

Fast and sensitive protein alignment using DIAMOND

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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.	1.2	16
7	Entropy-Scaling Search of Massive Biological Data. Cell Systems, 2015, 1, 130-140.	2.9	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.	1.6	28
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28	Functional Metagenomics of Spacecraft Assembly Cleanrooms: Presence of Virulence Factors Associated with Human Pathogens. <i>Frontiers in Microbiology</i> , 2016, 7, 1321.	1.5	24
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93	Novel mycoviruses discovered from metatranscriptomics survey of soybean phyllosphere phytobiomes. <i>Virus Research</i> , 2016, 213, 332-342.	1.1	136
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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1198	The transcriptome of <i>Pinus pinaster</i> under <i>Fusarium circinatum</i> challenge. <i>BMC Genomics</i> , 2020, 21, 28.	1.2	19
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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.	2.2	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.	1.6	16
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1520	Gamma proteobacteria mediating utilization of methyl-, sulfur- and petroleum organic compounds in deep ocean hydrothermal plumes. <i>ISME Journal</i> , 2020, 14, 3136-3148.	4.4	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.	1.5	26
1522	Gut Microbiota-Associated Activation of TLR5 Induces Apolipoprotein A1 Production in the Liver. <i>Circulation Research</i> , 2020, 127, 1236-1252.	2.0	32
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1524	Termite mounds contain soil-derived methanotroph communities kinetically adapted to elevated methane concentrations. <i>ISME Journal</i> , 2020, 14, 2715-2731.	4.4	21
1525	REINDEER: efficient indexing of <i>k</i> -mer presence and abundance in sequencing datasets. <i>Bioinformatics</i> , 2020, 36, i177-i185.	1.8	40
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1541	First Draft Genome Assembly of the Malaysian Stingless Bee, <i>Heterotrigona itama</i> (Apidae, Meliponinae). <i>Data</i> , 2020, 5, 112.	1.2	0
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1545	Benchmarking Orthogroup Inference Accuracy: Revisiting Orthobench. <i>Genome Biology and Evolution</i> , 2020, 12, 2258-2266.	1.1	23
1546	Shotgun metagenomic analysis reveals new insights into bacterial community profiles in tempeh. <i>BMC Research Notes</i> , 2020, 13, 562.	0.6	6

#	ARTICLE	IF	CITATIONS
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1557	A Comparative Evaluation of Tools to Predict Metabolite Profiles From Microbiome Sequencing Data. <i>Frontiers in Microbiology</i> , 2020, 11, 595910.	1.5	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.	1.5	4
1559	Metabolic impact of persistent organic pollutants on gut microbiota. <i>Gut Microbes</i> , 2020, 12, 1848209.	4.3	22
1560	Coding-Complete Genome Sequence of Yada Yada Virus, a Novel Alphavirus Detected in Australian Mosquitoes. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	10
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1566	The CtrA Regulon of <i>Rhodobacter sphaeroides</i> Favors Adaptation to a Particular Lifestyle. <i>Journal of Bacteriology</i> , 2020, 202, .	1.0	8
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1569	Draft Genome Sequence of Psychrotolerant <i>Clostridium</i> sp. Strain M14, Isolated from Spoiled Uncooked Venison. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	3
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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, .	1.4	6
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1577	Selective carbon sources influence the end products of microbial nitrate respiration. <i>ISME Journal</i> , 2020, 14, 2034-2045.	4.4	61
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1591	Progression of regeneration in demosponge Cinachyrella cf cavernosa based on wound location. Hydrobiologia, 2020, 847, 2555-2571.	1.0	1
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1607	Comparative Genomic and Proteomic Analyses of Three Widespread Phytophthora Species: <i>Phytophthora chlamydospora</i> , <i>Phytophthora gonapodyides</i> and <i>Phytophthora pseudosyringae</i> . <i>Microorganisms</i> , 2020, 8, 653.	1.6	36
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#	ARTICLE	IF	CITATIONS
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1627	Tax4Fun2: prediction of habitat-specific functional profiles and functional redundancy based on 16S rRNA gene sequences. <i>Environmental Microbiomes</i> , 2020, 15, 11.	2.2	323
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#	ARTICLE	IF	CITATIONS
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1726	Systematic and Comparative Evaluation of Software Programs for Template-Based Modeling of Protein Structures. <i>Biotechnology Journal</i> , 2020, 15, e1900343.	1.8	5
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#	ARTICLE	IF	CITATIONS
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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.	3.9	17
1730	The First Draft Genome Assembly of Snow Sheep (<i>Ovis nivicola</i>). <i>Genome Biology and Evolution</i> , 2020, 12, 1330-1336.	1.1	14
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1734	Transcriptome and cell wall degrading enzyme-related gene analysis of <i>Pestalotiopsis neglecta</i> in response to sodium phophorbide a. <i>Pesticide Biochemistry and Physiology</i> , 2020, 169, 104639.	1.6	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.	1.5	1
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1744	<i>Deinococcus detaillensis</i> sp. nov., isolated from humus soil in Antarctica. <i>Archives of Microbiology</i> , 2020, 202, 2493-2498.	1.0	8
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#	ARTICLE	IF	CITATIONS
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1748	Broccoli: Combining Phylogenetic and Network Analyses for Orthology Assignment. <i>Molecular Biology and Evolution</i> , 2020, 37, 3389-3396.	3.5	65
1749	BlobToolKit – Interactive Quality Assessment of Genome Assemblies. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1361-1374.	0.8	883
1750	Phenylalanine increases chrysanthemum flower immunity against <i>Botrytis cinerea</i> attack. <i>Plant Journal</i> , 2020, 104, 226-240.	2.8	30
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1752	Shotgun metagenomics of dust microbiome from flight deck and cabin in civil aviation aircraft. <i>Indoor Air</i> , 2020, 30, 1199-1212.	2.0	19
1753	The genome, transcriptome, and proteome of the fish parasite <i>Pomphorhynchus laevis</i> (Acanthocephala). <i>PLoS ONE</i> , 2020, 15, e0232973.	1.1	19
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1755	Mulching practices alter soil microbial functional diversity and benefit to soil quality in orchards on the Loess Plateau. <i>Journal of Environmental Management</i> , 2020, 271, 110985.	3.8	34
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1757	Metatranscriptomic Analysis of Virus Diversity in Urban Wild Birds with Parectic Disease. <i>Journal of Virology</i> , 2020, 94, .	1.5	21
1758	Advantages and Limits of Metagenomic Assembly and Binning of a Giant Virus. <i>MSystems</i> , 2020, 5, .	1.7	14
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1762	ZEAMAP, a Comprehensive Database Adapted to the Maize Multi-Omics Era. <i>IScience</i> , 2020, 23, 101241.	1.9	63
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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.	3.9	16
1767	<i>Bacillus tepidophilus</i> sp. nov., isolated from tepid spring. <i>Archives of Microbiology</i> , 2020, 202, 2367-2371.	1.0	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.	4.8	44
1769	Effects of forced taxonomic transitions on metabolic composition and function in microbial microcosms. <i>Environmental Microbiology Reports</i> , 2020, 12, 514-524.	1.0	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.	1.7	31
1771	The <i>Seminavis robusta</i> genome provides insights into the evolutionary adaptations of benthic diatoms. <i>Nature Communications</i> , 2020, 11, 3320.	5.8	55
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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.	1.3	9
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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.	3.4	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.	2.8	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.	0.8	10
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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.	4.8	80
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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.	1.6	26

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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.	6.1	42
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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.	2.0	12
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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.	1.5	7
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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.	0.4	5
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1822	Clades of huge phages from across Earth's ecosystems. <i>Nature</i> , 2020, 578, 425-431.	13.7	331
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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.	1.8	7
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1842	Precision Medicine Informatics: Principles, Prospects, and Challenges. <i>IEEE Access</i> , 2020, 8, 13593-13612.	2.6	26
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1847	Piphillin predicts metagenomic composition and dynamics from DADA2-corrected 16S rDNA sequences. <i>BMC Genomics</i> , 2020, 21, 56.	1.2	54
1848	Are viruses associated with disc herniation? A clinical case series. <i>BMC Musculoskeletal Disorders</i> , 2020, 21, 27.	0.8	5
1849	Whole genome sequence of an edible and medicinal mushroom, <i>Hericium erinaceus</i> (Basidiomycota,) Tj ETQq1 1 0,784314 rsgBT /Over	1.3	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. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	27
1851	Enrichment of novel Actinomycetales and the detection of monooxygenases during aerobic 1,4-dioxane biodegradation with uncontaminated and contaminated inocula. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 2255-2269.	1.7	12
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1857	Functional profiles of phycospheric microorganisms during a marine dinoflagellate bloom. <i>Water Research</i> , 2020, 173, 115554.	5.3	26
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1859	Metagenomics methods for the study of plant-associated microbial communities: A review. <i>Journal of Microbiological Methods</i> , 2020, 170, 105860.	0.7	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.	3.9	86
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1862	Diversity and Host Interactions among Virulent and Temperate Baltic Sea Flavobacterium Phages. <i>Viruses</i> , 2020, 12, 158.	1.5	11
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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.	6.5	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.	2.4	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.	1.0	9
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1870	CCMetagen: comprehensive and accurate identification of eukaryotes and prokaryotes in metagenomic data. <i>Genome Biology</i> , 2020, 21, 103.	3.8	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.	1.1	2

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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.	2.2	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.	1.8	42
1875	NGS-based characterization of microbial diversity and functional profiling of solid tannery waste metagenomes. <i>Genomics</i> , 2020, 112, 2903-2913.	1.3	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, .	1.7	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.	0.8	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.	1.8	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.	2.0	15
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1882	Parallel Evolution in the Integration of a Co-obligate Aphid Symbiosis. <i>Current Biology</i> , 2020, 30, 1949-1957.e6.	1.8	54
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1884	Tracking resistomes, virulence genes, and bacterial pathogens in long-term manure-amended greenhouse soils. <i>Journal of Hazardous Materials</i> , 2020, 396, 122618.	6.5	55
1885	Overexpression of <i>LITPS2</i> 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.	2.8	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.	3.9	44
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1888	Phylogenomics of <i>Rhodocyclales</i> and its distribution in wastewater treatment systems. <i>Scientific Reports</i> , 2020, 10, 3883.	1.6	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.	0.6	8

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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.	1.1	34
1892	Draft Genome Sequences of Novel <i>Campylobacter</i> Species Isolated from Nonhuman Primates. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	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, .	0.3	1
1894	Genomic Sequence of a New <i>Alphavirus</i> Detected in Comber (<i>Serranus cabrilla</i>). <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	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, .	1.7	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.	2.2	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.	1.6	59
1898	No More Tears: Mining Sequencing Data for Novel Bt Cry Toxins with CryProcessor. <i>Toxins</i> , 2020, 12, 204.	1.5	19
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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, .	1.4	41
1902	Reference Human Rotavirus A Genome Sequence from a Previously Vaccinated Child with Diarrhea in Nigeria. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	0
1903	Altered gut microbial profile is associated with abnormal metabolism activity of Autism Spectrum Disorder. <i>Gut Microbes</i> , 2020, 11, 1246-1267.	4.3	166
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1905	Metagenomic Next-Generation Sequencing in Clinical Microbiology. <i>Clinical Microbiology Newsletter</i> , 2020, 42, 53-59.	0.4	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.	1.8	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.	1.2	20

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1909	Abundance and diversity of microbial arsenic biotransformation genes in the sludge of full-scale anaerobic digesters from a municipal wastewater treatment plant. <i>Environment International</i> , 2020, 138, 105535.	4.8	33
1910	Deep DNA metagenomic sequencing reveals oral microbiome divergence between monozygotic twins discordant for multiple sclerosis severity. <i>Journal of Neuroimmunology</i> , 2020, 343, 577237.	1.1	4
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1912	Insights into response to food intake in anadromous <i>Coilia nasus</i> through stomach transcriptome analysis. <i>Aquaculture Research</i> , 2020, 51, 2799-2812.	0.9	7
1913	Linking extracellular enzymes to phylogeny indicates a predominantly particle-associated lifestyle of deep-sea prokaryotes. <i>Science Advances</i> , 2020, 6, eaaz4354.	4.7	63
1914	Annotated Genome Sequence of <i>Aspergillus tanneri</i> NIH1004. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	2
1915	Complementary Metagenomic Approaches Improve Reconstruction of Microbial Diversity in a Forest Soil. <i>MSystems</i> , 2020, 5, .	1.7	45
1916	Transcriptomic analysis of sea cucumber (<i>Holothuria leucospilota</i>) coelomocytes revealed the echinoderm cytokine response during immune challenge. <i>BMC Genomics</i> , 2020, 21, 306.	1.2	10
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1918	Immune Suppressive Extracellular Vesicle Proteins of <i>Leptopilina heterotoma</i> Are Encoded in the Wasp Genome. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1-12.	0.8	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. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 455-466.	0.8	21
1920	Comprehensive metagenomic analysis of blastic plasmacytoid dendritic cell neoplasm. <i>Blood Advances</i> , 2020, 4, 1006-1011.	2.5	10
1921	Small and mighty: adaptation of superphylum Patescibacteria to groundwater environment drives their genome simplicity. <i>Microbiome</i> , 2020, 8, 51.	4.9	205
1922	Structure and function of the Arctic and Antarctic marine microbiota as revealed by metagenomics. <i>Microbiome</i> , 2020, 8, 47.	4.9	61
1923	Postnatal Gut Immunity and Microbiota Development Is Minimally Affected by Prenatal Inflammation in Preterm Pigs. <i>Frontiers in Immunology</i> , 2020, 11, 420.	2.2	11
1924	De novo Sequencing and Analysis of <i>Salvia hispanica</i> Tissue-Specific Transcriptome and Identification of Genes Involved in Terpenoid Biosynthesis. <i>Plants</i> , 2020, 9, 405.	1.6	11
1925	Molecular Drivers of Lymphocyte Organization in Vertebrate Mucosal Surfaces: Revisiting the TNF Superfamily Hypothesis. <i>Journal of Immunology</i> , 2020, 204, 2697-2711.	0.4	11

#	ARTICLE	IF	CITATIONS
1926	Sustained RNA virome diversity in Antarctic penguins and their ticks. <i>ISME Journal</i> , 2020, 14, 1768-1782.	4.4	56
1927	Microbial Diversity and Metabolic Potential in the Stratified Sansha Yongle Blue Hole in the South China Sea. <i>Scientific Reports</i> , 2020, 10, 5949.	1.6	27
1928	Diversity and potential biogeochemical impacts of viruses in bulk and rhizosphere soils. <i>Environmental Microbiology</i> , 2021, 23, 588-599.	1.8	62
1929	Taxonomic and functional analysis of soil microbial communities in a mining site across a metal(loid) contamination gradient. <i>European Journal of Soil Science</i> , 2021, 72, 1190-1205.	1.8	13
1930	High throughput BLAST algorithm using spark and cassandra. <i>Journal of Supercomputing</i> , 2021, 77, 1879-1896.	2.4	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. <i>Environmental Microbiology</i> , 2021, 23, 728-743.	1.8	27
1933	Post-glacial establishment of locally adapted fish populations over a steep salinity gradient. <i>Journal of Evolutionary Biology</i> , 2021, 34, 138-156.	0.8	28
1934	Toward a high-quality pan-genome landscape of <i>Bacillus subtilis</i> by removal of confounding strains. <i>Briefings in Bioinformatics</i> , 2021, 22, 1951-1971.	3.2	46
1935	Advanced nitrogen removal in a fixed-bed anaerobic ammonia oxidation reactor following an anoxic/oxic reactor: Nitrogen removal contributions and mechanisms. <i>Bioresource Technology</i> , 2021, 320, 124297.	4.8	8
1936	ALeS: adaptive-length spaced-seed design. <i>Bioinformatics</i> , 2021, 37, 1206-1210.	1.8	2
1937	Genomic Architecture of Rapid Parallel Adaptation to Fresh Water in a Wild Fish. <i>Molecular Biology and Evolution</i> , 2021, 38, 1317-1329.	3.5	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. <i>Plant Pathology</i> , 2021, 70, 249-258.	1.2	24
1939	Side effects of free nitrous acid on the sewer resistome and mobilome. <i>Chemical Engineering Journal</i> , 2021, 405, 126657.	6.6	3
1940	Exploring transcriptional switches from pairwise, temporal and population RNA-Seq data using deepTS. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	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> . <i>Journal of Applied Microbiology</i> , 2021, 130, 405-415.	1.4	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> . <i>Phytopathology</i> , 2021, 111, 268-280.	1.1	26
1943	A unified catalog of 204,938 reference genomes from the human gut microbiome. <i>Nature Biotechnology</i> , 2021, 39, 105-114.	9.4	628

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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.	1.4	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.	3.5	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.	2.2	40
1947	Analysis of heavy metal-related indices in the Eboing permafrost on the Tibetan Plateau. <i>Catena</i> , 2021, 196, 104907.	2.2	8
1948	Genomic Features of Parthenogenetic Animals. <i>Journal of Heredity</i> , 2021, 112, 19-33.	1.0	55
1949	Benchmarking orthology methods using phylogenetic patterns defined at the base of Eukaryotes. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	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.	2.2	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.	4.4	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.	4.1	62
1953	Ecogenomics and metabolic potential of the South Atlantic Ocean microbiome. <i>Science of the Total Environment</i> , 2021, 765, 142758.	3.9	16
1954	Draft genomes of <i>Perkinsus olseni</i> and <i>Perkinsus chesapeaki</i> reveal polyploidy and regional differences in heterozygosity. <i>Genomics</i> , 2021, 113, 677-688.	1.3	11
1955	Interpreting lacustrine bulk sediment $\delta^{15}N$ values using metagenomics in a tropical hypersaline lake system. <i>Journal of Paleolimnology</i> , 2021, 65, 151-168.	0.8	4
1956	Functional metagenomic landscape of polluted river reveals potential genes involved in degradation of xenobiotic pollutants. <i>Environmental Research</i> , 2021, 192, 110332.	3.7	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.	6.5	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.	1.8	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.	4.8	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.	3.9	33
1961	New insight into microbial degradation of mycotoxins during anaerobic digestion. <i>Waste Management</i> , 2021, 119, 215-225.	3.7	12

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1962	Precision targeting of bacterial pathogen via bi-functional nanozyme activated by biofilm microenvironment. <i>Biomaterials</i> , 2021, 268, 120581.	5.7	54
1963	The communities and functional profiles of virioplankton along a salinity gradient in a subtropical estuary. <i>Science of the Total Environment</i> , 2021, 759, 143499.	3.9	16
1964	Marine <i>Dadabacteria</i> exhibit genome streamlining and phototrophy-driven niche partitioning. <i>ISME Journal</i> , 2021, 15, 1248-1256.	4.4	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.	1.0	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.	1.4	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.	0.5	4
1968	Metagenomic assessment of the global diversity and distribution of bacteria and fungi. <i>Environmental Microbiology</i> , 2021, 23, 316-326.	1.8	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.	2.1	13
1970	Geographic pattern of antibiotic resistance genes in the metagenomes of the giant panda. <i>Microbial Biotechnology</i> , 2021, 14, 186-197.	2.0	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.	3.9	19
1972	A metagenomic assessment of microbial communities in anaerobic bioreactors and sediments: Taxonomic and functional relationships. <i>Anaerobe</i> , 2021, 68, 102296.	1.0	4
1973	State-of-the-art genome inference in the human MHC. <i>International Journal of Biochemistry and Cell Biology</i> , 2021, 131, 105882.	1.2	22
1974	Virome characterization of <i>Cryphonectria parasitica</i> isolates from Azerbaijan unveiled a new myomonavirus and a putative new RNA virus unrelated to described viral sequences. <i>Virology</i> , 2021, 553, 51-61.	1.1	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.	3.9	9
1976	Probing periodontal microbial dark matter using metataxonomics and metagenomics. <i>Periodontology 2000</i> , 2021, 85, 12-27.	6.3	16
1977	GreenPhylDB v5: a comparative pangenomic database for plant genomes. <i>Nucleic Acids Research</i> , 2021, 49, D1464-D1471.	6.5	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.	1.7	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.	2.9	10

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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.	4.4	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.	4.4	30
1982	Identification of Natural CRISPR Systems and Targets in the Human Microbiome. <i>Cell Host and Microbe</i> , 2021, 29, 94-106.e4.	5.1	20
1983	Anaerobic bacterial degradation of protein and lipid macromolecules in subarctic marine sediment. <i>ISME Journal</i> , 2021, 15, 833-847.	4.4	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.	1.4	14
1985	Responses of the sugarcane rhizosphere microbiota to different levels of water stress. <i>Applied Soil Ecology</i> , 2021, 159, 103817.	2.1	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.	5.1	22
1987	Comparative genomics of <i>Clostridium</i> species associated with vacuum-packed meat spoilage. <i>Food Microbiology</i> , 2021, 95, 103687.	2.1	25
1988	Cyanobacterial blooms in wastewater treatment facilities: Significance and emerging monitoring strategies. <i>Journal of Microbiological Methods</i> , 2021, 180, 106123.	0.7	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.	1.3	7
1990	The Developmental and Genetic Architecture of the Sexually Selected Male Ornament of Swordtails. <i>Current Biology</i> , 2021, 31, 911-922.e4.	1.8	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.	2.9	21
1992	Heavy metal could drive co-selection of antibiotic resistance in terrestrial subsurface soils. <i>Journal of Hazardous Materials</i> , 2021, 411, 124848.	6.5	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.	4.4	29
1994	Transcriptional landscape of rice roots at the single-cell resolution. <i>Molecular Plant</i> , 2021, 14, 384-394.	3.9	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.	3.5	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.	1.5	13
1997	CheckV assesses the quality and completeness of metagenome-assembled viral genomes. <i>Nature Biotechnology</i> , 2021, 39, 578-585.	9.4	569

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1998	Isolation, identification and artificial inoculation of <i>Ustilago esculenta</i> on <i>Zizania latifolia</i> . Horticultural Plant Journal, 2021, 7, 347-358.	2.3	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.	1.2	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.	3.6	12
2001	High-accuracy long-read amplicon sequences using unique molecular identifiers with Nanopore or PacBio sequencing. Nature Methods, 2021, 18, 165-169.	9.0	198
2002	High-throughput Metagenomics for Identification of Pathogens in the Clinical Settings. Small Methods, 2021, 5, 2000792.	4.6	96
2003	Mini-metagenome analysis of psychrophilic electroactive biofilms based on single cell sorting. Science of the Total Environment, 2021, 762, 144328.	3.9	9
2004	SCycDB: A curated functional gene database for metagenomic profiling of sulphur cycling pathways. Molecular Ecology Resources, 2021, 21, 924-940.	2.2	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.	0.9	1
2006	TOA: A software package for automated functional annotation in non-model plant species. Molecular Ecology Resources, 2021, 21, 621-636.	2.2	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.	2.8	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.	3.5	19
2009	The Function and Evolution of Motile DNA Replication Systems in Ciliates. Current Biology, 2021, 31, 66-76.e6.	1.8	76
2010	Virome of Bat Guano from Nine Northern California Roosts. Journal of Virology, 2021, 95, .	1.5	24
2011	Genome analysis reveals probiotic propensities of <i>Paenibacillus polymyxa</i> HK4. Genomics, 2021, 113, 861-873.	1.3	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.	1.2	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.	4.8	20
2014	Timing the origin of eukaryotic cellular complexity with ancient duplications. Nature Ecology and Evolution, 2021, 5, 92-100.	3.4	61
2015	<i>Bacillus alkalicellulosilyticus</i> sp. nov., isolated from extremely alkaline bauxite residue (red mud) site. Archives of Microbiology, 2021, 203, 719-723.	1.0	12

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2016	Phylogenomic inference of the interrelationships of Lake Baikal sponges. <i>Systematics and Biodiversity</i> , 2021, 19, 209-217.	0.5	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.	4.6	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.	4.1	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.	4.4	14
2020	Wolbachia affects reproduction in the spider mite <i>Tetranychus truncatus</i> (Acari: Tetranychidae) by regulating chorion protein S38 like and <i>Rep</i> . <i>Insect Molecular Biology</i> , 2021, 30, 18-29.	1.0	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.	2.5	15
2022	Biofilm matrix disrupts nematode motility and predatory behavior. <i>ISME Journal</i> , 2021, 15, 260-269.	4.4	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.	2.2	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.	1.5	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.	4.4	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.	2.2	13
2027	A metagenomic-based method to study hospital air dust resistome. <i>Chemical Engineering Journal</i> , 2021, 406, 126854.	6.6	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.	0.4	6
2029	Challenges in gene-oriented approaches for pangenome content discovery. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	8
2030	Gene expression during bacterivorous growth of a widespread marine heterotrophic flagellate. <i>ISME Journal</i> , 2021, 15, 154-167.	4.4	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.	4.4	62
2032	Comparative genomics reveals insights into cyanobacterial evolution and habitat adaptation. <i>ISME Journal</i> , 2021, 15, 211-227.	4.4	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.	0.8	3

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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.	2.2	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.	1.4	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.	1.7	7
2037	Current challenges and best-practice protocols for microbiome analysis. <i>Briefings in Bioinformatics</i> , 2021, 22, 178-193.	3.2	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.	1.1	15
2039	Metagenomic Assembly: Reconstructing Genomes from Metagenomes. <i>Methods in Molecular Biology</i> , 2021, 2242, 139-152.	0.4	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.	4.4	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.	0.5	13
2045	Viral evolution sustains a dengue outbreak of enhanced severity. <i>Emerging Microbes and Infections</i> , 2021, 10, 536-544.	3.0	6
2047	Metagenomic analysis of the cow, sheep, reindeer and red deer rumen. <i>Scientific Reports</i> , 2021, 11, 1990.	1.6	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, .	1.1	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.	0.9	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.	2.2	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.	2.0	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.	1.9	19

#	ARTICLE	IF	CITATIONS
2055	Interpopulation differences of retroduplication variations (RDVs) in rice retrogenes and their phenotypic correlations. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 600-611.	1.9	1
2056	The Gut Microbiome Is Altered in Postmenopausal Women With Osteoporosis and Osteopenia. <i>JBMR Plus</i> , 2021, 5, e10452.	1.3	48
2057	Transcriptome Profiles in the Spleen of the Chinese Giant Salamander (<i>Andrias davidianus</i>) Challenged with <i>Citrobacter freundii</i> . <i>Russian Journal of Bioorganic Chemistry</i> , 2021, 47, 252-260.	0.3	1
2058	Comparative genomics reveals new functional insights in uncultured MAST species. <i>ISME Journal</i> , 2021, 15, 1767-1781.	4.4	18
2059	Competitive Exclusion and Metabolic Dependency among Microorganisms Structure the Cellulose Economy of an Agricultural Soil. <i>MBio</i> , 2021, 12, .	1.8	23
2060	Oxford nanopore sequencing in clinical microbiology and infection diagnostics. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	28
2061	Integrated mRNA and miRNA expression profile analysis of female and male gonads in <i>Hyriopsis cumingii</i> . <i>Scientific Reports</i> , 2021, 11, 665.	1.6	11
2062	Prediction and analysis of metagenomic operons via MetaRon: a pipeline for prediction of Metagenome and whole-genome opeRons. <i>BMC Genomics</i> , 2021, 22, 60.	1.2	2
2064	Harnessing CRISPR-Cas system diversity for gene editing technologies. <i>Journal of Biomedical Research</i> , 2021, 35, 91.	0.7	1
2065	A draft transcriptome of a parasite <i>Neocamacolaimus parasiticus</i> (Camacolaimidae, Plectida). <i>Journal of Nematology</i> , 2021, 53, 1-4.	0.4	4
2066	Diversity analysis of thermophilic hydrogenogenic carboxydrotrophs by carbon monoxide dehydrogenase amplicon sequencing using new primers. <i>Extremophiles</i> , 2021, 25, 61-76.	0.9	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. <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 127-130.	1.4	11
2071	Genomic signatures of the evolution of defence against its natural enemies in the poisonous and medicinal plant <i>Datura stramonium</i> (Solanaceae). <i>Scientific Reports</i> , 2021, 11, 882.	1.6	17
2072	Expansion and persistence of antibiotic-specific resistance genes following antibiotic treatment. <i>Gut Microbes</i> , 2021, 13, 1-19.	4.3	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. <i>Italian Journal of Animal Science</i> , 2021, 20, 1147-1155.	0.8	5
2076	Computational Genomics. , 2021, , 213-241.		0

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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.	2.2	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, .	3.3	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.	2.0	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.	4.4	40
2081	Comparative Analysis of Core and Accessory Genes in Coexpression Network. <i>Methods in Molecular Biology</i> , 2021, 2242, 45-58.	0.4	2
2083	Combined genomic, transcriptomic, and metabolomic analyses provide insights into chayote (<i>Sechium</i>) Tj ETQq1 1,0784314,rgBT /Ome	2.9	39
2084	A Multi-Omics Characterization of the Natural Product Potential of Tropical Filamentous Marine Cyanobacteria. <i>Marine Drugs</i> , 2021, 19, 20.	2.2	19
2085	Polinton-like viruses are abundant in aquatic ecosystems. <i>Microbiome</i> , 2021, 9, 13.	4.9	32
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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2280	Expression analysis of genes related to cold tolerance in <i>Dendroctonus valens</i> . <i>PeerJ</i> , 2021, 9, e10864.	0.9	9
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2314	MetaPrism: A versatile toolkit for joint taxa/gene analysis of metagenomic sequencing data. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	1
2316	PhotoModPlus: A web server for photosynthetic protein prediction from genome neighborhood features. <i>PLoS ONE</i> , 2021, 16, e0248682.	1.1	0
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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.	1.0	2
2344	The chromosome-scale 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.	4.1	60

#	ARTICLE	IF	CITATIONS
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2379	Metabolic pathways inferred from a bacterial marker gene illuminate ecological changes across South Pacific frontal boundaries. <i>Nature Communications</i> , 2021, 12, 2213.	5.8	25
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#	ARTICLE	IF	CITATIONS
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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.	2.3	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, .	1.8	26
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2409	Proteomic Identification and Meta-Analysis in <i>Salvia hispanica</i> RNA-Seq de novo Assemblies. <i>Plants</i> , 2021, 10, 765.	1.6	2
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2419	GeneMark-HM: improving gene prediction in DNA sequences of human microbiome. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab047.	1.5	4
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2425	NGScloud2: optimized bioinformatic analysis using Amazon Web Services. <i>PeerJ</i> , 2021, 9, e11237.	0.9	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.	3.3	37
2427	Genome sequence, transcriptome, and annotation of rodent malaria parasite <i>Plasmodium yoelii nigeriensis</i> N67. <i>BMC Genomics</i> , 2021, 22, 303.	1.2	7
2428	Tissue-specific transcriptome analysis of drought stress and rehydration in <i>Trachycarpus fortunei</i> at seedling. <i>PeerJ</i> , 2021, 9, e10933.	0.9	4
2429	iBLAST: Incremental BLAST of new sequences via automated e-value correction. <i>PLoS ONE</i> , 2021, 16, e0249410.	1.1	3
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#	ARTICLE	IF	CITATIONS
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2448	Prophage Genomics and Ecology in the Family Rhodobacteraceae. <i>Microorganisms</i> , 2021, 9, 1115.	1.6	22
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2451	The Presence of Ancient Core Genes Reveals Endogenization from Diverse Viral Ancestors in Parasitoid Wasps. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	14
2452	Challenges in benchmarking metagenomic profilers. <i>Nature Methods</i> , 2021, 18, 618-626.	9.0	63
2453	Bacteriophage-Host Association in the Phytoplasma Insect Vector <i>Euscelidius variegatus</i> . <i>Pathogens</i> , 2021, 10, 612.	1.2	9
2454	The Significance of Genotypic Diversity in Coral Competitive Interaction: A Transcriptomic Perspective. <i>Frontiers in Ecology and Evolution</i> , 2021, 9, .	1.1	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.	1.6	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, .	1.5	3
2457	DNA adenine methylation is involved in persister formation in <i>E. coli</i> . <i>Microbiological Research</i> , 2021, 246, 126709.	2.5	16
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2459	Metatranscriptome Library Preparation Influences Analyses of Viral Community Activity During a Brown Tide Bloom. <i>Frontiers in Microbiology</i> , 2021, 12, 664189.	1.5	12

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2463	Diversity and distribution of viruses inhabiting the deepest ocean on Earth. <i>ISME Journal</i> , 2021, 15, 3094-3110.	4.4	55
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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.	1.6	20
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2479	Beyond taxonomy: Validating functional inference approaches in the context of fish farm impact assessments. <i>Molecular Ecology Resources</i> , 2021, 21, 2264-2277.	2.2	8

#	ARTICLE	IF	CITATIONS
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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.	1.7	5
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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.	0.9	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.	2.2	22
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2495	Gene-level metagenomic architectures across diseases yield high-resolution microbiome diagnostic indicators. <i>Nature Communications</i> , 2021, 12, 2907.	5.8	33
2498	Transcriptome analysis reveals significant difference in gene expression and pathways between two peanut cultivars under AI stress. <i>Gene</i> , 2021, 781, 145535.	1.0	19
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#	ARTICLE	IF	CITATIONS
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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.	1.5	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.	1.6	1
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2508	Virus Diversity and Loads in Crickets Reared for Feed: Implications for Husbandry. <i>Frontiers in Veterinary Science</i> , 2021, 8, 642085.	0.9	11
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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.	1.3	12
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2513	Deep ocean metagenomes provide insight into the metabolic architecture of bathypelagic microbial communities. <i>Communications Biology</i> , 2021, 4, 604.	2.0	107
2514	Metabolic flexibility allows bacterial habitat generalists to become dominant in a frequently disturbed ecosystem. <i>ISME Journal</i> , 2021, 15, 2986-3004.	4.4	89
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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.	13.5	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, .	3.3	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.	2.2	13
2522	antiSMASH 6.0: improving cluster detection and comparison capabilities. <i>Nucleic Acids Research</i> , 2021, 49, W29-W35.	6.5	1,520

#	ARTICLE	IF	CITATIONS
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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 (Basel)</i> , 2021, 7, 1041.	1.0	1
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.	3.7	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.	1.5	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.	1.8	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.	1.7	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.	4.4	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.	1.0	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.	3.5	32
2533	Molecular mechanisms of mutualistic and antagonistic interactions in a plant-pollinator association. <i>Nature Ecology and Evolution</i> , 2021, 5, 974-986.	3.4	30
2534	A molecular survey of canine respiratory viruses in New Zealand. <i>New Zealand Veterinary Journal</i> , 2021, 69, 224-233.	0.4	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.	1.5	31
2540	Long-read metagenomics retrieves complete single-contig bacterial genomes from canine feces. <i>BMC Genomics</i> , 2021, 22, 330.	1.2	41
2541	Enlightening the taxonomy darkness of human gut microbiomes with a cultured biobank. <i>Microbiome</i> , 2021, 9, 119.	4.9	479
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2546	Early-Life Immune System Maturation in Chickens Using a Synthetic Community of Cultured Gut Bacteria. <i>MSystems</i> , 2021, 6, .	1.7	68
2547	Pests, diseases, and aridity have shaped the genome of <i>Corymbia citriodora</i> . <i>Communications Biology</i> , 2021, 4, 537.	2.0	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.	1.2	12
2549	Responses of cyanobacterial aggregate microbial communities to algal blooms. <i>Water Research</i> , 2021, 196, 117014.	5.3	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, .	3.3	42
2552	The diversity of opsins in Lake Baikal amphipods (Amphipoda: Gammaridae). <i>Bmc Ecology and Evolution</i> , 2021, 21, 81.	0.7	9
2553	Variation of Metagenome From Feedstock to Digestate in Full-Scale Biogas Plants. <i>Frontiers in Microbiology</i> , 2021, 12, 660225.	1.5	7
2554	Rhizomal Reclassification of Living Organisms. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5643.	1.8	16
2555	Comparison of nodule endophyte composition, diversity, and gene content between <i>Medicago truncatula</i> genotypes. <i>Phytobiomes Journal</i> , 0, , .	1.4	1
2556	Four novel picornaviruses detected in Magellanic Penguins (<i>Spheniscus magellanicus</i>) in Chile. <i>Virology</i> , 2021, 560, 116-123.	1.1	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.	6.5	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.	1.6	39
2560	Gut microbiota in healthy and unhealthy long-living people. <i>Gene</i> , 2021, 779, 145510.	1.0	17
2561	A Chromosome-Level Genome Assembly of <i>Ephesia elutella</i> (Hübner, 1796) (Lepidoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	8.1	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, .	0.8	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.	4.4	48
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#	ARTICLE	IF	CITATIONS
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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.	1.3	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.	1.1	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.	2.1	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.	1.3	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.	2.9	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.	1.6	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.	1.2	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.	2.2	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.	0.3	4
2580	HIV-1 Infection Alters the Viral Composition of Plasma in Men Who Have Sex with Men. <i>MSphere</i> , 2021, 6, .	1.3	16
2581	Database-independent de novo metaproteomics of complex microbial communities. <i>Cell Systems</i> , 2021, 12, 375-383.e5.	2.9	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, .	1.4	19
2583	Studying the Genetic Diversity of Yam Bean Using a New Draft Genome Assembly. <i>Agronomy</i> , 2021, 11, 953.	1.3	7
2584	Particulate Metabolites and Transcripts Reflect Diel Oscillations of Microbial Activity in the Surface Ocean. <i>MSystems</i> , 2021, 6, .	1.7	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.	3.7	31
2586	Insight into the function and evolution of the Woodâ€™Ljungdahl pathway in <i>Actinobacteria</i> . <i>ISME Journal</i> , 2021, 15, 3005-3018.	4.4	55

#	ARTICLE	IF	CITATIONS
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2589	Novel Mycoviruses Discovered in the Mycovirome of a Necrotrophic Fungus. <i>MBio</i> , 2021, 12, .	1.8	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.	2.9	21
2592	PHROG: families of prokaryotic virus proteins clustered using remote homology. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab067.	1.5	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.	1.8	0
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2596	De novo genome sequencing of mycoparasite <i>Mycogone pernicioso</i> strain MgR1 sheds new light on its biological complexity. <i>Brazilian Journal of Microbiology</i> , 2021, 52, 1545-1556.	0.8	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.	1.5	4
2599	The Genomic Impact of Mycoheterotrophy in Orchids. <i>Frontiers in Plant Science</i> , 2021, 12, 632033.	1.7	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.	1.5	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.	3.5	93
2607	Metagenomic compendium of 189,680 DNA viruses from the human gut microbiome. <i>Nature Microbiology</i> , 2021, 6, 960-970.	5.9	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.	1.0	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.	1.2	5
2610	Evaluating microbiome-directed fibre snacks in gnotobiotic mice and humans. <i>Nature</i> , 2021, 595, 91-95.	13.7	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.	4.9	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.	1.0	12

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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.	1.2	1
2617	Simulation study and comparative evaluation of viral contiguous sequence identification tools. <i>BMC Bioinformatics</i> , 2021, 22, 329.	1.2	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.	1.4	7
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2620	Metagenomics of mine tailing rhizospheric communities and its selection for plant establishment towards bioremediation. <i>Microbiological Research</i> , 2021, 247, 126732.	2.5	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.	2.0	9
2622	Viromes in marine ecosystems reveal remarkable invertebrate RNA virus diversity. <i>Science China Life Sciences</i> , 2022, 65, 426-437.	2.3	22
2623	Freshwater <i>Chlorobia</i> Exhibit Metabolic Specialization among Cosmopolitan and Endemic Populations. <i>MSystems</i> , 2021, 6, .	1.7	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.	1.6	2
2626	Arabinogalactan-proteins from non-coniferous gymnosperms have unusual structural features. <i>Carbohydrate Polymers</i> , 2021, 261, 117831.	5.1	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.	1.6	4
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2630	Microbial species performance responses to environmental changes: genomic traits and nutrient availability. <i>Ecology</i> , 2021, 102, e03382.	1.5	3
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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, .	1.1	19
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#	ARTICLE	IF	CITATIONS
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2687	Transcriptome analysis provides insights into copper toxicology in piebald naked carp (<i>Gymnocypris</i>) Tj ETQq0 0 0 rBT /Overlock 10 Tf	1.2	3
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2699	Whole-genome microsynteny-based phylogeny of angiosperms. <i>Nature Communications</i> , 2021, 12, 3498.	5.8	53
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#	ARTICLE	IF	CITATIONS
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2709	Insights into Autotrophic Activities and Carbon Flow in Iron-Rich Pelagic Aggregates (Iron Snow). <i>Microorganisms</i> , 2021, 9, 1368.	1.6	2
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2717	Optimizing experimental design for genome sequencing and assembly with Oxford Nanopore Technologies. <i>GigaByte</i> , 0, 2021, 1-26.	0.0	10
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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.	1.3	13
2722	RaFAH: Host prediction for viruses of Bacteria and Archaea based on protein content. <i>Patterns</i> , 2021, 2, 100274.	3.1	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.	4.4	40
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#	ARTICLE	IF	CITATIONS
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2731	<i>Paraliobacillus salinarum</i> sp. nov., isolated from saline soil in Yingkou, China. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	4
2732	A microbial consortium-based product promotes potato yield by recruiting rhizosphere bacteria involved in nitrogen and carbon metabolisms. <i>Microbial Biotechnology</i> , 2021, 14, 1961-1975.	2.0	8
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2736	Characterization of Spacesuit Associated Microbial Communities and Their Implications for NASA Missions. <i>Frontiers in Microbiology</i> , 2021, 12, 608478.	1.5	5
2737	Root Endophytes and <i>Ginkgo biloba</i> Are Likely to Share and Compensate Secondary Metabolic Processes, and Potentially Exchange Genetic Information by LTR-RTs. <i>Frontiers in Plant Science</i> , 2021, 12, 704985.	1.7	12
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#	ARTICLE	IF	CITATIONS
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2757	Holocene life and microbiome profiling in ancient tropical Lake Chalco, Mexico. <i>Scientific Reports</i> , 2021, 11, 13848.	1.6	8
2758	Sulfate differentially stimulates but is not respired by diverse anaerobic methanotrophic archaea. <i>ISME Journal</i> , 2022, 16, 168-177.	4.4	21
2760	PON-Sol2: Prediction of Effects of Variants on Protein Solubility. <i>International Journal of Molecular Sciences</i> , 2021, 22, 8027.	1.8	10
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2766	orthofisher: a broadly applicable tool for automated gene identification and retrieval. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	12
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#	ARTICLE	IF	CITATIONS
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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, .	1.0	10
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2773	SAUTE: sequence assembly using target enrichment. <i>BMC Bioinformatics</i> , 2021, 22, 375.	1.2	9
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2778	Disproportionate microbial responses to decadal drainage on a Siberian floodplain. <i>Global Change Biology</i> , 2021, 27, 5124-5140.	4.2	8
2780	Dynamics of Baltic Sea phages driven by environmental changes. <i>Environmental Microbiology</i> , 2021, 23, 4576-4594.	1.8	5
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2785	Fishing for the Virome of Tropical Tuna. <i>Viruses</i> , 2021, 13, 1291.	1.5	8
2786	Four chromosome scale genomes and a pan-genome annotation to accelerate pecan tree breeding. <i>Nature Communications</i> , 2021, 12, 4125.	5.8	49
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2788	Complexity and Local Specificity of the Virome Associated with Tospovirus-Transmitting Thrips Species. <i>Journal of Virology</i> , 2021, 95, e0059721.	1.5	25
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2791	Transcriptomic response of <i>Daphnia magna</i> to nitrogen- or phosphorus-limited diet. <i>Ecology and Evolution</i> , 2021, 11, 11009-11019.	0.8	3
2792	Deep Ancestral Introgression Shapes Evolutionary History of Dragonflies and Damselflies. <i>Systematic Biology</i> , 2022, 71, 526-546.	2.7	32
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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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.	0.6	5
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2964	Dynamics of the fecal microbiome and antimicrobial resistome in commercial piglets during the weaning period. <i>Scientific Reports</i> , 2021, 11, 18091.	1.6	5
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2966	Microbiome degrading linear alkylbenzene sulfonate in activated sludge. <i>Journal of Hazardous Materials</i> , 2021, 418, 126365.	6.5	9

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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.	5.3	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.	1.5	7
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#	ARTICLE	IF	CITATIONS
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2988	Comparative analysis of long non-coding RNA expression profiles induced by resveratrol and metformin treatment for hepatic insulin resistance. <i>International Journal of Molecular Medicine</i> , 2021, 48, .	1.8	7
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2992	Chromosome-Level Genome Sequence of <i>Aspergillus chevalieri</i> M1, Isolated from Katsuobushi. <i>Microbiology Resource Announcements</i> , 2021, 10, e0038521.	0.3	1
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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.	3.9	56
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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.	1.6	4
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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.	1.5	3
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3017	OrtSuite: from genomes to prediction of microbial interactions within targeted ecosystem processes. <i>Life Science Alliance</i> , 2021, 4, e202101167.	1.3	4
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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, .	1.5	11
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3032	RNA virome abundance and diversity is associated with host age in a bird species. <i>Virology</i> , 2021, 561, 98-106.	1.1	19
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3041	MINTIA: a metagenomic INserT integrated assembly and annotation tool. <i>PeerJ</i> , 2021, 9, e11885.	0.9	0
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3043	Genomic and Phenotypic Analysis of COVID-19-Associated Pulmonary Aspergillosis Isolates of <i>Aspergillus fumigatus</i> . <i>Microbiology Spectrum</i> , 2021, 9, e0001021.	1.2	31
3044	Comparison of DNA and RNA sequencing of total nucleic acids from human cervix for metagenomics. <i>Scientific Reports</i> , 2021, 11, 18852.	1.6	9
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3051	Struo2: efficient metagenome profiling database construction for ever-expanding microbial genome datasets. <i>PeerJ</i> , 2021, 9, e12198.	0.9	24
3053	Ectomycorrhizal access to organic nitrogen mediates CO2 fertilization response in a dominant temperate tree. <i>Nature Communications</i> , 2021, 12, 5403.	5.8	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.	1.2	6
3056	Genomic Insights into the Ecological Role and Evolution of a Novel <i>Thermoplasmata</i> Order, <i>Ca</i> Candidatus <i>Sysuiplasmatales</i> . <i>Applied and Environmental Microbiology</i> , 2021, 87, e0106521.	1.4	3
3057	Mining nematode protein secretomes to explain lifestyle and host specificity. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009828.	1.3	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.	6.5	24
3060	The Human Gut Resistome up to Extreme Longevity. <i>MSphere</i> , 2021, 6, e0069121.	1.3	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.	1.1	1
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3071	Metagenomics reveals contrasting energy utilization efficiencies of captive and wild camels (<i>Camelus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tff	1.3	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.	1.2	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.	1.3	1
3074	Chromosome-Level Genome Sequence of <i>Aspergillus puulauensis</i> MK2, a Fungus Isolated from a Dead Hard Tick. <i>Microbiology Resource Announcements</i> , 2021, 10, e0037221.	0.3	1
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3076	Microbial Phylogenetic Context Using Phylogenetic Outlines. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	6
3077	The influence of alfalfaâ€switchgrass intercropping on microbial community structure and function. <i>Environmental Microbiology</i> , 2021, 23, 6828-6843.	1.8	5
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3081	The role of pollination in controlling <i>Ginkgo biloba</i> ovule development. <i>New Phytologist</i> , 2021, 232, 2353-2368.	3.5	8
3082	Hydrodynamic disturbance controls microbial community assembly and biogeochemical processes in coastal sediments. <i>ISME Journal</i> , 2022, 16, 750-763.	4.4	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.	1.8	9
3084	Novel Freshwater Cyanophages Provide New Insights into Evolutionary Relationships between Freshwater and Marine Cyanophages. <i>Microbiology Spectrum</i> , 2021, 9, e0059321.	1.2	10
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3087	Effects of Rotations With Legume on Soil Functional Microbial Communities Involved in Phosphorus Transformation. <i>Frontiers in Microbiology</i> , 2021, 12, 661100.	1.5	19
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3098	Infants with cystic fibrosis have altered fecal functional capacities with potential clinical and metabolic consequences. <i>BMC Microbiology</i> , 2021, 21, 247.	1.3	6
3099	Disease-induced changes in plant microbiome assembly and functional adaptation. <i>Microbiome</i> , 2021, 9, 187.	4.9	157
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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.	1.5	7
3104	Belowground responses of bacterial communities to foliar SA application over four plant generations. <i>Plant and Soil</i> , 2022, 470, 65-79.	1.8	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.	4.2	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.	4.8	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.	3.9	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.	2.3	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.	3.9	31

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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.	0.4	1
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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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.	1.8	3
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#	ARTICLE	IF	CITATIONS
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4555	House crickets (Orthoptera: 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.	2.1	0
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#	ARTICLE	IF	CITATIONS
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4574	A mouse model of occult intestinal colonization demonstrating antibiotic-induced outgrowth of carbapenem-resistant <i>Enterobacteriaceae</i> . <i>Microbiome</i> , 2022, 10, 43.	4.9	8
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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4622	Identification and molecular characterization of highly divergent RNA viruses in cattle, Uganda.. <i>Virus Research</i> , 2022, 313, 198739.	1.1	4
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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5560	Identification and genome characterization of novel parechovirus sequences from <i>Hipposideros armiger</i> in China. <i>Virology Journal</i> , 2022, 19, 80.	1.4	0
5561	Tracing RNA viruses associated with <i>Nudibranchia</i> gastropods. <i>PeerJ</i> , 2022, 10, e13410.	0.9	4
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5608	Metagenomic mining of Indian river confluence reveal functional microbial community with lignocellulolytic potential. <i>3 Biotech</i> , 2022, 12, .	1.1	1

#	ARTICLE	IF	CITATIONS
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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, .	1.7	5
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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.	0.8	8
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5651	Influence of Tire Wear Particle Input on Water Purification Efficiency of Bioretention System. <i>SSRN Electronic Journal</i> , 0, .	0.4	0
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5654	The Gut Microbiota Composition of <i>Cnaphalocrocis medinalis</i> and Their Predicted Contribution to Larval Nutrition. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
5655	Mechanisms of Pine Disease Susceptibility Under Experimental Climate Change. <i>Frontiers in Forests and Global Change</i> , 0, 5, .	1.0	3
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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.	1.1	7
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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.	0.7	4
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5671	A phylogenetic and proteomic reconstruction of eukaryotic chromatin evolution. <i>Nature Ecology and Evolution</i> , 2022, 6, 1007-1023.	3.4	26
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5683	SeqScreen: accurate and sensitive functional screening of pathogenic sequences via ensemble learning. <i>Genome Biology</i> , 2022, 23, .	3.8	13
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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