i> , 2024, 13, .	6.4	0
8348	Identification of potential microbial risk factors associated with fecal indicator exceedances at recreational beaches. <i>Environmental Microbiomes</i> , 2024, 19, .	5.0	0
8349	Hybrid <i>de novo</i> genome assembly of the sexually dimorphic Lady Amherst's pheasant. <i>DNA Research</i> , 2024, 31, .	3.4	0
8350	Hagfish genome elucidates vertebrate whole-genome duplication events and their evolutionary consequences. <i>Nature Ecology and Evolution</i> , 2024, 8, 519-535.	7.8	4
8351	Near-chromosomal-level genome of the red palm weevil (<i>Rhynchophorus ferrugineus</i>), a potential resource for genome-based pest control. <i>Scientific Data</i> , 2024, 11, .	5.3	0
8352	New clades of viruses infecting the obligatory biotroph <i>Bremia lactucae</i> representing distinct evolutionary trajectory for viruses infecting oomycetes. <i>Virus Evolution</i> , 2024, 10, .	4.9	1
8353	Genome sequencing and molecular networking analysis of the wild fungus <i>Anthostomella pinea</i> reveal its ability to produce a diverse range of secondary metabolites. <i>Fungal Biology and Biotechnology</i> , 2024, 11, .	5.1	0
8354	Comparative omics analysis of a new deep-sea barnacle species (Cirripedia, Scalpellomorpha) and shallow-water barnacle species provides insights into deep-sea adaptation. <i>Frontiers in Marine Science</i> , 0, 10, .	2.5	0
8355	The effects of primary and secondary bacterial exposure on the seahorse (<i>Hippocampus erectus</i>) immune response. <i>Developmental and Comparative Immunology</i> , 2024, 153, 105136.	2.3	0
8356	Microbially mediated mechanisms underlie soil carbon accrual by conservation agriculture under decade-long warming. <i>Nature Communications</i> , 2024, 15, .	12.8	2
8357	Non-negligible N ₂ O emission hotspots: Rivers impacted by ion-adsorption rare earth mining. <i>Water Research</i> , 2024, 251, 121124.	11.3	1
8358	Insights into the effects of anthropogenic activities on oil reservoir microbiome and metabolic potential. <i>New Biotechnology</i> , 2024, 79, 30-38.	4.4	1
8359	A chromosome-level genome assembly for <i>Onobrychis viciifolia</i> reveals gene copy number gain underlying enhanced proanthocyanidin biosynthesis. <i>Communications Biology</i> , 2024, 7, .	4.4	1
8360	Investigating the etiologies of non-malarial febrile illness in Senegal using metagenomic sequencing. <i>Nature Communications</i> , 2024, 15, .	12.8	0
8361	SpliceProt 2.0: A Sequence Repository of Human, Mouse, and Rat Proteoforms. <i>International Journal of Molecular Sciences</i> , 2024, 25, 1183.	4.1	0
8362	First Genome Sequence of the Microcolonial Black Fungus <i>Saxispiralis lemnorm</i> MUM 23.14: Insights into the Unique Genomic Traits of the Aeminiaceae Family. <i>Microorganisms</i> , 2024, 12, 104.	3.6	0
8363	Pervasive associations between dark septate endophytic fungi with tree root and soil microbiomes across Europe. <i>Nature Communications</i> , 2024, 15, .	12.8	2
8364	Targeted Metagenomic Databases Provide Improved Analysis of Microbiota Samples. <i>Microorganisms</i> , 2024, 12, 135.	3.6	0

#	ARTICLE	IF	CITATIONS
8365	The chromosome-scale genome of <i>Magnolia sinica</i> (Magnoliaceae) provides insights into the conservation of plant species with extremely small populations (PSESP). <i>GigaScience</i> , 2024, 13, .	6.4	0
8366	Genome sequence of the <i>Klebsiella quasipneumoniae</i> bacteriophage EKq1 with activity against <i>Klebsiella pneumoniae</i> . <i>Microbiology Resource Announcements</i> , 2024, 13, .	0.6	0
8367	Genomics and transcriptomics of the Chinese mitten crabs (<i>Eriocheir sinensis</i>). <i>Scientific Data</i> , 2023, 10, .	5.3	0
8368	Virophages Found in Viromes from Lake Baikal. <i>Biomolecules</i> , 2023, 13, 1773.	4.0	0
8369	A chromosome-level genome assembly of <i>Agave hybrid</i> NO.11648 provides insights into the CAM photosynthesis. <i>Horticulture Research</i> , 2024, 11, .	6.3	0
8371	Semi-Supervised and Incremental Sequence Analysis for Taxonomic Classification. , 2023, , .		0
8373	Strain-level diversity in sulfonamide biodegradation: adaptation of <i>Paenarthrobacter</i> to sulfonamides. <i>ISME Journal</i> , 2024, 18, .	9.8	0
8374	A chromosome-level genome assembly of the Rhus gall aphid <i>Schlechtendalia chinensis</i> provides insight into the endogenization of Parvovirus-like DNA sequences. <i>BMC Genomics</i> , 2024, 25, .	2.8	0
8375	Precision run-on sequencing (PRO-seq) for microbiome transcriptomics. <i>Nature Microbiology</i> , 2024, 9, 241-250.	13.3	0
8376	Deciphering the gut microbiome of grass carp through multi-omics approach. <i>Microbiome</i> , 2024, 12, .	11.1	0
8378	Gut microbiome and serum metabolome analyses identify <i>Bacteroides fragilis</i> as regulators of serotonin content and PRL secretion in broody geese1. <i>Journal of Integrative Agriculture</i> , 2024, , .	3.5	0
8379	Virome analysis of <i>Desmodus rotundus</i> tissue samples from the Amazon region. <i>BMC Genomics</i> , 2024, 25, .	2.8	0
8380	Potential environmental risks of field bio/non-degradable microplastic from mulching residues in farmland: Evidence from metagenomic analysis of plastisphere. <i>Journal of Hazardous Materials</i> , 2024, 465, 133428.	12.4	0
8381	Differential expression and gene correlation analyses reveal core <i>CAZymes</i> in <i>Fusarium oxysporum</i> f.sp. <i>lycopersici</i> exposed to mutagen and heat stress. <i>Journal of Phytopathology</i> , 2024, 172, .	1.0	0
8383	Draft genome sequence of a black yeast fungus <i>Exophiala xenobiotica</i> isolated from La Brea Tar Pits. <i>Microbiology Resource Announcements</i> , 2024, 13, .	0.6	0
8385	Ruminal microbiota-host crosstalks promote ruminal epithelial development in neonatal lambs with alfalfa hay introduction. <i>MSystems</i> , 2024, 9, .	3.8	0
8386	Phased genome assemblies reveal haplotype-specific genetic load in the critically endangered Chinese <i>Bahaba</i> (Teleostei, Sciaenidae). <i>Molecular Ecology</i> , 2024, 33, .	3.9	0
8387	Changes in Microbiota Composition during the Anaerobic Digestion of Macroalgae in a Three-Stage Bioreactor. <i>Microorganisms</i> , 2024, 12, 109.	3.6	0

#	ARTICLE	IF	CITATIONS
8388	Gene modelling and annotation for the Hawaiian bobtail squid, <i>Euprymna scolopes</i> . <i>Scientific Data</i> , 2024, 11, .	5.3	1
8389	Chromosome-scale assembly and gene editing of <i>Solanum americanum</i> genome reveals the basis for thermotolerance and fruit anthocyanin composition. <i>Theoretical and Applied Genetics</i> , 2024, 137, .	3.6	0
8391	Comparative genomics reveals probable adaptations for xylose use in <i>Thermoanaerobacterium saccharolyticum</i> . <i>Extremophiles</i> , 2024, 28, .	2.3	0
8393	Temporal development and potential interactions between the gut microbiome and resistome in early childhood. <i>Microbiology Spectrum</i> , 2024, 12, .	3.0	0
8395	Genome-wide analysis of the <i>Tritipyrum</i> NAC gene family and the response of TtNAC477 in salt tolerance. <i>BMC Plant Biology</i> , 2024, 24, .	3.6	0
8396	Skin microbe-dependent TSLP-ILC2 priming axis in early life is co-opted in allergic inflammation. <i>Cell Host and Microbe</i> , 2024, 32, 244-260.e11.	11.0	0
8397	Virus–prokaryote infection pairs associated with prokaryotic production in a freshwater lake. <i>MSystems</i> , 2024, 9, .	3.8	0
8398	Assessing the metabolism, phylogenomic, and taxonomic classification of the halophilic genus <i>Halarchaeum</i> . <i>FEMS Microbiology Letters</i> , 2024, 371, .	1.8	0
8399	Virome profiling of fig wasps (<i>Ceratosolen</i> spp.) reveals virus diversity spanning four realms. <i>Virology</i> , 2024, 591, 109992.	2.4	0
8400	Distinct microbial hydrogen and reductant disposal pathways explain interbreed variations in ruminant methane yield. <i>ISME Journal</i> , 2024, 18, .	9.8	0
8401	Nitrate-driven anaerobic oxidation of ethane and butane by bacteria. <i>ISME Journal</i> , 2024, 18, .	9.8	0
8402	Evaluation of Genomic Contamination Detection Tools and Influence of Horizontal Gene Transfer on Their Efficiency through Contamination Simulations at Various Taxonomic Ranks. <i>Applied Microbiology</i> , 2024, 4, 124-132.	1.6	0
8403	Novel order-level lineage of ammonia-oxidizing archaea widespread in marine and terrestrial environments. <i>ISME Journal</i> , 2024, 18, .	9.8	1
8404	Declines in ice cover are accompanied by light limitation responses and community change in freshwater diatoms. <i>ISME Journal</i> , 2024, 18, .	9.8	0
8405	Temperature, pH, and oxygen availability contributed to the functional differentiation of ancient <i>Nitrososphaeria</i> . <i>ISME Journal</i> , 2024, 18, .	9.8	0
8407	Gut microbiota reflect adaptation of cave-dwelling tadpoles to resource scarcity. <i>ISME Journal</i> , 2024, 18, .	9.8	0
8408	Nitric oxide delays the postharvest nutritional quality decline of ‘Golden Hook’ beans. <i>Food Frontiers</i> , 2024, 5, 636-655.	7.4	0
8409	Diversity of <i>Bathyarchaeia</i> viruses in metagenomes and virus-encoded CRISPR system components. <i>ISME Communications</i> , 2024, 4, .	4.2	1

#	ARTICLE	IF	CITATIONS
8412	Identification of commensal gut bacterial strains with lipogenic effects contributing to NAFLD in children. IScience, 2024, 27, 108861.	4.1	0
8413	Near chromosome-level and highly repetitive genome assembly of the snake pipefish <i>Entelurus aequoreus</i> (Syngnathiformes: Syngnathidae). GigaByte, 0, 2024, 1-13.	0.0	0
8414	Transcriptional landscape of the <scp>pMP7017</scp> megaplasmid and its impact on the <i>Bifidobacterium breve</i><scp>UCC2003</scp> transcriptome. Microbial Biotechnology, 2024, 17, .	4.2	0
8415	Draft genome sequence of <i>Wigglesworthia glossinidia</i> âœœpalpalis gambiensisâœœ isolate. Microbiology Resource Announcements, 2024, 13, .	0.6	0
8416	Comparative analysis of metagenomic classifiers for long-read sequencing datasets. BMC Bioinformatics, 2024, 25, .	2.6	1
8418	Genomic and morphological characterization of a new <i>Thiothrix</i> species from a sulfide hot spring of the Zmeinaya bay (Northern Baikal, Russia). Antonie Van Leeuwenhoek, 2024, 117, .	1.7	0
8419	<i>Helicovermis profundus</i> gen. nov., sp. nov., a novel mesophilic, asporogenous bacterium within the Clostridia isolated from a deep-sea hydrothermal vent chimney. Antonie Van Leeuwenhoek, 2024, 117, .	1.7	0
8420	Chromosome-level assembly and gene annotation of <i>Decapterus maruadsi</i> genome using Nanopore and Hi-C technologies. Scientific Data, 2024, 11, .	5.3	0
8421	Enhanced nitrate reduction in hypotrophic waters with integrated photocatalysis and biodegradation. Environmental Science and Ecotechnology, 2024, 21, 100390.	13.5	0
8423	Dynamics of soil microbial communities involved in carbon cycling along three successional forests in southern China. Frontiers in Microbiology, 0, 14, .	3.5	0
8424	Integrated omics analysis reveals the alteration of gut microbiota and fecal metabolites in <i>Cervus elaphus kansuensis</i> . Applied Microbiology and Biotechnology, 2024, 108, .	3.6	0
8425	Towards estimating the number of strains that make up a natural bacterial population. Nature Communications, 2024, 15, .	12.8	2
8426	Human milk cream alters intestinal microbiome of preterm infants: a prospective cohort study. Pediatric Research, 0, , .	2.3	1
8429	Long-term conservation tillage with reduced nitrogen fertilization intensity can improve winter wheat health via positive plantâœœmicroorganism feedback in the rhizosphere. FEMS Microbiology Ecology, 2024, 100, .	2.7	1
8430	Competitive enrichment of comammox <i>Nitrospira</i> in floccular sludge. Water Research, 2024, 251, 121151.	11.3	1
8431	Chromosomeâœœlevel genome assembly of <i>Prunella vulgaris</i> L.Âœprovides insights into pentacyclic triterpenoid biosynthesis. Plant Journal, 2024, 118, 731-752.	5.7	0
8432	Accessory genes define species-specific routes to antibiotic resistance. Life Science Alliance, 2024, 7, e202302420.	2.8	0
8433	Functional characterization of LcTPS1 and LcTPS14 explains the biosynthesis of citronellol, citronellal and linalool in <i>Lagerstroemia caudata</i> . Industrial Crops and Products, 2024, 209, 118033.	5.2	0

#	ARTICLE	IF	CITATIONS
8434	Associations Between Gut Microbial Features and Sickness Symptoms in Kidney Transplant Recipients. Biological Research for Nursing, 0, , .	1.9	0
8437	A chromosome-level genome for the nudibranch gastropod <i>Berghia stephanieae</i> helps parse clade-specific gene expression in novel and conserved phenotypes. BMC Biology, 2024, 22, .	3.8	0
8438	An in situ digital synthesis strategy for the discovery and description of ocean life. Science Advances, 2024, 10, .	10.3	0
8439	Oral microbiome associated with differential ratios of <i>Porphyromonas gingivalis</i> and <i>Streptococcus cristatus</i> . Microbiology Spectrum, 2024, 12, .	3.0	0
8441	MulAxialGO: Multi-Modal Feature-Enhanced Deep Learning Model for Protein Function Prediction. , 2023, , .		0
8443	<i>Prevotella copri</i> variants among a single host diverge in sphingolipid production. MBio, 2024, 15, .	4.1	0
8444	Comparative Transcriptome Analysis Reveals Changes in Gene Expression Associated with Anthocyanin Metabolism in <i>Begonia semperflorens</i> under Light Conditions. Horticulturae, 2024, 10, 96.	2.8	0
8446	A tradeoff evolution between acoustic fat bodies and skull muscles in toothed whales. Gene, 2024, 901, 148167.	2.2	0
8447	Metagenomic of Liver Tissue Identified at Least Two Genera of Totivirus-like Viruses in <i>Molossus molossus</i> Bats. Microorganisms, 2024, 12, 206.	3.6	0
8448	Co-evolution of gene transfer agents and their alphaproteobacterial hosts. Journal of Bacteriology, 2024, 206, .	2.2	1
8450	Dataset from RNAseq analysis of differential gene expression among developmental stages of two non-marine ostracodes. Data in Brief, 2024, 53, 110070.	1.0	0
8451	Community-scale models of microbiomes: Articulating metabolic modelling and metagenome sequencing. Microbial Biotechnology, 2024, 17, .	4.2	1
8452	A systematic screen for co-option of transposable elements across the fungal kingdom. Mobile DNA, 2024, 15, .	3.6	0
8453	Alkali-Activated Foams Coated with Colloidal Ag for Point-of-Use Water Disinfection. ACS ES&T Water, 2024, 4, 687-697.	4.6	1
8457	Virome analysis of New Zealand bats reveals cross-species viral transmission among the <i>Coronaviridae</i> . Virus Evolution, 2024, 10, .	4.9	0
8458	Metatranscriptomic profiles reveal the biotransformation potential of azithromycin in river periphyton. Water Research, 2024, 251, 121140.	11.3	0
8459	NeuralBeds: Neural embeddings for efficient DNA data compression and optimized similarity search. Computational and Structural Biotechnology Journal, 2024, 23, 732-741.	4.1	0
8461	Metagenomics reveals differences in the composition of bacterial antimicrobial resistance and antibiotic resistance genes in pasteurized yogurt and probiotic bacteria yogurt from China. Journal of Dairy Science, 2024, , .	3.4	0

#	ARTICLE	IF	CITATIONS
8463	Direct observations of microbial community succession on sinking marine particles. ISME Journal, 2024, 18, .	9.8	0
8464	Metagenomics reveals the temporal dynamics of the rumen resistome and microbiome in goat kids. Microbiome, 2024, 12, .	11.1	0
8465	Uptake and effect of carboxyl-modified polystyrene microplastics on cotton plants. Journal of Hazardous Materials, 2024, 466, 133581.	12.4	0
8466	Microbiologic surveys for Baijiu fermentation are affected by experimental design. International Journal of Food Microbiology, 2024, 413, 110588.	4.7	0
8467	T4SEpp: A pipeline integrating protein language models to predict bacterial type IV secreted effectors. Computational and Structural Biotechnology Journal, 2024, 23, 801-812.	4.1	0
8468	ASAP: a platform for gene functional analysis in Angelica sinensis. BMC Genomics, 2024, 25, .	2.8	0
8469	Metagenomic insights into the dynamic degradation of brown algal polysaccharides by kelp-associated microbiota. Applied and Environmental Microbiology, 2024, 90, .	3.1	0
8470	The Gut Microbiome Correlated to Chemotherapy Efficacy in Diffuse Large B-Cell Lymphoma Patients. Hematology Reports, 2024, 16, 63-75.	0.8	0
8471	Transcriptome profiling of the gills to air exposure in mud crab <i>Scylla paramamosain</i>. Israeli Journal of Aquaculture - Bamidgah, 2024, 76, .	0.0	0
8473	Unraveling the phylogenomic diversity of Methanomassiliicoccales and implications for mitigating ruminant methane emissions. Genome Biology, 2024, 25, .	8.8	0
8474	Hiding in plain sight: The discovery of complete genomes of 11 hypothetical spindle-shaped viruses that putatively infect mesophilic ammonia-oxidizing archaea. Environmental Microbiology Reports, 2024, 16, .	2.4	1
8477	Impact of Anthropogenic Activities on Microbial Community Structure in Riverbed Sediments of East Kazakhstan. Microorganisms, 2024, 12, 246.	3.6	0
8478	Three Rounds of Read Correction Significantly Improve Eukaryotic Protein Detection in ONT Reads. Microorganisms, 2024, 12, 247.	3.6	0
8479	Metagenomics reveals microbial communities and functional differences during chili pepper (<i>Capsicum frutescens</i> L.) natural fermentation: Effects of brines and containers. Food Frontiers, 2024, 5, 753-770.	7.4	0
8480	Chromosome-level genome of spider Pardosa pseudoannulata and cuticle protein genes in environmental stresses. Scientific Data, 2024, 11, .	5.3	0
8482	<sc>GH136</sc>-encoding gene (<sc><i>per</i>B</sc>) is involved in gut colonization and persistence by <i>Bifidobacterium bifidum</i> <sc>PRL2010</sc>. Microbial Biotechnology, 2024, 17, .	4.2	1
8485	Rhizosphere assembly alters along a chronosequence in the Hallstätter glacier forefield (Dachstein,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	2.7	0
8486	Role of genes encoding microbial carbohydrate-active enzymes in the accumulation and dynamics of organic carbon in subtropical forest soils. Science of the Total Environment, 2024, 918, 170295.	8.0	0

#	ARTICLE	IF	CITATIONS
8487	Metatranscriptomic Sequencing of Medically Important Mosquitoes Reveals Extensive Diversity of RNA Viruses and Other Microbial Communities in Western Australia. <i>Pathogens</i> , 2024, 13, 107.	2.8	0
8488	The Mediterranean mussel <i>Mytilus galloprovincialis</i> : a novel model for developmental studies in mollusks. <i>Development (Cambridge)</i> , 2024, 151, .	2.5	0
8489	Chromosome-level genome assembly of <i>Hippophae gyantsensis</i> . <i>Scientific Data</i> , 2024, 11, .	5.3	0
8490	Characterization and analysis of multi-organ full-length transcriptomes in <i>Sphaeropteris brunoniana</i> and <i>Alsophila latebrosa</i> highlight secondary metabolism and chloroplast RNA editing pattern of tree ferns. <i>BMC Plant Biology</i> , 2024, 24, .	3.6	0
8491	Microorganisms oxidize glucose through distinct pathways in permeable and cohesive sediments. <i>ISME Journal</i> , 2024, 18, .	9.8	0
8492	Numerical stability of DeepGOPlus inference. <i>PLoS ONE</i> , 2024, 19, e0296725.	2.5	0
8493	Morphological, phylogenetic, and genomic evidence reveals the causal agent of thread blight disease of cacao in Peru is a new species of <i>Marasmius</i> in the section <i>Neosessiles</i> , <i>Marasmius infestans</i> sp. nov.. <i>F1000Research</i> , 0, 12, 1327.	1.6	0
8495	Exploring virus-host-environment interactions in a chemotrophic-based underground estuary. <i>Environmental Microbiomes</i> , 2024, 19, .	5.0	0
8496	Genome-centric analyses of 165 metagenomes show that mobile genetic elements are crucial for the transmission of antimicrobial resistance genes to pathogens in activated sludge and wastewater. <i>Microbiology Spectrum</i> , 2024, 12, .	3.0	0
8498	Genetic constraints in genes exhibiting splicing plasticity in facultative diapause. <i>Heredity</i> , 2024, 132, 142-155.	2.6	1
8499	Prokaryotic Microbial Diversity Analysis and Preliminary Prediction of Metabolic Function in Salt Lakes on the Qinghai-Tibet Plateau. <i>Water (Switzerland)</i> , 2024, 16, 451.	2.7	0
8500	Lignite-steel slag constructed wetland with multi-functionality and effluent reuse. <i>Journal of Environmental Management</i> , 2024, 353, 120183.	7.8	1
8501	Heat Shock Protein Genes Affect the Rapid Cold Hardening Ability of Two Invasive Tephritids. <i>Insects</i> , 2024, 15, 90.	2.2	0
8502	Integrated Transcriptomics and Metabolomics Analysis Reveals the Effects of Cutting on the Synthesis of Flavonoids and Saponins in Chinese Herbal Medicine <i>Astragalus mongholioides</i> . <i>Metabolites</i> , 2024, 14, 97.	2.9	0
8503	Functional characterization of the <i>dbu</i> locus for D-branched-chain amino acid catabolism in <i>Pseudomonas putida</i> . <i>Applied and Environmental Microbiology</i> , 2024, 90, .	3.1	0
8504	Metabolic shifts in glycogen-accumulating organisms: Exploring carbon and phosphorus dynamics under two distinct phosphorus limitation modes. <i>Journal of Cleaner Production</i> , 2024, 443, 141042.	9.3	0
8505	Host-gut microbiota interactions shape parasite infections in farmed Atlantic salmon. <i>MSystems</i> , 2024, 9, .	3.8	0
8506	Effects of sublethal fipronil exposure on cross-generational functional responses and gene expression in <i>Binodoxys communis</i> . <i>Environmental Science and Pollution Research</i> , 0, , .	5.3	0

#	ARTICLE	IF	CITATIONS
8507	GeNLP: a web tool for NLP-based exploration and prediction of microbial gene function. Bioinformatics, 2024, 40, .	4.1	0
8508	ContScout: sensitive detection and removal of contamination from annotated genomes. Nature Communications, 2024, 15, .	12.8	0
8510	Metagenomic exploration of Andaman region of the Indian Ocean. Scientific Reports, 2024, 14, .	3.3	0
8511	Draft genome sequence of <i>Dietzia</i> sp. strain CH92 isolated from oil reservoir. Microbiology Resource Announcements, 2024, 13, .	0.6	0
8512	Infant age inversely correlates with gut carriage of resistance genes, reflecting modifications in microbial carbohydrate metabolism during early life. , 2024, 3, .		0
8513	Unveiling CRESS DNA Virus Diversity in Oysters by Virome. Viruses, 2024, 16, 228.	3.3	0
8515	Genome report: chromosome-scale genome assembly of the West Indian fruit fly <i>Anastrepha obliqua</i> (Diptera: Tephritidae). G3: Genes, Genomes, Genetics, 2024, 14, .	1.8	0
8517	Mechanism of 2- <i>fucosyllactose</i> degradation by human-associated <i>Akkermansia</i> . Journal of Bacteriology, 2024, 206, .	2.2	0
8518	Marine picoplankton metagenomes and MAGs from eleven vertical profiles obtained by the Malaspina Expedition. Scientific Data, 2024, 11, .	5.3	0
8519	Biotic interactions between benthic infauna and aerobic methanotrophs mediate methane fluxes from coastal sediments. ISME Journal, 2024, 18, .	9.8	0
8520	How microbial communities shape peatland carbon dynamics: New insights and implications. Soil Biology and Biochemistry, 2024, 191, 109345.	8.8	0
8521	Metagenomic insight into the pathogenic-related characteristics and resistome profiles within microbiome residing on the Angkor sandstone monuments in Cambodia. Science of the Total Environment, 2024, 918, 170402.	8.0	0
8522	Analysis of the gut microbiome associated to PVC biodegradation in yellow mealworms. Ecotoxicology and Environmental Safety, 2024, 272, 116046.	6.0	0
8523	The genome of the blind bee louse fly reveals deep convergences with its social host and illuminates <i>Drosophila</i> origins. Current Biology, 2024, 34, 1122-1132.e5.	3.9	1
8524	Genomic analysis of <i>Ralstonia pickettii</i> reveals the genetic features for potential pathogenicity and adaptive evolution in drinking water. Frontiers in Microbiology, 0, 14, .	3.5	0
8525	FEEDS, the Food waste biopEptiDe claSsifier: From microbial genomes and substrates to biopeptides function. Current Research in Biotechnology, 2024, 7, 100186.	3.7	0
8526	Comprehensive whole-genome sequencing reveals genetic characteristics of <i>Colletotrichum fruticola</i> (Nara gc5) the causative organism of circular leaf spot disease of rubber (<i>Hevea</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf60 97 Td (
8528	Protein language models meet reduced amino acid alphabets. Bioinformatics, 2024, 40, .	4.1	0

#	ARTICLE	IF	CITATIONS
8529	Human pangenome analysis of sequences missing from the reference genome reveals their widespread evolutionary, phenotypic, and functional roles. <i>Nucleic Acids Research</i> , 2024, 52, 2212-2230.	14.5	0
8531	Contribution of sulfur-containing precursors to release of hydrogen sulfide in sludge composting. <i>Journal of Environmental Management</i> , 2024, 353, 120195.	7.8	0
8532	Significance of phosphorus deficiency for the mitigation of mercury toxicity in the Robinia pseudoacacia L. rhizobia symbiotic association. <i>Journal of Hazardous Materials</i> , 2024, 467, 133717.	12.4	0
8533	Loss of symbiotic and increase of virulent bacteria through microbial networks in Lynch syndrome colon carcinogenesis. <i>Frontiers in Oncology</i> , 0, 13, .	2.8	0
8534	High-quality genomes of Bombax ceiba and Ceiba pentandra provide insights into the evolution of Malvaceae species and differences in their natural fiber development. <i>Plant Communications</i> , 2024, , 100832.	7.7	0
8535	Single-cell transcriptomic analysis reveals genome evolution in predatory litostomatean ciliates. <i>European Journal of Protistology</i> , 2024, 93, 126062.	1.5	0
8536	Stability of gut microbiome after COVID-19 vaccination in healthy and immuno-compromised individuals. <i>Life Science Alliance</i> , 2024, 7, e202302529.	2.8	0
8537	Water quality drives the reconfiguration of riverine planktonic microbial food webs. <i>Environmental Research</i> , 2024, 249, 118379.	7.5	0
8540	Effect of Isopropyl Ester of Hydroxy Analogue of Methionine on Rumen Microbiome, Active Enzymes, and Protein Metabolism Pathways of Yak. <i>Fermentation</i> , 2024, 10, 94.	3.0	0
8542	Identification of drought stress genes expressed in Jatropha curcas by using RNA sequencing. <i>AIP Conference Proceedings</i> , 2024, , .	0.4	0
8543	Australian terrestrial environments harbour extensive RNA virus diversity. <i>Virology</i> , 2024, 593, 110007.	2.4	0
8544	Enhancing transcriptome analysis in medicinal plants: multiple unigene sets in Astragalus membranaceus. <i>Frontiers in Plant Science</i> , 0, 15, .	3.6	0
8545	Five Species of Wild Freshwater Sport Fish in Wisconsin, USA, Reveal Highly Diverse Viromes. <i>Pathogens</i> , 2024, 13, 150.	2.8	0
8546	Long read genome assembly of <i>Automeris io</i> (Lepidoptera: Saturniidae) an emerging model for the evolution of deimatic displays. <i>G3: Genes, Genomes, Genetics</i> , 2024, 14, .	1.8	0
8547	Influence of weeding methods on rhizosphere soil and root endophytic microbial communities in tea plants. <i>Frontiers in Microbiology</i> , 0, 15, .	3.5	0
8548	Preliminary exploratory research on the application value of oral and intestinal meta-genomics in predicting subjects' occupations—A case study of the distinction between students and migrant workers. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	0
8550	Molecular mechanism of <i>Serratia marcescens</i> Bizio infection in <i>Reticulitermes chinensis</i> Snyder based on full-length SMRT transcriptome sequencing. <i>Bulletin of Entomological Research</i> , 0, , 1-13.	1.0	0
8551	Analysis of insecticide resistance and <i>de novo</i> transcriptome assembly of resistance associated genes in the European grapevine moth, <i>Lobesia botrana</i> (Lepidoptera: Tortricidae). <i>Bulletin of Entomological Research</i> , 2024, 114, 88-98.	1.0	0

#	ARTICLE	IF	CITATIONS
8552	Microbial-derived imidazole propionate links the heart failure-associated microbiome alterations to disease severity. <i>Genome Medicine</i> , 2024, 16, .	8.2	0
8553	Biogenic manganese oxides promote metal(loid) remediation by shaping microbial communities in biological aqua crust. <i>Water Research</i> , 2024, 253, 121287.	11.3	1
8554	Microbial community succession of cow manure and tobacco straw composting. , 0, 3, .		0
8555	Snowprint: a predictive tool for genetic biosensor discovery. <i>Communications Biology</i> , 2024, 7, .	4.4	0
8556	Assessing microbial diversity in Yellowstone National Park hot springs using a field deployable automated nucleic acid extraction system. <i>Frontiers in Ecology and Evolution</i> , 0, 12, .	2.2	0
8558	The short-term effect of simulated acid rain and nitrogen deposition on the soil microbial functional profile targeting C, N, and P cycling. <i>Applied Soil Ecology</i> , 2024, 197, 105327.	4.3	0
8559	Antibiotic resistance genes and mobile genetic elements in different rivers: The link with antibiotics, microbial communities, and human activities. <i>Science of the Total Environment</i> , 2024, 919, 170788.	8.0	1
8560	Metagenomic insights into the impact of litter from poultry Concentrated Animal Feeding Operations (CAFOs) to adjacent soil and water microbial communities. <i>Science of the Total Environment</i> , 2024, 920, 170772.	8.0	0
8561	Unravelling the main immune repertoire of <i>Paracentrotus lividus</i> following <i>Vibrio anguillarum</i> bath challenge. <i>Fish and Shellfish Immunology</i> , 2024, 147, 109431.	3.6	0
8562	Distribution patterns and functional diversity of DNA viruses determined by ecological niches in huge river ecosystems. <i>Virology</i> , 2024, 593, 110015.	2.4	0
8564	Nutrient structure dynamics and microbial communities at the waterâ€sediment interface in an extremely acidic lake in northern Patagonia. <i>Frontiers in Microbiology</i> , 0, 15, .	3.5	0
8565	Pan-transcriptomic analysis reveals alternative splicing control of cold tolerance in rice. <i>Plant Cell</i> , 0, , .	6.6	0
8566	From germline genome to highly fragmented somatic genome: genome-wide DNA rearrangement during the sexual process in ciliated protists. <i>Marine Life Science and Technology</i> , 2024, 6, 31-49.	4.6	1
8567	Microbial antagonistic mechanisms of Hg(II) and Se(IV) in efficient wastewater treatment using granular sludge. <i>Water Research</i> , 2024, 253, 121311.	11.3	0
8568	A high-quality genome assembly of the waterlily aphid <i>Rhopalosiphum nymphaeae</i> . <i>Scientific Data</i> , 2024, 11, .	5.3	0
8569	Gut Microbiota Disorders in Obesity-Associated Benign Prostatic Hyperplasia in Rats. <i>Biochemical Genetics</i> , 0, , .	1.7	0
8570	Isolation of potentially novel species expands the genomic and functional diversity of Lachnospiraceae. , 2024, 3, .		0
8571	Utilizing a Metagenome Assembled Genome Approach Revealed Further Insights into Microbially Mediated Heavy-Metal Resistance in Soils from a Former Nuclear Materials Production Facility. <i>Applied Microbiology</i> , 2024, 4, 376-389.	1.6	0

#	ARTICLE	IF	CITATIONS
8572	Complete genome sequences of <i>Rhizobium</i> sp. strain SL42 and <i>Hydrogenophaga</i> sp. strain SL48, microsymbionts of <i>Amphicarpaea bracteata</i> . , 0, 3, .		0
8573	Protein function prediction as approximate semantic entailment. <i>Nature Machine Intelligence</i> , 2024, 6, 220-228.	16.0	0
8574	Novel insights into the rhizosphere and seawater microbiome of <i>Zostera marina</i> in diverse mariculture zones. <i>Microbiome</i> , 2024, 12, .	11.1	0
8575	Whole Genome Duplication Events Likely Contributed to the Aquatic Adaptive Evolution of <i>Parkerioideae</i> . <i>Plants</i> , 2024, 13, 521.	3.5	0
8576	Spatiotemporal Changes of Antibiotic Resistance, Potential Pathogens, and Health Risk in Kindergarten Dust. <i>Environmental Science & Technology</i> , 2024, 58, 3919-3930.	10.0	0
8577	Long non-coding RNAs mediate fish gene expression in response to ocean acidification. <i>Evolutionary Applications</i> , 2024, 17, .	3.1	0
8578	Nitrogen and phosphorus limitations promoted bacterial nitrate metabolism and propagation of antibiotic resistome in the phycosphere of <i>Auxenochlorella pyrenoidosa</i> . <i>Journal of Hazardous Materials</i> , 2024, 468, 133786.	12.4	0
8579	Regulation of wheat growth by soil multifunctionality and metagenomic-based microbial functional profiles under mulching treatments. <i>Science of the Total Environment</i> , 2024, 920, 170881.	8.0	0
8580	Sponges on shifting reefs: holobionts show similar molecular and physiological responses to coral versus macroalgal food. <i>Frontiers in Marine Science</i> , 0, 11, .	2.5	0
8581	Ammonia stress-induced heat shock factor 1 enhances white spot syndrome virus infection by targeting the interferon-like system in shrimp. <i>MBio</i> , 2024, 15, .	4.1	0
8583	A genome and gene catalog of the aquatic microbiomes of the Tibetan Plateau. <i>Nature Communications</i> , 2024, 15, .	12.8	0
8584	Distinct regulatory networks control toxin gene expression in elapid and viperid snakes. <i>BMC Genomics</i> , 2024, 25, .	2.8	0
8585	Microbiological risk assessment and resistome analysis from shotgun metagenomics of bovine colostrum microbiome. <i>Saudi Journal of Biological Sciences</i> , 2024, 31, 103957.	3.8	0
8586	Sesame bacterial wilt significantly alters rhizosphere soil bacterial community structure, function, and metabolites in continuous cropping systems. <i>Microbiological Research</i> , 2024, 282, 127649.	5.3	0
8587	The genome of a globally invasive passerine, the common myna, <i>Acridotheres tristis</i> . <i>DNA Research</i> , 2024, 31, .	3.4	0
8588	Genome analysis of three isolates of <i>Stemphylium lycopersici</i> differ in their virulence and sporulation ability: Identification of effectors, pathogenesis and virulence factors. <i>Plant Pathology</i> , 2024, 73, 1156-1168.	2.4	0
8589	Microbiology of <i>Big Soda Lake</i> , a multi-extreme meromictic volcanic crater lake in the <i>Nevada</i> desert. <i>Environmental Microbiology</i> , 2024, 26, .	3.8	0
8590	Biochemical, molecular, and physiological assessments of crude oil dietary exposure in sub-adult red drum (<i>Sciaenops ocellatus</i>). <i>Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology</i> , 2024, 278, 109864.	2.6	0

#	ARTICLE	IF	CITATIONS
8591	Metabolic analysis of the CAZy class glycosyltransferases in rhizospheric soil fungione of the plant species <i>Moringa oleifera</i> . Saudi Journal of Biological Sciences, 2024, 31, 103956.	3.8	0
8592	Paleocene origin of a streamlined digestive symbiosis in leaf beetles. Current Biology, 2024, 34, 1621-1634.e9.	3.9	0
8593	The gut microbiome regulates the clinical efficacy of sulfasalazine therapy for IBD-associated spondyloarthritis. Cell Reports Medicine, 2024, 5, 101431.	6.5	0
8594	Shotgun Metagenomic Approaches. , 2024, , 43-54.		0
8595	The Genome of <i>Plasmodium gonderi</i> : Insights into the Evolution of Human Malaria Parasites. Genome Biology and Evolution, 2024, 16, .	2.5	0
8596	Residue quality drives SOC sequestration by altering microbial taxonomic composition and ecophysiological function in desert ecosystem. Environmental Research, 2024, 250, 118518.	7.5	0
8597	Characterization of the genomic sequence of a circo-like virus and of three chaphamaparvoviruses detected in mute swan (<i>Cygnus olor</i>). Microbiology Resource Announcements, 2024, 13, .	0.6	0
8598	Human papillomavirus negative high grade cervical lesions and cancers: Suggested guidance for HPV testing quality assurance. Journal of Clinical Virology, 2024, 171, 105657.	3.1	0
8599	Efficient encoding of large antigenic spaces by epitope prioritization with Dolphyn. Nature Communications, 2024, 15, .	12.8	0
8600	Effects of Glucagon-Like Peptide-1 Receptor Agonists on Gut Microbiota in Dehydroepiandrosterone-Induced Polycystic Ovary Syndrome Mice: Compared Evaluation of Liraglutide and Semaglutide Intervention. Diabetes, Metabolic Syndrome and Obesity: Targets and Therapy, 0, Volume 17, 865-880.	2.4	0
8601	Immunosuppressive role of <i>BDNF</i> in therapy-induced neuroendocrine prostate cancer. Molecular Oncology, 0, , .	4.6	0
8602	High <i>Frankia</i> abundance and low diversity of microbial community are associated with nodulation specificity and stability of sea buckthorn root nodule. Frontiers in Plant Science, 0, 15, .	3.6	0
8603	Aberrant splicing of a nicotinic acetylcholine receptor alpha 6 subunit is associated with spinosad tolerance in the thrips predator <i>Orius laevigatus</i> . Pesticide Biochemistry and Physiology, 2024, 200, 105837.	3.6	0
8604	Chromosome-level genome assembly of the silver pomfret <i>Pampus argenteus</i> . Scientific Data, 2024, 11, .	5.3	0
8605	Multi-omics reveal mechanisms of high enteral starch diet mediated colonic dysbiosis via microbiome-host interactions in young ruminant. Microbiome, 2024, 12, .	11.1	0
8606	PHDtools: A platform for pathogen detection and multi-dimensional genetic signatures decoding to realize pathogen genomics data analyses online. Gene, 2024, 909, 148306.	2.2	0
8607	EcoGenoRisk: Developing a computational ecological risk assessment tool for synthetic biology. Environmental Pollution, 2024, 346, 123647.	7.5	0
8608	Perception of the Biocontrol Potential and Palmitic Acid Biosynthesis Pathway of <i>Bacillus subtilis</i> H2 through Merging Genome Mining with Chemical Analysis. Journal of Agricultural and Food Chemistry, 2024, 72, 4834-4848.	5.2	0

#	ARTICLE	IF	CITATIONS
8609	Classic human astrovirus 4, 8, MLBâ€³, and likely new genotype 5 sublineage in stool samples of children in Nigeria. <i>Journal of Medical Virology</i> , 2024, 96, .	5.0	0
8610	Integrative transcriptome and metabolome analysis reveals the discrepancy in the accumulation of active ingredients between <i>Lycium barbarum</i> cultivars. <i>Planta</i> , 2024, 259, .	3.2	0
8611	Time-shifted expression of acetoclastic and methylotrophic methanogenesis by a single <i>Methanosarcina</i> genomospecies predominates the methanogen dynamics in Philippine rice field soil. <i>Microbiome</i> , 2024, 12, .	11.1	0
8612	Endophytic fungi as a potential source of anti-cancer drug. <i>Archives of Microbiology</i> , 2024, 206, .	2.2	0
8613	In situ membrane separation drives nitrous oxide enrichment from nitrate denitrification for energy recovery. <i>Journal of Water Process Engineering</i> , 2024, 59, 105064.	5.6	0
8614	Extreme precipitation alters soil nitrogen cycling related microbial community in karst abandoned farmland. <i>Applied Soil Ecology</i> , 2024, 197, 105345.	4.3	0
8617	An historical â€œwreckâ€ A transcriptome assembly of the naval shipworm, <i>Teredo navalis</i> Linnaeus, 1978. <i>Marine Genomics</i> , 2024, 74, 101097.	1.1	0
8618	Uncovering the Role of Hydroxycinnamoyl Transferase in Boosting Chlorogenic Acid Accumulation in <i>Carthamus tinctorius</i> Cells under Methyl Jasmonate Elicitation. <i>International Journal of Molecular Sciences</i> , 2024, 25, 2710.	4.1	0
8619	Strain-Specific Anti-Inflammatory Effects of <i>Faecalibacterium prausnitzii</i> Strain KBL1027 in Koreans. <i>Probiotics and Antimicrobial Proteins</i> , 0, , .	3.9	0
8620	Exploring the resistome and virulome in major sequence types of <i>Acinetobacter baumannii</i> genomes: Correlations with genome divergence and sequence types. <i>Infection, Genetics and Evolution</i> , 2024, 119, 105579.	2.3	0
8622	Screening potential biomarkers associated with insulin resistance in high-fat diet-fed mice by integrating metagenomics and untargeted metabolomics. <i>Microbiology Spectrum</i> , 2024, 12, .	3.0	0
8623	Possible Spreading of SARS-CoV-2 from Humans to Captive Non-Human Primates in the Peruvian Amazon. <i>Animals</i> , 2024, 14, 732.	2.3	0
8624	Using Deep Learning for the Taxonomic Classification of Microbial Sequences. , 2024, 19, 8-14.		0
8625	Genome assembly provides insights into the genome evolution of <i>Baccaurea ramiflora</i> Lour.. <i>Scientific Reports</i> , 2024, 14, .	3.3	0
8626	Deficient butyrate metabolism in the intestinal microbiome is a potential risk factor for recurrent kidney stone disease. <i>Urolithiasis</i> , 2024, 52, .	2.0	0
8627	The Rhizosphere Functional Microbial Community: A Key Driver of Phosphorus Utilization Efficiency in Karst Forest Plants. <i>Forests</i> , 2024, 15, 453.	2.1	0
8628	A Distinct <i>Arabidopsis</i> Latent Virus 1 Isolate Was Found in Wild <i>Brassica hirta</i> Plants and Bees, Suggesting the Potential Involvement of Pollinators in Virus Spread. <i>Plants</i> , 2024, 13, 671.	3.5	0
8629	A metagenomic catalog of the early-life human gut virome. <i>Nature Communications</i> , 2024, 15, .	12.8	0

#	ARTICLE	IF	CITATIONS
8630	Host adaptive radiation is associated with rapid virus diversification and cross-species transmission in African cichlid fishes. <i>Current Biology</i> , 2024, 34, 1247-1257.e3.	3.9	0
8631	Detecting and characterizing new endofungal bacteria in new hosts: <i>Pandora</i> sputorum and <i>Mycetohabitans endofungorum</i> in <i>Rhizopus arrhizus</i> . <i>Frontiers in Microbiology</i> , 0, 15, .	3.5	0
8632	Comparative genomics reveals distinct diversification patterns among LysR-type transcriptional regulators in the ESKAPE pathogen <i>Pseudomonas aeruginosa</i> . <i>Microbial Genomics</i> , 2024, 10, .	2.0	0
8633	Viral potential to modulate microbial methane metabolism varies by habitat. <i>Nature Communications</i> , 2024, 15, .	12.8	0
8634	Red pandas with different diets and environments exhibit different gut microbial functional composition and capacity. <i>Integrative Zoology</i> , 0, , .	2.6	0
8635	Altered microbial bile acid metabolism exacerbates T cell-driven inflammation during graft-versus-host disease. <i>Nature Microbiology</i> , 2024, 9, 614-630.	13.3	0
8636	Seagrass-mediated rhizosphere redox gradients are linked with ammonium accumulation driven by diazotrophs. <i>Microbiology Spectrum</i> , 2024, 12, .	3.0	0
8637	Body size mediates the functional potential of soil organisms by diversity and community assembly across soil aggregates. <i>Microbiological Research</i> , 2024, 282, 127669.	5.3	0
8638	Identification and molecular characterization of a novel totivirus from <i>Mangifera indica</i> . <i>Archives of Virology</i> , 2024, 169, .	2.1	0
8639	A Synthetic Microbiome Based on Dominant Microbes in Wild Rice Rhizosphere to Promote Sulfur Utilization. <i>Rice</i> , 2024, 17, .	4.0	0
8640	<i>Fluctibacter corallii</i> gen. nov., sp. nov., isolated from the coral <i>Montipora capitata</i> on a reef in Kāneʻohe Bay, Oʻahu, Hawaiʻi, reclassification of <i>Aestuariibacter halophilus</i> as <i>Fluctibacter halophilus</i> comb. nov., and <i>Paraglaciecola oceanifecundans</i> as a later heterotypic synonym of <i>Paraglaciecola agarilytica</i> . <i>Antonie Van Leeuwenhoek</i> , 2024, 117, .	1.7	0
8641	Metabolomic and transcriptomic analysis of bitter compounds in <i>Dendrocalamopsis oldhamii</i> shoots. <i>Journal of Food Composition and Analysis</i> , 2024, 130, 106140.	3.9	0
8642	Ploidy variation on gene differential expression in cowpea. <i>Ciencia Rural</i> , 2024, 54, .	0.5	0
8643	In Silico Screening of Bacteriocin Gene Clusters within a Set of Marine Bacillota Genomes. <i>International Journal of Molecular Sciences</i> , 2024, 25, 2566.	4.1	0
8644	Comparative transcriptome and metabolome analysis revealed diversity in the response of resistant and susceptible rose (<i>Rosa hybrida</i>) varieties to <i>Marssonina rosae</i> . <i>Frontiers in Plant Science</i> , 0, 15, .	3.6	0
8645	Diagnosing and reintegrating traceability of infectious diseases via metagenomic next-generation sequencing: Study of a severe case of <i>Rickettsia japonica</i> infection. , 2024, 3, 100094.		0
8646	A high-quality chromosomal-level reference genome of <i>Dendrobium nobile</i> Lindl. provides new insights into the biosynthesis and accumulation of picrotoxane-type sesquiterpenoid alkaloids. <i>Industrial Crops and Products</i> , 2024, 211, 118243.	5.2	0
8649	Study on somatic embryogenesis of <i>cinnamomum camphora</i> based on transcriptome sequencing. <i>Revista Brasileira De Botanica</i> , 0, , .	1.3	0

#	ARTICLE	IF	CITATIONS
8650	Tips and tools to obtain and assess mosquito viromes. Archives of Microbiology, 2024, 206, .	2.2	0
8651	Early-life ruminal microbiome-derived indole-3-carboxaldehyde and prostaglandin D2 are effective promoters of rumen development. Genome Biology, 2024, 25, .	8.8	0
8652	Diverse plasmid systems and their ecology across human gut metagenomes revealed by PlasX and MobMess. Nature Microbiology, 2024, 9, 830-847.	13.3	0
8653	Integrated Metagenomics and 15N Isotope Tracing Reveal the Mechanisms Through which the Nitrogen-Planting Density Interaction Impacts Rice Root Nitrogen Uptake Efficiency. Journal of Soil Science and Plant Nutrition, 0, , .	3.4	0
8654	Identification of plantsâ€™ functional counterpart of the metazoan mediator of DNA Damage checkpoint 1. EMBO Reports, 2024, 25, 1936-1961.	4.5	0
8655	Exploring Cereal Metagenomics: Unravelling Microbial Communities for Improved Food Security. Microorganisms, 2024, 12, 510.	3.6	0
8656	Exploring the dynamics of antibiotic resistome on plastic debris traveling from the river to the sea along a representative estuary based on field sequential transfer incubations. Science of the Total Environment, 2024, 923, 171464.	8.0	0
8657	Chromosome-scale genome assemblies of Himalopsyche anomala and Eubasilissa splendida (Insecta: Tj ETQq1 1 0,784314 rgBT /Overlo	5.3	0
8658	To what extent do water reuse treatments reduce antibiotic resistance indicators? A comparison of two full-scale systems. Water Research, 2024, 254, 121425.	11.3	0
8659	Genome evolution and divergence in cis-regulatory architecture is associated with condition-responsive development in horned dung beetles. PLoS Genetics, 2024, 20, e1011165.	3.5	0
8660	Bacterial hypothetical proteins may be of functional interest. , 0, 3, .		0
8661	Rubisco is evolving for improved catalytic efficiency and CO ₂ assimilation in plants. Proceedings of the National Academy of Sciences of the United States of America, 2024, 121, .	7.1	0
8662	Discovery and characterization of novel DNA viruses in <i>Apis mellifera</i> : expanding the honey bee virome through metagenomic analysis. MSysystems, 2024, 9, .	3.8	0
8664	Forty-nine metagenomic-assembled genomes from an aquatic virome expand Caudoviricetes by 45 potential new families and the newly uncovered Gossevirus of Bamfordvirae. Journal of General Virology, 2024, 105, .	2.9	0
8665	Transcriptome analysis of genes involved in the pathogenesis mechanism of potato virus Y in potato cultivar Youjin. Frontiers in Microbiology, 0, 15, .	3.5	0
8666	The Idesia polycarpa genome provides insights into its evolution and oil biosynthesis. Cell Reports, 2024, 43, 113909.	6.4	0
8668	Comprehensive profiling of antibiotic resistance genes in diverse environments and novel function discovery. , 2024, 2, 100054.		0
8669	Seasonal and geographical impact on the Irish raw milk microbiota correlates with chemical composition and climatic variables. MSysystems, 2024, 9, .	3.8	0

#	ARTICLE	IF	CITATIONS
8671	Pod-shattering characteristic differences between shattering-resistant and shattering-susceptible common vetch accessions are associated with lignin biosynthesis. <i>Journal of Integrative Agriculture</i> , 2024, , .	3.5	0
8672	Graphene promotes the growth of <i>Vigna angularis</i> by regulating the nitrogen metabolism and photosynthesis. <i>PLoS ONE</i> , 2024, 19, e0297892.	2.5	0
8673	Do bed bugs transmit human viruses, or do humans spread bed bugs and their viruses? A worldwide survey of the bed bug RNA virosphere. <i>Virus Research</i> , 2024, 343, 199349.	2.2	0
8674	Comparative analysis of the vaginal bacteriome and virome in healthy women living in high-altitude and sea-level areas. <i>European Journal of Medical Research</i> , 2024, 29, .	2.2	0
8675	baCLIFE: a user-friendly computational workflow for genome analysis and prediction of lifestyle-associated genes in bacteria. <i>Nature Communications</i> , 2024, 15, .	12.8	0
8676	Performance evaluation and metagenomic analysis of sequencing batch reactor under transient 2,4,6-trichlorophenol shock. <i>Journal of Hazardous Materials</i> , 2024, 469, 133983.	12.4	0
8677	Application of computation in the study of biosynthesis of phytochemicals. , 2024, , 321-355.		0
8679	Multi-omics reveals the mechanism of rumen microbiome and its metabolome together with host metabolome participating in the regulation of milk production traits in dairy buffaloes. <i>Frontiers in Microbiology</i> , 0, 15, .	3.5	0
8680	Quantification of microbially induced soil N ₂ O emissions by an inhibitory cocktail in mountain forest ecosystems. <i>Geoderma</i> , 2024, 443, 116835.	5.1	0
8681	Whole-genome sequencing and analysis of <i>Chryseobacterium arthrosphaerae</i> from <i>Rana nigromaculata</i> . <i>BMC Microbiology</i> , 2024, 24, .	3.3	0
8682	High-quality draft genome of Gammaproteobacterial SUP05 cluster from non-buoyant hydrothermal plumes of ultraslow spreading Gakkel Ridge (Central Arctic Ocean). <i>Microbiology Resource Announcements</i> , 2024, 13, .	0.6	0
8683	Metagenomic Characterization of Poultry Cloacal and Oropharyngeal Swabs in Kenya Reveals Bacterial Pathogens and Their Antimicrobial Resistance Genes. <i>International Journal of Microbiology</i> , 2024, 2024, 1-18.	2.3	0
8684	Field application of de novo transcriptomic analysis to evaluate the effects of sublethal freshwater salinization on <i>Gasterosteus aculeatus</i> in urban streams. <i>PLoS ONE</i> , 2024, 19, e0298213.	2.5	0
8685	Genomic insights into the chromosomal elongation in a family of Collembola. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2024, 291, .	2.6	0
8686	Lambda3: homology search for protein, nucleotide, and bisulfite-converted sequences. <i>Bioinformatics</i> , 2024, 40, .	4.1	0
8687	Improvement of <i>Panax notoginseng</i> saponin accumulation triggered by methyl jasmonate under arbuscular mycorrhizal fungi. <i>Frontiers in Plant Science</i> , 0, 15, .	3.6	0
8690	Biosynthesis of the highly oxygenated tetracyclic core skeleton of Taxol. <i>Nature Communications</i> , 2024, 15, .	12.8	0
8691	A novel hantavirus identified in bats (<i>Carollia perspicillata</i>) in Brazil. <i>Scientific Reports</i> , 2024, 14, .	3.3	0

#	ARTICLE	IF	CITATIONS
8693	Multi-omics analysis reveals the biosynthesis of flavonoids during the browning process of <i>Malus sieversii</i> explants. <i>Physiologia Plantarum</i> , 2024, 176, .	5.2	0
8694	Arbuscular mycorrhizal fungi promote functional gene regulation of phosphorus cycling in rhizosphere microorganisms of <i>Iris tectorum</i> under Cr stress. <i>Journal of Environmental Sciences</i> , 0, 151, 187-199.	6.1	0
8695	DeTox: a pipeline for the detection of toxins in venomous organisms. <i>Briefings in Bioinformatics</i> , 2024, 25, .	6.5	0
8696	Co-infecting viruses of species Bovine rhinitis B virus (Picornaviridae) and Bovine nidovirus 1 (Tobaniviridae) identified for the first time from a post-mortem respiratory sample of a sheep (<i>Ovis</i>)	1.7	0
8697	The effects of food provisioning on the gut microbiota community and antibiotic resistance genes of Yunnan snub-nosed monkey. <i>Frontiers in Microbiology</i> , 0, 15, .	3.5	0
8699	Microbiota-derived indoles alleviate intestinal inflammation and modulate microbiome by microbial cross-feeding. <i>Microbiome</i> , 2024, 12, .	11.1	0
8700	Vaginal microbiota are associated with in vitro fertilization during female infertility. , 0, , .		0
8701	Magnesium oxide nanoparticles reduce clubroot by regulating plant defense response and rhizosphere microbial community of tumorous stem mustard (<i>Brassica juncea</i> var. <i>tumida</i>). <i>Frontiers in Microbiology</i> , 0, 15, .	3.5	0
8702	Metagenomic Detection and Genetic Characterization of Human Sapoviruses among Children with Acute Flaccid Paralysis in Nigeria. <i>Pathogens</i> , 2024, 13, 264.	2.8	0
8703	Expanded phylogeny of extremely halophilic archaea shows multiple independent adaptations to hypersaline environments. <i>Nature Microbiology</i> , 2024, 9, 964-975.	13.3	0
8704	Duplicated CHSs (chalcone synthase) genes modulate flavonoid production in tea plants in response to light stress1. <i>Journal of Integrative Agriculture</i> , 2024, , .	3.5	0
8705	Comparative Genomic Analysis of the Mutant <i>Rhodotorula mucilaginosa</i> JH-R23 Provides Insight into the High-Yield Carotenoid Mechanism. <i>Fermentation</i> , 2024, 10, 176.	3.0	0
8706	Kinetic, electrochemical and spectral characterization of bacterial and archaeal rusticyanins; unexpected stability issues and consequences for applications in biotechnology. <i>Journal of Inorganic Biochemistry</i> , 2024, 256, 112539.	3.5	0
8707	Sugar accumulation stage in sugar beets is a key stage in response to continuous cropping soil microbial community assembly. <i>Plant and Soil</i> , 0, , .	3.7	0
8709	Emerging resistome diversity in clinical <i>Vibrio cholerae</i> strains revealing their role as potential reservoirs of antimicrobial resistance. <i>Molecular Biology Reports</i> , 2024, 51, .	2.3	0
8710	Challenges in computational discovery of bioactive peptides in ¹⁶ S rRNA omics data. <i>Proteomics</i> , 0, , .	2.2	0
8711	Airway commensal bacteria in cystic fibrosis inhibit the growth of <i>P. aeruginosa</i> via a released metabolite. <i>Microbiological Research</i> , 2024, 283, 127680.	5.3	0
8712	The transcription factor MYB1 activates DGAT2 transcription to promote triacylglycerol accumulation in <i>Sacha inchi</i> (<i>Plukenetia volubilis</i> L.) leaves under heat stress. <i>Plant Physiology and Biochemistry</i> , 2024, 208, 108517.	5.8	0

#	ARTICLE	IF	CITATIONS
8713	Effects of crop rotation on sugar beet growth through improving soil physicochemical properties and microbiome. <i>Industrial Crops and Products</i> , 2024, 212, 118331.	5.2	0
8715	Multi-Omics integration can be used to rescue metabolic information for some of the dark region of the <i>Pseudomonas putida</i> proteome. <i>BMC Genomics</i> , 2024, 25, .	2.8	0
8716	Metagenomic sequencing reveals viral diversity of mosquitoes from Shandong Province, China. <i>Microbiology Spectrum</i> , 2024, 12, .	3.0	0
8717	BASALT refines binning from metagenomic data and increases resolution of genome-resolved metagenomic analysis. <i>Nature Communications</i> , 2024, 15, .	12.8	0
8719	Integrated metabolome–metagenome analysis provides new insights into the impacts of sea cucumber (<i>Apostichopus japonicus</i>) aestivation on marine sediment composition. <i>Aquaculture</i> , 2024, 586, 740800.	3.5	0
8720	Metagenomic sequencing identified microbial species in the rumen and cecum microbiome responsible for niacin treatment and related to intramuscular fat content in finishing cattle. <i>Frontiers in Microbiology</i> , 0, 15, .	3.5	0
8721	Dynamic DNA N ⁶ -adenine methylation (6mA) governs the encystment process, showcased in the unicellular eukaryote <i>Pseudocohnilembus persalinus</i> . <i>Genome Research</i> , 2024, 34, 256-271.	5.5	0
8722	<i>Anaerostipes hadrus</i> , a butyrate-producing bacterium capable of metabolizing 5-fluorouracil. <i>MSphere</i> , 2024, 9, .	2.9	0
8723	Comparative transcriptome combined with physiological analyses revealed key genes and pathways for cadmium tolerance in wild-type and mutant microalgae <i>Dunaliella salina</i> . <i>Algal Research</i> , 2024, 79, 103475.	4.6	0
8724	Comparative genomics and secretome profiling of <i>Enterobacter cloacae</i> SBP-8. , 0, , .		0
8725	Identification of Viruses in Molossus Bats from the Brazilian Amazon: A Descriptive Metagenomic Analysis. <i>Microorganisms</i> , 2024, 12, 593.	3.6	0
8726	Effects of different nitrogen applications and straw return depth on straw microbial and carbon and nitrogen cycles in paddy fields in the cool zone. <i>Scientific Reports</i> , 2024, 14, .	3.3	0
8727	Transcriptome Sequencing Reveals the Mechanism of Auxin Regulation during Root Expansion in Carrot. <i>International Journal of Molecular Sciences</i> , 2024, 25, 3425.	4.1	0
8729	A novel glycoside hydrolase 43-like enzyme from <i>Clostridium boliviensis</i> is an endo-xylanase and a candidate for xylooligosaccharide production from different xylan substrates. <i>Applied and Environmental Microbiology</i> , 2024, 90, .	3.1	0
8730	Integrated Metagenomic and Metabolomic Analysis on Two Competing Mussels, <i>Mytella strigata</i> and <i>Perna viridis</i> , in China. <i>Animals</i> , 2024, 14, 918.	2.3	0
8731	Physiological and molecular mechanisms of radicle development of somatic embryos in <i>Schisandra chinensis</i> cultured in the dark. <i>Plant Cell, Tissue and Organ Culture</i> , 2024, 157, .	2.3	0
8732	Exploring associations between the teat apex metagenome and <i>Staphylococcus aureus</i> intramammary infections in primiparous cows under organic directives. <i>Applied and Environmental Microbiology</i> , 2024, 90, .	3.1	0
8733	Extremely oligotrophic and complex-carbon-degrading microaerobic bacteria from Arabian Sea oxygen minimum zone sediments. <i>Archives of Microbiology</i> , 2024, 206, .	2.2	0

#	ARTICLE	IF	CITATIONS
8735	A Novel Strain of <i>Bacillus cereus</i> with a Strong Antagonistic Effect Specific to <i>Sclerotinia</i> and Its Genomic and Transcriptomic Analysis. <i>Microorganisms</i> , 2024, 12, 611.	3.6	0
8736	<i>Rhizoctonia solani</i> disease suppression: addition of keratin-rich soil amendment leads to functional shifts in soil microbial communities. <i>FEMS Microbiology Ecology</i> , 2024, 100, .	2.7	0
8737	Diverse winter communities and biogeochemical cycling potential in the under-ice microbial plankton of a subarctic river-to-sea continuum. <i>Microbiology Spectrum</i> , 2024, 12, .	3.0	0
8738	Decoupling between the genetic potential and the metabolic regulation and expression in microbial organic matter cleavage across microbiomes. <i>Microbiology Spectrum</i> , 2024, 12, .	3.0	0
8739	Revealing the specific regulations of nitric oxide on the postharvest ripening and senescence of bitter melon fruit. <i>ABIOTECH</i> , 2024, 5, 29-45.	3.9	0
8741	Enriched rhizospheric functional microbiome may enhance adaptability of <i>Artemisia lavandulaefolia</i> and <i>Betula luminifera</i> in antimony mining areas. <i>Frontiers in Microbiology</i> , 0, 15, .	3.5	0
8742	Genomic characteristics of nine Nitrospirota metagenome-assembled genomes in deep-sea sediments from East Pacific polymetallic nodules zone. <i>Marine Genomics</i> , 2024, 75, 101107.	1.1	0
8743	New duck papillomavirus type identified in a mallard in Missouri, USA. <i>Archives of Virology</i> , 2024, 169, .	2.1	0
8746	Multi-Omics Analysis of the Co-Regulation of Wood Alcohol Accumulation in Baijiu Fermentation. <i>Fermentation</i> , 2024, 10, 175.	3.0	0
8747	Taxonomic and functional dynamics of nirS denitrifiers along a salinity gradient in the Pearl River Estuary. <i>Frontiers in Marine Science</i> , 0, 11, .	2.5	0
8748	Revisiting a pollen-transmitted ilarvirus previously associated with angular mosaic of grapevine. <i>Virus Research</i> , 2024, 344, 199362.	2.2	0
8750	De novo transcriptomic analysis of Doum Palm (<i>Hyphaene compressa</i>) revealed an insight into its potential drought tolerance. <i>PLoS ONE</i> , 2024, 19, e0292543.	2.5	0
8751	Response of soil bacteria to PUREX chemicals suggests biomarker utility and bioremediation potential. <i>Journal of Radioanalytical and Nuclear Chemistry</i> , 2024, 333, 1899-1909.	1.5	0
8753	<i>Natronoglopus mannanivorans</i> gen. nov., sp. nov., beta-1,4-mannan utilizing natronoarchaea from hypersaline soda lakes. <i>Frontiers in Microbiology</i> , 0, 15, .	3.5	0
8754	Impact of rumen microbiome on cattle carcass traits. <i>Scientific Reports</i> , 2024, 14, .	3.3	0
8755	Intestinal dual-specificity phosphatase 6 regulates the cold-induced gut microbiota remodeling to promote white adipose browning. <i>Npj Biofilms and Microbiomes</i> , 2024, 10, .	6.4	0
8756	Planetary Protection Knowledge Gap Closure Enabling Crewed Missions to Mars. <i>Astrobiology</i> , 2024, 24, 230-274.	3.0	0
8757	Polyphyletic origin of saxitoxin biosynthesis genes in the marine dinoflagellate <i>Alexandrium</i> revealed by comparative transcriptomics. <i>Harmful Algae</i> , 2024, 134, 102620.	4.8	0

#	ARTICLE	IF	CITATIONS
8758	Transcriptomic and Metabolomic Analyses Reveal the Response Mechanism of <i>Ophiopogon japonicus</i> to Waterlogging Stress. <i>Biology</i> , 2024, 13, 197.	2.8	0
8759	The Home Environment Is a Reservoir for Methicillin-Resistant Coagulase-Negative Staphylococci and Mammaliicocci. <i>Antibiotics</i> , 2024, 13, 279.	3.7	0
8760	Multi-Trophic Species Diversity Contributes to the Restoration of Soil Multifunctionality in Degraded Karst Forests through Cascading Effects. <i>Forests</i> , 2024, 15, 559.	2.1	0