

Interactive Tree Of Life (iTOL) v5: an online tool for phylogenetic annotation

Nucleic Acids Research

49, W293-W296

DOI: [10.1093/nar/gkab301](https://doi.org/10.1093/nar/gkab301)

Citation Report

#	ARTICLE	IF	CITATIONS
1	OUP accepted manuscript. JAC-Antimicrobial Resistance, 2021, 3, dlab147.	0.9	4
8	Identification of a Novel Biosynthetic Gene Cluster in <i>Aspergillus niger</i> Using Comparative Genomics. <i>Journal of Fungi</i> (Basel, Switzerland), 2021, 7, 374.	1.5	8
10	Genomics of Adaptations in Ungulates. <i>Animals</i> , 2021, 11, 1617.	1.0	3
11	Feedborne <i>Salmonella enterica</i> Serovar Jerusalem Outbreak in Different Organic Poultry Flocks in Switzerland and Italy Linked to Soya Expeller. <i>Microorganisms</i> , 2021, 9, 1367.	1.6	2
14	A Molecular Perspective on Colistin and <i>Klebsiella pneumoniae</i> : Mode of Action, Resistance Genetics, and Phenotypic Susceptibility. <i>Diagnostics</i> , 2021, 11, 1165.	1.3	15
16	Gotree/Goalign: toolkit and Go API to facilitate the development of phylogenetic workflows. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab075.	1.5	50
17	Integrated SMRT Technology with UMI RNA-Seq Reveals the Hub Genes in Stamen Petalody in <i>Camellia oleifera</i> . <i>Forests</i> , 2021, 12, 749.	0.9	3
18	Microbial Communities of <i>Cladonia</i> Lichens and Their Biosynthetic Gene Clusters Potentially Encoding Natural Products. <i>Microorganisms</i> , 2021, 9, 1347.	1.6	10
20	Identification of a neural basis for cold acclimation in <i>Drosophila</i> larvae. <i>IScience</i> , 2021, 24, 102657.	1.9	12
21	Genome-wide identification and expression profiling of DREB genes in <i>Saccharum spontaneum</i> . <i>BMC Genomics</i> , 2021, 22, 456.	1.2	20
22	Investigation of <i>Salmonella</i> Phage "Bacteria Infection Profiles: Network Structure Reveals a Gradient of Target-Range from Generalist to Specialist Phage Clones in Nested Subsets. <i>Viruses</i> , 2021, 13, 1261.	1.5	3
23	Taxonomic Revision of the Banana <i>Fusarium</i> Wilt TR4 Pathogen Is Premature. <i>Phytopathology</i> , 2021, 111, 2141-2145.	1.1	14
30	Complete mitochondrial genome of <i>Gazella subgutturosa reginae</i> (Bovidae: Antilopinae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2310-2312.	0.2	3
33	Co-Infection of Infectious Hypodermal and Hematopoietic Necrosis Virus (IHHNV) and White Spot Syndrome Virus (WSSV) in the Wild Crustaceans of Andaman and Nicobar Archipelago, India. <i>Viruses</i> , 2021, 13, 1378.	1.5	6
34	Structure "Activity Relationships of the Enterococcal Cytolysin. <i>ACS Infectious Diseases</i> , 2021, 7, 2445-2454.	1.8	7
35	Systematic Structure-Based Search for Ochratoxin-Degrading Enzymes in Proteomes from Filamentous Fungi. <i>Biomolecules</i> , 2021, 11, 1040.	1.8	10
37	Maternal Phylogenetic Relationships and Genetic Variation among Rare, Phenotypically Similar Donkey Breeds. <i>Genes</i> , 2021, 12, 1109.	1.0	3
38	Seeing the Forest through the (Phylogenetic) Trees: Functional Characterisation of Grapevine Terpene Synthase (VviTPS) Paralogues and Orthologues. <i>Plants</i> , 2021, 10, 1520.	1.6	1

#	ARTICLE	IF	CITATIONS
40	Emergence of IncHI2 Plasmids With Mobilized Colistin Resistance (mcr)-9 Gene in ESBL-Producing, Multidrug-Resistant Salmonella Typhimurium and Its Monophasic Variant ST34 From Food-Producing Animals in Italy. <i>Frontiers in Microbiology</i> , 2021, 12, 705230.	1.5	15
41	Molecular Phylogenetic Analysis of the AIG Family in Vertebrates. <i>Genes</i> , 2021, 12, 1190.	1.0	1
43	Microsatellite-Based Genetic Structure and Hybrid Detection in Alpacas Bred in Poland. <i>Animals</i> , 2021, 11, 2193.	1.0	3
46	Flavonoid-Modifying Capabilities of the Human Gut Microbiome—An In Silico Study. <i>Nutrients</i> , 2021, 13, 2688.	1.7	18
48	Draft Genome Sequence of <i>Bacillus amyloliquefaciens</i> Strain CB, a Biological Control Agent and Plant Growth-Promoting Bacterium Isolated From Cotton (<i>Gossypium L.</i>) Rhizosphere in Coimbatore, Tamil Nadu, India. <i>Frontiers in Genetics</i> , 2021, 12, 704165.	1.1	0
51	Isolation and genetic characterization of a relapsing fever spirochete isolated from <i>Ornithodoros puertoricensis</i> collected in central Panama. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009642.	1.3	14
52	Clandestinovirus: A Giant Virus With Chromatin Proteins and a Potential to Manipulate the Cell Cycle of Its Host <i>Vermamoeba vermiformis</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 715608.	1.5	17
53	Pan-Genome of Novel <i>Pantoea stewartii</i> subsp. <i>indologenes</i> Reveals Genes Involved in Onion Pathogenicity and Evidence of Lateral Gene Transfer. <i>Microorganisms</i> , 2021, 9, 1761.	1.6	5
54	Rapid identification of methylase specificity (RIMS-seq) jointly identifies methylated motifs and generates shotgun sequencing of bacterial genomes. <i>Nucleic Acids Research</i> , 2021, 49, e113-e113.	6.5	9
56	Distribution of SARS-CoV-2 Lineages in the Czech Republic, Analysis of Data from the First Year of the Pandemic. <i>Microorganisms</i> , 2021, 9, 1671.	1.6	7
58	Mitochondrial genomes of five <i>Hyphessobrycon</i> tetras and their phylogenetic implications. <i>Ecology and Evolution</i> , 2021, 11, 12754-12764.	0.8	11
64	SARS-CoV-2 testing and sequencing for international arrivals reveals significant cross border transmission of high risk variants into the United Kingdom. <i>EClinicalMedicine</i> , 2021, 38, 101021.	3.2	24
66	Evidence of an epidemic spread of KPC-producing Enterobacterales in Czech hospitals. <i>Scientific Reports</i> , 2021, 11, 15732.	1.6	12
71	Conditional stomatal closure in a fern shares molecular features with flowering plant active stomatal responses. <i>Current Biology</i> , 2021, 31, 4560-4570.e5.	1.8	12
72	Active Circulation of Madariaga Virus, a Member of the Eastern Equine Encephalitis Virus Complex, in Northeast Brazil. <i>Pathogens</i> , 2021, 10, 983.	1.2	7
74	Isolation and Characterisation of the Bundooravirus Genus and Phylogenetic Investigation of the Salasmaviridae Bacteriophages. <i>Viruses</i> , 2021, 13, 1557.	1.5	7
75	Gene-Metabolite Network Analysis Revealed Tissue-Specific Accumulation of Therapeutic Metabolites in <i>Mallotus japonicus</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 8835.	1.8	3
78	Mixed Acid Fermentation of Carbohydrate-Rich Dairy Manure Hydrolysate. <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 724304.	2.0	11

#	ARTICLE	IF	CITATIONS
81	An exquisitely preserved tiny bark-eating beetle (Coleoptera: Trogossitidae) from mid-Cretaceous Burmese amber and the phylogeny of Trogossitidae. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 0, .	0.6	3
83	Whole genome sequencing of clinical samples reveals extensively drug resistant tuberculosis (XDR) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 42	1.6	8
84	Re-examining the association of AmpC variants with Enterobacter species in the context of updated taxonomy. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, e0159621.	1.4	6
85	Non-Penicillin-Susceptible <i>Streptococcus suis</i> Isolated from Humans. <i>Pathogens</i> , 2021, 10, 1178.	1.2	14
86	Feruloyl esterase Fae1 is required specifically for host colonisation by the rice-blast fungus <i>Magnaporthe oryzae</i> . <i>Current Genetics</i> , 2022, 68, 97-113.	0.8	5
88	<i>Haleganticoccus tardaogens</i> sp. nov., an extremely halophilic archaeon isolated from a saline soil. <i>Extremophiles</i> , 2021, 25, 483-492.	0.9	6
90	Widespread prevalence and molecular epidemiology of tet(X4) and mcr-1 harboring <i>Escherichia coli</i> isolated from chickens in Pakistan. <i>Science of the Total Environment</i> , 2022, 806, 150689.	3.9	17
91	Comparative Analysis of SLA-1, SLA-2, and DQB1 Genetic Diversity in Locally-Adapted Kenyan Pigs and Their Wild Relatives, Warthogs. <i>Veterinary Sciences</i> , 2021, 8, 180.	0.6	2
92	Characterization and identification of lactic acid bacteria from Mexican stingless bees (Apidae:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 42	0.2	4
94	Ongoing Outbreak of Extensively Drug-Resistant <i>Campylobacter jejuni</i> Infections Associated With US Pet Store Puppies, 2016-2020. <i>JAMA Network Open</i> , 2021, 4, e2125203.	2.8	9
95	Tracing Eukaryotic Ribosome Biogenesis Factors Into the Archaeal Domain Sheds Light on the Evolution of Functional Complexity. <i>Frontiers in Microbiology</i> , 2021, 12, 739000.	1.5	11
96	Integrating perspectives in actinomycete research: an ActinoBase review of 2020-21. <i>Microbiology (United Kingdom)</i> , 2021, 167, .	0.7	4
97	Molecular Phylogeny of <i>Trifolium</i> L. Section <i>Trifolium</i> with Reference to Chromosome Number and Subsections Delimitation. <i>Plants</i> , 2021, 10, 1985.	1.6	4
99	Effects of laboratory domestication on the rodent gut microbiome. <i>ISME Communications</i> , 2021, 1, .	1.7	21
102	The taxonomic distribution of histamine-secreting bacteria in the human gut microbiome. <i>BMC Genomics</i> , 2021, 22, 695.	1.2	22
103	Clinical Molecular and Genomic Epidemiology of <i>Morganella morganii</i> in China. <i>Frontiers in Microbiology</i> , 2021, 12, 744291.	1.5	9
107	Cydrasil 3, a curated 16S rRNA gene reference package and web app for cyanobacterial phylogenetic placement. <i>Scientific Data</i> , 2021, 8, 230.	2.4	22
108	Mining nematode protein secretomes to explain lifestyle and host specificity. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009828.	1.3	11

#	ARTICLE	IF	CITATIONS
109	Members of the ELMOD protein family specify formation of distinct aperture domains on the Arabidopsis pollen surface. <i>ELife</i> , 2021, 10, .	2.8	9
110	Primordial Germ Cell Specification in Vertebrate Embryos: Phylogenetic Distribution and Conserved Molecular Features of Preformation and Induction. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 730332.	1.8	21
114	Development of Genome-Wide Functional Markers Using Draft Genome Assembly of Guava (<i>Psidium</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 708332.	1.7	8
115	Discovery of ancestral L-ornithine and L-lysine decarboxylases reveals parallel, pseudoconvergent evolution of polyamine biosynthesis. <i>Journal of Biological Chemistry</i> , 2021, 297, 101219.	1.6	10
116	Genome-Based Taxonomic Rearrangement of the Order Geobacterales Including the Description of <i>Geomonas azotofigans</i> sp. nov. and <i>Geomonas diazotrophica</i> sp. nov.. <i>Frontiers in Microbiology</i> , 2021, 12, 737531.	1.5	59
117	Taxonomy update for the family Alphasatellitidae: new subfamily, genera, and species. <i>Archives of Virology</i> , 2021, 166, 3503-3511.	0.9	15
118	Plasmidome of <i>Listeria</i> spp.â€”The repA-Family Business. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10320.	1.8	7
119	Final Destination? Pinpointing <i>Hyella disjuncta</i> sp. nov. PCC 6712 (Cyanobacteria) Based on Taxonomic Aspects, Multicellularity, Nitrogen Fixation and Biosynthetic Gene Clusters. <i>Life</i> , 2021, 11, 916.	1.1	2
120	Phenogenomic Characterization of a Newly Domesticated and Novel Species from the Genus <i>Verrucosipora</i> . <i>Applied and Environmental Microbiology</i> , 2021, 87, e0132721.	1.4	2
122	Incomplete tricarboxylic acid cycle and proton gradient in <i>Pandoravirus massiliensis</i> : is it still a virus?. <i>ISME Journal</i> , 2022, 16, 695-704.	4.4	16
123	Complete mitochondrial genomes of three reef forming <i>Acropora</i> corals (Acroporidae, Scleractinia) from Chagos Archipelago, Indian Ocean. <i>Biodiversity Data Journal</i> , 2021, 9, e72762.	0.4	5
124	Arbidol targeting influenza virus A Hemagglutinin; A comparative study. <i>Biophysical Chemistry</i> , 2021, 277, 106663.	1.5	9
125	Extracellular Vesicle Proteomes Shed Light on the Evolutionary, Interactive, and Functional Divergence of Their Biogenesis Mechanisms. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 734950.	1.8	7
126	Characterization of a blaNDM-1-Bearing IncHI5-Like Plasmid From <i>Klebsiella pneumoniae</i> of Infant Origin. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 738053.	1.8	9
127	A novel screening method for the detection of <i>Pseudoalteromonas shioyasakiensis</i> , an emerging opportunistic pathogen that caused the mass mortality of juvenile Pacific abalone (<i>Haliotis discus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.7	1
128	Hyaluronidases and hyaluronate lyases: From humans to bacteriophages. <i>Colloids and Surfaces B: Biointerfaces</i> , 2021, 208, 112095.	2.5	9
129	A novel SARS-CoV-2 related coronavirus with complex recombination isolated from bats in Yunnan province, China. <i>Emerging Microbes and Infections</i> , 2021, 10, 1683-1690.	3.0	39
130	The current state of <i>SubtiWiki</i> , the database for the model organism <i>Bacillus subtilis</i> . <i>Nucleic Acids Research</i> , 2022, 50, D875-D882.	6.5	89

#	ARTICLE	IF	CITATIONS
133	BRAD V3.0: an upgraded Brassicaceae database. <i>Nucleic Acids Research</i> , 2022, 50, D1432-D1441.	6.5	89
134	Genomic analysis of 600 vancomycin-resistant <i>Enterococcus faecium</i> reveals a high prevalence of ST80 and spread of similar <i>vanA</i> regions via IS1216E and plasmid transfer in diverse genetic lineages in Ireland. <i>Journal of Antimicrobial Chemotherapy</i> , 2022, 77, 320-330.	1.3	13
136	Phylogeography and Antioxidant Activity of Proso Millet (<i>Panicum miliaceum</i> L.). <i>Plants</i> , 2021, 10, 2112.	1.6	2
138	Development and validation of simultaneous identification of 26 mammalian and poultry species by a multiplex assay. <i>International Journal of Legal Medicine</i> , 2022, 136, 1-12.	1.2	7
140	Hallstatt miners consumed blue cheese and beer during the Iron Age and retained a non-Westernized gut microbiome until the Baroque period. <i>Current Biology</i> , 2021, 31, 5149-5162.e6.	1.8	22
141	Genetic Diversity and Population Structure Revealed by SSR Markers on Endemic Species <i>Osmanthus serrulatus</i> Rehder from Southwestern Sichuan Basin, China. <i>Forests</i> , 2021, 12, 1365.	0.9	4
142	Chromosome-Level Genome Assembly of <i>Cyrtotrachelus buqueti</i> and Mining of Its Specific Genes. <i>Frontiers in Ecology and Evolution</i> , 2021, 9, .	1.1	2
143	Comprehensive Comparative Genomics and Phenotyping of <i>Methylobacterium</i> Species. <i>Frontiers in Microbiology</i> , 2021, 12, 740610.	1.5	20
144	Transmission Dynamics of Carbapenem-Resistant <i>Klebsiella pneumoniae</i> Sequence Type 11 Strains Carrying Capsular Loci KL64 and <i>rmpA/rmpA2</i> Genes. <i>Frontiers in Microbiology</i> , 2021, 12, 736896.	1.5	11
145	Ammonia Oxidizing Prokaryotes Respond Differently to Fertilization and Termination Methods in Common Oat's Rhizosphere. <i>Frontiers in Microbiology</i> , 2021, 12, 746524.	1.5	2
146	More than meets the eye: decrypting diversity reveals hidden interaction specificity between frogs and frog-biting midges. <i>Ecological Entomology</i> , 2022, 47, 95-108.	1.1	6
147	Identification, Molecular Characteristic, and Expression Analysis of PIFs Related to Chlorophyll Metabolism in Tea Plant (<i>Camellia sinensis</i>). <i>International Journal of Molecular Sciences</i> , 2021, 22, 10949.	1.8	4
148	Discovery of a Kojibiose Hydrolase by Analysis of Specificity-Determining Correlated Positions in Glycoside Hydrolase Family 65. <i>Molecules</i> , 2021, 26, 6321.	1.7	6
151	Characterization of HIV-1 Epidemic in Kyrgyzstan. <i>Frontiers in Microbiology</i> , 2021, 12, 753675.	1.5	10
152	A tale of two STs: molecular and clinical epidemiology of MRSA t304 in Norway 2008–2016. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2022, 41, 209-218.	1.3	5
153	CRISPR-Cas systems are widespread accessory elements across bacterial and archaeal plasmids. <i>Nucleic Acids Research</i> , 2022, 50, 4315-4328.	6.5	44
154	Study on the Characteristic Codon Usage Pattern in Porcine Epidemic Diarrhea Virus Genomes and Its Host Adaptation Phenotype. <i>Frontiers in Microbiology</i> , 2021, 12, 738082.	1.5	14
156	Functional Characterization of the Nep1-Like Protein Effectors of the Necrotrophic Pathogen " <i>Alternaria brassicae</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 738617.	1.5	11

#	ARTICLE	IF	CITATIONS
157	Novel Binding Partners for CCT and PhLP1 Suggest a Common Folding Mechanism for WD40 Proteins with a 7-Bladed Beta-Propeller Structure. <i>Proteomes</i> , 2021, 9, 40.	1.7	0
158	The first third-generation HIV-1 circulating recombinant form (CRF114_0155) identified in central China. <i>Archives of Virology</i> , 2021, 166, 3409-3416.	0.9	2
159	Phylogenomics of Haloarchaea: The Controversy of the Genera <i>Natrinema</i> - <i>Haloterrigena</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 740909.	1.5	66
162	Sugar transporters in grasses: Function and modulation in source and storage tissues. <i>Journal of Plant Physiology</i> , 2021, 266, 153541.	1.6	9
163	Virome analysis of three Ixodidae ticks species from Colombia: A potential strategy for discovering and surveying tick-borne viruses. <i>Infection, Genetics and Evolution</i> , 2021, 96, 105103.	1.0	5
164	Identification and molecular characterization of the high-affinity copper transporters family in <i>Solanum lycopersicum</i> . <i>International Journal of Biological Macromolecules</i> , 2021, 192, 600-610.	3.6	10
165	Galloway-Mowat syndrome: New insights from bioinformatics and expression during <i>Xenopus</i> embryogenesis. <i>Gene Expression Patterns</i> , 2021, 42, 119215.	0.3	4
166	An Explorative Tool for Mutation Tracking in the Spike Glycoprotein of SARS-CoV-2. , 2021, , .		0
167	Genomic Epidemiology Reveals Multiple Introductions of Severe Acute Respiratory Syndrome Coronavirus 2 in Niigata City, Japan, Between February and May 2020. <i>Frontiers in Microbiology</i> , 2021, 12, 749149.	1.5	4
168	Establishment of a Publicly Available Core Genome Multilocus Sequence Typing Scheme for <i>Clostridium perfringens</i> . <i>Microbiology Spectrum</i> , 2021, 9, e0053321.	1.2	5
170	<i>Clarireedia hainanense</i>: A New Species Is Associated with Dollar Spot of Turfgrass in Hainan, China. <i>Plant Disease</i> , 2022, 106, 996-1002.	0.7	6
171	Evolutionary genomics and biosynthetic potential of novel environmental Actinobacteria. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 8805-8822.	1.7	3
172	Status quo of <i>tet</i> regulation in bacteria. <i>Microbial Biotechnology</i> , 2022, 15, 1101-1119.	2.0	16
173	Discovery of two novel oxidases using a high-throughput activity screen. <i>ChemBioChem</i> , 2021, , .	1.3	4
174	Sacbrood viruses cross-infection between <i>Apis cerana</i> and <i>Apis mellifera</i> : Rapid detection, viral dynamics, evolution and spillover risk assessment. <i>Journal of Invertebrate Pathology</i> , 2021, 186, 107687.	1.5	3
176	Identification of defense related gene families and their response against powdery and downy mildew infections in <i>Vitis vinifera</i> . <i>BMC Genomics</i> , 2021, 22, 776.	1.2	8
177	Emergence of Tigecycline Nonsusceptible and IMP-4 Carbapenemase-Producing K2-ST65 Hypervirulent <i>Klebsiella pneumoniae</i> in China. <i>Microbiology Spectrum</i> , 2021, 9, e0130521.	1.2	17
178	Whole Genome Sequencing and Comparative Genome Analyses of <i>Chlamydia abortus</i> Strains of Avian Origin Suggests That <i>Chlamydia abortus</i> Species Should Be Expanded to Include Avian and Mammalian Subgroups. <i>Pathogens</i> , 2021, 10, 1405.	1.2	14

#	ARTICLE	IF	CITATIONS
179	Genomic Analysis of Prophages from <i>Klebsiella pneumoniae</i> Clinical Isolates. <i>Microorganisms</i> , 2021, 9, 2252.	1.6	14
180	High molecular weight glutenin gene diversity in <i>Aegilops tauschii</i> demonstrates unique origin of superior wheat quality. <i>Communications Biology</i> , 2021, 4, 1242.	2.0	14
183	Lipid synthesis at the trophic base as the source for energy management to build complex structures. <i>Current Opinion in Biotechnology</i> , 2022, 73, 364-373.	3.3	1
184	Investigation of a Limited but Explosive COVID-19 Outbreak in a German Secondary School. <i>SSRN Electronic Journal</i> , 0, , .	0.4	2
185	Glue Genes Are Subjected to Diverse Selective Forces during <i>Drosophila</i> Development. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	5
186	The Evolutionary Landscape of SARS-CoV-2 Variant B.1.1.519 and Its Clinical Impact in Mexico City. <i>Viruses</i> , 2021, 13, 2182.	1.5	31
188	Chloroplast Genome Draft of <i>Dryobalanops aromatica</i> Generated Using Oxford Nanopore Technology and Its Potential Application for Phylogenetic Study. <i>Forests</i> , 2021, 12, 1515.	0.9	1
189	Identification and characterization of a noncanonical menaquinone-linked formate dehydrogenase. <i>Journal of Biological Chemistry</i> , 2022, 298, 101384.	1.6	11
190	Sequencing of the Complete Mitochondrial Genome of <i>Pingus sinensis</i> (Spirurina: Quimperidae): Gene Arrangements and Phylogenetic Implications. <i>Genes</i> , 2021, 12, 1772.	1.0	4
191	Phylogenetic Analysis Reveals Source Attribution Patterns for <i>Campylobacter</i> spp. in Tennessee and Pennsylvania. <i>Microorganisms</i> , 2021, 9, 2300.	1.6	9
194	Identification of Glutathione Peroxidase Gene Family in <i>Ricinus communis</i> and Functional Characterization of RcGPX4 in Cold Tolerance. <i>Frontiers in Plant Science</i> , 2021, 12, 707127.	1.7	6
196	The and beta-tubulin genes cannot substitute for loss of the beta-tubulin gene. <i>MicroPublication Biology</i> , 2021, 2021, .	0.1	1
197	In silico genome mining of potential novel biosynthetic gene clusters for drug discovery from <i>Burkholderia</i> bacteria. <i>Computers in Biology and Medicine</i> , 2022, 140, 105046.	3.9	6
198	Genome-wide analysis of V-ATPase genes in <i>Plutella xylostella</i> (L.) and the potential role of PxVHA-G1 in resistance to <i>Bacillus thuringiensis</i> Cry1Ac toxin. <i>International Journal of Biological Macromolecules</i> , 2022, 194, 74-83.	3.6	4
199	Molecular detection and characterization of the endosymbiont <i>Wolbachia</i> in the European hedgehog flea, <i>Archaeopsylla erinacei</i> . <i>Infection, Genetics and Evolution</i> , 2022, 97, 105161.	1.0	2
200	Functional genomic analyses reveal an open pan-genome for the chloroviruses and a potential for genetic innovation in new isolates. <i>Journal of Virology</i> , 2021, , JVI0136721.	1.5	8
201	Identification and characterization of histones in <i>Physarum polycephalum</i> evidence a phylogenetic vicinity of Mycetozoans to the animal kingdom. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab107.	1.5	3
202	Metabolism of key atmospheric volatile organic compounds by the marine heterotrophic bacterium <i>Pelagibacter</i> HTCC1062 (<sc>SAR11</sc>). <i>Environmental Microbiology</i> , 2022, 24, 212-222.	1.8	9

#	ARTICLE	IF	CITATIONS
207	Population genetic and genomic analyses of Western Massasauga (<i>Sistrurus tergeminus</i> ssp.): implications for subspecies delimitation and conservation. <i>Conservation Genetics</i> , 2022, 23, 271-283.	0.8	3
208	Going Forward and Back: The Complex Evolutionary History of the GPx. <i>Biology</i> , 2021, 10, 1165.	1.3	15
209	Absence of Resistance Mutations in the Integrase Coding Region among ART-Experienced Patients in the Republic of the Congo. <i>Microorganisms</i> , 2021, 9, 2355.	1.6	0
210	Maturation of 23S rRNA includes removal of helix H1 in many bacteria. <i>RNA Biology</i> , 2021, , 1-10.	1.5	3
211	First Record of <i>Trichobilharzia physellae</i> (Talbot, 1936) in Europe, a Possible Causative Agent of Cercarial Dermatitis. <i>Pathogens</i> , 2021, 10, 1473.	1.2	8
213	Can the SARS-CoV-2 Spike Protein Bind Integrins Independent of the RGD Sequence?. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 765300.	1.8	12
214	Comparative Analysis of Herbaceous and Woody Cell Wall Digestibility by Pathogenic Fungi. <i>Molecules</i> , 2021, 26, 7220.	1.7	2
216	Presence and Persistence of Putative Lytic and Temperate Bacteriophages in Vaginal Metagenomes from South African Adolescents. <i>Viruses</i> , 2021, 13, 2341.	1.5	8
217	Evolution of Rosaceae Plastomes Highlights Unique <i>Cerasus</i> Diversification and Independent Origins of Fruiting Cherry. <i>Frontiers in Plant Science</i> , 2021, 12, 736053.	1.7	10
218	Carbapenem-Resistant <i>Citrobacter</i> spp. as an Emerging Concern in the Hospital-Setting: Results From a Genome-Based Regional Surveillance Study. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 744431.	1.8	23
219	β -elimination of hyaluronate by red king crab hyaluronidase. <i>Scientific Reports</i> , 2021, 11, 22600.	1.6	7
220	Emergence of novel avian origin H7N9 viruses after introduction of H7N9 and rLN79 vaccine strains to China. <i>Transboundary and Emerging Diseases</i> , 2022, 69, 213-220.	1.3	10
221	Genome-wide identification and expression analysis of ethylene responsive factor family transcription factors in <i>Juglans regia</i> . <i>PeerJ</i> , 2021, 9, e12429.	0.9	9
227	Genome-wide survey and characterization of transcription factors in the silk gland of the silkworm, <i>Bombyx mori</i> . <i>PLoS ONE</i> , 2021, 16, e0259870.	1.1	3
228	Intraspecies Genomic Divergence of a Fig Wasp Species Is Due to Geographical Barrier and Adaptation. <i>Frontiers in Ecology and Evolution</i> , 2021, 9, .	1.1	1
229	A phosphorus limitation induced, functionally conserved DUF506 protein is a repressor of root hair elongation in plants. <i>New Phytologist</i> , 2022, 233, 1153-1171.	3.5	10
231	Comprehensive Analysis of the SUV Gene Family in Allopolyploid <i>Brassica napus</i> and Its Diploid Ancestors. <i>Genes</i> , 2021, 12, 1848.	1.0	1
232	Metagenome-assembled genomes and gene catalog from the chicken gut microbiome aid in deciphering antibiotic resistomes. <i>Communications Biology</i> , 2021, 4, 1305.	2.0	49

#	ARTICLE	IF	CITATIONS
233	Comparative Genomic and Pan-Genomic Characterization of <i>Staphylococcus epidermidis</i> From Different Sources Unveils the Molecular Basis and Potential Biomarkers of Pathogenic Strains. <i>Frontiers in Microbiology</i> , 2021, 12, 770191.	1.5	4
234	Lipid transfer protein allergy: A review of current controversies. <i>Clinical and Experimental Allergy</i> , 2022, 52, 222-230.	1.4	13
238	A class I histone deacetylase HDA-2 is essential for embryonic development and size regulation of fertilized eggs in <i>Caenorhabditis elegans</i> . <i>Genes and Genomics</i> , 2021, , 1.	0.5	1
239	The Diversity and Nitrogen Metabolism of Culturable Nitrate-Utilizing Bacteria Within the Oxygen Minimum Zone of the Changjiang (Yangtze River) Estuary. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	4
240	Genomic surveillance of <i>Neisseria meningitidis</i> serogroup W in Portugal from 2003 to 2019. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2022, 41, 289-298.	1.3	3
241	Detecting Flavobacterial Fish Pathogens in the Environment via High-Throughput Community Analysis. <i>Applied and Environmental Microbiology</i> , 2022, 88, AEM0209221.	1.4	6
242	A spatial&temporal understanding of gene regulatory networks and NtARF-mediated regulation of potassium accumulation in tobacco. <i>Planta</i> , 2022, 255, 9.	1.6	5
243	De novo leaf transcriptome of a triploid linalool chemotype of <i>Lippia alba</i> (Mill.) N.E.Br. ex Britton & P. Wilson. <i>Revista Brasileira De Botanica</i> , 2021, 44, 889-901.	0.5	2
245	LectinOracle: A Generalizable Deep Learning Model for Lectin&Glycan Binding Prediction. <i>Advanced Science</i> , 2022, 9, e21103807.	5.6	18
246	Genomic evidence of SARS&CoV&2 reinfection in the Republic of Korea. <i>Journal of Medical Virology</i> , 2022, 94, 1717-1722.	2.5	2
247	Saline lakes on the Qinghai-Tibet Plateau harbor unique viral assemblages mediating microbial environmental adaptation. <i>IScience</i> , 2021, 24, 103439.	1.9	13
248	The <sc>miR</sc>â&282&5p regulates larval moulting process by targeting chitinase 5 in <i>Bombyx mori</i>. <i>Insect Molecular Biology</i> , 2022, 31, 190-201.	1.0	9
249	Bacterial microcompartments in food-related microbes. <i>Current Opinion in Food Science</i> , 2022, 43, 128-135.	4.1	4
252	<i>Streptomyces aureorectus</i> DSM 41692 and <i>Streptomyces virens</i> DSM 41465 are producers of the antibiotic nucleocidin and 4&2-fluoroadenosine is identified as a co-product. <i>Organic and Biomolecular Chemistry</i> , 2021, 19, 10081-10084.	1.5	7
253	The Power of Universal Contextualized Protein Embeddings in Cross-species Protein Function Prediction. <i>Evolutionary Bioinformatics</i> , 2021, 17, 117693432110626.	0.6	4
254	Genome-Wide Identification of R2R3-MYB Transcription Factors: Discovery of a &DiacuteDual-Function&Diacute Regulator of Gypenoside and Flavonol Biosynthesis in <i>Gynostemma pentaphyllum</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 796248.	1.7	6
255	The Sperm Protein Spaca6 is Essential for Fertilization in Zebrafish. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 806982.	1.8	13
257	Sequence Divergence and Functional Specializations of the Ancient Spliceosomal SF3b: Implications in Flexibility and Adaptations of the Multi-Protein Complex. <i>Frontiers in Genetics</i> , 2021, 12, 747344.	1.1	1

#	ARTICLE	IF	CITATIONS
258	Evolution of holocentric chromosomes: Drivers, diversity, and deterrents. <i>Seminars in Cell and Developmental Biology</i> , 2022, 127, 90-99.	2.3	15
261	Genome-Wide Identification and Characterization of the RCI2 Gene Family in Allotetraploid <i>Brassica napus</i> Compared with Its Diploid Progenitors. <i>International Journal of Molecular Sciences</i> , 2022, 23, 614.	1.8	5
262	On the expansion of biological functions of lytic polysaccharide monooxygenases. <i>New Phytologist</i> , 2022, 233, 2380-2396.	3.5	59
264	Investigation of a Limited but Explosive COVID-19 Outbreak in a German Secondary School. <i>Viruses</i> , 2022, 14, 87.	1.5	16
265	The CbbQO-type rubisco activases encoded in carboxysome gene clusters can activate carboxysomal form IA rubiscos. <i>Journal of Biological Chemistry</i> , 2022, 298, 101476.	1.6	5
266	A novel gene order and remolded tRNAs revealed in the mitogenome of Asian gecarcinucid freshwater crabs (<i>Brachyura</i> , <i>Gecarcinucidae</i>). <i>Gene</i> , 2022, 813, 146102.	1.0	1
267	Potential epigenetic regulation of RNA 5' terminal NAD decapping associated with cellular energy status of postharvest <i>Fragaria</i> — <i>ananassa</i> in response to <i>Botrytis cinerea</i> invasion. <i>Postharvest Biology and Technology</i> , 2022, 186, 111840.	2.9	16
268	Diversity and Function of Wolf Spider Gut Microbiota Revealed by Shotgun Metagenomics. <i>Frontiers in Microbiology</i> , 2021, 12, 758794.	1.5	7
269	Alterations in chromosomal genes <i>nfsA</i> , <i>nfsB</i> , and <i>ribE</i> are associated with nitrofurantoin resistance in <i>Escherichia coli</i> from the United Kingdom. <i>Microbial Genomics</i> , 2021, 7, .	1.0	9
270	Genomic Characterization of Carbapenem-Non-susceptible <i>Pseudomonas aeruginosa</i> Clinical Isolates From Saudi Arabia Revealed a Global Dissemination of GES-5-Producing ST235 and VIM-2-Producing ST233 Sub-Lineages. <i>Frontiers in Microbiology</i> , 2021, 12, 765113.	1.5	13
272	Actinoporin-like Proteins Are Widely Distributed in the Phylum Porifera. <i>Marine Drugs</i> , 2022, 20, 74.	2.2	2
273	The Mouse Gastrointestinal Bacteria Catalogue enables translation between the mouse and human gut microbiotas via functional mapping. <i>Cell Host and Microbe</i> , 2022, 30, 124-138.e8.	5.1	59
275	The Landscape of Autophagy-Related (ATG) Genes and Functional Characterization of TaVAMP727 to Autophagy in Wheat. <i>International Journal of Molecular Sciences</i> , 2022, 23, 891.	1.8	2
276	Comparative Transcriptome Analysis in <i>Taraxacum koksaghyz</i> to Identify Genes that Determine Root Volume and Root Length. <i>Frontiers in Genetics</i> , 2021, 12, 784883.	1.1	1
278	Synthesis of Nuclear and Chloroplast Data Combined With Network Analyses Supports the Polyploid Origin of the Apple Tribe and the Hybrid Origin of the Maleae "Gillenieae" Clade. <i>Frontiers in Plant Science</i> , 2021, 12, 820997.	1.7	16
279	ITS DNA Barcoding Reveals That <i>Halophila stipulacea</i> Still Remains the Only Non-Indigenous Seagrass of the Mediterranean Sea. <i>Diversity</i> , 2022, 14, 76.	0.7	5
280	Genome Analysis of <i>Klebsiella oxytoca</i> Complex for Antimicrobial Resistance and Virulence Genes. <i>Antimicrobial Agents and Chemotherapy</i> , 2022, 66, aac0218321.	1.4	8
281	Genomic Epidemiology of <i>Salmonella enterica</i> Circulating in Surface Waters Used in Agriculture and Aquaculture in Central Mexico. <i>Applied and Environmental Microbiology</i> , 2022, 88, aem0214921.	1.4	6

#	ARTICLE	IF	CITATIONS
282	From Genome Sequencing to CRISPR-Based Genome Editing for Climate-Resilient Forest Trees. <i>International Journal of Molecular Sciences</i> , 2022, 23, 966.	1.8	16
285	Analysis of glucose and xylose metabolism in new indigenous <i>Meyerozyma caribbica</i> strains isolated from corn residues. <i>World Journal of Microbiology and Biotechnology</i> , 2022, 38, 35.	1.7	10
286	Identification of methicillin-resistant <i>Staphylococcus aureus</i> ST8 isolates in China with potential high virulence. <i>Emerging Microbes and Infections</i> , 2022, 11, 507-518.	3.0	7
287	Negative Modulation of the Angiogenic Cascade Induced by Allosteric Kinesin Eg5 Inhibitors in a Gastric Adenocarcinoma In Vitro Model. <i>Molecules</i> , 2022, 27, 957.	1.7	10
288	C Proteins: Controllers of Orderly Paramyxovirus Replication and of the Innate Immune Response. <i>Viruses</i> , 2022, 14, 137.	1.5	9
289	Molecular Evolution of Tubulins in Diatoms. <i>International Journal of Molecular Sciences</i> , 2022, 23, 618.	1.8	4
291	Redefining the coenzyme A transferase superfamily with a large set of manually annotated proteins. <i>Protein Science</i> , 2022, 31, 864-881.	3.1	9
292	Evolutionary and mechanistic diversity of Type I-F CRISPR-associated transposons. <i>Molecular Cell</i> , 2022, 82, 616-628.e5.	4.5	36
293	Whole-Genome Sequence of a Porcine Circovirus Type 2 Strain Detected in Assam, India. <i>Microbiology Resource Announcements</i> , 2022, 11, e0059321.	0.3	1
295	Phylum Gemmatimonadota and Its Role in the Environment. <i>Microorganisms</i> , 2022, 10, 151.	1.6	69
296	In Silico Predictions of Ecological Plasticity Mediated by Protein Family Expansions in Early-Diverging Fungi. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 67.	1.5	3
297	Wheat stem rust recorded for the first time in decades in Ireland. <i>Plant Pathology</i> , 2022, 71, 890-900.	1.2	7
298	Born in the mitochondrion and raised in the nucleus: Evolution of a novel tandem repeat family in <i>Medicago polymorpha</i> (Fabaceae). <i>Plant Journal</i> , 2022, , .	2.8	5
299	Exploring the role of framework mutations in enabling breadth of a cross-reactive antibody (CR3022) against the SARS-CoV-2 RBD and its variants of concern. <i>Journal of Biomolecular Structure and Dynamics</i> , 2023, 41, 2341-2354.	2.0	5
300	Microbial Consortia Involved in Traditional Sicilian Sourdough: Characterization of Lactic Acid Bacteria and Yeast Populations. <i>Microorganisms</i> , 2022, 10, 283.	1.6	13
301	Replication initiator proteins of <i>Acinetobacter baumannii</i> plasmids: An update note. <i>Plasmid</i> , 2022, 119-120, 102616.	0.4	6
302	Assessment of marine benthic diatom communities: insights from a combined morphological and metabarcoding approach in Mediterranean shallow coastal waters. <i>Marine Pollution Bulletin</i> , 2022, 174, 113183.	2.3	13
303	Occurrence of Rotavirus A Genotypes and Other Enteric Pathogens in Diarrheic Suckling Piglets from Spanish Swine Farms. <i>Animals</i> , 2022, 12, 251.	1.0	6

#	ARTICLE	IF	CITATIONS
305	Evolutionary analyses of the gasdermin family suggest conserved roles in infection response despite loss of pore-forming functionality. <i>BMC Biology</i> , 2022, 20, 9.	1.7	35
306	Genome-Wide Prediction, Functional Divergence, and Characterization of Stress-Responsive BZR Transcription Factors in <i>B. napus</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 790655.	1.7	12
307	Connexins evolved after early chordates lost innexin diversity. <i>ELife</i> , 2022, 11, .	2.8	7
308	Lifespan prolonging mechanisms and insulin upregulation without fat accumulation in long-lived reproductives of a higher termite. <i>Communications Biology</i> , 2022, 5, 44.	2.0	27
309	Clues to reaction specificity in PLP-dependent fold type I aminotransferases of monosaccharide biosynthesis. <i>Proteins: Structure, Function and Bioinformatics</i> , 2022, 90, 1247-1258.	1.5	0
310	Characterisation of tetraspanins from <i>Schistosoma haematobium</i> and evaluation of their potential as novel diagnostic markers. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010151.	1.3	5
311	Characteristics of SARS-CoV-2 transmission in a medium-sized city with traditional communities during the early COVID-19 epidemic in China. <i>Virologica Sinica</i> , 2022, 37, 187-197.	1.2	4
313	Epidemiology and Genetic Analysis of SARS-CoV-2 in Myanmar during the Community Outbreaks in 2020. <i>Viruses</i> , 2022, 14, 259.	1.5	2
314	Revisiting the intragenetic structure of the genus <i>Pseudomonas</i> with complete whole genome sequence information: Insights into diversity and pathogen-related genetic determinants. <i>Infection, Genetics and Evolution</i> , 2022, 97, 105183.	1.0	6
316	Genomic Changes within a Subset of IncI2 Plasmids Associated with Dissemination of mcr-1 Genes and Other Important Antimicrobial Resistance Determinants. <i>Antibiotics</i> , 2022, 11, 181.	1.5	3
317	Identifying temporal and spatial patterns of variation from multimodal data using MEFISTO. <i>Nature Methods</i> , 2022, 19, 179-186.	9.0	63
318	The Planctomycetia: an overview of the currently largest class within the phylum Planctomycetes. <i>Antonie Van Leeuwenhoek</i> , 2022, 115, 169-201.	0.7	24
319	A Brief History of Giant Viruses™ Studies in Brazilian Biomes. <i>Viruses</i> , 2022, 14, 191.	1.5	4
320	Complete chloroplast genome of <i>Campsis grandiflora</i> (Thunb.) schum and systematic and comparative analysis within the family Bignoniaceae. <i>Molecular Biology Reports</i> , 2022, 49, 3085-3098.	1.0	6
321	Co-occurrence Interaction Networks of Extremophile Species Living in a Copper Mining Tailing. <i>Frontiers in Microbiology</i> , 2021, 12, 791127.	1.5	6
322	Newly identified HMO-2011-type phages reveal genomic diversity and biogeographic distributions of this marine viral group. <i>ISME Journal</i> , 2022, 16, 1363-1375.	4.4	8
323	Comparative Genome Analysis Reveals Accumulation of Single-Nucleotide Repeats in Pathogenic <i>Escherichia</i> Lineages. <i>Current Issues in Molecular Biology</i> , 2022, 44, 498-504.	1.0	0
324	Genomic insights into versatile lifestyle of three new bacterial candidate phyla. <i>Science China Life Sciences</i> , 2022, 65, 1547-1562.	2.3	8

#	ARTICLE	IF	CITATIONS
325	Population structure analysis and laboratory monitoring of <i>Shigella</i> by core-genome multilocus sequence typing. <i>Nature Communications</i> , 2022, 13, 551.	5.8	17
326	Predicting the capsid architecture of phages from metagenomic data. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 721-732.	1.9	10
328	Genomic Diversity of Bacteriophages Infecting the Genus <i>Acinetobacter</i> . <i>Viruses</i> , 2022, 14, 181.	1.5	12
330	Comparative Genome Analysis of Three <i>Komagataeibacter</i> Strains Used for Practical Production of Nata-de-Coco. <i>Frontiers in Microbiology</i> , 2021, 12, 798010.	1.5	1
331	Integrated Analysis of Transcriptome and Proteome to Reveal Pupal Color Switch in <i>Papilio xuthus</i> Butterflies. <i>Frontiers in Genetics</i> , 2021, 12, 795115.	1.1	1
332	Research note: The resistome of commensal <i>Escherichia coli</i> isolated from broiler carcasses produced without the use of antibiotics. <i>Poultry Science</i> , 2022, 101, 101770.	1.5	6
333	The complete mitochondrial genome of <i>Hyalomma rufipes</i> (Acari: Ixodidae) from China and comparative analysis of mitogenomes in genus <i>Hyalomma</i> . <i>International Journal of Acarology</i> , 0, , 1-11.	0.3	2
334	Sentinel Surveillance Reveals Emerging Daptomycin-Resistant ST736 <i>Enterococcus faecium</i> and Multiple Mechanisms of Linezolid Resistance in <i>Enterococci</i> in the United States. <i>Frontiers in Microbiology</i> , 2021, 12, 807398.	1.5	2
335	Discrimination between Carbapenem-Resistant and Carbapenem-Sensitive <i>Klebsiella pneumoniae</i> Strains through Computational Analysis of Surface-Enhanced Raman Spectra: a Pilot Study. <i>Microbiology Spectrum</i> , 2022, 10, e0240921.	1.2	22
336	Large-Scale Phylogenetic Analysis Reveals a New Genetic Clade among <i>Escherichia coli</i> O26 Strains. <i>Microbiology Spectrum</i> , 2022, 10, e0252521.	1.2	1
337	Comparative Study in Zebrafish and Medaka Unravels the Mechanisms of Tissue Regeneration. <i>Frontiers in Ecology and Evolution</i> , 2022, 10, .	1.1	8
338	A novel C-terminal DxRSDxE motif in ceramide synthases involved in dimer formation. <i>Journal of Biological Chemistry</i> , 2022, 298, 101517.	1.6	12
339	Phylogenomic classification and synteny network analyses deciphered the evolutionary landscape of aldo-keto reductase (AKR) gene superfamily in the plant kingdom. <i>Gene</i> , 2022, 816, 146169.	1.0	4
340	Classical aquaporins from Pacific white shrimp (<i>Litopenaeus vannamei</i>): Molecular characterization and expression analysis in hypersalinity. <i>Aquaculture Reports</i> , 2022, 23, 101016.	0.7	3
341	Viral metagenomics unveiled extensive communications of viruses within giant pandas and their associated organisms in the same ecosystem. <i>Science of the Total Environment</i> , 2022, 820, 153317.	3.9	22
342	Antarctic fungi applied to textile dye bioremediation. <i>Anais Da Academia Brasileira De Ciencias</i> , 2022, 94, e20210234.	0.3	4
343	Mitochondrial Genome Architecture and Evolutionary Origin of the Yao Silkworm, a Living Fossil of the Domestic Silkworm <i>Bombyx mori</i> (Lepidoptera: Bombycidae). <i>Journal of Insect Science</i> , 2022, 22, .	0.6	1
344	KaruBioNet: a network and discussion group for a better collaboration and structuring of bioinformatics in Guadeloupe (French West Indies). <i>Bioinformatics Advances</i> , 2022, 2, .	0.9	7

#	ARTICLE	IF	CITATIONS
345	Identification of Olfactory Genes in <i>Monochamus saltuarius</i> and Effects of <i>Bursaphelenchus xylophilus</i> Infestation on Their Expression. <i>Forests</i> , 2022, 13, 258.	0.9	5
347	Aquaporins in Pacific White Shrimp (<i>Litopenaeus vannamei</i>): Molecular Characterization, Expression Patterns, and Transcriptome Analysis in Response to Salinity Stress. <i>Frontiers in Marine Science</i> , 2022, 9, .	1.2	4
348	Specificity of mouse and human Fcγ receptors and their polymorphic variants for IgG subclasses of different species. <i>European Journal of Immunology</i> , 2022, 52, 753-759.	1.6	15
350	Plant GATA Factors: Their Biology, Phylogeny, and Phylogenomics. <i>Annual Review of Plant Biology</i> , 2022, 73, 123-148.	8.6	28
352	Polymerase chain reaction and loop-mediated isothermal amplification targeting <i>lic13162</i> , <i>lic20239</i> , and <i>lipL32</i> genes for leptospirosis diagnosis. <i>Brazilian Journal of Microbiology</i> , 2022, 53, 1029-1037.	0.8	1
353	Genome-Wide Analysis of U-box E3 Ubiquitin Ligase Family in Response to ABA Treatment in <i>Salvia miltiorrhiza</i> . <i>Frontiers in Plant Science</i> , 2022, 13, 829447.	1.7	5
355	Molecular characterization of the phytopathogen <i>C. theae</i> (Petch) "Causative of birds eye spot infection in <i>Camellia sinensis</i> host through DNA polymorphism and proteome analysis techniques. <i>Physiological and Molecular Plant Pathology</i> , 2022, 118, 101809.	1.3	0
359	<i>Pseudonocardia humida</i> sp. nov., an Actinomycete Isolated from Mangrove Soil Showing Distinct Distribution Pattern of Biosynthetic Gene Clusters. <i>Current Microbiology</i> , 2022, 79, 87.	1.0	1
361	Species Composition and Distribution of the Vector Aphids of PVY and PLRV in India. <i>Potato Research</i> , 0, , 1.	1.2	0
364	A novel mitochondrial genome haplotype in <i>Parantica sita sita</i> (Lepidoptera: Nymphalidae: Danainae) indicates substantial intraspecific genetic divergence. <i>Applied Entomology and Zoology</i> , 2022, 57, 109.	0.6	1
365	Genome-wide analysis and expression profiling of Cation/H ⁺ exchanger (CAX) family genes reveal likely functions in cadmium stress responses in poplar. <i>International Journal of Biological Macromolecules</i> , 2022, 204, 76-88.	3.6	16
366	Plasmid Mediated <i>mcr-1.1</i> Colistin-Resistance in Clinical Extraintestinal <i>Escherichia coli</i> Strains Isolated in Poland. <i>Frontiers in Microbiology</i> , 2021, 12, 547020.	1.5	10
367	Rapid discovery of diverse neutralizing SARS-CoV-2 antibodies from large-scale synthetic phage libraries. <i>MAbs</i> , 2022, 14, 2002236.	2.6	14
368	Cargo Genes of Tn <i><i>7</i></i> -Like Transposons Comprise an Enormous Diversity of Defense Systems, Mobile Genetic Elements, and Antibiotic Resistance Genes. <i>MBio</i> , 2021, 12, e0293821.	1.8	34
369	Research and Innovation Supporting the European Sustainable and Smart Mobility Strategy: A Technology Perspective from Recent European Union Projects. <i>Applied Sciences (Switzerland)</i> , 2021, 11, 11981.	1.3	11
370	Antimicrobial Susceptibility of <i>Lactobacillus delbrueckii</i> subsp. <i>lactis</i> from Milk Products and Other Habitats. <i>Foods</i> , 2021, 10, 3145.	1.9	5
371	Genomic Analysis of the First European Bacteriophages with Depolymerase Activity and Biocontrol Efficacy against the Phytopathogen <i>Ralstonia solanacearum</i> . <i>Viruses</i> , 2021, 13, 2539.	1.5	9
372	First record of <i>Telenomus fariai</i> Costa Lima, 1927 (Hymenoptera, Scelionidae, Telenominae) as a parasitoid of <i>Triatoma dimidiata</i> (Latreille, 1811) (Hemiptera, Reduviidae, Triatominae) eggs in Mexico. <i>Journal of Hymenoptera Research</i> , 0, 87, 309-322.	0.8	3

#	ARTICLE	IF	CITATIONS
373	<i>Psix striaticeps</i> (Dodd) (Hymenoptera, Scelionidae): an Old World parasitoid of stink bug eggs arrives in Florida, USA. <i>Journal of Hymenoptera Research</i> , 0, 87, 503-521.	0.8	5
374	<i>In silico</i> identification of tetraspanins in monopisthocotylean (Platyhelminthes: Monogenea) parasites of fish. <i>Journal of Helminthology</i> , 2022, 96, e23.	0.4	0
375	Using a pupal exuvia to designate the undamaged neotype of a species belonging to a complex of sibling species – the case of <i>Aedes coluzzii</i> (Diptera, Culicidae). <i>Parasite</i> , 2022, 29, 19.	0.8	1
376	Trans-Regional and Cross-Host Spread of β -Carrying Plasmids Revealed by Complete Plasmid Sequences – 44 Countries, 1998–2020. <i>China CDC Weekly</i> , 2022, 4, 242-248.	1.0	6
377	Genome-wide diversity of Zika virus: Exploring spatio-temporal dynamics to guide a new nomenclature proposal. <i>Virus Evolution</i> , 2022, 8, veac029.	2.2	5
378	Exploring a prolonged enterovirus C104 infection in a severely ill patient using nanopore sequencing. <i>Virus Evolution</i> , 2022, 8, veab109.	2.2	4
379	Omics and Mechanistic Insights into Di-(2-Ethylhexyl) Phthalate Degradation in the O ₂ -Fluctuating Estuarine Sediments. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
380	Prevalence of Antifungal Resistance, Genetic Basis of Acquired Azole and Echinocandin Resistance, and Genotyping of <i>Candida krusei</i> Recovered from an International Collection. <i>Antimicrobial Agents and Chemotherapy</i> , 2022, 66, AAC0185621.	1.4	4
381	Simple molecular based method for selected Oligochaeta (Annelida: Clitellata) genera identification. <i>Biologia (Poland)</i> , 2022, 77, 1083-1087.	0.8	2
382	A Case Building Ciliate in the Genus <i>Pseudoblepharisma</i> Found in Subtropical Fresh Water. <i>Diversity</i> , 2022, 14, 174.	0.7	2
383	<i>Pseudomonas bijieensis</i> Strain XL17 within the <i>P. corrugata</i> Subgroup Producing 2,4-Diacetylphloroglucinol and Lipopeptides Controls Bacterial Canker and Gray Mold Pathogens of Kiwifruit. <i>Microorganisms</i> , 2022, 10, 425.	1.6	15
384	Proteoform Profiles Reveal That Alpha-1-Antitrypsin in Human Serum and Milk Is Derived From a Common Source. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 858856.	1.6	6
386	The Phyllosymbiosis Pattern Between the Fig Wasps of the Same Genus and Their Associated Microbiota. <i>Frontiers in Microbiology</i> , 2021, 12, 800190.	1.5	1
387	Unraveling Nitrogen, Sulfur, and Carbon Metabolic Pathways and Microbial Community Transcriptional Responses to Substrate Deprivation and Toxicity Stresses in a Bioreactor Mimicking Anoxic Brackish Coastal Sediment Conditions. <i>Frontiers in Microbiology</i> , 2022, 13, 798906.	1.5	2
389	A holistic genome dataset of bacteria, archaea and viruses of the Pearl River estuary. <i>Scientific Data</i> , 2022, 9, 49.	2.4	12
390	Genetic Characterization of Multidrug-Resistant <i>E. coli</i> Isolates from Bloodstream Infections in Lithuania. <i>Microorganisms</i> , 2022, 10, 449.	1.6	5
391	Molecular Characterization of the 2020 Outbreak of Lumpy Skin Disease in Nepal. <i>Microorganisms</i> , 2022, 10, 539.	1.6	19
392	<i>Macrococcus armenti</i> sp. nov., a novel bacterium isolated from the skin and nasal cavities of healthy pigs and calves. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	16

#	ARTICLE	IF	CITATIONS
393	Distinct Expansion of Group II Introns During Evolution of Prokaryotes and Possible Factors Involved in Its Regulation. <i>Frontiers in Microbiology</i> , 2022, 13, 849080.	1.5	4
394	Short- and long-read metagenomics of urban and rural South African gut microbiomes reveal a transitional composition and undescribed taxa. <i>Nature Communications</i> , 2022, 13, 926.	5.8	26
395	Protease activities of vaginal <i>Porphyromonas</i> species disrupt coagulation and extracellular matrix in the cervicovaginal niche. <i>Npj Biofilms and Microbiomes</i> , 2022, 8, 8.	2.9	10
398	In-Flight Transmission of a SARS-CoV-2 Lineage B.1.617.2 Harboring the Rare S:E484Q Immune Escape Mutation. <i>Viruses</i> , 2022, 14, 504.	1.5	2
399	Highly Resolved Papilionoid Legume Phylogeny Based on Plastid Phylogenomics. <i>Frontiers in Plant Science</i> , 2022, 13, 823190.	1.7	25
400	Evolutionary adaptation of the Polycomb repressive complex 2. <i>Epigenetics and Chromatin</i> , 2022, 15, 7.	1.8	15
401	Alphaflexivirus Genomes in Stony Coral Tissue Loss Disease-Affected, Disease-Exposed, and Disease-Unexposed Coral Colonies in the U.S. Virgin Islands. <i>Microbiology Resource Announcements</i> , 2022, 11, e0119921.	0.3	10
402	Was the Last Bacterial Common Ancestor a Monoderm after All?. <i>Genes</i> , 2022, 13, 376.	1.0	6
403	Insights Into the Species-Specific Microbiota of Greenideinae (Hemiptera: Aphididae) With Evidence of Phylosymbiosis. <i>Frontiers in Microbiology</i> , 2022, 13, 828170.	1.5	3
404	Active anaerobic methane oxidation and sulfur disproportionation in the deep terrestrial subsurface. <i>ISME Journal</i> , 2022, 16, 1583-1593.	4.4	16
405	A Descriptive Analysis of Urinary ESBL-Producing- <i>Escherichia coli</i> in Cerdanya Hospital. <i>Microorganisms</i> , 2022, 10, 488.	1.6	5
406	Discovery and Characterization of a New Crustin Antimicrobial Peptide from <i>Amphibalanus amphitrite</i> . <i>Pharmaceutics</i> , 2022, 14, 413.	2.0	8
407	Genome-Annotated Bacterial Collection of the Barley Rhizosphere Microbiota. <i>Microbiology Resource Announcements</i> , 2022, 11, e0106421.	0.3	3
408	Comprehensive Analysis of Imipenemase (IMP)-Type Metallo- β -Lactamase: A Global Distribution Threatening Asia. <i>Antibiotics</i> , 2022, 11, 236.	1.5	7
409	Genome-Wide Comparative Analysis of the R2R3-MYB Gene Family in Five Solanaceae Species and Identification of Members Regulating Carotenoid Biosynthesis in Wolfberry. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2259.	1.8	19
410	SINE-Based Phylogenomics Reveal Extensive Introgression and Incomplete Lineage Sorting in <i>Myotis</i> . <i>Genes</i> , 2022, 13, 399.	1.0	8
411	<i>Curtobacterium</i> spp. and <i>Curtobacterium flaccumfaciens</i> : Phylogeny, Genomics-Based Taxonomy, Pathogenicity, and Diagnostics. <i>Current Issues in Molecular Biology</i> , 2022, 44, 889-927.	1.0	15
412	Degradation of 2,6-dichlorophenol by <i>Trichoderma longibraciatum</i> Isolated from an industrial Soil Sample in Dammam, Saudi Arabia. <i>Scientific Reports</i> , 2022, 12, 2940.	1.6	2

#	ARTICLE	IF	CITATIONS
414	Evolutionary transition from a single RNA replicator to a multiple replicator network. <i>Nature Communications</i> , 2022, 13, 1460.	5.8	25
415	Identification of distinct capsule types associated with <i>Serratia marcescens</i> infection isolates. <i>PLoS Pathogens</i> , 2022, 18, e1010423.	2.1	6
417	High-Density Genetic Variation Map Reveals Key Candidate Loci and Genes Associated With Important Agronomic Traits in Peanut. <i>Frontiers in Genetics</i> , 2022, 13, 845602.	1.1	3
418	Pan-Genome Analysis of <i>Laribacter hongkongensis</i> : Virulence Gene Profiles, Carbohydrate-Active Enzyme Prediction, and Antimicrobial Resistance Characterization. <i>Frontiers in Microbiology</i> , 2022, 13, 862776.	1.5	2
419	Taxonomic distribution and evolutionary analysis of the equol biosynthesis gene cluster. <i>BMC Genomics</i> , 2022, 23, 182.	1.2	10
421	Behavioral, ecological and evolutionary mechanisms underlying caterpillar-ant symbioses. <i>Current Opinion in Insect Science</i> , 2022, 52, 100898.	2.2	7
422	Associating life stages and sexes of Nearctic <i>Polycentropus</i> Curtis, 1835 (Trichoptera: Tj ETQq0 0 0 rgBT /Oyerlock 10 Tf 50 502	0.8	5
423	Taxonomic synopsis of <i>Berberis</i> (Berberidaceae) from the northern Hengduan mountains region in China, with descriptions of seven new species. <i>Plant Diversity</i> , 2022, 44, 505-517.	1.8	3
424	Automatic identification and annotation of MYB gene family members in plants. <i>BMC Genomics</i> , 2022, 23, 220.	1.2	26
425	Total Phenolic Levels, In Vitro Antioxidant Properties, and Fatty Acid Profile of Two Microalgae, <i>Tetraselmis marina</i> Strain IMA043 and Naviculoid Diatom Strain IMA053, Isolated from the North Adriatic Sea. <i>Marine Drugs</i> , 2022, 20, 207.	2.2	9
426	Characterization of genome-wide long terminal repeat retrotransposons provide insights into trait evolution of four grapevine species. <i>Journal of Systematics and Evolution</i> , 2023, 61, 414-427.	1.6	4
427	Characterization of an Unknown Region Linked to the Glycoside Hydrolase Family 17 Î²-1,3-Glucanase of <i>Vibrio vulnificus</i> Reveals a Novel Glucan-Binding Domain. <i>Marine Drugs</i> , 2022, 20, 250.	2.2	4
428	Reliable and Scalable Identification and Prioritization of Putative Cellulolytic Anaerobes With Large Genome Data. <i>Frontiers in Bioinformatics</i> , 2022, 2, .	1.0	0
429	Healthcare-associated infections caused by chlorhexidine-tolerant <i>Serratia marcescens</i> carrying a promiscuous IncHI2 multi-drug resistance plasmid in a veterinary hospital. <i>PLoS ONE</i> , 2022, 17, e0264848.	1.1	6
430	Genotype to ecotype in niche environments: adaptation of <i>Arthrobacter</i> to carbon availability and environmental conditions. <i>ISME Communications</i> , 2022, 2, .	1.7	9
432	<i>Brachybacterium epidermidis</i> Sp. Nov., a Novel Bacterial Species Isolated from the Back of the Right Hand, in a 67-Year-Old Healthy Woman. <i>International Journal of Microbiology</i> , 2022, 2022, 1-8.	0.9	0
433	Identifying SARS-CoV-2 Lineage Mutation Hallmarks and Correlating Them With Clinical Outcomes in Egypt: A Pilot Study. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 817735.	1.6	1
434	SARS-CoV-2 Nsp13 encodes for an HLA-E-stabilizing peptide that abrogates inhibition of NKG2A-expressing NK cells. <i>Cell Reports</i> , 2022, 38, 110503.	2.9	31

#	ARTICLE	IF	CITATIONS
435	A Novel Lineage of Cile-Like Viruses Discloses the Phylogenetic Continuum Across the Family Kitaviridae. <i>Frontiers in Microbiology</i> , 2022, 13, 836076.	1.5	9
436	Genome-wide analysis suggests multiple domestication events of Chinese local pigs. <i>Animal Genetics</i> , 2022, 53, 293-306.	0.6	5
437	Multidrug-resistant <i>Klebsiella pneumoniae</i> : a retrospective study in Manaus, Brazil. <i>Archives of Microbiology</i> , 2022, 204, 202.	1.0	15
438	Correlational networking guides the discovery of unclustered lanthipeptide protease-encoding genes. <i>Nature Communications</i> , 2022, 13, 1647.	5.8	12
439	Alphacoronavirus in a Daubenton's Myotis Bat (<i>Myotis daubentonii</i>) in Sweden. <i>Viruses</i> , 2022, 14, 556.	1.5	5
440	Complete genome analysis of African swine fever virus isolated from domestic pigs during the first ASF outbreaks in India. <i>Transboundary and Emerging Diseases</i> , 2022, 69, .	1.3	9
441	Evolutionary genomic relationships and coupling in MK-STYX and STYX pseudophosphatases. <i>Scientific Reports</i> , 2022, 12, 4139.	1.6	3
442	Genome-Wide Identification of BAHD Superfamily and Functional Characterization of Bornyl Acetyltransferases Involved in the Bornyl Acetate Biosynthesis in <i>Wurfbainia villosa</i> . <i>Frontiers in Plant Science</i> , 2022, 13, 860152.	1.7	5
443	Localized outbreaks of <i>Pseudomonas aeruginosa</i> belonging to international high-risk clones in a south Indian hospital. <i>Journal of Medical Microbiology</i> , 2022, 71, .	0.7	2
444	Arabidopsis RBV is a conserved WD40 repeat protein that promotes microRNA biogenesis and ARGONAUTE1 loading. <i>Nature Communications</i> , 2022, 13, 1217.	5.8	19
445	Contrasting Strategies for Sucrose Utilization in a Floral Yeast Clade. <i>MSphere</i> , 2022, 7, e0003522.	1.3	4
448	Chickensplash! Exploring the health concerns of washing raw chicken. <i>Physics of Fluids</i> , 2022, 34, 031910.	1.6	2
449	Genome-Wide Identification and Expression Profile Reveal Potential Roles of Peanut ZIP Family Genes in Zinc/Iron-Deficiency Tolerance. <i>Plants</i> , 2022, 11, 786.	1.6	7
450	Genomic prediction of morphometric and colorimetric traits in Solanaceous fruits. <i>Horticulture Research</i> , 2022, 9, .	2.9	10
451	Insight into the cryptic diversity and phylogeography of the peculiar fried egg jellyfish <i>Phacellophora</i> (Cnidaria, Scyphozoa, Ulmaridae). <i>PeerJ</i> , 2022, 10, e13125.	0.9	3
452	Genome wide association study of <i>Escherichia coli</i> bloodstream infection isolates identifies genetic determinants for the portal of entry but not fatal outcome. <i>PLoS Genetics</i> , 2022, 18, e1010112.	1.5	22
453	Severe acute respiratory coronavirus virus 2 (SARS-CoV-2) exposure investigations using genomic sequencing among healthcare workers and patients in a large academic center. <i>Infection Control and Hospital Epidemiology</i> , 2022, , 1-4.	1.0	1
454	Epidemiological Dynamics of SARS-CoV-2 Variants During Social Protests in Cali, Colombia. <i>Frontiers in Medicine</i> , 2022, 9, 863911.	1.2	4

#	ARTICLE	IF	CITATIONS
456	Microbial Identification Using rRNA Operon Region: Database and Tool for Metataxonomics with Long-Read Sequence. <i>Microbiology Spectrum</i> , 2022, 10, e0201721.	1.2	11
457	Convergent Evolution of Antibiotic Tolerance in Patients with Persistent Methicillin-Resistant <i>Staphylococcus aureus</i> Bacteremia. <i>Infection and Immunity</i> , 2022, 90, e0000122.	1.0	8
458	Apoplasmic class III peroxidases PRX62 and PRX69 promote <i>Arabidopsis</i> root hair growth at low temperature. <i>Nature Communications</i> , 2022, 13, 1310.	5.8	25
459	The impacts of allopolyploidization on Methyl-CpG-Binding Domain (MBD) gene family in <i>Brassica napus</i> . <i>BMC Plant Biology</i> , 2022, 22, 103.	1.6	3
461	The Use of Long-Read Sequencing to Study the Phylogenetic Diversity of the Potato Varieties Plastome of the Ural Selection. <i>Agronomy</i> , 2022, 12, 846.	1.3	2
462	Horizontal Gene Transfer of Fluoroquinolone Resistance-Confering Genes From Commensal <i>Neisseria</i> to <i>Neisseria gonorrhoeae</i> : A Global Phylogenetic Analysis of 20,047 Isolates. <i>Frontiers in Microbiology</i> , 2022, 13, 793612.	1.5	9
463	The molecular basis of FimT-mediated DNA uptake during bacterial natural transformation. <i>Nature Communications</i> , 2022, 13, 1065.	5.8	10
464	<i>Peptostreptococcus faecalis</i> sp. nov., new bacterial species isolated from healthy indigenous congolese volunteer. <i>Heliyon</i> , 2022, 8, e09102.	1.4	4
466	A chromosome-scale genome assembly of the false clownfish, <i>Amphiprion ocellaris</i> . <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	11
467	Convergent selection of a WD40 protein that enhances grain yield in maize and rice. <i>Science</i> , 2022, 375, eabg7985.	6.0	110
468	Prevalence and characteristics of the mcr-1 gene in retail meat samples in Zhejiang Province, China. <i>Journal of Microbiology</i> , 2022, 60, 610-619.	1.3	7
470	BURP domain-containing genes in legumes: genome-wide identification, structure, and expression analysis under stresses and development. <i>Plant Biotechnology Reports</i> , 2022, 16, 369-388.	0.9	4
471	Comparative Genome Analysis Across 128 <i>Phytophthora</i> Isolates Reveal Species-Specific Microsatellite Distribution and Localized Evolution of Compartmentalized Genomes. <i>Frontiers in Microbiology</i> , 2022, 13, 806398.	1.5	2
472	High diversity in the regulatory region of Shiga toxin encoding bacteriophages. <i>BMC Genomics</i> , 2022, 23, 230.	1.2	8
473	StrainGE: a toolkit to track and characterize low-abundance strains in complex microbial communities. <i>Genome Biology</i> , 2022, 23, 74.	3.8	35
475	Hypothesis: Transâ€¦licing Generates Evolutionary Novelty in the Photosynthetic Amoeba <i>Paulinella</i> . <i>Journal of Phycology</i> , 2022, 58, 392-405.	1.0	2
476	TAL effectors and the predicted host targets of pomegranate bacterial blight pathogen <i>Xanthomonas citri</i> pv. <i>punicae</i> . <i>Current Genetics</i> , 2022, , 1.	0.8	3
477	Whole genome sequencing and molecular epidemiology of paediatric <i>Staphylococcus aureus</i> bacteraemia. <i>Journal of Global Antimicrobial Resistance</i> , 2022, 29, 197-206.	0.9	6

#	ARTICLE	IF	CITATIONS
478	Expanding the Medfly Virome: Viral Diversity, Prevalence, and sRNA Profiling in Mass-Reared and Field-Derived Medflies. <i>Viruses</i> , 2022, 14, 623.	1.5	8
479	Classification of 27 <i>Corynebacterium kroppenstedtii</i> -Like Isolates Associated with Mastitis in China and Descriptions of <i>C. parakroppenstedtii</i> sp. nov. and <i>C. pseudokroppenstedtii</i> sp. nov. <i>Microbiology Spectrum</i> , 2022, 10, e0137221.	1.2	12
480	Mechanistic basis of choline import involved in teichoic acids and lipopolysaccharide modification. <i>Science Advances</i> , 2022, 8, eabm1122.	4.7	11
481	Protein targeting to starch 1, a functional protein of starch biosynthesis in wheat (<i>Triticum aestivum</i>) Tj ETQq1 1 0.784314 rgBT /Ove	2.0	7
482	Bacterial Competition Systems Share a Domain Required for Inner Membrane Transport of the Bacteriocin Pyocin G from <i>Pseudomonas aeruginosa</i> . <i>MBio</i> , 2022, 13, e0339621.	1.8	6
483	Comparative Genomics on Cultivated and Uncultivated Freshwater and Marine <i>Candidatus</i> Manganitrophaceae Species Implies Their Worldwide Reach in Manganese Chemolithoautotrophy. <i>MBio</i> , 2022, 13, e0342121.	1.8	4
484	Usutu virus in blackbirds (<i>Turdus merula</i>) with clinical signs, a case study from northern Italy. <i>European Journal of Wildlife Research</i> , 2022, 68, 1.	0.7	5
485	A Systematic Phylogenomic Classification of the Multidrug and Toxic Compound Extrusion Transporter Gene Family in Plants. <i>Frontiers in Plant Science</i> , 2022, 13, 774885.	1.7	8
486	Genome Assembly and Genome Annotation of <i>Leishmania martiniquensis</i> Isolated from a Leishmaniasis Patient in Thailand. <i>Journal of Parasitology Research</i> , 2022, 2022, 1-7.	0.5	1
487	Insight into the Phylogeny and Binding Ability of WRKY Transcription Factors. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2895.	1.8	9
489	Deciphering Genomes: Genetic Signatures of Plant-Associated Micromonospora. <i>Frontiers in Plant Science</i> , 2022, 13, 872356.	1.7	3
490	Genetic Diversity, Distribution, and Genomic Characterization of Antibiotic Resistance and Virulence of Clinical <i>Pseudomonas aeruginosa</i> Strains in Kenya. <i>Frontiers in Microbiology</i> , 2022, 13, 835403.	1.5	12
491	The Ribosomal DNA Loci of the Ancient Monocot <i>Pistia stratiotes</i> L. (Araceae) Contain Different Variants of the 35S and 5S Ribosomal RNA Gene Units. <i>Frontiers in Plant Science</i> , 2022, 13, 819750.	1.7	6
492	In Silico Characterisation of the Late Embryogenesis Abundant (LEA) Protein Families and Their Role in Desiccation Tolerance in <i>Ramonda serbica</i> Panc. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3547.	1.8	11
495	Population Structure Analysis and Association Mapping for Turcicum Leaf Blight Resistance in Tropical Maize Using SSR Markers. <i>Genes</i> , 2022, 13, 618.	1.0	9
496	Detection and characterisation of 16S rRNA methyltransferase-producing <i>Pseudomonas aeruginosa</i> from the UK and Republic of Ireland from 2003–2015. <i>International Journal of Antimicrobial Agents</i> , 2022, 59, 106550.	1.1	8
497	Antimicrobial Resistance, Biofilm Formation, and Virulence Genes in <i>Enterococcus</i> Species from Small Backyard Chicken Flocks. <i>Antibiotics</i> , 2022, 11, 380.	1.5	14
498	Whole-genome sequencing and gene sharing network analysis powered by machine learning identifies antibiotic resistance sharing between animals, humans and environment in livestock farming. <i>PLoS Computational Biology</i> , 2022, 18, e1010018.	1.5	19

#	ARTICLE	IF	CITATIONS
499	Remarkable genomic diversity among <i>Escherichia</i> isolates recovered from healthy chickens. <i>PeerJ</i> , 2022, 10, e12935.	0.9	6
501	Metagenome-Assembled Genomes From <i>Pyropia haitanensis</i> Microbiome Provide Insights Into the Potential Metabolic Functions to the Seaweed. <i>Frontiers in Microbiology</i> , 2022, 13, 857901.	1.5	9
502	SNPs in Genes Related to DNA Damage Repair in <i>Mycobacterium Tuberculosis</i> : Their Association with Type 2 Diabetes Mellitus and Drug Resistance. <i>Genes</i> , 2022, 13, 609.	1.0	3
503	Comparison of Reptilian Genomes Reveals Deletions Associated with the Natural Loss of $\gamma\delta$ T Cells in Squamates. <i>Journal of Immunology</i> , 2022, 208, 1960-1967.	0.4	10
504	Phylogeography and evolutionary dynamics analysis of porcine delta-coronavirus with host expansion to humans. <i>Transboundary and Emerging Diseases</i> , 2022, 69, .	1.3	8
505	First Record of <i>Ophidonais serpentina</i> (Müller, 1773) (Oligochaeta: Naididae) in China: The Occurrence or Absence of Needles Are Intraspecific Differences. <i>Diversity</i> , 2022, 14, 265.	0.7	0
506	A Comprehensive Analysis of Calmodulin-Like Proteins of <i>Glycine max</i> Indicates Their Role in Calcium Signaling and Plant Defense Against Insect Attack. <i>Frontiers in Plant Science</i> , 2022, 13, 817950.	1.7	16
507	Extensive/Multidrug-Resistant Pneumococci Detected in Clinical Respiratory Tract Samples in Southern Sweden Are Closely Related to International Multidrug-Resistant Lineages. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 824449.	1.8	3
508	Impact of Modular Architecture on Activity of Glycoside Hydrolase Family 5 Subfamily 8 Mannanases. <i>Molecules</i> , 2022, 27, 1915.	1.7	5
509	Role of Wheat Phosphorus Starvation Tolerance 1 Genes in Phosphorus Acquisition and Root Architecture. <i>Genes</i> , 2022, 13, 487.	1.0	7
510	Ni ²⁺ -Assisted Hydrolysis May Affect the Human Proteome; Filaggrin Degradation Ex Vivo as an Example of Possible Consequences. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 828674.	1.6	1
511	Nitrate-Induced MtCLE34 Gene Lacks the Ability to Reduce Symbiotic Nodule Number and Carries Nonsense Mutation in a Few Accessions of <i>Medicago truncatula</i> . <i>Agronomy</i> , 2022, 12, 842.	1.3	3
513	Unraveling the <i>Tropaeolum majus</i> L. (<i>Nasturtium</i>) Root-Associated Bacterial Community in Search of Potential Biofertilizers. <i>Microorganisms</i> , 2022, 10, 638.	1.6	4
515	Association of Mannose-Binding Lectin 2 Gene Polymorphism with Tuberculosis Based on <i>Mycobacterium tuberculosis</i> Lineages. <i>Infection and Drug Resistance</i> , 2022, Volume 15, 1225-1234.	1.1	1
516	First Report of a Methicillin-Resistant, High-Level Mupirocin-Resistant <i>Staphylococcus argenteus</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 860163.	1.8	1
517	Migration Drives the Replacement of <i>Xanthomonas perforans</i> Races in the Absence of Widely Deployed Resistance. <i>Frontiers in Microbiology</i> , 2022, 13, 826386.	1.5	4
518	Genome-Wide Identification and Expression Analysis of SNARE Genes in <i>Brassica napus</i> . <i>Plants</i> , 2022, 11, 711.	1.6	4
519	Characterization of the glutathione S-transferase genes in the sand flies <i>Phlebotomus papatasi</i> and <i>Lutzomyia longipalpis</i> shows expansion of the novel glutathione S-transferase (X) class. <i>Insect Molecular Biology</i> , 2022, 31, 417-433.	1.0	4

#	ARTICLE	IF	CITATIONS
520	Anaerobic single-cell dispensing facilitates the cultivation of human gut bacteria. <i>Environmental Microbiology</i> , 2022, 24, 3861-3881.	1.8	15
521	Phylogenomics and Comparative Genomics Highlight Specific Genetic Features in <i>Ganoderma</i> Species. <i>Journal of Fungi</i> (Basel, Switzerland), 2022, 8, 311.	1.5	10
522	Comparative analysis of the kinomes of <i>Plasmodium falciparum</i> , <i>Plasmodium vivax</i> and their host <i>Homo sapiens</i> . <i>BMC Genomics</i> , 2022, 23, 237.	1.2	9
523	Nontoxicogenic <i>Vibrio cholerae</i> Challenge Strains for Evaluating Vaccine Efficacy and Inferring Mechanisms of Protection. <i>MBio</i> , 2022, 13, e0053922.	1.8	4
524	<i>Listeria monocytogenes</i> isolates from <i>Cornu aspersum</i> snails: Whole genome-based characterization and host-pathogen interactions in a snail infection model. <i>Fish and Shellfish Immunology</i> , 2022, 123, 469-478.	1.6	1
526	Genomic Surveillance of COVID-19 Variants With Language Models and Machine Learning. <i>Frontiers in Genetics</i> , 2022, 13, 858252.	1.1	8
527	Short prokaryotic Argonaute systems trigger cell death upon detection of invading DNA. <i>Cell</i> , 2022, 185, 1471-1486.e19.	13.5	85
528	The mycobacterial <i>guaB1</i> gene encodes a guanosine 5'-monophosphate reductase with a cystathionine synthase domain. <i>FEBS Journal</i> , 2022, 289, 5571-5598.	2.2	2
529	Incidence of toxigenic <i>Aspergillus</i> and <i>Fusarium</i> species occurring in maize kernels from Kenyan households. <i>World Mycotoxin Journal</i> , 2022, 15, 407-416.	0.8	1
530	Assembly and Functional Role of PACE Transporter PA2880 from <i>Pseudomonas aeruginosa</i> . <i>Microbiology Spectrum</i> , 2022, 10, e0145321.	1.2	7
531	Residual risk of mother-to-child transmission of hepatitis B virus infection despite timely birth-dose vaccination in Cameroon (ANRS 12303): a single-centre, longitudinal observational study. <i>The Lancet Global Health</i> , 2022, 10, e521-e529.	2.9	24
532	Transposon activity, local duplications and propagation of structural variants across haplotypes drive the evolution of the <i>Drosophila</i> S2 cell line. <i>BMC Genomics</i> , 2022, 23, 276.	1.2	4
533	Amplicon-Based Next-Generation Sequencing as a Diagnostic Tool for the Detection of Phylotypes of <i>Cutibacterium acnes</i> in Orthopedic Implant-Associated Infections. <i>Frontiers in Microbiology</i> , 2022, 13, 866893.	1.5	4
534	From rags to enriched: metagenomic insights into ammonia-oxidizing archaea following ammonia enrichment of a denuded oligotrophic soil ecosystem. <i>Environmental Microbiology</i> , 2022, 24, 3097-3110.	1.8	4
535	Multifunctional biocatalyst for conjugate reduction and reductive amination. <i>Nature</i> , 2022, 604, 86-91.	13.7	48
536	Phage anti-CBASS and anti-Pycsar nucleases subvert bacterial immunity. <i>Nature</i> , 2022, 605, 522-526.	13.7	70
538	Multiple genetic analyses for Chinese Hunan Han population via 46 A-STRs. <i>Annals of Human Biology</i> , 2022, , 1-26.	0.4	0
539	First record of <i>Pheretima vungtauensis</i> (Clitellata: Megascolecidae) in India and its phylogenetic relationship with <i>Metaphire houlleti</i> . , 0, , 1.		0

#	ARTICLE	IF	CITATIONS
540	Genomic Insights into the Distribution of Peptidases and Proteolytic Capacity among <i>Prevotella</i> and <i>Paraprevotella</i> Species. <i>Microbiology Spectrum</i> , 2022, 10, e0218521.	1.2	10
541	Cross-kingdom expression of synthetic genetic elements promotes discovery of metabolites in the human microbiome. <i>Cell</i> , 2022, 185, 1487-1505.e14.	13.5	17
543	The non-specific lipid transfer protein GmLtp1.3 is involved in drought and salt tolerance in soybean. <i>Environmental and Experimental Botany</i> , 2022, 196, 104823.	2.0	3
546	Identification and characterization of Crumbs polarity complex proteins in <i>Caenorhabditis elegans</i> . <i>Journal of Biological Chemistry</i> , 2022, 298, 101786.	1.6	2
547	Phylogenetic study to analyse the evolutionary relationship of taxonomically diverse α -amylases. <i>Rendiconti Lincei</i> , 0, , 1.	1.0	0
548	Molecular biology and modeling analysis reveal functional roles of propionate to acetate ratios on microbial syntrophy and competition in electro-assisted anaerobic digestion. <i>Water Research</i> , 2022, 216, 118335.	5.3	17
549	Antimicrobial resistance in commensal <i>Staphylococcus aureus</i> from wild ungulates is driven by agricultural land cover and livestock farming. <i>Environmental Pollution</i> , 2022, 303, 119116.	3.7	10
550	Is methicillin-susceptible <i>Staphylococcus aureus</i> (MSSA) CC398 a true animal-independent pathogen?. <i>Journal of Global Antimicrobial Resistance</i> , 2022, 29, 120-123.	0.9	6
551	Genome sequence of a carbapenemase-encoding <i>Acinetobacter baumannii</i> isolate of the sequence type 231 isolated from hospital wastewater in South Africa. <i>Journal of Global Antimicrobial Resistance</i> , 2022, 29, 150-154.	0.9	5
552	Examination of D-loop region and DBY gene as tools for identifying hybridisation in alpacas (<i>Vicugna</i>) Tj ETQq1 1 0.784314 rgBT /Ove	0.6	1
553	Comparative genomics reveals the evidence of aromatic hydrocarbons degradation potential in genus <i>Roseovarius</i> in marine environment. <i>International Biodeterioration and Biodegradation</i> , 2022, 171, 105408.	1.9	16
554	Omics and mechanistic insights into di-(2-ethylhexyl) phthalate degradation in the O ₂ -fluctuating estuarine sediments. <i>Chemosphere</i> , 2022, 299, 134406.	4.2	7
555	Extension of Mitogenome Enrichment Based on Single Long-Range PCR: mtDNAs and Putative Mitochondrial-Derived Peptides of Five Rodent Hibernators. <i>Frontiers in Genetics</i> , 2021, 12, 685806.	1.1	8
556	New Insights into Interspecific Hybridization in <i>Lemna L. Sect. Lemna</i> (Lemnaceae Martinov). <i>Plants</i> , 2021, 10, 2767.	1.6	21
557	Reassessment of <i>Annamocarya sinensis</i> (<i>Carya sinensis</i>) Taxonomy through Concatenation and Coalescence Phylogenetic Analysis. <i>Plants</i> , 2022, 11, 52.	1.6	3
558	Evolution of 14-3-3 Proteins in Angiosperm Plants: Recurring Gene Duplication and Loss. <i>Plants</i> , 2021, 10, 2724.	1.6	8
559	Comparative Analysis of anti-Shine-Dalgarno Function in <i>Flavobacterium johnsoniae</i> and <i>Escherichia coli</i> . <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 787388.	1.6	5
560	Complete Genome Sequence, Molecular Characterization and Phylogenetic Relationships of a Novel Tern Adenovirus. <i>Microorganisms</i> , 2022, 10, 31.	1.6	3

#	ARTICLE	IF	CITATIONS
562	Interstitial Arabidopsis-Type Telomeric Repeats in Asteraceae. <i>Plants</i> , 2021, 10, 2794.	1.6	3
563	Comparative Genomic Study of Vinyl Chloride Cluster and Description of Novel Species, <i>Mycolicibacterium vinylchloridicum</i> sp. nov.. <i>Frontiers in Microbiology</i> , 2021, 12, 767895.	1.5	2
565	Transposable Prophages in <i>Leptospira</i> : An Ancient, Now Diverse, Group Predominant in Causative Agents of Weil's Disease. <i>International Journal of Molecular Sciences</i> , 2021, 22, 13434.	1.8	4
566	Identification and classification of reverse transcriptases in bacterial genomes and metagenomes. <i>Nucleic Acids Research</i> , 2022, 50, e29-e29.	6.5	11
567	Investigating the role of carbohydrate-binding module 34 in cyclomaltodextrinase from <i>Geobacillus thermopakistaniensis</i> : structural and functional analyses. <i>3 Biotech</i> , 2022, 12, 25.	1.1	2
568	Microbial Communities in Retail Draft Beers and the Biofilms They Produce. <i>Microbiology Spectrum</i> , 2021, 9, e0140421.	1.2	2
569	Diverse Single-Stranded DNA Viruses Identified in Chicken Buccal Swabs. <i>Microorganisms</i> , 2021, 9, 2602.	1.6	6
570	<i>Phosphitispora fastidiosa</i> gen. nov. sp. nov., a new dissimilatory phosphite-oxidizing anaerobic bacterium isolated from anaerobic sewage sludge. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	14
572	Mutational landscape of SARS-CoV-2 genome in Turkey and impact of mutations on spike protein structure. <i>PLoS ONE</i> , 2021, 16, e0260438.	1.1	6
574	Ruminant-associated <i>Listeria monocytogenes</i> isolates belong preferentially to dairy-associated hypervirulent clones: a longitudinal study in 19 farms. <i>Environmental Microbiology</i> , 2021, 23, 7617-7631.	1.8	17
576	Genetic diversity and aggressiveness of <i>Fusarium virguliforme</i> isolates across the Midwestern United States. <i>Phytopathology</i> , 2021, , .	1.1	0
577	Chromosomally Located <i>fosA7</i> in <i>Salmonella</i> Isolates From China. <i>Frontiers in Microbiology</i> , 2021, 12, 781306.	1.5	11
580	In situ visualization of glycoside hydrolase family 92 genes in marine flavobacteria. <i>ISME Communications</i> , 2021, 1, .	1.7	1
581	Taxon-Specific Shifts in Bacterial and Archaeal Transcription of Dissolved Organic Matter Cycling Genes in a Stratified Fjord. <i>MSystems</i> , 2021, 6, e0057521.	1.7	1
582	Evaluation of Genotypes for Major Diseases of Pepper Genetic Resources Using the Fluidigm System. <i>Han'guk Yukchong Hakhoe Chi</i> , 2021, 53, 432-449.	0.2	0
585	Eco-phylogenetic analyses reveal divergent evolution of vitamin B ₁₂ metabolism in the marine bacterial family <i>Psychromonadaceae</i> . <i>Environmental Microbiology Reports</i> , 2022, 14, 147-163.	1.0	2
586	Genome-Wide Analysis of WRKY Gene Family and the Dynamic Responses of Key WRKY Genes Involved in <i>Ostrinia furnacalis</i> Attack in <i>Zea mays</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 13045.	1.8	16
589	Recent Advances in Structure, Function, and Pharmacology of Class A Lipid GPCRs: Opportunities and Challenges for Drug Discovery. <i>Pharmaceuticals</i> , 2022, 15, 12.	1.7	12

#	ARTICLE	IF	CITATIONS
590	The pseudokinase domain in receptor guanylyl cyclases. <i>Methods in Enzymology</i> , 2022, 667, 535-574.	0.4	2
591	Standardized genome-wide function prediction enables comparative functional genomics: a new application area for Gene Ontologies in plants. <i>GigaScience</i> , 2022, 11, .	3.3	2
592	Deciphering the Molecular Mechanisms of Insecticide Resistance From the Transcriptome Data of Field Evolved Spinosad Resistant and Susceptible Populations of <i>Plutella xylostella</i> (Lepidoptera: Tj ETQq0 0 0 rgBTg/Overlook 10 Tf 50		
593	Comparative genome analyses of five <i>Vibrio penaeicida</i> strains provide insights into their virulence-related factors. <i>Microbial Genomics</i> , 2022, 8, .	1.0	3
594	Metagenomic analysis reveals mixed <i>Mycobacterium tuberculosis</i> infection in a 18th century Hungarian midwife. <i>Tuberculosis</i> , 2022, , 102181.	0.8	3
595	Prevalence and Molecular Typing of Carbapenemase-Producing Enterobacterales among Newborn Patients in Italy. <i>Antibiotics</i> , 2022, 11, 431.	1.5	3
596	Characterization of <i>Escherichia coli</i> harboring colibactin genes (clb) isolated from beef production and processing systems. <i>Scientific Reports</i> , 2022, 12, 5305.	1.6	2
597	Genome-wide identification and evolution of interleukins and their potential roles in response to CCRV and <i>Aeromonas hydrophila</i> challenge in grass carp (<i>Ctenopharyngodon idella</i>). <i>Aquaculture</i> , 2022, 556, 738266.	1.7	1
598	<i>Solanum galapagense</i> derived purple tomato fruit color is conferred by novel alleles of the <i>anthocyanin fruit</i> and <i>atrorubrum</i> loci. <i>Plant Direct</i> , 2022, 6, e394.	0.8	5
599	Best practices in metabarcoding of fungi: From experimental design to results. <i>Molecular Ecology</i> , 2022, 31, 2769-2795.	2.0	87
600	Genomic characterisation of an entomopathogenic strain of <i>Serratia ureilytica</i> in the critically endangered phasmid <i>Dryococelus australis</i> . <i>PLoS ONE</i> , 2022, 17, e0265967.	1.1	0
602	Epidemiology of <i>Klebsiella michiganensis</i> Carrying Multidrug-Resistant IncHI5 Plasmids in the Southeast Coastal Area of China. <i>Infection and Drug Resistance</i> , 2022, Volume 15, 1831-1843.	1.1	5
603	Molecular Characterization Reveals the Involvement of Calcium Dependent Protein Kinases in Abiotic Stress Signaling and Development in Chickpea (<i>Cicer arietinum</i>). <i>Frontiers in Plant Science</i> , 2022, 13, 831265.	1.7	3
604	Prevalence of Tick-Borne Pathogens in Questing <i>Ixodes ricinus</i> and <i>Dermacentor reticulatus</i> Ticks Collected from Recreational Areas in Northeastern Poland with Analysis of Environmental Factors. <i>Pathogens</i> , 2022, 11, 468.	1.2	7
605	Metagenomic signatures of balancing selection in the human gut. <i>Molecular Ecology</i> , 2023, 32, 2582-2591.	2.0	4
607	Assessment of the Transmission Dynamics of <i>Clostridioides difficile</i> in a Farm Environment Reveals the Presence of a New Toxigenic Strain Connected to Swine Production. <i>Frontiers in Microbiology</i> , 2022, 13, 858310.	1.5	5
608	Mutational meltdown or controlled chain reaction: The dynamics of rapid plastome evolution in the hyperdiversity of Poaceae. <i>Journal of Systematics and Evolution</i> , 2023, 61, 328-344.	1.6	5
610	Understanding Diversity, Evolution, and Structure of Small Heat Shock Proteins in Annelida Through in Silico Analyses. <i>Frontiers in Physiology</i> , 2022, 13, 817272.	1.3	2

#	ARTICLE	IF	CITATIONS
611	A GH115 β -glucuronidase structure reveals dimerization-mediated substrate binding and a proton wire potentially important for catalysis. <i>Acta Crystallographica Section D: Structural Biology</i> , 2022, 78, 658-668.	1.1	2
612	Regulatory Evolution of the <i>phoH</i> Ancestral Gene in <i>Salmonella enterica</i> Serovar Typhimurium. <i>Journal of Bacteriology</i> , 2022, 204, e0058521.	1.0	2
614	Complete Genome Characterization of Reticuloendotheliosis Virus Detected in Chickens with Multiple Viral Coinfections. <i>Viruses</i> , 2022, 14, 798.	1.5	3
615	Reclassification of 11 Members of the Family Rhodobacteraceae at Genus and Species Levels and Proposal of <i>Pseudogemmobacter hezensis</i> sp. nov.. <i>Frontiers in Microbiology</i> , 2022, 13, 849695.	1.5	47
617	Insights into the biosynthesis pathway of phenolic compounds in microalgae. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 1901-1913.	1.9	27
618	Methods for the Cost-Effective Production of Bacteria-Derived Double-Stranded RNA for in vitro Knockdown Studies. <i>Frontiers in Physiology</i> , 2022, 13, 836106.	1.3	11
619	The specific DNA barcodes based on chloroplast genes for species identification of Theaceae plants. <i>Physiology and Molecular Biology of Plants</i> , 2022, 28, 837-848.	1.4	8
620	Functional, transcriptional, and microbial shifts associated with healthy pulmonary aging in rhesus macaques. <i>Cell Reports</i> , 2022, 39, 110725.	2.9	7
621	Rapid Identification and Source Tracing of a <i>Salmonella</i> Typhimurium Outbreak in China by Metagenomic and Whole-Genome Sequencing. <i>Foodborne Pathogens and Disease</i> , 2022, 19, 259-265.	0.8	1
622	Genetic evidence of transoceanic migration of the small brown planthopper between China and Japan. <i>Pest Management Science</i> , 2022, , .	1.7	4
623	Epidemiology and Comparative Analyses of the S Gene on Feline Coronavirus in Central China. <i>Pathogens</i> , 2022, 11, 460.	1.2	8
624	Prediction of Prophages and Their Host Ranges in Pathogenic and Commensal <i>Neisseria</i> Species. <i>MSystems</i> , 2022, 7, e0008322.	1.7	9
626	Identification, Characterization, and Preliminary X-ray Diffraction Analysis of a Single Stranded DNA Binding Protein (LjSSB) from Psychrophilic <i>Lacinutrix jangbogonensis</i> PAMC 27137. <i>Crystals</i> , 2022, 12, 538.	1.0	1
627	A single point mutation in a member of FAD2 multigene family resulted in the generation of a high oleic line of <i>Silybum marianum</i> (L.) Gaertn.. <i>Industrial Crops and Products</i> , 2022, 182, 114930.	2.5	2
628	Integrative Genomics Sheds Light on Evolutionary Forces Shaping the Acidithiobacillia Class Acidophilic Lifestyle. <i>Frontiers in Microbiology</i> , 2021, 12, 822229.	1.5	10
629	Genetic and geographical delineation of zoonotic vector-borne helminths of canids. <i>Scientific Reports</i> , 2022, 12, 6699.	1.6	6
630	MtEFD and MtEFD2: Two transcription factors with distinct neofunctionalization in symbiotic nodule development. <i>Plant Physiology</i> , 2022, 189, 1587-1607.	2.3	9
631	Characterization of CRISPR-Cas systems in <i>Bifidobacterium breve</i> . <i>Microbial Genomics</i> , 2022, 8, .	1.0	1

#	ARTICLE	IF	CITATIONS
632	Reevaluation of the Phylogenetic Diversity and Global Distribution of the Genus <i>Candidatus</i> <i>Accumulibacter</i> . <i>MSystems</i> , 2022, 7, e0001622.	1.7	22
634	Genome Mining Shows Ubiquitous Presence and Extensive Diversity of Toxin-Antitoxin Systems in <i>Pseudomonas syringae</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 815911.	1.5	5
635	Integrating Venom Peptide Libraries Into a Phylogenetic and Broader Biological Framework. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 784419.	1.6	1
636	A Bioinformatics Workflow for Investigating Fungal Biosynthetic Gene Clusters. <i>Methods in Molecular Biology</i> , 2022, 2489, 1-21.	0.4	2
637	The new phylogenetic relationships in Veneridae (Bivalvia: Venerida). <i>Zoological Journal of the Linnean Society</i> , 2022, 196, 346-365.	1.0	3
638	Enhanced Cultured Diversity of the Mouse Gut Microbiota Enables Custom-Made Synthetic Communities. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1
639	CLMB: Deep Contrastive Learning for Robust Metagenomic Binning. <i>Lecture Notes in Computer Science</i> , 2022, , 326-348.	1.0	4
641	Improving Lipid Production of <i>Yarrowia lipolytica</i> by the Aldehyde Dehydrogenase-Mediated Furfural Detoxification. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4761.	1.8	6
642	SARS-CoV-2 Omicron Variant in Croatia – Rapid Detection of the First Case and Cross-Border Spread. <i>Pathogens</i> , 2022, 11, 511.	1.2	4
643	Two Hidden mtDNA-Clades of Crown-of-Thorns Starfish in the Pacific Ocean. <i>Frontiers in Marine Science</i> , 2022, 9, .	1.2	3
644	Interactive, integrated analysis of single-cell transcriptomic and phylogenetic data with PhyloVision. <i>Cell Reports Methods</i> , 2022, 2, 100200.	1.4	5
646	First Identification of a Multidrug-Resistant <i>Pseudomonas putida</i> Co-Carrying Five β -Lactam Resistance Genes Recovered from a Urinary Tract Infection in China. <i>Infection and Drug Resistance</i> , 2022, Volume 15, 2229-2234.	1.1	1
647	Identification and Analysis of SARS-CoV-2 Alpha Variants in the Largest Taiwan COVID-19 Outbreak in 2021. <i>Frontiers in Medicine</i> , 2022, 9, 869818.	1.2	10
648	Systems-Based Approach for Optimization of Assembly-Free Bacterial MLST Mapping. <i>Life</i> , 2022, 12, 670.	1.1	0
649	Role of Diversity and Recombination in the Emergence of Chilli Leaf Curl Virus. <i>Pathogens</i> , 2022, 11, 529.	1.2	3
650	Diversity of Giant Viruses Infecting <i>Vermamoeba vermiformis</i> . <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	1
652	Comprehensive role of SARS-CoV-2 spike glycoprotein in regulating host signaling pathway. <i>Journal of Medical Virology</i> , 2022, 94, 4071-4087.	2.5	5
653	The essential <i>M. tuberculosis</i> Clp protease is functionally asymmetric in vivo. <i>Science Advances</i> , 2022, 8, eabn7943.	4.7	6

#	ARTICLE	IF	CITATIONS
654	A family of conserved bacterial virulence factors dampens interferon responses by blocking calcium signaling. <i>Cell</i> , 2022, 185, 2354-2369.e17.	13.5	26
656	Whole genome sequencing of multidrug-resistant <i>Mycobacterium tuberculosis</i> isolates collected in the Czech Republic, 2005–2020. <i>Scientific Reports</i> , 2022, 12, 7149.	1.6	14
657	Compendium of specialized metabolite biosynthetic diversity encoded in bacterial genomes. <i>Nature Microbiology</i> , 2022, 7, 726-735.	5.9	106
659	Regulatory phosphorylation event of phosphoglucomutase 1 tunes its activity to regulate glycogen metabolism. <i>FEBS Journal</i> , 2022, 289, 6005-6020.	2.2	6
660	The co-occurrence of antibiotic resistance genes between dogs and their owners in families. , 2022, 1, .		14
661	Repeated transmission of SARS-CoV-2 in an overcrowded Irish emergency department elucidated by whole-genome sequencing. <i>Journal of Hospital Infection</i> , 2022, 126, 1-9.	1.4	4
662	Comparative Genomics Reveals Insights into the Divergent Evolution of Astigmatic Mites and Household Pest Adaptations. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	13
663	Exploring the microbial influence on seasonal nitrous oxide concentration in a full-scale wastewater treatment plant using metagenome assembled genomes. <i>Water Research</i> , 2022, 219, 118563.	5.3	5
664	Cloning and Functional Characterization of the Polyketide Synthases Based on Genome Mining of <i>Preussia isomera</i> XL-1326. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	5
665	Pangenome analysis of Enterobacteria reveals richness of secondary metabolite gene clusters and their associated gene sets. <i>Synthetic and Systems Biotechnology</i> , 2022, 7, 900-910.	1.8	9
666	Combined GWAS and Transcriptome Analyses Provide New Insights Into the Response Mechanisms of Sunflower Against Drought Stress. <i>Frontiers in Plant Science</i> , 2022, 13, 847435.	1.7	14
667	Human-to-dog transmission of SARS-CoV-2, Colombia. <i>Scientific Reports</i> , 2022, 12, 7880.	1.6	9
668	The Mycovirome in a Worldwide Collection of the Brown Rot Fungus <i>Monilinia fructicola</i> . <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 481.	1.5	6
669	The flying spider-monkey tree fern genome provides insights into fern evolution and arborescence. <i>Nature Plants</i> , 2022, 8, 500-512.	4.7	42
670	<i>Copranaerobaculum intestinale</i> gen. nov., sp. nov., a novel anaerobic bacterium isolated from human faeces. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	6
671	Identification and Comparative Genomic Analysis of Type VI Secretion Systems and Effectors in <i>Klebsiella pneumoniae</i> . <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	8
672	Nitric oxide signaling controls collective contractions in a colonial choanoflagellate. <i>Current Biology</i> , 2022, 32, 2539-2547.e5.	1.8	8
673	Comparative Genomics Unveils the Habitat Adaptation and Metabolic Profiles of <i>Clostridium</i> in an Artificial Ecosystem for Liquor Production. <i>MSystems</i> , 2022, 7, e0029722.	1.7	13

#	ARTICLE	IF	CITATIONS
674	Elevational Gradients Impose Dispersal Limitation on Streptomyces. <i>Frontiers in Microbiology</i> , 2022, 13, 856263.	1.5	1
676	PhyloCloud: an online platform for making sense of phylogenomic data. <i>Nucleic Acids Research</i> , 2022, , .	6.5	4
677	The First Cbk-Like Phage Infecting Erythrobacter, Representing a Novel Siphoviral Genus. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	1
678	Metagenomic exploration of antibiotic resistance genes and their hosts in aquaculture waters of the semi-closed Dongshan Bay (China). <i>Science of the Total Environment</i> , 2022, 838, 155784.	3.9	12
679	Absence of some cytochrome P450 (CYP) and hydroxysteroid dehydrogenase (HSD) enzymes in hagfishes. <i>General and Comparative Endocrinology</i> , 2022, 323-324, 114045.	0.8	0
680	Microbially mediated arsenic mobilization in the clay layer and underlying aquifer in the Hetao Basin, Inner Mongolia, China. <i>Science of the Total Environment</i> , 2022, 836, 155597.	3.9	5
681	Species Identification of Larval Fish in Hawaiian Waters Using DNA Barcoding. <i>Frontiers in Marine Science</i> , 2022, 9, .	1.2	3
682	True-atomic-resolution insights into the structure and functional role of linear chains and low-barrier hydrogen bonds in proteins. <i>Nature Structural and Molecular Biology</i> , 2022, 29, 440-450.	3.6	21
683	Genomic Analyses of SUT and TST Sugar Transporter Families in Low and High Sugar Accumulating Sugarcane Species (<i>Saccharum spontaneum</i> and <i>Saccharum officinarum</i>). <i>Tropical Plant Biology</i> , 2022, 15, 181-196.	1.0	3
684	Viola shiweii, a new species of Viola (Violaceae) from karst forest in Guizhou, China. <i>PhytoKeys</i> , 0, 196, 63-89.	0.4	3
685	Undibacter mobilis gen. nov., sp. nov. isolated from an artificial wetland in Okcheon, Korea. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	10
686	Minimizing tillage modifies fungal denitrifier communities, increases denitrification rates and enhances the genetic potential for fungal, relative to bacterial, denitrification. <i>Soil Biology and Biochemistry</i> , 2022, 170, 108718.	4.2	6
687	Analysis of rhodopsin G protein-coupled receptor orthologs reveals semiochemical peptides for parasite (<i>Schistosoma mansoni</i>) and host (<i>Biomphalaria glabrata</i>) interplay. <i>Scientific Reports</i> , 2022, 12, 8243.	1.6	5
688	Novel Screening System of Virulent Strains for the Establishment of a <i>Mycobacterium avium</i> Complex Lung Disease Mouse Model Using Whole-Genome Sequencing. <i>Microbiology Spectrum</i> , 2022, 10, e0045122.	1.2	4
689	Phylogeny of NF-YA trans-activation splicing isoforms in vertebrate evolution. <i>Genomics</i> , 2022, 114, 110390.	1.3	4
690	High Prevalence of blaCTXM β /IncI1- β /ST3 Plasmids in Extended-Spectrum β -Lactamase-Producing Escherichia coli Isolates Collected From Domestic Animals in Guadeloupe (French West Indies). <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	3
691	Characterization of a Novel Esterase Est33 From an Antarctic Bacterium: A Representative of a New Esterase Family. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	0
692	Prevalence and Characterization of the Cefazolin Inoculum Effect in North American Methicillin-Susceptible Staphylococcus aureus Isolates. <i>Journal of Clinical Microbiology</i> , 2022, 60, e0249521.	1.8	7

#	ARTICLE	IF	CITATIONS
693	Multiple long-range host shifts of major <i>Wolbachia</i> supergroups infecting arthropods. <i>Scientific Reports</i> , 2022, 12, 8131.	1.6	10
694	Comprehensive genome analysis of <i>Lentzea</i> reveals repertoire of polymer-degrading enzymes and bioactive compounds with clinical relevance. <i>Scientific Reports</i> , 2022, 12, 8409.	1.6	3
695	SARS-CoV-2 delta variant infection in domestic dogs and cats, Thailand. <i>Scientific Reports</i> , 2022, 12, 8403.	1.6	33
696	Genotyping of respiratory syncytial virus among influenza-like illness and severe acute respiratory infection cases of children in the Philippines from 2006 to 2016. <i>Influenza and Other Respiratory Viruses</i> , 2022, 16, 942-951.	1.5	4
697	Molecular data reallocates <i>Sorosphaerula radicalis</i> (Plasmodiophorida, Phytomyxea, Rhizaria) to the genus <i>Hillenburgia</i> . <i>Journal of Eukaryotic Microbiology</i> , 2022, , e12924.	0.8	3
698	The loss of polyphenol oxidase function is associated with hilum pigmentation and has been selected during pea domestication. <i>New Phytologist</i> , 2022, 235, 1807-1821.	3.5	14
699	Molecular Evolution of Porcine Reproductive and Respiratory Syndrome Virus Field Strains from Two Swine Production Systems in the Midwestern United States from 2001 to 2020. <i>Microbiology Spectrum</i> , 2022, 10, e0263421.	1.2	12
700	Genome-wide identification and expression analysis of <i>CPP</i> -like gene family in <i>Triticum aestivum</i> L. under different hormone and stress conditions. <i>Open Life Sciences</i> , 2022, 17, 544-562.	0.6	4
707	High prevalence of an alpha variant lineage with a premature stop codon in ORF7a in Iraq, winter 2020-2021. <i>PLoS ONE</i> , 2022, 17, e0267295.	1.1	8
708	The Impact of Chromate on <i>Pseudomonas aeruginosa</i> Molybdenum Homeostasis. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	4
714	A Defined Medium for Cultivation and Exometabolite Profiling of Soil Bacteria. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	11
715	A catalog of 48,425 nonredundant viruses from oral metagenomes expands the horizon of the human oral virome. <i>IScience</i> , 2022, 25, 104418.	1.9	20
716	The Identification of Fish Eggs From Four Economically Important Species in Guanghai Bay (China). <i>Frontiers in Marine Science</i> , 2022, 9, .	1.2	0
717	A single amino acid residue controls acyltransferase activity in a polyketide synthase from <i>Toxoplasma gondii</i> . <i>IScience</i> , 2022, 25, 104443.	1.9	7
719	Evolution-Informed Discovery of the Naphthalenone Biosynthetic Pathway in Fungi. <i>MBio</i> , 0, , .	1.8	5
721	Identification of <i>Pseudomonas asiatica</i> subsp. <i>bavariensis</i> str. <i>JM1</i> as the first <i>N</i> - μ -carboxy(m)ethyllysine-degrading soil bacterium. <i>Environmental Microbiology</i> , 2022, 24, 3229-3241.	1.8	4
722	Symbiosis with Dinoflagellates Alters Cnidarian Cell-Cycle Gene Expression. <i>Cellular Microbiology</i> , 2022, 2022, 1-20.	1.1	4
724	Phenotypic and Genetic Characterization of <i>Klebsiella pneumoniae</i> Isolates from Wild Animals in Central Italy. <i>Animals</i> , 2022, 12, 1347.	1.0	7

#	ARTICLE	IF	CITATIONS
725	Mechanism-Based Strategy for Optimizing HaloTag Protein Labeling. <i>Jacs Au</i> , 2022, 2, 1324-1337.	3.6	7
726	Exploring the Evolutionary History and Phylodynamics of Human Immunodeficiency Virus Type 1 Outbreak From Unnao, India Using Phylogenetic Approach. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	1
727	Ancient Origins of Cytoskeletal Crosstalk: Spectraplaklin-like Proteins Precede the Emergence of Cortical Microtubule Stabilization Complexes as Crosslinkers. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5594.	1.8	3
728	Evidence for an Independent Hydrogenosome-to-Mitosome Transition in the CL3 Lineage of Fornicates. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	3
729	Lebanese SARS-CoV-2 genomics: 24 months of the pandemic. <i>Virus Research</i> , 2022, 317, 198824.	1.1	2
730	The Complex Genomic Diversity of <i>Yersinia pestis</i> on the Long-Term Plague Foci in Qinghai-Tibet Plateau. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
731	Origin and Global Expansion of <i>Mycobacterium tuberculosis</i> Complex Lineage 3. <i>Genes</i> , 2022, 13, 990.	1.0	13
732	An Epistatic Network Describes <i>oppA</i> and <i>glgB</i> as Relevant Genes for <i>Mycobacterium tuberculosis</i> . <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	1.6	1
733	Substantiation of propitious "Enzybiotic" from two novel bacteriophages isolated from a wastewater treatment plant in Qatar. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
735	Genomic epidemiology and temperature dependency of hypermucoviscous <i>Klebsiella pneumoniae</i> in Japan. <i>Microbial Genomics</i> , 2022, 8, .	1.0	5
736	Whole-Genome Analysis Reveals That Bacteriophages Promote Environmental Adaptation of <i>Staphylococcus aureus</i> via Gene Exchange, Acquisition, and Loss. <i>Viruses</i> , 2022, 14, 1199.	1.5	8
737	A Toolbox for the Generation of Chemical Probes for Baculovirus IAP Repeat Containing Proteins. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, .	1.8	6
738	The Emerging Role of Proline in the Establishment and Functioning of Legume-Rhizobium Symbiosis. <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	2
739	Widespread stop-codon recoding in bacteriophages may regulate translation of lytic genes. <i>Nature Microbiology</i> , 2022, 7, 918-927.	5.9	25
741	Community Origins of Healthcare-Associated CC59 Methicillin-Resistant <i>Staphylococcus aureus</i> in China. <i>Journal of Infectious Diseases</i> , 0, , .	1.9	0
743	Genetic Diversity and Differentiation of MHC Class I Genes in Red-Crowned Crane Populations. <i>Frontiers in Ecology and Evolution</i> , 0, 10, .	1.1	2
744	Characterization of Three SEPALLATA-Like MADS-Box Genes Associated With Floral Development in <i>Paphiopedilum henryanum</i> (Orchidaceae). <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	2
745	Evolution of Heme Peroxygenases: Ancient Roots and Later Evolved Branches. <i>Antioxidants</i> , 2022, 11, 1011.	2.2	1

#	ARTICLE	IF	CITATIONS
746	Comprehensive Bioinformatics and Expression Analysis of the TLP Gene Family Revealed Its Role in Regulating the Response of <i>Oryza sativa</i> to <i>Nilaparvata lugens</i> , <i>Laodelphax striatellus</i> , and Jinggaangmycin. <i>Agronomy</i> , 2022, 12, 1297.	1.3	12
747	Alternative splicing of <i>REGULATOR OF LEAF INCLINATION 1</i> modulates phosphate starvation signaling and growth in plants. <i>Plant Cell</i> , 2022, 34, 3319-3338.	3.1	24
748	Venomics of the Central European Myrmicine Ants <i>Myrmica rubra</i> and <i>Myrmica ruginodis</i> . <i>Toxins</i> , 2022, 14, 358.	1.5	6
749	GSDMEa-mediated pyroptosis is bi-directionally regulated by caspase and required for effective bacterial clearance in teleost. <i>Cell Death and Disease</i> , 2022, 13, .	2.7	19
750	Whole-Genome Resequencing of Xiangxi Cattle Identifies Genomic Diversity and Selection Signatures. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	3
751	DARHD: A sequence database for aromatic ring-hydroxylating dioxygenase analysis and primer evaluation. <i>Journal of Hazardous Materials</i> , 2022, 436, 129230.	6.5	7
752	Detection of SARS-CoV-2 Variants of Concern with Tiling Amplicon Sequencing from Wastewater. <i>ACS ES&T Water</i> , 2022, 2, 2185-2193.	2.3	5
754	Molecular and Pathogenic Characterization of <i>Fusarium</i> Species Associated with Corm Rot Disease in Saffron from China. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 515.	1.5	9
755	Genomic and Biological Profile of a Novel Bacteriophage, <i>Vibrio</i> phage <i>Virtus</i> , Which Improves Survival of <i>Sparus aurata</i> Larvae Challenged with <i>Vibrio harveyi</i> . <i>Pathogens</i> , 2022, 11, 630.	1.2	16
758	The importance of the urea cycle and its relationships to polyamine metabolism during ammonium stress in <i>Medicago truncatula</i> . <i>Journal of Experimental Botany</i> , 2022, 73, 5581-5595.	2.4	9
760	Interspecies commensal interactions have nonlinear impacts on host immunity. <i>Cell Host and Microbe</i> , 2022, 30, 988-1002.e6.	5.1	23
763	Genomic Surveillance of Clinical <i>Pseudomonas aeruginosa</i> Isolates Reveals an Additive Effect of Carbapenemase Production on Carbapenem Resistance. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	4
764	A glimpse into the past: phylogenesis and protein domain analysis of the group XIV of C-type lectins in vertebrates. <i>BMC Genomics</i> , 2022, 23, .	1.2	1
766	Microbial community diversity changes during voltage reversal repair in a 12-unit microbial fuel cell. <i>Chemical Engineering Journal</i> , 2022, 446, 137334.	6.6	9
767	High-throughput, single-microbe genomics with strain resolution, applied to a human gut microbiome. <i>Science</i> , 2022, 376, .	6.0	100
769	Comparative in silico characterization of <i>Klebsiella pneumoniae</i> hypervirulent plasmids and their antimicrobial resistance genes. <i>Annals of Clinical Microbiology and Antimicrobials</i> , 2022, 21, .	1.7	10
770	Genome-wide analysis of PTR transporters in <i>Candida</i> species and their functional characterization in <i>Candida auris</i> . <i>Applied Microbiology and Biotechnology</i> , 2022, 106, 4223-4235.	1.7	3
771	What complete mitochondrial genomes tell us about the evolutionary history of the black soldier fly, <i>Hermetia illucens</i> . <i>Bmc Ecology and Evolution</i> , 2022, 22, .	0.7	2

#	ARTICLE	IF	CITATIONS
773	Noncanonical prokaryotic X family DNA polymerases lack polymerase activity and act as exonucleases. <i>Nucleic Acids Research</i> , 0, , .	6.5	0
775	Stage-specific miRNAs regulate gene expression associated with growth, development and parasite-host interaction during the intra-mammalian migration of the zoonotic helminth parasite <i>Fasciola hepatica</i> . <i>BMC Genomics</i> , 2022, 23, .	1.2	10
776	Serological characterization of lineage II insect-specific flaviviruses compared with pathogenic mosquito-borne flaviviruses. <i>Biochemical and Biophysical Research Communications</i> , 2022, 616, 115-121.	1.0	1
777	Designing potential siRNA molecules for silencing the gene of the nucleocapsid protein of Nipah virus: A computational investigation. <i>Infection, Genetics and Evolution</i> , 2022, 102, 105310.	1.0	7
779	An Application of Zooms to Identify Archaeological Avian Fauna from Teotihuacan, Mexico. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
780	Masâ€Related G Proteinâ€Coupled Receptors X (MRGPRX): Orphan GPCRs with Potential as Targets for Future Drugs. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
781	Chromosome-level genome assembly of the black widow spider <i>Latrodectus elegans</i> illuminates composition and evolution of venom and silk proteins. <i>GigaScience</i> , 2022, 11, .	3.3	9
782	Flux Regulation Through Glycolysis and Respiration is Balanced by Inositol Pyrophosphates. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
783	High-Throughput Sequencing Covers Greater Nematode Diversity than Conventional Morphotyping on Natural Cedar Forests in Yakushima Island, Japan. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
784	Textile Industry Wastewater Microbiome: Recovery of Metagenome Assembled Genomes (Mags) Using Shotgun Sequencing Approach from Jetpur, Gujarat, India. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
787	Evolution of Phage Tail Sheath Protein. <i>Viruses</i> , 2022, 14, 1148.	1.5	8
788	Genetic Drift and Host-Adaptive Features Likely Underlie the Cladogenesis of Insect-Associated Lachnospiraceae. <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	4
789	Enterotoxin- and Antibiotic-Resistance-Encoding Genes Are Present in Both Coagulase-Positive and Coagulase-Negative Foodborne <i>Staphylococcus</i> Strains. <i>Applied Microbiology</i> , 2022, 2, 367-380.	0.7	6
791	Alaskan palaeosols in modern times: Deciphering unique microbial diversity within the late-Holocene. <i>Holocene</i> , 0, , 095968362211012.	0.9	0
792	Lignocellulose degradation in <i>Protaetia brevitarsis</i> larvae digestive tract: refining on a tightly designed microbial fermentation production line. <i>Microbiome</i> , 2022, 10, .	4.9	18
793	Genome-Wide Characterization of Superoxide Dismutase (SOD) Genes in <i>Daucus carota</i> : Novel Insights Into Structure, Expression, and Binding Interaction With Hydrogen Peroxide (H ₂ O ₂) Under Abiotic Stress Condition. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	13
794	Functional Characterization of Recombinant Raw Starch Degrading α -Amylase from <i>Roseateles terrae</i> HL11 and Its Application on Cassava Pulp Saccharification. <i>Catalysts</i> , 2022, 12, 647.	1.6	4
795	Genomic Characterization of Mobile Genetic Elements Associated With Carbapenem Resistance of <i>Acinetobacter baumannii</i> From India. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	9

#	ARTICLE	IF	CITATIONS
796	Identification of QTNs Associated With Flowering Time, Maturity, and Plant Height Traits in <i>Linum usitatissimum</i> L. Using Genome-Wide Association Study. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	7
797	High sorbic acid resistance of <i>Penicillium roqueforti</i> is mediated by the SORBUS gene cluster. <i>PLoS Genetics</i> , 2022, 18, e1010086.	1.5	4
799	Isolation of <i>Listeria ivanovii</i> from Bulk-Tank Milk of Sheep and Goat Farms—From Clinical Work to Bioinformatics Studies: Prevalence, Association with Milk Quality, Antibiotic Susceptibility, Predictors, Whole Genome Sequence and Phylogenetic Relationships. <i>Biology</i> , 2022, 11, 871.	1.3	3
802	Functional Nitrogenase Cofactor Maturase NifB in Mitochondria and Chloroplasts of <i>Nicotiana benthamiana</i> . <i>MBio</i> , 2022, 13, .	1.8	8
803	RNA Interference-Mediated Knockdown of <i>Bombyx mori</i> Haemocyte-Specific Cathepsin L (Cat L)-Like Cysteine Protease Gene Increases <i>Bacillus thuringiensis kurstaki</i> Toxicity and Reproduction in Insect Cadavers. <i>Toxins</i> , 2022, 14, 394.	1.5	8
804	Tree House Explorer: A Novel Genome Browser for Phylogenomics. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	4
805	Novel Gene Rearrangement in the Mitochondrial Genome of Three <i>Garra</i> and Insights Into the Phylogenetic Relationships of Labeoninae. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	2
806	Complete chloroplast genome of <i>Lilium ledebourii</i> (Baker) Boiss and its comparative analysis: lights into selective pressure and adaptive evolution. <i>Scientific Reports</i> , 2022, 12, .	1.6	14
807	Genetic diversity and demography of <i>Bufo japonicus</i> and <i>B. torrenticola</i> (Amphibia: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 18).	0.9	5
808	Obligate sexual reproduction of a homothallic fungus closely related to the <i>Cryptococcus</i> pathogenic species complex. <i>ELife</i> , 0, 11, .	2.8	4
809	An Update of Mobile Colistin Resistance in Non-Fermentative Gram-Negative Bacilli. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	13
811	A Ubiquitously Conserved Cyanobacterial Protein Phosphatase Essential for High Light Tolerance in a Fast-Growing Cyanobacterium. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	4
812	Morphology, molecular characterization and phylogeny of <i>Bolbosoma nipponicum</i> Yamaguti, 1939 (Acanthocephala: Polymorphidae), a potential zoonotic parasite of human acanthocephaliasis. <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2022, 18, 212-220.	0.6	4
813	miRNAs Copy Number Variations Repertoire as Hallmark Indicator of Cancer Species Predisposition. <i>Genes</i> , 2022, 13, 1046.	1.0	5
814	The First Fossil of Nossidiinae From Mid-Cretaceous Amber of Northern Myanmar (Coleoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 18).	1.1	4
815	The Complete Genome of the “Flavescence Dor”-Phytoplasma Reveals Characteristics of Low Genome Plasticity. <i>Biology</i> , 2022, 11, 953.	1.3	12
816	Whole genome sequencing analysis to evaluate the influence of T2DM on polymorphisms associated with drug resistance in <i>M. tuberculosis</i> . <i>BMC Genomics</i> , 2022, 23, .	1.2	1
817	Culturable Bacterial Diversity from the Basaltic Subsurface of the Young Volcanic Island of Surtsey, Iceland. <i>Microorganisms</i> , 2022, 10, 1177.	1.6	1

#	ARTICLE	IF	CITATIONS
818	Identification, Molecular Cloning, and Functional Characterization of a Coniferyl Alcohol Acyltransferase Involved in the Biosynthesis of Dibenzocyclooctadiene Lignans in <i>Schisandra chinensis</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	7
819	The molecular impact of life in an indoor environment. <i>Science Advances</i> , 2022, 8, .	4.7	3
820	500 metagenome-assembled microbial genomes from 30 subtropical estuaries in South China. <i>Scientific Data</i> , 2022, 9, .	2.4	9
821	Comparative Analysis of Diverse Acetyltransferase-Type Toxin-Antitoxin Loci in <i>Klebsiella pneumoniae</i> . <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	2
822	Odd one out? Functional tuning of <i>Zymomonas mobilis</i> pyruvate kinase is narrower than its allosteric, human counterpart. <i>Protein Science</i> , 2022, 31, .	3.1	5
824	Systematic analysis and identification of regulators for SRS genes in <i>Capsicum annuum</i> . <i>Plant Growth Regulation</i> , 2022, 98, 51-64.	1.8	2
825	Epidemiological characterization of SARS-CoV-2 variants in children over the four COVID-19 waves and correlation with clinical presentation. <i>Scientific Reports</i> , 2022, 12, .	1.6	12
827	Aminoglycoside resistance in <i>Pseudomonas aeruginosa</i> : the contribution of the MexXY-OprM efflux pump varies between isolates. <i>Journal of Medical Microbiology</i> , 2022, 71, .	0.7	9
828	In Silico Analyses of the Role of Codon Usage at the Hemagglutinin Cleavage Site in Highly Pathogenic Avian Influenza Genesis. <i>Viruses</i> , 2022, 14, 1352.	1.5	3
829	Kalium channelrhodopsins are natural light-gated potassium channels that mediate optogenetic inhibition. <i>Nature Neuroscience</i> , 2022, 25, 967-974.	7.1	56
830	Bacterial Enoyl-Reductases: The Ever-Growing List of Fabs, Their Mechanisms and Inhibition. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
831	Prevalence and Genomic Diversity of <i>Salmonella enterica</i> Recovered from River Water in a Major Agricultural Region in Northwestern Mexico. <i>Microorganisms</i> , 2022, 10, 1214.	1.6	4
832	Datasets are not enough: Challenges in labeling network traffic. <i>Computers and Security</i> , 2022, 120, 102810.	4.0	24
833	Genomic analysis of diversity, biogeography, and drug resistance in <i>Mycobacterium bovis</i> . <i>Transboundary and Emerging Diseases</i> , 2022, 69, .	1.3	2
834	Genetic diversity of <i>Plasmodium vivax</i> reticulocyte binding protein 2b in global parasite populations. <i>Parasites and Vectors</i> , 2022, 15, .	1.0	2
835	Megaviruses contain various genes encoding for eukaryotic vesicle trafficking factors. <i>Traffic</i> , 0, , .	1.3	5
836	Genome-Resolved Characterization of Structure and Potential Functions of the Zebrafish Stool Microbiome. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	3
837	An Outbreak of Human Systemic Anthrax, including One Case of Anthrax Meningitis, Occurred in Calabria Region (Italy): A Description of a Successful One Health Approach. <i>Life</i> , 2022, 12, 909.	1.1	2

#	ARTICLE	IF	CITATIONS
838	Fungal Communities of the Pine Wilt Disease Complex: Studying the Interaction of Ophiostomatales With Bursaphelenchus xylophilus. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	5
839	Development of Droplet Digital PCR Assay for Detection of Seed-Borne Burkholderia glumae and B. gladioli Causing Bacterial Panicle Blight Disease of Rice. <i>Microorganisms</i> , 2022, 10, 1223.	1.6	6
840	Isolation, diversity and antimicrobial activity of planctomycetes from the Tejo river estuary (Portugal). <i>FEMS Microbiology Ecology</i> , 2022, 98, .	1.3	8
841	Turnover in Life-Strategies Recapitulates Marine Microbial Succession Colonizing Model Particles. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5
844	Six-rowed wild-growing barleys are hybrids of diverse origins. <i>Plant Journal</i> , 2022, 111, 849-858.	2.8	1
846	Eco-Plastics in the Sea: Succession of Micro- and Macro-Fouling on a Biodegradable Polymer Augmented With Oyster Shell. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	5
847	Short- and long-read metagenomics expand individualized structural variations in gut microbiomes. <i>Nature Communications</i> , 2022, 13, .	5.8	35
848	The Zymoseptoria tritici white collar-1 gene, ZtWco-1, is required for development and virulence on wheat. <i>Fungal Genetics and Biology</i> , 2022, 161, 103715.	0.9	4
849	Probing the structure and function of polymerase λ helicase-like domain. <i>DNA Repair</i> , 2022, 116, 103358.	1.3	2
850	Comparative genomics analysis of Bacillus velezensis LOH112 isolated from a nonagenarian provides insights into its biocontrol and probiotic traits. <i>Gene</i> , 2022, 835, 146644.	1.0	4
851	FishExp: A comprehensive database and analysis platform for gene expression and alternative splicing of fish species. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 3676-3684.	1.9	3
852	Comparative genomic analysis reveals new evidence of genus boundary for family Iridoviridae and explores qualified hallmark genes. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 3493-3502.	1.9	5
853	Deciphering the cryptic nature of European rock-dwelling Pyramidula snails (Gastropoda: Tj ETQq0 0 0 rgBT /Overlock 10, Tf 50 262 0,2	0.2	2
854	Variants in Bedaquiline-Candidate-Resistance Genes: Prevalence in Bedaquiline-Naive Patients, Effect on MIC, and Association with Mycobacterium tuberculosis Lineage. <i>Antimicrobial Agents and Chemotherapy</i> , 2022, 66, .	1.4	5
855	DIP2 is a unique regulator of diacylglycerol lipid homeostasis in eukaryotes. <i>ELife</i> , 0, 11, .	2.8	5
856	Transcriptomic Identification of a Unique Set of Nodule-Specific Cysteine-Rich Peptides Expressed in the Nitrogen-Fixing Root Nodule of <i>Astragalus sinicus</i> . <i>Molecular Plant-Microbe Interactions</i> , 2022, 35, 893-905.	1.4	5
857	Genetic Diversity of Juglans mandshurica Populations in Northeast China Based on SSR Markers. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	6
858	A highly conserved core bacterial microbiota with nitrogen-fixation capacity inhabits the xylem sap in maize plants. <i>Nature Communications</i> , 2022, 13, .	5.8	44

#	ARTICLE	IF	CITATIONS
859	Transcriptomic modulation in response to an intoxication with deltamethrin in a population of <i>Triatoma infestans</i> with low resistance to pyrethroids. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010060.	1.3	6
861	Genetic Structure of Racing Pigeons (<i>Columba livia</i>) Kept in Poland Based on Microsatellite Markers. <i>Genes</i> , 2022, 13, 1175.	1.0	0
863	The Location of Missense Variants in the Human GIP Gene Is Indicative for Natural Selection. <i>Frontiers in Endocrinology</i> , 0, 13, .	1.5	1
864	Genome-Wide Characterization of QYYZ-Like PRRSV During 2018â€“2021. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	8
865	Screening and identification of azo dye decolorizers from mangrove rhizospheric soil. <i>Environmental Science and Pollution Research</i> , 2022, 29, 83496-83511.	2.7	2
866	Three families of Asgard archaeal viruses identified in metagenome-assembled genomes. <i>Nature Microbiology</i> , 2022, 7, 962-973.	5.9	21
867	Genomic Diversity of Bradyrhizobium from the Tree Legumes <i>Inga</i> and <i>Lysiloma</i> (Caesalpinioideae-Mimosoid Clade). <i>Diversity</i> , 2022, 14, 518.	0.7	3
868	Mixed-Mode Bacterial Transmission via Eggshells in an Oviparous Reptile Without Parental Care. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
869	Dehalogenation of Chlorinated Ethenes to Ethene by a Novel Isolate, <i>Dehalogenimonas etheniformans</i> . <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	14
870	A critical evaluation of <i>Mycobacterium bovis</i> pangenomics, with reference to its utility in outbreak investigation. <i>Microbial Genomics</i> , 2022, 8, .	1.0	7
871	PIWI Proteins Play an Antiviral Role in Lepidopteran Cell Lines. <i>Viruses</i> , 2022, 14, 1442.	1.5	7
872	Genomic Characterization of <i>Enterococcus hirae</i> From Beef Cattle Feedlots and Associated Environmental Continuum. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5
873	Identification and Functional Characterisation of Two Oat UDP-Glucosyltransferases Involved in Deoxynivalenol Detoxification. <i>Toxins</i> , 2022, 14, 446.	1.5	5
874	Genome-Resolved Metagenomic Analysis of Groundwater: Insights into Arsenic Mobilization in Biogeochemical Interaction Networks. <i>Environmental Science & Technology</i> , 2022, 56, 10105-10119.	4.6	25
875	Abundance and Niche Differentiation of Comammox in the Sludges of Wastewater Treatment Plants That Use the Anaerobicâ€“Anoxicâ€“Aerobic Process. <i>Life</i> , 2022, 12, 954.	1.1	1
876	Stable antibiotic resistance and rapid human adaptation in livestock-associated MRSA. <i>ELife</i> , 0, 11, .	2.8	28
878	Genomes of six viruses that infect Asgard archaea from deep-sea sediments. <i>Nature Microbiology</i> , 2022, 7, 953-961.	5.9	17
879	Clonal and Horizontal Transmission of <i>bla</i> _{NDM} among <i>Klebsiella pneumoniae</i> in Childrenâ€™s Intensive Care Units. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	12

#	ARTICLE	IF	CITATIONS
880	DNA Barcoding and Distribution of Gastropods and Malacostracans in the Lower Danube Region. <i>Diversity</i> , 2022, 14, 533.	0.7	1
881	Potential metabolic and genetic interaction among viruses, methanogen and methanotrophic archaea, and their syntrophic partners. <i>ISME Communications</i> , 2022, 2, .	1.7	5
882	Comprehensive identification and characterization of the HML-9 group in the human genome. <i>Retrovirology</i> , 2022, 19, .	0.9	8
883	Potent Protease Inhibitors of Highly Pathogenic Lagoviruses: Rabbit Hemorrhagic Disease Virus and European Brown Hare Syndrome Virus. <i>Microbiology Spectrum</i> , 0, , .	1.2	1
884	Genome-Wide Analysis and Profile of UDP-Glycosyltransferases Family in Alfalfa (<i>Medicago sativa</i> L.) under Drought Stress. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7243.	1.8	8
885	Whole genome resequencing reveals the genetic contribution of Kazakh and Swiss Brown cattle to a population of Xinjiang Brown cattle. <i>Gene</i> , 2022, 839, 146725.	1.0	2
888	Multilocus Sequence Typing and Antifungal Susceptibility of <i>Candida albicans</i> Isolates From Milk and Genital Tract of Dromedary Camel. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	2
889	Genome-Wide Study of Drug Resistant <i>Mycobacterium tuberculosis</i> and Its Intra-Host Evolution during Treatment. <i>Microorganisms</i> , 2022, 10, 1440.	1.6	5
891	Comparative phylogeny and evolutionary analysis of Dicer-like protein family in two plant monophyletic lineages. <i>Journal of Genetic Engineering and Biotechnology</i> , 2022, 20, 103.	1.5	0
892	The Mutational Landscape of SARS-CoV-2 Variants of Concern Recovered From Egyptian Patients in 2021. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
893	Identification of a Putative CodY Regulon in the Gram-Negative Phylum Synergistetes. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7911.	1.8	0
894	p53 Binding Sites in Long Terminal Repeat 5Hs (LTR5Hs) of Human Endogenous Retrovirus K Family (HML-2 Subgroup) Play Important Roles in the Regulation of LTR5Hs Transcriptional Activity. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	11
897	Many dissimilar NusG protein domains switch between α -helix and β -sheet folds. <i>Nature Communications</i> , 2022, 13, .	5.8	20
898	Microbial communities in developmental stages of lucinid bivalves. <i>ISME Communications</i> , 2022, 2, .	1.7	2
899	Expanded Dataset Reveals the Emergence and Evolution of DNA Gyrase in Archaea. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	4
900	A Candidate Gene Cluster for the Bioactive Natural Product Gyrophoric Acid in Lichen-Forming Fungi. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	12
901	Genome-Wide Identification, Characterization, and Comparative Analysis of NLR Resistance Genes in <i>Coffea</i> spp.. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
902	Characterization of <i>Bordetella pertussis</i> Strains Isolated from India. <i>Pathogens</i> , 2022, 11, 794.	1.2	1

#	ARTICLE	IF	CITATIONS
904	Genomic Diversity and Selection Signatures for Weining Cattle on the Border of Yunnan-Guizhou. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	7
905	Landscape of B Cell Receptor Repertoires in COVID-19 Patients Revealed Through CDR3 Sequencing of Immunoglobulin Heavy and Light Chains. <i>Immunological Investigations</i> , 2022, 51, 1994-2008.	1.0	3
906	Growing Maize Root: Lectins Involved in Consecutive Stages of Cell Development. <i>Plants</i> , 2022, 11, 1799.	1.6	0
907	Development of a Multi-Epitope Vaccine for <i>Mycoplasma hyopneumoniae</i> and Evaluation of Its Immune Responses in Mice and Piglets. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7899.	1.8	8
908	Comparative Genomics of Thaumarchaeota From Deep-Sea Sponges Reveal Their Niche Adaptation. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
909	Pan-phylum In Silico Analyses of Nematode Endocannabinoid Signalling Systems Highlight Novel Opportunities for Parasite Drug Target Discovery. <i>Frontiers in Endocrinology</i> , 0, 13, .	1.5	1
910	Characterization of the complete chloroplast genome sequences of six <i>Dalbergia</i> species and its comparative analysis in the subfamily of Papilionoideae (Fabaceae). <i>PeerJ</i> , 0, 10, e13570.	0.9	4
911	The Unique Seed Protein Composition of Quality Protein Popcorn Promotes Growth of Beneficial Bacteria From the Human Gut Microbiome. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
912	Genome Size Variation and Evolution Driven by Transposable Elements in the Genus <i>Oryza</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	10
913	Analysis of the Taxonomy, Synteny, and Virulence Factors for Soft Rot Pathogen <i>Pectobacterium aroidearum</i> in <i>Amorphophallus konjac</i> Using Comparative Genomics. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
914	Within-host evolution of a gut pathobiont facilitates liver translocation. <i>Nature</i> , 2022, 607, 563-570.	13.7	65
915	Systematic identification of cell-fate regulatory programs using a single-cell atlas of mouse development. <i>Nature Genetics</i> , 2022, 54, 1051-1061.	9.4	29
916	Gene Losses and Plastome Degradation in the Hemiparasitic Species <i>Plicosepalus acaciae</i> and <i>Plicosepalus curviflorus</i> : Comparative Analyses and Phylogenetic Relationships among Santalales Members. <i>Plants</i> , 2022, 11, 1869.	1.6	3
918	Structurally derived universal mechanism for the catalytic cycle of the tail-anchored targeting factor Get3. <i>Nature Structural and Molecular Biology</i> , 2022, 29, 820-830.	3.6	7
919	Microbial Diversity in Groundwater and Its Response to Seawater Intrusion in Beihai City, Southern China. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
920	Aminoglycoside-Modifying Enzymes Are Sufficient to Make <i>Pseudomonas aeruginosa</i> Clinically Resistant to Key Antibiotics. <i>Antibiotics</i> , 2022, 11, 884.	1.5	7
921	Warthog Genomes Resolve an Evolutionary Conundrum and Reveal Introgression of Disease Resistance Genes. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	11
923	Genome-Wide Analysis of CqCrRLK1L and CqRALF Gene Families in <i>Chenopodium quinoa</i> and Their Roles in Salt Stress Response. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	5

#	ARTICLE	IF	CITATIONS
924	Genomic surveillance for multidrug-resistant or hypervirulent <i>Klebsiella pneumoniae</i> among United States bloodstream isolates. <i>BMC Infectious Diseases</i> , 2022, 22, .	1.3	23
925	<i>Coframalaxius bletteryi</i> gen. et sp. nov. from subterranean habitat in Southern France (Hemiptera, Tj ETQq1 1 0,784314 rgBT /Ove	5.0	8
926	An invasive weed-associated bacteria confers enhanced heat stress tolerance in wheat. <i>Heliyon</i> , 2022, 8, e09893.	1.4	5
927	Evolution of the Inhibitory and Non-Inhibitory $\hat{\mu}$, $\hat{\eta}$, and IF1 Subunits of the F1FO-ATPase as Related to the Endosymbiotic Origin of Mitochondria. <i>Microorganisms</i> , 2022, 10, 1372.	1.6	5
928	A Novel <i>Alteromonas</i> Phage Lineage with a Broad Host Range and Small Burst Size. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	3
931	Diversity and Ecophysiology of the Genus OLB8 and Other Abundant Uncultured Saprospiraceae Genera in Global Wastewater Treatment Systems. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	32
932	Soil substrate culturing approaches recover diverse members of Actinomycetota from desert soils of Herring Island, East Antarctica. <i>Extremophiles</i> , 2022, 26, .	0.9	4
933	A super pan-genomic landscape of rice. <i>Cell Research</i> , 2022, 32, 878-896.	5.7	99
934	Antibiotic Resistance Properties among <i>Pseudomonas</i> spp. Associated with Salmon Processing Environments. <i>Microorganisms</i> , 2022, 10, 1420.	1.6	10
936	Comparative Analysis of Chloroplast Genome in <i>Saccharum</i> spp. and Related Members of <i>Saccharum</i> Complex™. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7661.	1.8	7
937	Cell competition and the regulative nature of early mammalian development. <i>Cell Stem Cell</i> , 2022, 29, 1018-1030.	5.2	11
938	Identification of Mobile Colistin Resistance Gene <i>mcr-10</i> in Disinfectant and Antibiotic Resistant <i>Escherichia coli</i> from Disinfected Tableware. <i>Antibiotics</i> , 2022, 11, 883.	1.5	3
939	Selection of <i>Anabaena</i> sp. PCC 7938 as a Cyanobacterium Model for Biological ISRU on Mars. <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	10
940	Broadly neutralizing antibodies target the coronavirus fusion peptide. <i>Science</i> , 2022, 377, 728-735.	6.0	111
941	Estimating the genetic structure of <i>Triatoma dimidiata</i> (Hemiptera: Reduviidae) and the transmission dynamics of <i>Trypanosoma cruzi</i> in Boyacá, eastern Colombia. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010534.	1.3	5
943	Beyond tuberculosis: Diversity and implications of non-tuberculous mycobacteria at the wildlife-livestock interface. <i>Transboundary and Emerging Diseases</i> , 2022, 69, .	1.3	13
945	Genome-Wide Analysis of DoSPX Genes and the Function of DoSPX4 in Low Phosphorus Response in <i>Dendrobium officinale</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	0
946	Co-Occurrence of <i>Francisella</i> , Spotted Fever Group Rickettsia, and <i>Midichloria</i> in Avian-Associated <i>Hyalomma rufipes</i> . <i>Microorganisms</i> , 2022, 10, 1393.	1.6	5

#	ARTICLE	IF	CITATIONS
949	Integrated Analysis of Single-Molecule Real-Time Sequencing and Next-Generation Sequencing Reveals Insights into Drought Tolerance Mechanism of <i>Lolium multiflorum</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 7921.	1.8	4
950	Cross-kingdom regulation of calcium- and/or calmodulin-dependent protein kinases by phospho-switches that relieve autoinhibition. <i>Current Opinion in Plant Biology</i> , 2022, 68, 102251.	3.5	4
951	Bending over backwards: BAR proteins and the actin cytoskeleton in mammalian receptor-mediated endocytosis. <i>European Journal of Cell Biology</i> , 2022, 101, 151257.	1.6	5
952	Comparison of S gene mutations in patients with occult and chronic hepatitis B virus infection. <i>Virus Research</i> , 2022, 318, 198855.	1.1	1
953	Antibiofilm activity of secondary metabolites from bacterial endophytes of Red Sea soft corals. <i>International Biodeterioration and Biodegradation</i> , 2022, 173, 105462.	1.9	9
954	Genome-wide identification of the cytochrome P450 superfamily in <i>Olea europaea</i> helps elucidate the synthesis pathway of oleuropein to improve the quality of olive oil. <i>Scientia Horticulturae</i> , 2022, 304, 111291.	1.7	4
955	Dispersed emergence and protracted domestication of polyploid wheat uncovered by mosaic ancestral haplotype inference. <i>Nature Communications</i> , 2022, 13, .	5.8	27
957	A New Species of <i>Limnephilus</i> (Insecta: Trichoptera: Limnephilidae) from China, with Revision of the Genus <i>Limnephilus</i> on the Chinese Mainland. <i>Insects</i> , 2022, 13, 653.	1.0	2
958	The Complete Mitochondrial Genome of <i>Ophioglossum vulgatum</i> L. Is with Highly Repetitive Sequences: Intergenomic Fragment Transfer and Phylogenetic Analysis. <i>Genes</i> , 2022, 13, 1287.	1.0	6
959	Time Series Genomics of <i>Pseudomonas aeruginosa</i> Reveals the Emergence of a Hypermutator Phenotype and Within-Host Evolution in Clinical Inpatients. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	2
960	Identification and Characterization of DNA Demethylase Genes and Their Association With Thermal Stress in Wheat (<i>Triticum aestivum</i> L.). <i>Frontiers in Genetics</i> , 0, 13, .	1.1	3
961	Systematic whole-genome sequencing reveals an unexpected diversity among actinomycetoma pathogens and provides insights into their antibacterial susceptibilities. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010128.	1.3	4
962	Effect of pressure on biomethanation process and spatial stratification of microbial communities in trickle bed reactors under decreasing gas retention time. <i>Bioresource Technology</i> , 2022, 361, 127701.	4.8	19
963	Transcriptomic analysis of deceptively pollinated <i>Arum maculatum</i> (Araceae) reveals association between terpene synthase expression in floral trap chamber and species-specific pollinator attraction. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	3
964	Selection signature analyses and genome-wide association reveal genomic hotspot regions that reflect differences between breeds of horse with contrasting risk of degenerative suspensory ligament desmitis. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	3
966	Genomic epidemiology of SARS-CoV-2 in a university outbreak setting and implications for public health planning. <i>Scientific Reports</i> , 2022, 12, .	1.6	5
969	Genome-wide identification and expression pattern analysis of lipoxygenase gene family in turnip (<i>Brassica rapa</i> L. subsp. <i>rapa</i>). <i>PeerJ</i> , 0, 10, e13746.	0.9	5
970	Oral microbiome diversity: The curious case of <i>Corynebacterium</i> sp. isolation. <i>Molecular Oral Microbiology</i> , 2022, 37, 167-179.	1.3	2

#	ARTICLE	IF	CITATIONS
971	Identification of heptapeptides targeting a lethal bacterial strain in septic mice through an integrative approach. <i>Signal Transduction and Targeted Therapy</i> , 2022, 7, .	7.1	2
974	Bioinformatic Analysis of a Set of 14 Temperate Bacteriophages Isolated from <i>Staphylococcus aureus</i> Strains Highlights Their Massive Genetic Diversity. <i>Microbiology Spectrum</i> , 0, , .	1.2	1
975	Metagenome-Assembled Genomes from a Microbiome Grown in Dairy Manure Hydrolysate. <i>Microbiology Resource Announcements</i> , 2022, 11, .	0.3	2
976	The acquisition of clinically relevant amoxicillin resistance in <i>Streptococcus pneumoniae</i> requires ordered horizontal gene transfer of four loci. <i>PLoS Pathogens</i> , 2022, 18, e1010727.	2.1	6
978	Molecular Epidemiology and Baseline Resistance of Hepatitis C Virus to Direct Acting Antivirals in Croatia. <i>Pathogens</i> , 2022, 11, 808.	1.2	0
979	Molecular characterization, expression and response to immune challenges of 3 members of the toll-like receptor superfamily 11 in the golden pompano (<i>Trachinotus ovatus</i>). <i>Aquaculture Reports</i> , 2022, 25, 101268.	0.7	2
980	The microbiome and its association with antibiotic resistance genes in the hadal biosphere at the Yap Trench. <i>Journal of Hazardous Materials</i> , 2022, 439, 129543.	6.5	3
981	Investigation of healthcare-associated COVID-19 in a large French hospital group by whole-genome sequencing. <i>Microbiological Research</i> , 2022, 263, 127133.	2.5	7
982	A Vast World of Viroid-Like Circular RNAs Revealed by Mining Metatranscriptomes. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
983	New <i>Microviridae</i> isolated from <i>Sulfitobacter</i> reveals two cosmopolitan subfamilies of single-stranded DNA phages infecting marine and terrestrial Alphaproteobacteria. <i>Virus Evolution</i> , 2022, 8, .	2.2	5
984	Highly Virulent and Multidrug-Resistant <i>Escherichia coli</i> Sequence Type 58 from a Sausage in Germany. <i>Antibiotics</i> , 2022, 11, 1006.	1.5	7
985	Novel Insights into the Pig Gut Microbiome Using Metagenome-Assembled Genomes. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	16
986	Evolutionary history of metazoan TMEM16 family. <i>Molecular Phylogenetics and Evolution</i> , 2022, 177, 107595.	1.2	3
987	Travel-associated extensively drug-resistant typhoid fever: a case series to inform management in non-endemic regions. <i>Journal of Travel Medicine</i> , 2023, 30, .	1.4	4
988	Genome-Wide Identification and Analysis of the BBX Gene Family and Its Role in Carotenoid Biosynthesis in Wolfberry (<i>Lycium barbarum</i> L.). <i>International Journal of Molecular Sciences</i> , 2022, 23, 8440.	1.8	5
990	Genetic markers in Andean <i>Puya</i> species (Bromeliaceae) with implications on plastome evolution and phylogeny. <i>Ecology and Evolution</i> , 2022, 12, .	0.8	3
993	New insights into the evolutionary dynamic and lineage divergence of gasdermin E in metazoa. <i>Frontiers in Cell and Developmental Biology</i> , 0, 10, .	1.8	13
994	Mechanisms of Caspases 3/7/8/9 in the Degeneration of External Gills of Chinese Giant Salamanders (<i>Andrias davidianus</i>). <i>Genes</i> , 2022, 13, 1360.	1.0	0

#	ARTICLE	IF	CITATIONS
995	Comparative Genomic Analysis of Antarctic <i>Pseudomonas</i> Isolates with 2,4,6-Trinitrotoluene Transformation Capabilities Reveals Their Unique Features for Xenobiotics Degradation. <i>Genes</i> , 2022, 13, 1354.	1.0	12
996	Multilocus marker-based delimitation of <i>Salicornia persica</i> and its population discrimination assisted by supervised machine learning approach. <i>PLoS ONE</i> , 2022, 17, e0270463.	1.1	3
997	Developing Indicators of Nutrient Pollution in Streams Using 16S rRNA Gene Metabarcoding of Periphyton-Associated Bacteria. <i>Water (Switzerland)</i> , 2022, 14, 2361.	1.2	2
998	Glucose-1,6-Bisphosphate, a Key Metabolic Regulator, Is Synthesized by a Distinct Family of Î±-Phosphohexomutases Widely Distributed in Prokaryotes. <i>MBio</i> , 2022, 13, .	1.8	5
999	Abundance of Poloroviruses within Tasmanian Pea Crops and Surrounding Weeds, and the Genetic Diversity of TuYV Isolates Found. <i>Viruses</i> , 2022, 14, 1690.	1.5	4
1000	A Cocktail of Three Virulent Phages Controls Multidrug-Resistant <i>Salmonella</i> Enteritidis Infection in Poultry. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	6
1001	Islands Within Islands: Bacterial Phylogenetic Structure and Consortia in Hawaiian Lava Caves and Fumaroles. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	10
1003	Clinical and Genomic Epidemiology of <i>mcr-9</i> -Carrying Carbapenem-Resistant <i>Enterobacterales</i> Isolates in Metropolitan Atlanta, 2012 to 2017. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	4
1004	Analysis of <i>Streptomyces</i> Volatilomes Using Global Molecular Networking Reveals the Presence of Metabolites with Diverse Biological Activities. <i>Microbiology Spectrum</i> , 0, , .	1.2	2
1005	Dynamics of the Emerging Genogroup of Infectious Bursal Disease Virus Infection in Broiler Farms in South Korea: A Nationwide Study. <i>Viruses</i> , 2022, 14, 1604.	1.5	6
1006	Identification of Heat-Tolerant Genes in Non-Reference Sequences in Rice by Integrating Pan-Genome, Transcriptomics, and QTLs. <i>Genes</i> , 2022, 13, 1353.	1.0	2
1007	First Report of Zoonotic Tapeworms, <i>Dibothriocephalus latus</i> (Linnaeus, 1758) and <i>D. dendriticus</i> (Nitzsch, 1824), and Other Endohelminth Parasites in Chinook Salmon, <i>Oncorhynchus tshawytscha</i> , in Chile. <i>Comparative Parasitology</i> , 2022, 89, .	0.0	1
1008	Multi-omics profiling of the cold tolerant <i>Monoraphidium minutum</i> 26B-AM in response to abiotic stress. <i>Algal Research</i> , 2022, 66, 102794.	2.4	3
1009	Complete Genome Sequence, Molecular Characterization and Phylogenetic Relationships of a Temminck's Stint Calicivirus: Evidence for a New Genus within Caliciviridae Family. <i>Microorganisms</i> , 2022, 10, 1540.	1.6	2
1011	<i>Vibrio</i> Phage Artemius, a Novel Phage Infecting <i>Vibrio alginolyticus</i> . <i>Pathogens</i> , 2022, 11, 848.	1.2	6
1012	Intra-species diversity of <i>Clostridium perfringens</i> : A diverse genetic repertoire reveals its pathogenic potential. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	9
1013	Niche, not phylogeny, governs the response to oxygen availability among diverse <i>Pseudomonas aeruginosa</i> strains. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
1014	The type polyketide synthase supergene family in plants: complex evolutionary history and functional divergence. <i>Plant Journal</i> , 2022, 112, 414-428.	2.8	2

#	ARTICLE	IF	CITATIONS
1015	Two New <i>Rhizobiales</i> Species Isolated from Root Nodules of Common Sainfoin (<i>Onobrychis</i>)	1.2	6
1016	<i>Coprinus leucostictus</i> Rediscovered after a Century, Epitypified, and Its Generic Position in <i>Hausknechtia</i> Resolved by Multigene Phylogenetic Analysis of <i>Psathyrellaceae</i> . <i>Diversity</i> , 2022, 14, 699.	0.7	2
1017	High Prevalence and Varied Distribution of Antibiotic-Resistant Bacteria in the Rhizosphere and Rhizoplane of <i>Citrus medica</i> . <i>Microorganisms</i> , 2022, 10, 1708.	1.6	2
1018	The impacts of viral infection and subsequent antimicrobials on the microbiome-resistome of growing pigs. <i>Microbiome</i> , 2022, 10, .	4.9	9
1019	(Meta)Genomic Analysis Reveals Diverse Energy Conservation Strategies Employed by Globally Distributed <i>Gemmatimonadota</i> . <i>MSystems</i> , 2022, 7, .	1.7	6
1020	Phylogeny of <i>Membracoidea</i> (Hemiptera: Auchenorrhyncha) based on transcriptome data. <i>Systematic Entomology</i> , 2023, 48, 97-110.	1.7	8
1021	Oxygen-dependent regulation of E3(SCF)ubiquitin ligases and a Skp1-associated JmjD6 homolog in development of the social amoeba <i>Dictyostelium</i> . <i>Journal of Biological Chemistry</i> , 2022, 298, 102305.	1.6	3
1022	Global patterns and rates of habitat transitions across the eukaryotic tree of life. <i>Nature Ecology and Evolution</i> , 2022, 6, 1458-1470.	3.4	19
1025	Expression Profiling and MicroRNA Regulatory Networks of Homeobox Family Genes in Sugarcane <i>Saccharum spontaneum</i> L.. <i>International Journal of Molecular Sciences</i> , 2022, 23, 8724.	1.8	3
1027	A new species of the genus <i>Prosopistoma</i> Latreille, 1833 (Ephemeroptera, Prosopistomatidae) from Morocco. <i>ZooKeys</i> , 0, 1117, 203-218.	0.5	7
1028	Origination of LTR retroelement-derived <i>NYNRIN</i> coincides with therian placental emergence. <i>Molecular Biology and Evolution</i> , 0, , .	3.5	2
1029	Non-ribosomal peptide biosynthetic potential of the nematode symbiont <i>Photorhabdus</i> . <i>Environmental Microbiology Reports</i> , 0, , .	1.0	2
1030	Functional Testing to Characterize and Stratify PI3K Inhibitor Responses in Chronic Lymphocytic Leukemia. <i>Clinical Cancer Research</i> , 2022, 28, 4444-4455.	3.2	7
1031	Co-occurrence of <i>mcr-2</i> and <i>mcr-3</i> genes on chromosome of multidrug-resistant <i>Escherichia coli</i> isolated from healthy individuals in Thailand. <i>International Journal of Antimicrobial Agents</i> , 2022, 60, 106662.	1.1	8
1033	Structural plasticity enables evolution and innovation of RuBisCO assemblies. <i>Science Advances</i> , 2022, 8, .	4.7	9
1034	Molecular characterization of circulating <i>Salmonella Typhi</i> strains in an urban informal settlement in Kenya. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010704.	1.3	3
1037	Rhamnosyltransferases involved in the biosynthesis of flavone rutinosides in <i>Chrysanthemum</i> species. <i>Plant Physiology</i> , 2022, 190, 2122-2136.	2.3	6
1038	<i>Pseudovibrio flavus</i> sp. nov. isolated from the sea sponge <i>Verongula gigantea</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	0

#	ARTICLE	IF	CITATIONS
1039	Characterization and phylogenetic analysis of multiple C2 domain and transmembrane region proteins in maize. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	2
1040	Genetic determinants of antimicrobial resistance in three multi-drug resistant strains of <i>Cutibacterium acnes</i> isolated from patients with acne: a predictive in silico study. <i>Access Microbiology</i> , 2022, 4, .	0.2	3
1041	New Three-Finger Protein from Starfish <i>Asteria rubens</i> Shares Structure and Pharmacology with Human Brain Neuromodulator Lynx2. <i>Marine Drugs</i> , 2022, 20, 503.	2.2	2
1042	Chromosome-level reference genome for European flat oyster (<i>Ostrea edulis</i> L.). <i>Evolutionary Applications</i> , 2022, 15, 1713-1729.	1.5	10
1043	The chromosome-level holly (<i>Ilex latifolia</i>) genome reveals key enzymes in triterpenoid saponin biosynthesis and fruit color change. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	7
1044	Systematic Analysis of the Grafting-Related Glucanase-Encoding GH9 Family Genes in Pepper, Tomato and Tobacco. <i>Plants</i> , 2022, 11, 2092.	1.6	1
1045	Genome-Wide Characterization of Ascorbate Peroxidase Gene Family in Peanut (<i>Arachis hypogea</i> L.) Revealed Their Crucial Role in Growth and Multiple Stress Tolerance. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	17
1047	Phylogenetically and catabolically diverse diazotrophs reside in deep-sea cold seep sediments. <i>Nature Communications</i> , 2022, 13, .	5.8	29
1048	Characterizations of MYB Transcription Factors in <i>Camellia oleifera</i> Reveal the Key Regulators Involved in Oil Biosynthesis. <i>Horticulturae</i> , 2022, 8, 742.	1.2	3
1049	Cultivating marine bacteria under laboratory conditions: Overcoming the "unculturable" dogma. <i>Frontiers in Bioengineering and Biotechnology</i> , 0, 10, .	2.0	7
1050	Uninvited Guest: Arrival and Dissemination of Omicron Lineage SARS-CoV-2 in St. Petersburg, Russia. <i>Microorganisms</i> , 2022, 10, 1676.	1.6	5
1051	Molecular Epidemiology of Penicillin-Susceptible <i>Staphylococcus aureus</i> Bacteremia in Australia and Reliability of Diagnostic Phenotypic Susceptibility Methods to Detect Penicillin Susceptibility. <i>Microorganisms</i> , 2022, 10, 1650.	1.6	1
1052	Emergence of uncommon KL38-OCL6-ST220 carbapenem-resistant <i>Acinetobacter pittii</i> strain, co-producing chromosomal NDM-1 and OXA-820 carbapenemases. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	5
1053	The final piece of the Triangle of U: Evolution of the tetraploid <i>Brassica carinata</i> genome. <i>Plant Cell</i> , 2022, 34, 4143-4172.	3.1	18
1055	In silico analysis reveals the co-existence of CRISPR-Cas type I-F1 and type I-F2 systems and its association with restricted phage invasion in <i>Acinetobacter baumannii</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5
1056	Phage endolysins are adapted to specific hosts and are evolutionarily dynamic. <i>PLoS Biology</i> , 2022, 20, e3001740.	2.6	20
1057	Genomic Epidemiology of Carbapenemase-Producing and Colistin-Resistant <i>Enterobacteriaceae</i> among Sepsis Patients in Ethiopia: a Whole-Genome Analysis. <i>Antimicrobial Agents and Chemotherapy</i> , 2022, 66, .	1.4	4
1058	Sequencing introduced false positive rare taxa lead to biased microbial community diversity, assembly, and interaction interpretation in amplicon studies. <i>Environmental Microbiomes</i> , 2022, 17, .	2.2	17

#	ARTICLE	IF	CITATIONS
1060	Obligately aerobic human gut microbe expresses an oxygen resistant tungsten-containing oxidoreductase for detoxifying gut aldehydes. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
1061	Genomic Surveillance of SARS-CoV-2 in the Southern Province of Zambia: Detection and Characterization of Alpha, Beta, Delta, and Omicron Variants of Concern. <i>Viruses</i> , 2022, 14, 1865.	1.5	1
1062	MAS-related G protein-coupled receptors X (MRGPRX): Orphan GPCRs with potential as targets for future drugs. , 2022, 238, 108259.		16
1063	Cross-talk between the cytokinin, auxin, and gibberellin regulatory networks in determining parthenocary in cucumber. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	8
1064	Widespread repression of anti-CRISPR production by anti-CRISPR-associated proteins. <i>Nucleic Acids Research</i> , 2022, 50, 8615-8625.	6.5	16
1065	First report and whole-genome sequencing of <i>Pseudochrobactrum saccharolyticum</i> in Latin America. <i>Microbes and Infection</i> , 2023, 25, 105018.	1.0	0
1066	Invasive Group A Streptococcal Penicillin Binding Protein 2A— Variants Associated with Reduced Susceptibility to β -Lactam Antibiotics in the United States, 2015–2021. <i>Antimicrobial Agents and Chemotherapy</i> , 2022, 66, .	1.4	7
1067	Characterization of <i>Codonopsis pilosula</i> subsp. tangshen plastome and comparative analysis of <i>Codonopsis</i> species. <i>PLoS ONE</i> , 2022, 17, e0271813.	1.1	0
1068	Integrating metagenomic binning with flux balance analysis to unravel syntrophies in anaerobic CO ₂ methanation. <i>Microbiome</i> , 2022, 10, .	4.9	25
1069	Analysis of flavonol regulator evolution in the Brassicaceae reveals MYB12, MYB111 and MYB21 duplications and MYB11 and MYB24 gene loss. <i>BMC Genomics</i> , 2022, 23, .	1.2	5
1070	Microbiome of pear psyllids: A tale about closely related species sharing their endosymbionts. <i>Environmental Microbiology</i> , 2022, 24, 5788-5808.	1.8	13
1071	Phylogenetic and Phylogeographic Analysis of the Highly Pathogenic H5N6 Avian Influenza Virus in China. <i>Viruses</i> , 2022, 14, 1752.	1.5	5
1076	Ecophysiological and genomic analyses of a representative isolate of highly abundant <i>Bacillus cereus</i> strains in contaminated subsurface sediments. <i>Environmental Microbiology</i> , 2022, 24, 5546-5560.	1.8	4
1077	SARS-CoV-2 genome variations and evolution patterns in Egypt: a multi-center study. <i>Scientific Reports</i> , 2022, 12, .	1.6	1
1078	The human gut microbiota and glucose metabolism: a scoping review of key bacteria and the potential role of SCFAs. <i>American Journal of Clinical Nutrition</i> , 2022, 116, 862-874.	2.2	37
1080	Comprehensive investigation of antibiotic resistance gene content in <i>cfiA</i> -harboring <i>Bacteroides fragilis</i> isolates of human and animal origins by whole genome sequencing. <i>International Journal of Medical Microbiology</i> , 2022, 312, 151559.	1.5	8
1081	Homologous recombination between tandem paralogues drives evolution of a subset of type VII secretion system immunity genes in firmicute bacteria. <i>Microbial Genomics</i> , 2022, 8, .	1.0	5
1083	Genomic and functional insights into the diversification of the elongation factor eEF1B ³ in fungi. <i>Fungal Biology Reviews</i> , 2022, 42, 74-84.	1.9	1

#	ARTICLE	IF	CITATIONS
1084	Prokaryotic innate immunity through pattern recognition of conserved viral proteins. <i>Science</i> , 2022, 377, .	6.0	90
1085	Metabolism of Cysteine Conjugates and Production of Flavor Sulfur Compounds by a Carbon-14-Sulfur Lyase from the Oral Anaerobe <i>Fusobacterium nucleatum</i> . <i>Journal of Agricultural and Food Chemistry</i> , 2022, 70, 9969-9979.	2.4	9
1086	Comparative analysis of the plastid and mitochondrial genomes of <i>Artemisia giraldii</i> Pamp.. <i>Scientific Reports</i> , 2022, 12, .	1.6	7
1089	Genome characterization of a uropathogenic <i>Pseudomonas aeruginosa</i> isolate PA_HN002 with cyclic di-GMP-dependent hyper-biofilm production. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	3
1090	Insights into the Evolution of Aphid Mitogenome Features from New Data and Comparative Analysis. <i>Animals</i> , 2022, 12, 1970.	1.0	5
1092	Genomic reconstruction of short-chain fatty acid production by the human gut microbiota. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	1.6	18
1093	In Silico Study of Cell Surface Structures of <i>Parabacteroides distasonis</i> Involved in Its Maintenance within the Gut Microbiota. <i>International Journal of Molecular Sciences</i> , 2022, 23, 9411.	1.8	6
1094	The leaf beetle <i>Chelymorpha alternans</i> propagates a plant pathogen in exchange for pupal protection. <i>Current Biology</i> , 2022, 32, 4114-4127.e6.	1.8	16
1095	Evolution of the odorant-binding protein gene family in <i>Drosophila</i> . <i>Frontiers in Ecology and Evolution</i> , 0, 10, .	1.1	4
1096	ZccE is a Novel P-type ATPase That Protects <i>Streptococcus mutans</i> Against Zinc Intoxication. <i>PLoS Pathogens</i> , 2022, 18, e1010477.	2.1	7
1097	Transcriptome-Wide Analysis Revealed the Potential of the High-Affinity Potassium Transporter (HKT) Gene Family in Rice Salinity Tolerance via Ion Homeostasis. <i>Bioengineering</i> , 2022, 9, 410.	1.6	3
1098	A pan-Zea genome map for enhancing maize improvement. <i>Genome Biology</i> , 2022, 23, .	3.8	21
1099	Introduction, Spread and Impact of the SARS-CoV-2 Omicron Variants BA.1 and BA.2 in Cyprus. <i>Microorganisms</i> , 2022, 10, 1688.	1.6	2
1100	<i>Huaxiibacter chinensis</i> gen. nov., sp. nov., recovered from human sputum. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	3
1101	The Homeodomain-Leucine Zipper Genes Family Regulates the Jinglyngmycin Mediated Immune Response of <i>Oryza sativa</i> to <i>Nilaparvata lugens</i> , and <i>Laodelphax striatellus</i> . <i>Bioengineering</i> , 2022, 9, 398.	1.6	9
1102	Evidence for a Widespread Third System for Bacterial Polysaccharide Export across the Outer Membrane Comprising a Composite OPX/Î²-Barrel Translocon. <i>MBio</i> , 2022, 13, .	1.8	13
1104	Redefining the phylogenetic and metabolic diversity of phylum Omnitrophota. <i>Environmental Microbiology</i> , 2022, 24, 5437-5449.	1.8	5
1105	Ryhc Confers Extreme Resistance to Potato virus Y in Potato. <i>Cells</i> , 2022, 11, 2577.	1.8	12

#	ARTICLE	IF	CITATIONS
1107	The human gut serves as a reservoir of hypervirulent <i>Klebsiella pneumoniae</i> . <i>Gut Microbes</i> , 2022, 14, .	4.3	4
1108	Marine Bacteria from the Southeast Coast of Brazil as a Source of Insecticidal Compounds. <i>Revista Brasileira De Farmacognosia</i> , 0, , .	0.6	0
1110	Pervasive <i>Listeria monocytogenes</i> Is Common in the Norwegian Food System and Is Associated with Increased Prevalence of Stress Survival and Resistance Determinants. <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	24
1111	Genome-wide identification of the calcium-dependent protein kinase gene family in <i>Fragaria vesca</i> and expression analysis under different biotic stresses. <i>European Journal of Plant Pathology</i> , 0, , .	0.8	2
1112	Comprehensive characterization of Cysteine-rich protein-coding genes of <i>Giardia lamblia</i> and their role during antigenic variation. <i>Genomics</i> , 2022, 114, 110462.	1.3	6
1113	Deep Population Genomics Reveals Systematic and Parallel Evolution at a Lipopolysaccharide Biosynthetic Locus in <i>Xanthomonas</i> Pathogens That Infect Rice and Sugarcane. <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	1
1114	Occurrence of methane-oxidizing bacteria and methanogenic archaea in earth's cave systems: A metagenomic analysis. <i>Frontiers in Ecology and Evolution</i> , 0, 10, .	1.1	1
1115	Two divergent immune receptors of the allopolyploid <i>Nicotiana benthamiana</i> reinforce the recognition of a fungal microbe-associated molecular pattern VdEIX3. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	0
1116	Functional Prediction of trans-Prenyltransferases Reveals the Distribution of GFPPs in Species beyond the Brassicaceae Clade. <i>International Journal of Molecular Sciences</i> , 2022, 23, 9471.	1.8	1
1117	Genomic and phenotypic characterization of <i>Streptococcus mutans</i> isolates suggests key gene clusters in regulating its interaction with <i>Streptococcus gordonii</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
1118	Genomic Diversity, Antimicrobial Resistance, and Virulence Gene Profiles of <i>Salmonella</i> Serovar Kentucky Isolated from Humans, Food, and Animal Ceca Content Sources in the United States. <i>Foodborne Pathogens and Disease</i> , 2022, 19, 509-521.	0.8	9
1119	Quantitative and Qualitative Changes in the Genetic Diversity of Bacterial Communities in Anaerobic Bioreactors with the Diatomaceous Earth/Peat Cell Carrier. <i>Cells</i> , 2022, 11, 2571.	1.8	3
1121	Comparative genomics of <i>Leuconostoc lactis</i> strains isolated from human gastrointestinal system and fermented foods microbiomes. <i>BMC Genomic Data</i> , 2022, 23, .	0.7	2
1122	Virome of Giant Panda-Infesting Ticks Reveals Novel Bunyaviruses and Other Viruses That Are Genetically Close to Those from Giant Pandas. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	4
1123	Whole Genome Sequencing Suggests that "Nonpathogenicity on Banana (NPB)" is the Ancestral State of the <i>Ralstonia solanacearum</i> IIB-4 Lineage. <i>PhytoFrontiers</i> , 2023, 3, 262-267.	0.8	3
1124	Supplemental Oxygen Alters the Airway Microbiome in Cystic Fibrosis. <i>MSystems</i> , 2022, 7, .	1.7	1
1125	Population structure, susceptibility profile, phenotypic and mating properties of <i>Candida tropicalis</i> isolated from pediatric patients. <i>Microbial Pathogenesis</i> , 2022, 170, 105690.	1.3	1
1126	Detection of Endosymbiont <i>Candidatus</i> <i>Midichloria mitochondrii</i> and Tickborne Pathogens in Humans Exposed to Tick Bites, Italy. <i>Emerging Infectious Diseases</i> , 2022, 28, 1824-1832.	2.0	12

#	ARTICLE	IF	CITATIONS
1127	Structure of maize BZR1-type β -amylase BAM8 provides new insights into its noncatalytic adaptation. <i>Journal of Structural Biology</i> , 2022, 214, 107885.	1.3	3
1128	A core genome multilocus sequence typing (cgMLST) analysis of <i>Mycoplasma bovis</i> isolates. <i>Veterinary Microbiology</i> , 2022, 273, 109532.	0.8	4
1129	Therapeutic evaluation of the <i>Acinetobacter baumannii</i> phage Phab24 for clinical use. <i>Virus Research</i> , 2022, 320, 198889.	1.1	4
1130	HvGST4 enhances tolerance to multiple abiotic stresses in barley: Evidence from integrated meta-analysis to functional verification. <i>Plant Physiology and Biochemistry</i> , 2022, 188, 47-59.	2.8	5
1131	Expression of nuclear-encoded, haptophyte-derived <i>ftsH</i> genes support extremely rapid PSII repair and high-light photoacclimation in <i>Karenia brevis</i> (Dinophyceae). <i>Harmful Algae</i> , 2022, 118, 102295.	2.2	1
1132	Redefining Chlorobotryaceae as one of the principal and most diverse lineages of eustigmatophyte algae. <i>Molecular Phylogenetics and Evolution</i> , 2022, 177, 107607.	1.2	5
1135	Shiga Toxin Subtypes, Serogroups, Phylogroups, RAPD Genotypic Diversity, and Select Virulence Markers of Shiga-Toxigenic <i>Escherichia coli</i> Strains from Goats in Mid-Atlantic US. <i>Microorganisms</i> , 2022, 10, 1842.	1.6	2
1136	<i>Xanthomonas indica</i> sp. nov., a Novel Member of Non-Pathogenic <i>Xanthomonas</i> Community from Healthy Rice Seeds. <i>Current Microbiology</i> , 2022, 79, .	1.0	11
1137	Comparative Genomics of <i>Listeria</i> Species Recovered from Meat and Food Processing Facilities. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	5
1138	Genome-Wide Identification and Analysis of the R2R3-MYB Gene Family in <i>Theobroma cacao</i> . <i>Genes</i> , 2022, 13, 1572.	1.0	7
1139	Non-lysine ubiquitylation: Doing things differently. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	1.6	25
1140	Global genetic diversity and evolutionary patterns among Potato leafroll virus populations. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
1141	Full-Length Transcriptome Maps of Reef-Building Coral Illuminate the Molecular Basis of Calcification, Symbiosis, and Circadian Genes. <i>International Journal of Molecular Sciences</i> , 2022, 23, 11135.	1.8	0
1142	Detection of Alpha- and Betacoronaviruses in Frugivorous and Insectivorous Bats in Nigeria. <i>Pathogens</i> , 2022, 11, 1017.	1.2	2
1144	Mutations in <i>SCNM1</i> cause orofacioidigital syndrome due to minor intron splicing defects affecting primary cilia. <i>American Journal of Human Genetics</i> , 2022, 109, 1828-1849.	2.6	5
1145	Syntrophic Acetate-Oxidizing Microbial Consortia Enriched from Full-Scale Mesophilic Food Waste Anaerobic Digesters Showing High Biodiversity and Functional Redundancy. <i>MSystems</i> , 2022, 7, .	1.7	15
1146	Charting the landscape of the environmental exposome. , 2022, 1, .		12
1147	Analysis of complete chloroplast genome sequences and insight into the phylogenetic relationships of <i>Ferula</i> L. <i>BMC Genomics</i> , 2022, 23, .	1.2	11

#	ARTICLE	IF	CITATIONS
1150	Genome-wide characterization of three IGFs in hybrid yellow catfish (<i>Pseudobagrus fulvidraco</i> × <i>M. albus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T Reports, 2022, 26, 101315.	0.7	2
1151	Deciphering a novel chloramphenicol resistance mechanism: Oxidative inactivation of the propanediol pharmacophore. <i>Water Research</i> , 2022, 225, 119127.	5.3	10
1152	Dialysis Water Supply Faucet as Reservoir for Carbapenemase-Producing <i>Pseudomonas aeruginosa</i> . <i>Emerging Infectious Diseases</i> , 2022, 28, 2069-2073.	2.0	3
1153	Identification of TPS-d subfamily genes and functional characterization of three monoterpene synthases in slash pine. <i>Industrial Crops and Products</i> , 2022, 188, 115609.	2.5	4
1154	Genome-based taxonomic classification of the closest-to-Comamonadaceae group supports a new family Sphaerotilaceae fam. nov. and taxonomic revisions. <i>Systematic and Applied Microbiology</i> , 2022, 45, 126352.	1.2	12
1155	Characterisation of broad-spectrum phiKZ like jumbo phage and its utilisation in controlling multidrug-resistant <i>Pseudomonas aeruginosa</i> isolates. <i>Microbial Pathogenesis</i> , 2022, 172, 105767.	1.3	6
1156	Comparative genomic analysis of clinical <i>Acinetobacter nosocomialis</i> isolates from Terengganu, Malaysia led to the discovery of a novel tetracycline-resistant plasmid. <i>Journal of Global Antimicrobial Resistance</i> , 2022, 31, 104-109.	0.9	0
1157	Comparative evolutionary dynamics of the 5â€™ <i>mis</i> -regulatory elements (CREs) of miR167 genes in diploid and allopolyploid cotton species. <i>Plant Gene</i> , 2022, 32, 100380.	1.4	0
1158	Deciphering mixotrophic microbial electrosynthesis with shifting product spectrum by genome-centric metagenomics. <i>Chemical Engineering Journal</i> , 2023, 451, 139010.	6.6	7
1159	A song for the unsung: The relevance of <i>Plasmodium vinckei</i> as a laboratory rodent malaria system. <i>Parasitology International</i> , 2023, 92, 102680.	0.6	0
1160	Characterization of the complete mitochondrial genome of <i>Nippotaenia mogurndae</i> Yamaguti and Miyata, 1940 (Cestoda: Nippotaeniidae). <i>Journal of Helminthology</i> , 2022, 96, .	0.4	0
1161	Assembling a Reference Phylogenomic Tree of Bacteria and Archaea by Summarizing Many Gene Phylogenies. <i>Methods in Molecular Biology</i> , 2022, , 137-165.	0.4	1
1162	The Wastewater Resistome of Residential Aged Care Facilities Indicates a Role of Antimicrobial Stewardship in Reducing Resistance. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
1163	Evaluating the Hologenome Concept by the Analysis of the Root-Endosphere Microbiota of Chimeric Plants. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
1164	International Manufacturing and Trade in Colistin, its Implications in Polymyxin Resistance and One-Health Global Policies: A Microbiological, Economic and Anthropological Study. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
1165	Metagonia spiders of Galápagos: blind cave-dwellers and their epigean relatives (Araneae, Pholcidae). <i>Invertebrate Systematics</i> , 2022, 36, 647.	0.5	4
1166	Canavanine utilization <i>via</i> homoserine and hydroxyguanidine by a PLP-dependent β -lyase in <i>Pseudomonadaceae</i> and <i>Rhizobiales</i> . <i>RSC Chemical Biology</i> , 2022, 3, 1240-1250.	2.0	6
1167	TCM Analysis Data Resources, Web Services and Visualizations. <i>Translational Bioinformatics</i> , 2022, , 99-110.	0.0	0

#	ARTICLE	IF	CITATIONS
1168	Horizontal Gene Transfer Involving RNA Viruses and DNA Viruses. , 2022, , .		0
1169	Genome-Resolved Metagenomics Informs the Functional Ecology of Uncultured Acidobacteria in Redox Oscillated <i>Sphagnum</i> Peat. <i>MSystems</i> , 2022, 7, .	1.7	5
1171	Epidemiology of Plasmid Lineages Mediating the Spread of Extended-Spectrum Beta-Lactamases among Clinical <i>Escherichia coli</i> . <i>MSystems</i> , 2022, 7, .	1.7	6
1172	Emergent and Neglected Equine Filariasis in Egypt: Species Diversity and Host Immune Response. <i>Pathogens</i> , 2022, 11, 979.	1.2	1
1173	Identification of long-chain alkane-degrading (LadA) monooxygenases in <i>Aspergillus flavus</i> via in silico analysis. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5
1175	Bromate reduction by <i>Shewanella oneidensis</i> MR-1 is mediated by dimethylsulfoxide reductase. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
1177	Detection and Characterization of a Reassortant Mammalian Orthoreovirus Isolated from Bats in Xinjiang, China. <i>Viruses</i> , 2022, 14, 1897.	1.5	5
1178	Molecular Characterization of <i>Anopheles algeriensis</i> Theobald, 1903 (Diptera: Culicidae) Populations from Europe. <i>Pathogens</i> , 2022, 11, 990.	1.2	1
1179	Mass spectrometry data on specialized metabolome of medicinal plants used in East Asian traditional medicine. <i>Scientific Data</i> , 2022, 9, .	2.4	9
1180	Highly specific and sensitive detection of <i>Burkholderia pseudomallei</i> genomic DNA by CRISPR-Cas12a. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010659.	1.3	3
1182	The complete mitochondrial genome of <i>Parachiloglanis hodgarti</i> and its phylogenetic position within Sisoridae. <i>Journal of Oceanology and Limnology</i> , 2023, 41, 267-279.	0.6	2
1183	Key molecules of Mucorales for COVID-19-associated mucormycosis: a narrative review. <i>Journal of Bio-X Research</i> , 2022, 5, 104-111.	0.3	0
1184	Identification of <i>Leuconostoc</i> species based on novel marker genes identified using real-time PCR via computational pangenome analysis. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
1185	Low SARS-CoV-2 viral load among vaccinated individuals infected with Delta B.1.617.2 and Omicron BA.1.1.529 but not with Omicron BA.1.1 and BA.2 variants. <i>Frontiers in Public Health</i> , 0, 10, .	1.3	7
1186	Epigenetic machinery is functionally conserved in cephalopods. <i>BMC Biology</i> , 2022, 20, .	1.7	6
1187	Atypical and Unique Transmission of Monkeypox Virus during the 2022 Outbreak: An Overview of the Current State of Knowledge. <i>Viruses</i> , 2022, 14, 2012.	1.5	23
1189	The Repertoire of Solute-Binding Proteins of Model Bacteria Reveals Large Differences in Number, Type, and Ligand Range. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	5
1190	High throughput genome scale modeling predicts microbial vitamin requirements contribute to gut microbiome community structure. <i>Gut Microbes</i> , 2022, 14, .	4.3	7

#	ARTICLE	IF	CITATIONS
1191	Home and hub: pet trade and traditional medicine impact reptile populations in source locations and destinations. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2022, 289, .	1.2	3
1192	Genetics and Pathogenicity of Natural Reassortant of Infectious Bursal Disease Virus Emerging in Latvia. <i>Pathogens</i> , 2022, 11, 1081.	1.2	2
1193	Response of the plant core microbiome to <i>Fusarium oxysporum</i> infection and identification of the pathobiome. <i>Environmental Microbiology</i> , 2022, 24, 4652-4669.	1.8	19
1194	Emergence of Extensively Drug-Resistant ST170 <i>Citrobacter portucalensis</i> with Plasmids pK218-KPC, pK218-NDM, and pK218-SHV from a Tertiary Hospital, China. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	3
1195	Tick-Borne-Agents Detection in Patients with Acute Febrile Syndrome and Ticks from Magdalena Medio, Colombia. <i>Pathogens</i> , 2022, 11, 1090.	1.2	5
1197	The predatory soil bacterium <i>Myxococcus xanthus</i> combines a Tad- and an atypical type 3-like protein secretion system to kill bacterial cells. <i>Cell Reports</i> , 2022, 40, 111340.	2.9	16
1198	Calmodulin in <i>Paramecium</i> : Focus on Genomic Data. <i>Microorganisms</i> , 2022, 10, 1915.	1.6	1
1199	Arbovirus-vector protein interactomics identifies Loquacious as a co-factor for dengue virus replication in <i>Aedes</i> mosquitoes. <i>PLoS Pathogens</i> , 2022, 18, e1010329.	2.1	6
1200	Emergence of Asian endemic begomoviruses as a pandemic threat. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	5
1201	Molecular genetics and epidemiological characteristics of HIV-1 epidemic strains in various sexual risk behaviour groups in developed Eastern China, 2017–2020. <i>Emerging Microbes and Infections</i> , 2022, 11, 2326-2339.	3.0	5
1202	Limited Transmission of <i>Klebsiella pneumoniae</i> among Humans, Animals, and the Environment in a Caribbean Island, Guadeloupe (French West Indies). <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	7
1203	Impact of LTR-Retrotransposons on Genome Structure, Evolution, and Function in <i>Curcubitaceae</i> Species. <i>International Journal of Molecular Sciences</i> , 2022, 23, 10158.	1.8	9
1204	Protein Conformational Space at the Edge of Allostery: Turning a Nonallosteric Malate Dehydrogenase into an α -Allosterized-Enzyme Using Evolution-Guided Punctual Mutations. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	4
1205	In silico identification of bacterial seaweed-degrading bioplastic producers. <i>Microbial Genomics</i> , 2022, 8, .	1.0	3
1206	Extended genomic analyses of the broad-host-range phages vB_KmiM-2Di and vB_KmiM-4Dii reveal slopekviruses have highly conserved genomes. <i>Microbiology (United Kingdom)</i> , 2022, 168, .	0.7	5
1207	Phylogenetic survey of the subtilase family and a data-mining-based search for new subtilisins from <i>Bacillaceae</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
1208	Genome analysis of a new sulphur disproportionating species <i>Thermosulfurimonas</i> strain F29 and comparative genomics of sulfur-disproportionating bacteria from marine hydrothermal vents. <i>Microbial Genomics</i> , 2022, 8, .	1.0	1
1209	Dissecting the role of the human microbiome in COVID-19 via metagenome-assembled genomes. <i>Nature Communications</i> , 2022, 13, .	5.8	24

#	ARTICLE	IF	CITATIONS
1210	Identification of WRKY transcription factor family genes in <i>Pinus massoniana</i> Lamb. and their expression patterns and functions in response to drought stress. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	7
1211	Nebulous without <i>white</i> : annotated long-read genome assembly and CRISPR/Cas9 genome engineering in <i>Drosophila nebulosa</i> . <i>G3: Genes, Genomes, Genetics</i> , 0, , .	0.8	3
1212	Withdrawal of antibiotic growth promoters in China and its impact on the foodborne pathogen <i>Campylobacter coli</i> of swine origin. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	13
1213	Improving environmental monitoring of <i>Vibrionaceae</i> in coastal ecosystems through 16S rRNA gene amplicon sequencing. <i>Environmental Science and Pollution Research</i> , 2022, 29, 67466-67482.	2.7	5
1214	Origin of the Unexpected Enantioselectivity in the Enzymatic Reductions of 5-Membered-Ring Heterocyclic Ketones Catalyzed by <i>Candida parapsilosis</i> Carbonyl Reductases. <i>Catalysts</i> , 2022, 12, 1086.	1.6	4
1215	Plastomes Provide Insights into Differences between Morphology and Molecular Phylogeny: <i>Ostericum</i> and <i>Angelica</i> (<i>Apiaceae</i>) as an Example. <i>Diversity</i> , 2022, 14, 776.	0.7	3
1216	Resistance to Fluoroquinolones in <i>Pseudomonas aeruginosa</i> from Human, Animal, Food and Environmental Origin: The Role of CrpP and Mobilizable ICEs. <i>Antibiotics</i> , 2022, 11, 1271.	1.5	4
1217	Steroidogenic Effects of Salinity Change on the Hypothalamusâ€Pituitaryâ€Gonad (HPG) Axis of Male Chinese Sea Bass (<i>Lateolabrax maculatus</i>). <i>International Journal of Molecular Sciences</i> , 2022, 23, 10905.	1.8	1
1218	Genomic analysis reveals cryptic diversity in aphelids and sheds light on the emergence of Fungi. <i>Current Biology</i> , 2022, 32, 4607-4619.e7.	1.8	10
1220	CCIVR facilitates comprehensive identification of cis-natural antisense transcripts with their structural characteristics and expression profiles. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
1222	Emergence of a novel PRRSV-1 strain in mainland China: A recombinant strain derived from the two commercial modified live viruses Amervac and DV. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	10
1223	Genome-wide analysis of tandem duplicated genes and their expression under salt stress in seashore <i>paspalum</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	5
1224	Viruses inhibit TIR gcADPR signalling to overcome bacterial defence. <i>Nature</i> , 2022, 611, 326-331.	13.7	66
1225	First report of <i>Porcine respirovirus 1</i> in South Korea. <i>Transboundary and Emerging Diseases</i> , 2022, 69, 4041-4047.	1.3	6
1227	Whole genome sequencing of OXA-232-producing wzi93-KL112-O1 carbapenem-resistant <i>Klebsiella pneumoniae</i> in human bloodstream infection co-harboring chromosomal ISEcp1-based blaCTX-M-15 and one rmpA2-associated virulence plasmid. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	4
1229	Taxol and $\hat{1}^2$ -tubulins from endophytic fungi isolated from the Himalayan Yew, <i>Taxus wallichiana</i> Zucc.. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
1230	Colistin Resistance Mechanism in <i>Enterobacter hormaechei</i> subsp. <i>steigerwaltii</i> Isolated from Wild Boar (<i>Sus scrofa</i>) in France. <i>Pathogens</i> , 2022, 11, 1022.	1.2	1
1231	SARS-CoV-2 chronological genomic evolution and epidemiology in the Middle East and North Africa (MENA) region as affected by vaccination, conflict and socioeconomical disparities: a population-based cohort study. <i>BMJ Open</i> , 2022, 12, e060775.	0.8	1

#	ARTICLE	IF	CITATIONS
1232	Whole-genome resequencing reveals signature of local adaptation and divergence in wild soybean. <i>Evolutionary Applications</i> , 2022, 15, 1820-1833.	1.5	10
1236	A Novel Gene Alignment in <i>Dorea</i> sp. AM58-8 Produces 7-Dehydroxy-3 β Bile Acids from Primary Bile Acids. <i>Biochemistry</i> , 2022, 61, 2870-2878.	1.2	4
1237	Enzymatic and antifungal susceptibility profiles of <i>Candida glabrata</i> isolates from paediatric patients and their genetic diversity based on microsatellite length polymorphism. <i>Letters in Applied Microbiology</i> , 0, , .	1.0	1
1238	Comparative study of neuropeptide signaling systems in Hemiptera. <i>Insect Science</i> , 2023, 30, 705-724.	1.5	2
1239	Stem rust on barberry species in Europe: Host specificities and genetic diversity. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	3
1240	First Patient-to-Patient Intrahospital Transmission of Clade I <i>Candida auris</i> in France Revealed after a Two-Month Incubation Period. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	3
1241	The Mitogenome Structure of Righteye Flounders (Pleuronectidae): Molecular Phylogeny and Systematics of the Family in East Asia. <i>Diversity</i> , 2022, 14, 805.	0.7	1
1242	High-throughput sequencing covers greater nematode diversity than conventional morphotyping on natural cedar forests in Yakushima Island, Japan. <i>European Journal of Soil Biology</i> , 2022, 112, 103432.	1.4	3
1243	Genomic Diversity, Competition, and Toxin Production by Group I and II <i>Clostridium botulinum</i> Strains Used in Food Challenge Studies. <i>Microorganisms</i> , 2022, 10, 1895.	1.6	3
1244	Interference and co-existence of staphylococci and <i>Cutibacterium acnes</i> within the healthy human skin microbiome. <i>Communications Biology</i> , 2022, 5, .	2.0	14
1245	Genome-Wide Identification and Characterization of Heat Shock Protein 20 Genes in Maize. <i>Life</i> , 2022, 12, 1397.	1.1	3
1246	More than just hitchhikers: a survey of bacterial communities associated with diatoms originating from sea turtles. <i>FEMS Microbiology Ecology</i> , 2022, 98, .	1.3	2
1248	Functional and Structural Characterization of OXA-935, a Novel OXA-10-Family β -Lactamase from <i>Pseudomonas aeruginosa</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2022, 66, .	1.4	3
1252	A stable home for an equine pathogen: valid publication of the binomial <i>Prescottella equi</i> gen. nov., comb. nov., and reclassification of four rhodococcal species into the genus <i>Prescottella</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	11
1253	Multifaceted roles of GRAS transcription factors in growth and stress responses in plants. <i>IScience</i> , 2022, 25, 105026.	1.9	16
1255	Genetic analysis of seed traits in <i>Sorghum bicolor</i> that affect the human gut microbiome. <i>Nature Communications</i> , 2022, 13, .	5.8	7
1256	Reconstitution of monoterpene indole alkaloid biosynthesis in genome engineered <i>Nicotiana benthamiana</i> . <i>Communications Biology</i> , 2022, 5, .	2.0	27
1257	<i>Ecdyonurus aurasius</i> sp. nov. (Insecta, Ephemeroptera, Heptageniidae, Ecdyonurinae), a new micro-endemic mayfly species from Aurès Mountains (north-eastern Algeria). <i>ZooKeys</i> , 0, 1121, 17-37.	0.5	3

#	ARTICLE	IF	CITATIONS
1259	Recurrent emergence of <i>Klebsiella pneumoniae</i> carbapenem resistance mediated by an inhibitory <i>ompK36</i> mRNA secondary structure. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	8
1260	Rotavirus A in Domestic Pigs and Wild Boars: High Genetic Diversity and Interspecies Transmission. Viruses, 2022, 14, 2028.	1.5	5
1261	The Origin of Teratogenic Retinoids in Cyanobacteria. Toxins, 2022, 14, 636.	1.5	5
1262	Identification of orphan ligand-receptor relationships using a cell-based CRISPRa enrichment screening platform. ELife, 0, 11, .	2.8	9
1263	Global phylogenetic analysis of the RNA-dependent RNA polymerase with OrViT (OrthornaVirae Tree). Frontiers in Virology, 0, 2, .	0.7	0
1264	Genome-Wide Identification and Molecular Evolution of the Magnesium Transporter (MGT) Gene Family in <i>Citrullus lanatus</i> and <i>Cucumis sativus</i> . Agronomy, 2022, 12, 2253.	1.3	16
1265	Genome-wide identification and expression analysis of the calmodulin-binding transcription activator (CAMTA) family genes in tea plant. BMC Genomics, 2022, 23, .	1.2	5
1266	Codiversification of gut microbiota with humans. Science, 2022, 377, 1328-1332.	6.0	67
1267	Phylogeny and adaptative evolution to chemosynthetic habitat in barnacle (Cirripedia: Thoracica) revealed by mitogenomes. Frontiers in Marine Science, 0, 9, .	1.2	2
1268	The moss-specific transcription factor PpERF24 positively modulates immunity against fungal pathogens in <i>Physcomitrium patens</i> . Frontiers in Plant Science, 0, 13, .	1.7	5
1269	The mitochondrial genomes of <i>Enoplolambrus validus</i> (De Haan, 1837) and <i>Jonas distinctus</i> (De Haan, 1835) (Decapoda: Brachyura: Parthenopoidea, Crystoidea): a novel gene rearrangement and phylogenetic implications. Journal of Crustacean Biology, 2022, 42, .	0.3	0
1270	LSQP-DB: a species-specific quantitative PCR primer database for 307 Lactobacillaceae species. Systems Microbiology and Biomanufacturing, 0, , .	1.5	2
1271	Functional characterization of the pUceS8.3 promoter and its potential use for ectopic gene overexpression. Planta, 2022, 256, .	1.6	3
1272	The coral <i>Acropora loripes</i> genome reveals an alternative pathway for cysteine biosynthesis in animals. Science Advances, 2022, 8, .	4.7	10
1273	Dissecting microbial communities and resistomes for interconnected humans, soil, and livestock. ISME Journal, 2023, 17, 21-35.	4.4	14
1274	Whole-genome sequence analysis for evaluating the safety and probiotic potential of <i>Lactiplantibacillus pentosus</i> 9D3, a gamma-aminobutyric acid (GABA)-producing strain isolated from Thai pickled weed. Frontiers in Microbiology, 0, 13, .	1.5	8
1275	Whole-Genome Sequencing and Comparative Genomic Analysis of <i>Enterococcus</i> spp. Isolated from Dairy Products: Genomic Diversity, Functional Characteristics, and Pathogenic Potential. Applied Sciences (Switzerland), 2022, 12, 9620.	1.3	2
1276	Assigning <i>Culicoides</i> larvae to species using DNA barcoding of adult females and phylogenetic associations. Parasites and Vectors, 2022, 15, .	1.0	3

#	ARTICLE	IF	CITATIONS
1277	Low levels of tetracyclines select for a mutation that prevents the evolution of high-level resistance to tigecycline. <i>PLoS Biology</i> , 2022, 20, e3001808.	2.6	2
1278	SNP discovery in proso millet (<i>Panicum miliaceum</i> L.) using low-pass genome sequencing. <i>Plant Direct</i> , 2022, 6, .	0.8	4
1279	Investigating CRISPR spacer targets and their impact on genomic diversification of <i>Streptococcus mutans</i> . <i>Frontiers in Genetics</i> , 0, 13, .	1.1	4
1280	Liposomal Delivery of Newly Identified Prophage Lysins in a <i>Pseudomonas aeruginosa</i> Model. <i>International Journal of Molecular Sciences</i> , 2022, 23, 10143.	1.8	4
1282	Methyltransferases of Riboviria. <i>Biomolecules</i> , 2022, 12, 1247.	1.8	3
1283	Widespread yet persistent low abundance of TIM5-like cyanophages in the oceans. <i>Environmental Microbiology</i> , 2022, 24, 6476-6492.	1.8	2
1284	Ribosomal MLST nucleotide identity (rMLST-NI), a rapid bacterial species identification method: application to <i>Klebsiella</i> and <i>Raoultella</i> genomic species validation. <i>Microbial Genomics</i> , 2022, 8, .	1.0	2
1285	Deciphering microbial gene function using natural language processing. <i>Nature Communications</i> , 2022, 13, .	5.8	13
1286	Genetic Diversity in Leatherback Turtles (<i>Dermochelys coriacea</i>) along the Andaman Sea of Thailand. <i>Diversity</i> , 2022, 14, 764.	0.7	2
1289	Genetic structure of reconstituted native Carpathian goat breed based on information from microsatellite markers. <i>Annals of Animal Science</i> , 2022, 22, 1235-1244.	0.6	3
1291	Sources of variation in community composition of the hindgut microbiota in two tropical <i>Kyphosus</i> species. <i>Coral Reefs</i> , 2022, 41, 1523-1535.	0.9	3
1292	Whole-genome sequencing reveals the genetic mechanisms of domestication in classical inbred mice. <i>Genome Biology</i> , 2022, 23, .	3.8	6
1293	Identification of AP2/ERF Transcription Factor Family Genes and Expression Patterns in Response to Drought Stress in <i>Pinus massoniana</i> . <i>Forests</i> , 2022, 13, 1430.	0.9	2
1294	Transcriptome-wide identification of walnut PP2C family genes in response to external stimulus. <i>BMC Genomics</i> , 2022, 23, .	1.2	5
1295	Occurrence of SARS-CoV-2 reinfections at regular intervals in Ecuador. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	0
1296	Metagenomic analysis reveals the microbiome and antibiotic resistance genes in indigenous Chinese yellow-feathered chickens. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	6
1298	A bacterial pan-genome makes gene essentiality strain-dependent and evolvable. <i>Nature Microbiology</i> , 2022, 7, 1580-1592.	5.9	38
1299	Asymmetrical dose responses shape the evolutionary trade-off between antifungal resistance and nutrient use. <i>Nature Ecology and Evolution</i> , 2022, 6, 1501-1515.	3.4	11

#	ARTICLE	IF	CITATIONS
1300	Singular value decomposition of protein sequences as a method to visualize sequence and residue space. <i>Protein Science</i> , 2022, 31, .	3.1	1
1302	Converting the genomic knowledge base to build protein specific machine learning prediction models; a classification study on thermophilic serine protease. , 0, , .		0
1303	A Case of Persistent Human Pegivirus Infection in Two Separate Pregnancies of a Woman. <i>Microorganisms</i> , 2022, 10, 1925.	1.6	1
1304	Distribution and diversity of ROS-generating enzymes across the animal kingdom, with a focus on sponges (Porifera). <i>BMC Biology</i> , 2022, 20, .	1.7	7
1305	Genome-wide identification, phylogeny, and gene duplication of the epigenetic regulators in Fagaceae. <i>Physiologia Plantarum</i> , 0, , .	2.6	3
1306	Marine DNA methylation patterns are associated with microbial community composition and inform virus-host dynamics. <i>Microbiome</i> , 2022, 10, .	4.9	8
1307	Insights into the global freshwater virome. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	8
1308	A novel alkane monooxygenase (<i>alkB</i>) clade revealed by massive genomic survey and its dissemination association with IS elements. <i>PeerJ</i> , 0, 10, e14147.	0.9	4
1309	<i>PpyABF3</i> recruits the <i>COMPASS</i> -like complex to regulate bud dormancy maintenance via integrating <i>ABA</i> signaling and <i>GA</i> catabolism. <i>New Phytologist</i> , 2023, 237, 192-203.	3.5	10
1310	Genome-wide association mapping of Fusarium crown rot resistance in <i>Aegilops tauschii</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
1311	<i>Fusarium verticillioides</i> <i>NAT1</i> (<i>FDB2</i>) <i>N</i> -malonyltransferase is structurally, functionally and phylogenetically distinct from its <i>N</i> -acetyltransferase (<i>NAT</i>) homologues. <i>FEBS Journal</i> , 2023, 290, 2412-2436.	2.2	3
1312	Visualizing translation dynamics at atomic detail inside a bacterial cell. <i>Nature</i> , 2022, 610, 205-211.	13.7	61
1313	Genome-Wide Analysis of the SPL Gene Family and Expression Analysis during Flowering Induction in <i>Prunus yedoensis</i> "Somei-yoshino". <i>International Journal of Molecular Sciences</i> , 2022, 23, 10052.	1.8	3
1314	Comparative Analysis of Chloroplast Genomes within <i>Saxifraga</i> (Saxifragaceae) Takes Insights into Their Genomic Evolution and Adaption to the High-Elevation Environment. <i>Genes</i> , 2022, 13, 1673.	1.0	4
1315	Assessing the Role of Ancestral Fragments and Selection Signatures by Whole-Genome Scanning in Dehong Humped Cattle at the China-Myanmar Border. <i>Biology</i> , 2022, 11, 1331.	1.3	0
1316	Molecular phylogeny and historical biogeography of marine palaemonid shrimps (Palaemonidae:). <i>TJ ETQq1</i> 1 0.784314 rgBT /Overlock	1.6	8
1317	Pan-genome evolution and its association with divergence of metabolic functions in <i>Bifidobacterium</i> genus. <i>World Journal of Microbiology and Biotechnology</i> , 2022, 38, .	1.7	1
1318	<i>Anaeromyxobacter oryzae</i> sp. nov., <i>Anaeromyxobacter diazotrophicus</i> sp. nov. and <i>Anaeromyxobacter paludicola</i> sp. nov., isolated from paddy soils. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	4

#	ARTICLE	IF	CITATIONS
1319	Wolbachia infection dynamics in a natural population of the pear psyllid <i>Cacopsylla pyri</i> (Hemiptera: Tj ETQq0 0 0 ggBT /Overlock 10 Tf	1.6	16
1320	Identification and expression analysis of BURP domain-containing genes in jujube and their involvement in low temperature and drought response. <i>BMC Genomics</i> , 2022, 23, .	1.2	2
1322	Genome-wide identification, phylogenetic and expression pattern analysis of Dof transcription factors in blueberry (<i>Vaccinium corymbosum</i> L.). <i>PeerJ</i> , 0, 10, e14087.	0.9	3
1323	Genome dynamics mediated by repetitive and mobile elements in <i>Xanthomonas citri</i> pv. <i>durantae</i> . <i>Access Microbiology</i> , 2022, 4, .	0.2	1
1324	Lipopolysaccharide detection by the innate immune system may be an uncommon defence strategy used in nature. <i>Open Biology</i> , 2022, 12, .	1.5	16
1325	Host generalists dominate fungal communities associated with alpine knotweed roots: a study of Sebaciales. <i>PeerJ</i> , 0, 10, e14047.	0.9	0
1328	Endophytic fungi from kale (<i>Brassica oleracea</i> var. <i>acephala</i>) modify roots-glucosinolate profile and promote plant growth in cultivated Brassica species. First description of <i>Pyrenophora gallaeciana</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
1329	Photoactive Yellow Protein Represents a Distinct, Evolutionarily Novel Family of PAS Domains. <i>Journal of Bacteriology</i> , 2022, 204, .	1.0	4
1330	The complete chloroplast genome of the medical plant <i>Huperzia crispata</i> from the Huperziaceae family: structure, comparative analysis, and phylogenetic relationships. <i>Molecular Biology Reports</i> , 2022, 49, 11729-11741.	1.0	3
1331	Whole genome sequence analysis of ESBL-producing <i>Escherichia coli</i> recovered from New Zealand freshwater sites. <i>Microbial Genomics</i> , 2022, 8, .	1.0	2
1332	First report of the whole genome of <i>Moraxella bovoculi</i> genotype 1 from India and comparative genomics of <i>Moraxella bovoculi</i> to identify genotype-specific markers. <i>Archives of Microbiology</i> , 2022, 204, .	1.0	1
1333	Early defoliation induces auxin redistribution, promoting paradormancy release in pear buds. <i>Plant Physiology</i> , 0, , .	2.3	7
1334	Enhanced cultured diversity of the mouse gut microbiota enables custom-made synthetic communities. <i>Cell Host and Microbe</i> , 2022, 30, 1630-1645.e25.	5.1	26
1335	Niche differentiation and symbiotic association among ammonia/nitrite oxidizers in a full-scale rotating biological contactor. <i>Water Research</i> , 2022, 225, 119137.	5.3	3
1336	Deciphering the virulence potential of <i>Listeria monocytogenes</i> in the Norwegian meat and salmon processing industry by combining whole genome sequencing and in vitro data. <i>International Journal of Food Microbiology</i> , 2022, 383, 109962.	2.1	9
1337	Identification of a novel polyomavirus from a marsupial host. <i>Virus Evolution</i> , 2022, 8, .	2.2	2
1338	Bacterial Outer Membrane Polysaccharide Export (OPX) Proteins Occupy Three Structural Classes with Selective β -Barrel Porin Requirements for Polymer Secretion. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	5
1340	SPACA9 is a luminal protein of human ciliary singlet and doublet microtubules. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	25

#	ARTICLE	IF	CITATIONS
1342	Insight into co-hosts of nitrate reduction genes and antibiotic resistance genes in an urban river of the qinghai-tibet plateau. <i>Water Research</i> , 2022, 225, 119189.	5.3	12
1343	The <i>LeuO</i> regulator and quiescence: About transcriptional roadblocks, multiple promoters, and <i>crispr</i> . <i>Molecular Microbiology</i> , 2022, 118, 503-509.	1.2	2
1344	Evolutionary origin and functional specialization of Dormancy-Associated MADS box (DAM) proteins in perennial crops. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	3
1345	Phylogeny and taxonomy of <i>Cinnamomum</i> (Lauraceae). <i>Ecology and Evolution</i> , 2022, 12, .	0.8	6
1346	Transmission pathways of campylobacter spp. at broiler farms and their environment in Brandenburg, Germany. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5
1347	Drug resistance and population structure of <i>Plasmodium falciparum</i> and <i>Plasmodium vivax</i> in the Peruvian Amazon. <i>Scientific Reports</i> , 2022, 12, .	1.6	5
1348	Oral and Rectal Colonization by Antimicrobial-Resistant Gram-Negative Bacteria and Their Association with Death among Residents of Long-Term Care Facilities: A Prospective, Multicenter, Observational, Cohort Study. <i>Gerontology</i> , 2023, 69, 261-272.	1.4	5
1349	Exploring Cluster-Dependent Antibacterial Activities and Resistance Pathways of NOSO-502 and Colistin against <i>Enterobacter cloacae</i> Complex Species. <i>Antimicrobial Agents and Chemotherapy</i> , 2022, 66, .	1.4	7
1350	An ancient respiratory system in the widespread sedimentary archaea Thermopfundales. <i>Molecular Biology and Evolution</i> , 0, , .	3.5	2
1351	Deciphering the kinome of <i>Theileria annulata</i> for identification of drug targets and anti-theilerial drug. <i>Ticks and Tick-borne Diseases</i> , 2022, 13, 102049.	1.1	0
1352	Transxylosylation of stevioside by a novel GH39 β -xylosidase, and simultaneous valorization of agroindustrial byproducts. <i>Food and Bioproducts Processing</i> , 2022, 136, 130-140.	1.8	0
1353	Bedaquiline resistant <i>Mycobacterium tuberculosis</i> clinical isolates with and without rv0678 mutations have similar growth patterns under varying BDQ drug pressure. <i>Tuberculosis</i> , 2022, 137, 102266.	0.8	1
1354	Diversity-triggered bottom-up trophic interactions impair key soil functions under lindane pollution stress. <i>Environmental Pollution</i> , 2022, 314, 120293.	3.7	2
1355	A monograph of <i>Aspergillus</i> section <i>Candidi</i> . <i>Studies in Mycology</i> , 2022, 102, 1-51.	4.5	8
1356	Identification of 146 Metagenome-assembled Genomes from the Rumen Microbiome of Cattle in Japan. <i>Microbes and Environments</i> , 2022, 37, n/a.	0.7	4
1357	First Polycipivirus and Unmapped RNA Virus Diversity in the Yellow Crazy Ant, <i>Anoplolepis gracilipes</i> . <i>Viruses</i> , 2022, 14, 2161.	1.5	1
1358	Genome-Wide Identification and Salt Stress Response Analysis of the bZIP Transcription Factor Family in Sugar Beet. <i>International Journal of Molecular Sciences</i> , 2022, 23, 11573.	1.8	3
1359	Characterization, High-Density Fermentation, and the Production of a Directed Vat Set Starter of Lactobacilli Used in the Food Industry: A Review. <i>Foods</i> , 2022, 11, 3063.	1.9	10

#	ARTICLE	IF	CITATIONS
1360	Identification and Genome-Wide Association Analysis for Fusarium Crown Rot Resistance in Wheat. <i>Plant Disease</i> , 2023, 107, 1151-1158.	0.7	4
1362	Comparative Analysis of Molecular RFLP and SNP Markers in Assessing and Understanding the Genetic Diversity of Various Chicken Breeds. <i>Genes</i> , 2022, 13, 1876.	1.0	3
1363	Functional Characterization of <i>Saccharomyces cerevisiae</i> P5C Reductase, the Enzyme at the Converging Point of Proline and Arginine Metabolism. <i>Microorganisms</i> , 2022, 10, 2077.	1.6	2
1364	Comparative Analysis of Mesophilic YqfB-Type Amidohydrolases. <i>Biomolecules</i> , 2022, 12, 1492.	1.8	1
1365	Identification of Fungal Species Associated with Apple Canker in Tarim Basin, China. <i>Plant Disease</i> , 2023, 107, 1284-1298.	0.7	3
1366	Structural insights into light-driven anion pumping in cyanobacteria. <i>Nature Communications</i> , 2022, 13, .	5.8	4
1367	MGCEP 1.0: A Genetic-Engineered Marine-Derived Chassis Cell for a Scaled Heterologous Expression Platform of Microbial Bioactive Metabolites. <i>ACS Synthetic Biology</i> , 2022, 11, 3772-3784.	1.9	3
1371	Variation in plant traits and phylogenetic structure associated with native and nonnative species in an industrialized flora. <i>NeoBiota</i> , 0, 77, 101-123.	1.0	0
1373	Bioinformatic Assessment of Factors Affecting the Correlation between Protein Abundance and Elongation Efficiency in Prokaryotes. <i>International Journal of Molecular Sciences</i> , 2022, 23, 11996.	1.8	3
1374	Deciphering chloramphenicol biotransformation mechanisms and microbial interactions via integrated multi-omics and cultivation-dependent approaches. <i>Microbiome</i> , 2022, 10, .	4.9	8
1375	Reshaping the Binding Pocket of the Neurotransmitter:Solute Symporter (NSS) Family Transporter SLC6A14 (ATB0,+) Selectively Reduces Access for Cationic Amino Acids and Derivatives. <i>Biomolecules</i> , 2022, 12, 1404.	1.8	3
1376	Comparative mitogenomes provide new insights into phylogeny and taxonomy of the subfamily Xenocyprinae (Cypriniformes: Cyprinidae). <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0
1377	Genome-wide identification and expression profiling of WUSCHEL-related homeobox (WOX) genes confer their roles in somatic embryogenesis, growth and abiotic stresses in banana. <i>3 Biotech</i> , 2022, 12, .	1.1	4
1378	HiFi metagenomic sequencing enables assembly of accurate and complete genomes from human gut microbiota. <i>Nature Communications</i> , 2022, 13, .	5.8	22
1379	Investigation of a vanA linezolid- and vancomycin-resistant <i>Enterococcus faecium</i> outbreak in the Southwest Indian Ocean (Reunion Island). <i>International Journal of Antimicrobial Agents</i> , 2022, 60, 106686.	1.1	3
1381	Infección natural por SARS-CoV-2 en gatos y perros domésticos de personas con diagnóstico de COVID-19 en el Valle de Aburrá, Antioquia. <i>Biomedica</i> , 2022, 42, 48-58.	0.3	2
1382	Variation analysis of SARS-CoV-2 complete sequences from Iran. <i>Future Virology</i> , 0, , .	0.9	0
1383	The Function of BBX Gene Family under Multiple Stresses in <i>Nicotiana tabacum</i> . <i>Genes</i> , 2022, 13, 1841.	1.0	4

#	ARTICLE	IF	CITATIONS
1384	Emergence of a Novel Lineage and Wide Spread of a blaCTX-M-15/IncHI2/ST1 Plasmid among Nosocomial Enterobacter in Guadeloupe. <i>Antibiotics</i> , 2022, 11, 1443.	1.5	1
1385	Biochemical and Structural Characterization of Chi-Class Glutathione Transferases: A Snapshot on the Glutathione Transferase Encoded by sll0067 Gene in the Cyanobacterium <i>Synechocystis</i> sp. Strain PCC 6803. <i>Biomolecules</i> , 2022, 12, 1466.	1.8	2
1387	Microbial ecology of the Southern Ocean. <i>FEMS Microbiology Ecology</i> , 2022, 98, .	1.3	3
1388	The First Telomere-to-Telomere Chromosome-Level Genome Assembly of <i>Stagonospora tainanensis</i> Causing Sugarcane Leaf Blight. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 1088.	1.5	4
1389	Sequential action of a tRNA base editor in conversion of cytidine to pseudouridine. <i>Nature Communications</i> , 2022, 13, .	5.8	9
1390	Single-cell Raman-activated sorting and cultivation (scRACS-Culture) for assessing and mining in situ phosphate-solubilizing microbes from nature. <i>ISME Communications</i> , 2022, 2, .	1.7	5
1391	SARS-CoV-2 Transmission from Human to Pet and Suspected Transmission from Pet to Human, Thailand. <i>Journal of Clinical Microbiology</i> , 2022, 60, .	1.8	16
1392	Identification of microbial taxa present in <i>Ctenocephalides felis</i> (cat flea) reveals widespread co-infection and associations with vector phylogeny. <i>Parasites and Vectors</i> , 2022, 15, .	1.0	7
1393	Recovery and genome reconstruction of novel magnetotactic <i>Elusimicrobiota</i> from bog soil. <i>ISME Journal</i> , 2023, 17, 204-214.	4.4	5
1394	Mitochondrial gene rearrangements suggest a new genus in the subfamily Cantharinae (Coleoptera). <i>Zoologica Scripta</i> , 0, , .	0.7	0
1395	Concerted expansion and contraction of immune receptor gene repertoires in plant genomes. <i>Nature Plants</i> , 2022, 8, 1146-1152.	4.7	37
1396	Occurrence and Characterization of NDM-1-Producing <i>Shewanella</i> spp. and <i>Acinetobacter portensis</i> Co-Harboring tet(X3) in a Chinese Dairy Farm. <i>Antibiotics</i> , 2022, 11, 1422.	1.5	1
1397	Genomic characterization of antifungal <i>Acinetobacter</i> bacteria isolated from the skin of the frogs <i>Agalychnis callidryas</i> and <i>Craugastor fitzingeri</i> . <i>FEMS Microbiology Ecology</i> , 2022, 98, .	1.3	3
1398	Complete genome of <i>Vibrio japonicus</i> strain JCM 31412 and assessment of the <i>Nereis</i> clade of the genus <i>Vibrio</i> . <i>Antonie Van Leeuwenhoek</i> , 0, , .	0.7	0
1399	Ethanol-lactate transition of <i>Lachancea thermotolerans</i> is linked to nitrogen metabolism. <i>Food Microbiology</i> , 2023, 110, 104167.	2.1	8
1400	Identification and genomic characterization of a novel HIV-1 unique recombinant form (CRF01_AE/CRF07_BC) in Zhejiang Province, China. <i>Virus Genes</i> , 2023, 59, 142-147.	0.7	1
1401	Impact of Early Pandemic SARS-CoV-2 Lineages Replacement with the Variant of Concern P.1 (Gamma) in Western Bahia, Brazil. <i>Viruses</i> , 2022, 14, 2314.	1.5	5
1402	Identification and genomic characterization of major effect bacterial blight resistance locus (BB-13) in Upland cotton (<i>Gossypium hirsutum</i> L.). <i>Theoretical and Applied Genetics</i> , 2022, 135, 4421-4436.	1.8	2

#	ARTICLE	IF	CITATIONS
1403	Spatial and diel patterns of volatile organic compounds, DMSP-derived compounds, and planktonic microorganisms around a tropical scleractinian coral colony. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	3
1404	Antarctic aldehyde dehydrogenase from <i>Flavobacterium</i> PL002 as a potent catalyst for acetaldehyde determination in wine. <i>Scientific Reports</i> , 2022, 12, .	1.6	4
1409	Identification and expression analysis of G protein-coupled receptors in the cotton aphid, <i>Aphis gossypii</i> Glover. <i>International Journal of Biological Macromolecules</i> , 2023, 224, 115-124.	3.6	3
1410	Multidrug-Resistant High-Risk <i>Escherichia coli</i> and <i>Klebsiella pneumoniae</i> Clonal Lineages Occur in Black-Headed Gulls from Two Conservation Islands in Germany. <i>Antibiotics</i> , 2022, 11, 1357.	1.5	4
1412	Biogenic propane production by a marine <i>Photobacterium</i> strain isolated from the Western English Channel. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
1413	Putative Pathogenic Genes of <i>Leptospira interrogans</i> and <i>Leptospira weilii</i> Isolated from Patients with Acute Febrile Illness. <i>Tropical Medicine and Infectious Disease</i> , 2022, 7, 284.	0.9	1
1414	Plastome-based phylogeny and biogeography of <i>Lactuca L.</i> (Asteraceae) support revised lettuce gene pool categories. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4
1415	Identification and Investigation of the Genetic Variations and Candidate Genes Responsible for Seed Weight via GWAS in Paper Mulberry. <i>International Journal of Molecular Sciences</i> , 2022, 23, 12520.	1.8	2
1417	Formal recognition and classification of gene transfer agents as viriforms. <i>Virus Evolution</i> , 2022, 8, .	2.2	7
1418	Identification of the genes at S and Z reveals the molecular basis and evolution of grass self-incompatibility. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
1419	In silico investigation of the genus <i>Campylobacter</i> type VI secretion system reveals genetic diversity in organization and putative effectors. <i>Microbial Genomics</i> , 2022, 8, .	1.0	3
1420	Integrated Omic Approaches Reveal Molecular Mechanisms of Tolerance during Soybean and <i>Meloidogyne incognita</i> Interactions. <i>Plants</i> , 2022, 11, 2744.	1.6	4
1421	A stress-inducible protein regulates drought tolerance and flowering time in <i>Brachypodium</i> and <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2023, 191, 643-659.	2.3	8
1422	A putative bifunctional CPD/ (6-4) photolyase from the cyanobacteria <i>Synechococcus</i> sp. PCC 7335 is encoded by a UV-B inducible operon: New insights into the evolution of photolyases. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
1423	Comparative genomics and pangenomics of vancomycin-resistant and susceptible <i>Enterococcus faecium</i> from Irish hospitals. <i>Journal of Medical Microbiology</i> , 2022, 71, .	0.7	4
1424	Between Protein Fold and Nucleophile Identity: Multiscale Modeling of the TEV Protease Enzyme-Substrate Complex. <i>ACS Omega</i> , 2022, 7, 40279-40292.	1.6	4
1425	Genome-Wide Identification of the AGC Protein Kinase Gene Family Related to Photosynthesis in Rice (<i>Oryza sativa</i>). <i>International Journal of Molecular Sciences</i> , 2022, 23, 12557.	1.8	5
1426	Viral Small Terminase: A Divergent Structural Framework for a Conserved Biological Function. <i>Viruses</i> , 2022, 14, 2215.	1.5	11

#	ARTICLE	IF	CITATIONS
1428	Comprehensive Comparative Analysis and Development of Molecular Markers for <i>Dianthus</i> Species Based on Complete Chloroplast Genome Sequences. <i>International Journal of Molecular Sciences</i> , 2022, 23, 12567.	1.8	4
1429	Innovative Rhizosphere-Based Enrichment under P-Limitation Selects for Bacterial Isolates with High-Performance P-Solubilizing Traits. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	3
1432	Pangenome-wide analysis of cyclic nucleotide-gated channel (CNGC) gene family in citrus Spp. Revealed their intraspecies diversity and potential roles in abiotic stress tolerance. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	9
1433	Metagenomic Features Characterized with Microbial Iron Oxidoreduction and Mineral Interaction in Southwest Indian Ridge. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	7
1434	Genome-wide identification of Aux/IAA gene family and their expression analysis in <i>Prunus mume</i> . <i>Frontiers in Genetics</i> , 0, 13, .	1.1	4
1435	Molecular Epidemiology of mcr-1-Positive <i>Escherichia coli</i> and <i>Klebsiella pneumoniae</i> Isolates: Results from Russian Sentinel Surveillance (2013–2018). <i>Microorganisms</i> , 2022, 10, 2034.	1.6	2
1436	Bacterial hydrogen sulfide drives cryptic redox chemistry in gut microbial communities. <i>Nature Metabolism</i> , 2022, 4, 1260-1270.	5.1	9
1437	Geno- and Phenotypic Characteristics of a <i>Klebsiella pneumoniae</i> ST20 Isolate with Unusual Colony Morphology. <i>Microorganisms</i> , 2022, 10, 2063.	1.6	6
1438	Thionation toward High-Contrast ACQ-DIE Probes by Reprogramming the Aqueous Segregation Behavior: Enlightenment from a Sulfur-Substituted G-Quadruplex Ligand. <i>Analytical Chemistry</i> , 2022, 94, 15231-15239.	3.2	5
1439	Genome-wide characterization of the UDP-glycosyltransferase gene family reveals their potential roles in leaf senescence in cotton. <i>International Journal of Biological Macromolecules</i> , 2022, 222, 2648-2660.	3.6	6
1440	Mind the Gap—Deciphering GPCR Pharmacology Using 3D Pharmacophores and Artificial Intelligence. <i>Pharmaceuticals</i> , 2022, 15, 1304.	1.7	3
1441	Comparative Genomics of <i>Listeria monocytogenes</i> Isolates from Ruminant Listeriosis Cases in the Midwest United States. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	3
1442	Mobile Element Integration Reveals a Chromosome Dimer Resolution System in <i>Legionellales</i> . <i>MBio</i> , 2022, 13, .	1.8	1
1443	Within-patient evolution of plasmid-mediated antimicrobial resistance. <i>Nature Ecology and Evolution</i> , 2022, 6, 1980-1991.	3.4	21
1444	Hydrodynamic conditions affect the proteomic profile of marine biofilms formed by filamentous cyanobacterium. <i>Npj Biofilms and Microbiomes</i> , 2022, 8, .	2.9	3
1446	Variation in plant Toll/Interleukin-1 receptor domain protein dependence on <i>ENHANCED DISEASE SUSCEPTIBILITY 1</i> . <i>Plant Physiology</i> , 2023, 191, 626-642.	2.3	19
1447	Genome-Resolved Metagenomics and Metatranscriptomics Reveal that Aquificae Dominates Arsenate Reduction in Tengchong Geothermal Springs. <i>Environmental Science & Technology</i> , 2022, 56, 16473-16482.	4.6	11
1449	Molecular mechanisms leading to ceftolozane/tazobactam resistance in clinical isolates of <i>Pseudomonas aeruginosa</i> from five Latin American countries. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2

#	ARTICLE	IF	CITATIONS
1450	Overexpression of Î ² -Ketoacyl CoA Synthase 2B.1 from <i>Chenopodium quinoa</i> Promotes Suberin Monomersâ€™™ Production and Salt Tolerance in <i>Arabidopsis thaliana</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 13204.	1.8	4
1452	Clonal Spread of pESI-Positive Multidrug-Resistant ST32 <i>Salmonella enterica</i> Serovar <i>Infantis</i> Isolates among Broilers and Humans in Slovenia. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	5
1453	The genome sequence of <i>Hirschfeldia incana</i> , a new Brassicaceae model to improve photosynthetic light-use efficiency. <i>Plant Journal</i> , 0, , .	2.8	2
1454	Detection of beak and feather disease virus in India and its implications. <i>Transboundary and Emerging Diseases</i> , 2022, 69, .	1.3	4
1455	Asgard ESCRT-III and VPS4 reveal conserved chromatin binding properties of the ESCRT machinery. <i>ISME Journal</i> , 2023, 17, 117-129.	4.4	2
1456	Comparative Genomic Insights into the Evolution of <i>Halobacteria</i> -Associated <i>Candidatus</i> <i>Nanohaloarchaeota</i> . <i>MSystems</i> , 2022, 7, .	1.7	6
1457	An Analysis of the Current Status and Characteristics of Airborne Fungi in Indoor Air in Multi-Use Facilities Nationwide. <i>Korean Journal of Environmental Health Sciences</i> , 2022, 48, 282-289.	0.1	1
1458	The <i>Neurospora crassa</i> molybdate transporter: Characterizing a novel transporter homologous to the plant MOT1 family. <i>Fungal Genetics and Biology</i> , 2022, 163, 103745.	0.9	0
1459	Massively parallel single-cell genomics of microbiomes in rice paddies. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
1460	BACTERIAL NADQ (COG4111) IS A NUDIX-LIKE, ATP-RESPONSIVE REGULATOR OF NAD BIOSYNTHESIS. <i>Journal of Structural Biology</i> , 2022, , 107917.	1.3	0
1461	Epidemiological analysis of Legionnaires' disease in Scotland: a genomic study. <i>Lancet Microbe</i> , The, 2022, 3, e835-e845.	3.4	6
1463	An enigmatic beetle with affinity to <i>Lamingtoniidae</i> in mid-Cretaceous amber from northern Myanmar (Coleoptera: Cucujoidea). <i>Frontiers in Ecology and Evolution</i> , 0, 10, .	1.1	4
1464	Genome mining reveals abiotic stress resistance genes in plant genomes acquired from microbes via HGT. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4
1465	ABA biosynthesis gene <i>OsNCED3</i> contributes to preharvest sprouting resistance and grain development in rice. <i>Plant, Cell and Environment</i> , 2023, 46, 1384-1401.	2.8	12
1466	Isolation and characterization of novel <i>Fusobacterium nucleatum</i> bacteriophages. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5
1467	Genomic Insights into the Colistin Resistant <i>mcr</i> -Carrying <i>Escherichia coli</i> Strains in a Tertiary Hospital in China. <i>Antibiotics</i> , 2022, 11, 1522.	1.5	1
1468	Chromosome-level genome assembly of <i>Nibea coibor</i> using PacBio HiFi reads and Hi-C technologies. <i>Scientific Data</i> , 2022, 9, .	2.4	3
1469	Pan-Genome Analysis of <i>Staphylococcus aureus</i> Reveals Key Factors Influencing Genomic Plasticity. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	5

#	ARTICLE	IF	CITATIONS
1470	A Catalog of over 5,000 Metagenome-Assembled Microbial Genomes from the Caprinae Gut Microbiota. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	3
1471	Resistance potential of soil bacterial communities along a biodiversity gradient in forest ecosystems. , 2022, 1, 399-411.		2
1472	SARS-CoV-2 genomic surveillance in Malaysia: displacement of B.1.617.2 with AY lineages as the dominant Delta variants and the introduction of Omicron during the fourth epidemic wave. <i>International Journal of Infectious Diseases</i> , 2022, 125, 216-226.	1.5	10
1473	A reverse vaccinology approach identifies putative vaccination targets in the zoonotic nematode <i>Ascaris</i> . <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	4
1474	Unusual Class I Lanthipeptides from the Marine Bacteria <i>Thalassomonas viridans</i> . <i>ACS Synthetic Biology</i> , 2022, 11, 3608-3616.	1.9	5
1475	Genome-Wide Association Studies Identify an Association of Transferrin Binding Protein B Variation and Invasive Serogroup Y Meningococcal Disease in Older Adults. <i>Journal of Infectious Diseases</i> , 2022, 226, 2204-2214.	1.9	1
1476	Comparative Analysis of Novel Lytic Phages for Biological Control of Phytopathogenic <i>Xanthomonas</i> spp.. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	1
1477	Genomic and Phenotypic Trait Variation of the Opportunistic Human Pathogen <i>Aspergillus flavus</i> and Its Close Relatives. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	9
1478	First detection of <i>mcr-1</i> -producing <i>Escherichia coli</i> in Greece. <i>Journal of Global Antimicrobial Resistance</i> , 2022, 31, 252-255.	0.9	1
1479	An application of zooms to identify archaeological avian fauna from Teotihuacan, Mexico. <i>Journal of Archaeological Science</i> , 2022, 148, 105692.	1.2	4
1480	Genome-wide identification and expression analysis of fatty acid-binding proteins (FABPs) in Chinese perch <i>Siniperca chuatsi</i> and their circadian rhythm responses to cadmium exposure. <i>Aquaculture Reports</i> , 2022, 27, 101374.	0.7	0
1481	A partial duplication of an X-linked gene exclusive of a primate lineage (<i>Macaca</i>). <i>Gene</i> , 2023, 851, 146997.	1.0	0
1482	Genome Wide Characterization of CBL-CIPK Family Genes and Their Responsive Expression in <i>Rosa chinensis</i> . <i>Phyton</i> , 2023, 92, 349-368.	0.4	0
1483	Mango seedling genotyping reveals potential self-incompatibility and pollinator behavior. <i>Scientia Horticulturae</i> , 2023, 308, 111599.	1.7	0
1484	Study of antibiotic resistance in freshwater ecosystems with low anthropogenic impact. <i>Science of the Total Environment</i> , 2023, 857, 159378.	3.9	7
1485	Emergence of sulphonamide resistance in azithromycin-resistant pediatric strains of <i>Salmonella Typhi</i> and <i>Paratyphi A</i> : A genomics insight. <i>Gene</i> , 2023, 851, 146995.	1.0	5
1486	Whole-genome resequencing reveals recent signatures of selection in five populations of largemouth bass (<i>Micropterus salmoides</i>). <i>Zoological Research</i> , 2023, 44, 78-89.	0.9	3
1487	Insights into the effects of drying treatments on cultivable microbial diversity of marine sediments. <i>Microbiological Research</i> , 2023, 266, 127214.	2.5	3

#	ARTICLE	IF	CITATIONS
1488	Further studies on nicotianamine aminotransferase (NAAT) genes involved in biofortification in bread wheat (<i>Triticum aestivum</i> L.). <i>Plant Gene</i> , 2023, 33, 100389.	1.4	2
1490	BabyBoom: 3-Dimensional Structure-Based Ligand and Protein Interaction Prediction by Molecular Docking. <i>Biomolecules</i> , 2022, 12, 1633.	1.8	0
1491	The complete mitochondrial genome of <i>Hemigrapsus sinensis</i> (Brachyura, Grapsoidea, Varunidae) and its phylogenetic position within Grapsoidea. <i>Genes and Genomics</i> , 0, , .	0.5	3
1493	Genome-wide analysis of zinc finger-homeodomain (ZF-HD) transcription factors in diploid and tetraploid cotton. <i>Functional and Integrative Genomics</i> , 2022, 22, 1269-1281.	1.4	4
1494	KINN: An alignment-free accurate phylogeny reconstruction method based on inner distance distributions of k-mer pairs in biological sequences. <i>Molecular Phylogenetics and Evolution</i> , 2023, 179, 107662.	1.2	4
1495	Anaerobic Biohydrogenation of Isoprene by <i>Acetobacterium wieringae</i> Strain Y. <i>MBio</i> , 2022, 13, .	1.8	2
1496	Identification and Analysis of Stress-Associated Proteins (SAPs) Protein Family and Drought Tolerance of ZmSAP8 in Transgenic <i>Arabidopsis</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 14109.	1.8	1
1497	Longitudinal analysis of the Five Sisters hot springs in Yellowstone National Park reveals a dynamic thermoalkaline environment. <i>Scientific Reports</i> , 2022, 12, .	1.6	4
1498	Deeper genomic insights into tomato CLE genes repertoire identify new active peptides. <i>BMC Genomics</i> , 2022, 23, .	1.2	10
1499	Functional and Safety Characterization of <i>Weissella paramesenteroides</i> Strains Isolated from Dairy Products through Whole-Genome Sequencing and Comparative Genomics. <i>Dairy</i> , 2022, 3, 799-813.	0.7	9
1500	Assessment of Genetic Diversity among Wild <i>Ruta</i> <i>chalepensis</i> L. from the North of Jordan. <i>Diversity</i> , 2022, 14, 969.	0.7	0
1501	A Persistent Tuberculosis Outbreak in the UK Is Characterized by Hydrophobic <i>fadB4</i> -Deficient <i>Mycobacterium tuberculosis</i> That Replicates Rapidly in Macrophages. <i>MBio</i> , 0, , .	1.8	0
1502	Polymerization of the backbone of the pectic polysaccharide rhamnogalacturonan I. <i>Nature Plants</i> , 2022, 8, 1289-1303.	4.7	11
1503	Vetinformatics from functional genomics to drug discovery: Insights into decoding complex molecular mechanisms of livestock systems in veterinary science. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	7
1504	Genome-Wide Identification and Expression Profile Analysis of the WUSCHEL-Related Homeobox (WOX) Genes in Woodland Strawberry (<i>Fragaria vesca</i>). <i>Horticulturae</i> , 2022, 8, 1043.	1.2	2
1505	Six novel <i>Micromonospora</i> species associated with the phyllosphere and roots of leguminous plants: <i>Micromonospora alfalfae</i> sp. nov., <i>Micromonospora cabrerizensis</i> sp. nov., <i>Micromonospora foliorum</i> sp. nov., <i>Micromonospora hortensis</i> sp. nov., <i>Micromonospora salmantinae</i> sp. nov., and <i>Micromonospora trifolii</i> sp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	2
1506	Rare, convergent antibodies targeting the stem helix broadly neutralize diverse betacoronaviruses. <i>Cell Host and Microbe</i> , 2023, 31, 97-111.e12.	5.1	21
1507	Global analysis of common bean multidrug and toxic compound extrusion transporters (PvMATEs): PvMATE8 and pinto bean seed coat darkening. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3

#	ARTICLE	IF	CITATIONS
1508	An ancestral mycobacterial effector promotes dissemination of infection. <i>Cell</i> , 2022, 185, 4507-4525.e18.	13.5	16
1509	A short exposure to a semi-natural habitat alleviates the honey bee hive microbial imbalance caused by agricultural stress. <i>Scientific Reports</i> , 2022, 12, .	1.6	5
1510	Genome-Wide Identification and In Silico Analysis of ZF-HD Transcription Factor Genes in <i>Zea mays</i> L.. <i>Genes</i> , 2022, 13, 2112.	1.0	6
1511	Selection for Translational Efficiency in Genes Associated with Alphaproteobacterial Gene Transfer Agents. <i>MSystems</i> , 2022, 7, .	1.7	4
1512	Genome-Wide Identification and Expression Analysis of the NAC Gene Family in <i>Kandelia obovata</i> , a Typical Mangrove Plant. <i>Current Issues in Molecular Biology</i> , 2022, 44, 5622-5637.	1.0	6
1513	Taxonium, a web-based tool for exploring large phylogenetic trees. <i>ELife</i> , 0, 11, .	2.8	29
1515	Expanding the genomic encyclopedia of Actinobacteria with 824 isolate reference genomes. <i>Cell Genomics</i> , 2022, 2, 100213.	3.0	16
1516	Analyses of the Global Multilocus Genotypes of the Human Pathogenic Yeast <i>Cryptococcus neoformans</i> Species Complex. <i>Genes</i> , 2022, 13, 2045.	1.0	6
1517	Isolation of a New Infectious Pancreatic Necrosis Virus (IPNV) Variant from Genetically Resistant Farmed Atlantic Salmon (<i>Salmo salar</i>) during 2021â€“2022. <i>Pathogens</i> , 2022, 11, 1368.	1.2	3
1519	Whole-Genome Sequences of Human Monkeypox Virus Strains from Two 2022 Global Outbreak Cases in Western New York State. <i>Microbiology Resource Announcements</i> , 2022, 11, .	0.3	4
1521	A genomic snapshot of demographic and cultural dynamism in Upper Mesopotamia during the Neolithic Transition. <i>Science Advances</i> , 2022, 8, .	4.7	10
1522	Applying image clustering to phylogenetic analysis: A trial. <i>Plant Diversity</i> , 2023, 45, 234-237.	1.8	0
1523	Comparative genomics and informational content analysis uncovered internal regions of the core genes <i>rpoD</i> , <i>pepN</i> and <i>gltX</i> for an MLSA with genome-level resolving power within the genus <i>Pseudomonas</i> . <i>Molecular Phylogenetics and Evolution</i> , 2023, 179, 107663.	1.2	2
1525	The Genome of the Mitochondrion-Related Organelle in <i>Cepedea longa</i> , a Large Endosymbiotic Opalinid Inhabiting the Recta of Frogs. <i>International Journal of Molecular Sciences</i> , 2022, 23, 13472.	1.8	0
1526	Plant-associated <i>Bacillus</i> mobilizes its secondary metabolites upon perception of the siderophore pyochelin produced by a <i>Pseudomonas</i> competitor. <i>ISME Journal</i> , 2023, 17, 263-275.	4.4	24
1527	Genome-Wide Association Study Identifies a Rice Panicle Blast Resistance Gene <i>Pb3</i> Encoding NLR Protein. <i>International Journal of Molecular Sciences</i> , 2022, 23, 14032.	1.8	6
1528	Functional characterization of diverse type I-F CRISPR-associated transposons. <i>Nucleic Acids Research</i> , 2022, 50, 11670-11681.	6.5	7
1529	Web-based prediction of antimicrobial resistance in enterococcal clinical isolates by whole-genome sequencing. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2023, 42, 67-76.	1.3	3

#	ARTICLE	IF	CITATIONS
1530	Epidemiology, molecular characterization, and drug resistance of IncHI5 plasmids from Enterobacteriaceae. <i>International Microbiology</i> , 2023, 26, 371-378.	1.1	3
1531	Variations in the NSP4 gene of the type 2 porcine reproductive and respiratory syndrome virus isolated in China from 1996 to 2021. <i>Virus Genes</i> , 2023, 59, 109-120.	0.7	5
1532	Evolution of different rice ecotypes and genetic basis of flooding adaptability in Deepwater rice by GWAS. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	3
1533	Molecular Detection of Southern Tomato Amalgavirus Prevalent in Tomatoes and Its Genomic Characterization with Global Evolutionary Dynamics. <i>Viruses</i> , 2022, 14, 2481.	1.5	0
1534	The Hydrophobin Gene Family Confers a Fitness Trade-off between Spore Dispersal and Host Colonization in <i>Penicillium expansum</i> . <i>MBio</i> , 2022, 13, .	1.8	6
1535	Ancestral APOBEC3B Nuclear Localization Is Maintained in Humans and Apes and Altered in Most Other Old World Primate Species. <i>MSphere</i> , 2022, 7, .	1.3	6
1536	High diversity of the emerging pathogen <i>Acinetobacter baumannii</i> and other <i>Acinetobacter</i> spp. in raw manure, biogas plants digestates, and rural and urban wastewater treatment plants with system specific antimicrobial resistance profiles. <i>Science of the Total Environment</i> , 2023, 859, 160182.	3.9	6
1537	Outbreak of Parasitic Dinoflagellate <i>Piscinoodinium</i> sp. Infection in an Endangered Fish from India: <i>Arulius Barb</i> (<i>Dawkinsia arulius</i>). <i>Pathogens</i> , 2022, 11, 1350.	1.2	0
1538	<i>Sulfoacidibacillus ferrooxidans</i> , gen. nov., sp. nov., <i>Sulfoacidibacillus thermotolerans</i> , gen. nov., sp. nov., and <i>Ferroacidibacillus organovorans</i> , gen. nov., sp. nov.: Extremely acidophilic chemolitho-heterotrophic Firmicutes. <i>Research in Microbiology</i> , 2023, 174, 104008.	1.0	4
1539	Emergence and Genomic Characterization of <i>Neisseria gonorrhoeae</i> Isolates with High Levels of Ceftriaxone and Azithromycin Resistance in Guangdong, China, from 2016 to 2019. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	4
1540	Key players in syntrophic propionate oxidation revealed by metagenome-assembled genomes from anaerobic digesters bioaugmented with propionic acid enriched microbial consortia. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
1541	Specificity of a \hat{I}^2 -porphyranase produced by the carrageenophyte red alga <i>Chondrus crispus</i> and implications of this unexpected activity on red algal biology. <i>Journal of Biological Chemistry</i> , 2022, 298, 102707.	1.6	3
1542	Bacterial Dehydrogenases Facilitate Oxidative Inactivation and Bioremediation of Chloramphenicol. <i>ChemBioChem</i> , 2023, 24, .	1.3	2
1543	Amplification and sequencing of entire tick mitochondrial genomes for a phylogenomic analysis. <i>Scientific Reports</i> , 2022, 12, .	1.6	10
1544	Molecular characterization and genotyping of hepatitis C virus from Sudanese end-stage renal disease patients on haemodialysis. <i>BMC Infectious Diseases</i> , 2022, 22, .	1.3	1
1545	Two Subgroups within the GH43_36 \hat{I}^2 -l-Arabinofuranosidase Subfamily Hydrolyze Arabinosyl from Either Mono-or Disubstituted Xylosyl Units in Wheat Arabinoxylan. <i>International Journal of Molecular Sciences</i> , 2022, 23, 13790.	1.8	3
1547	Genetic Diversity and Characterization of Circular Replication (Rep)-Encoding Single-Stranded (CRESS) DNA Viruses. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	5
1549	Genomic remnants of ancestral methanogenesis and hydrogenotrophy in Archaea drive anaerobic carbon cycling. <i>Science Advances</i> , 2022, 8, .	4.7	17

#	ARTICLE	IF	CITATIONS
1550	Surveillance and Molecular Characterization of SARS-CoV-2 Infection in Non-Human Hosts in Gujarat, India. <i>International Journal of Environmental Research and Public Health</i> , 2022, 19, 14391.	1.2	4
1551	De Novo Hybrid Assembly of the <i>Salvia miltiorrhiza</i> Mitochondrial Genome Provides the First Evidence of the Multi-Chromosomal Mitochondrial DNA Structure of <i>Salvia</i> Species. <i>International Journal of Molecular Sciences</i> , 2022, 23, 14267.	1.8	10
1552	Characterization and analysis of linear epitopes corresponding to SARS-CoV-2 outbreak in Jilin Province, China. <i>Journal of Medical Virology</i> , 2023, 95, .	2.5	4
1555	Rho family GTPase signaling through type II p21-activated kinases. <i>Cellular and Molecular Life Sciences</i> , 2022, 79, .	2.4	3
1557	Adaptation of <i>Helicoverpa armigera</i> to Soybean Peptidase Inhibitors Is Associated with the Transgenerational Upregulation of Serine Peptidases. <i>International Journal of Molecular Sciences</i> , 2022, 23, 14301.	1.8	3
1558	Further Mining and Characterization of miRNA Resource in Chinese Fir (<i>Cunninghamia lanceolata</i>). <i>Genes</i> , 2022, 13, 2137.	1.0	1
1560	Evaluation of molecular typing for national surveillance of invasive clinical <i>Haemophilus influenzae</i> isolates from Denmark. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5
1561	Evidence of virulence and antibiotic resistance genes from the microbiome mapping in minimally processed vegetables producing facilities. <i>Food Research International</i> , 2022, 162, 112202.	2.9	7
1563	Deciphering the biodesulfurization potential of two novel <i>Rhodococcus</i> isolates from a unique Greek environment. <i>AIMS Microbiology</i> , 2022, 8, 484-506.	1.0	1
1564	Mutations in Spike Gene of SARS-CoV-2 that Are Associated with a Higher Viral Load: A Clinical Case Study. <i>Case Reports in Clinical Medicine</i> , 2022, 11, 474-486.	0.1	1
1565	Emergence of tet(X4)-positive hypervirulent <i>Klebsiella pneumoniae</i> of food origin in China. <i>LWT - Food Science and Technology</i> , 2023, 173, 114280.	2.5	2
1566	Community-integrated multi-omics facilitates the isolation of an organohalide dehalogenation microorganism. <i>Innovation(China)</i> , 2023, 4, 100355.	5.2	2
1567	Molting-related proteases in the brown planthopper, <i>Nilaparvata lugens</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2023, 152, 103893.	1.2	0
1568	Taxonomic proposal for a deep branching bacterial phylogenetic lineage: transfer of the family <i>Thermodesulfobiaceae</i> to <i>Thermodesulfobiales</i> ord. nov., <i>Thermodesulfobiiia</i> classis nov. and <i>Thermodesulfobiota</i> phyl. nov. <i>Systematic and Applied Microbiology</i> , 2023, 46, 126388.	1.2	6
1569	Opposite evolution of pathogenicity driven by in vivo <i>wzc</i> and <i>wcaJ</i> mutations in ST11-KL64 carbapenem-resistant <i>Klebsiella pneumoniae</i> . <i>Drug Resistance Updates</i> , 2023, 66, 100891.	6.5	7
1570	Ancient origin and conserved gene function in terpene pheromone and defense evolution of stink bugs and hemipteran insects. <i>Insect Biochemistry and Molecular Biology</i> , 2023, 152, 103879.	1.2	9
1571	Genomic characterization of tigeicycline-resistant tet(X4)-positive <i>E. coli</i> in slaughterhouses. <i>Veterinary Microbiology</i> , 2023, 276, 109606.	0.8	3
1572	Genome-wide identification and expression profiling of Wnt gene family in <i>Neocardina denticulata sinensis</i> . <i>Gene</i> , 2023, 854, 147122.	1.0	1

#	ARTICLE	IF	CITATIONS
1573	Contribution bias of parental genomes to the hybrid lineages of black Amur bream and topmouth culter revealed by low-coverage whole-genome sequencing. <i>Gene</i> , 2023, 852, 147058.	1.0	3
1574	Molecular typing and genome sequencing allow the identification of persistent <i>Listeria monocytogenes</i> strains and the tracking of the contamination source in food environments. <i>International Journal of Food Microbiology</i> , 2023, 386, 110025.	2.1	13
1575	Comparative phylogenomic analysis of 5â€™-regulatory elements (CREs) of miR160 gene family in diploid and allopolyploid cotton (<i>Gossypium</i>). <i>Gene Reports</i> , 2023, 30, 101721.	0.4	0
1576	Molecular epidemiology of Trichophyton infections among canines from Northern India. <i>Journal De Mycologie Medicale</i> , 2023, 33, 101352.	0.7	4
1577	Characterizing a novel CMK-EngA fusion protein from <i>Bifidobacterium</i> : Implications for inter-domain regulation. <i>Biochemistry and Biophysics Reports</i> , 2023, 33, 101410.	0.7	0
1578	Unexpected diversity of dye-decolorizing peroxidases. <i>Biochemistry and Biophysics Reports</i> , 2023, 33, 101401.	0.7	6
1579	First records of <i>Clusia</i> Haliday and <i>Clusiodes</i> Coquillett (Diptera: Clusiidae) from Korea. <i>Journal of Asia-Pacific Entomology</i> , 2023, 26, 102028.	0.4	0
1580	Whole-genome identification and expression analysis of basic leucine zipper genes under cadmium, drought and Orobanche cumana stresses in <i>Helianthus annuus</i> L.. <i>Industrial Crops and Products</i> , 2023, 193, 116123.	2.5	3
1581	InÂvitro and in silico characterization of a novel glutamate carboxypeptidase from <i>Cohnella</i> sp. A01. <i>Biochimie</i> , 2023, 207, 83-95.	1.3	2
1582	Textile industry wastewater microbiome: Recovery of metagenome assembled genomes (MAGs) using shotgun sequencing approach from Jetpur, Gujarat, India. <i>Ecological Genetics and Genomics</i> , 2023, 26, 100155.	0.3	1
1583	Prediction and verification of glycosyltransferase activity by bioinformatics analysis and protein engineering. <i>STAR Protocols</i> , 2023, 4, 101905.	0.5	1
1584	Characterisation of the photosynthetic complexes from the marine gammaproteobacterium <i>Congregibacter litoralis</i> KT71. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2023, 1864, 148946.	0.5	0
1585	Reducing the number of accepted species in <i>Aspergillus</i> series <i>Nigri</i> . <i>Studies in Mycology</i> , 2022, 102, 95-132.	4.5	11
1587	Molecular and Pharmacological Characterization of β -Adrenergic-like Octopamine Receptors in the Endoparasitoid <i>Cotesia chilonis</i> (Hymenoptera: Braconidae). <i>International Journal of Molecular Sciences</i> , 2022, 23, 14513.	1.8	1
1589	Distinct evolutionary trajectories in the <i>Escherichia coli</i> pangenome occur within sequence types. <i>Microbial Genomics</i> , 2022, 8, .	1.0	10
1590	New Insights into Avian Infectious Bronchitis Virus in Colombia from Whole-Genome Analysis. <i>Viruses</i> , 2022, 14, 2562.	1.5	3
1591	Two new species of <i>Centroptilum</i> Eaton, 1869 from North Africa (Ephemeroptera, Baetidae). <i>ZooKeys</i> , 0, 1131, 71-97.	0.5	8
1592	Revealing druggable cryptic pockets in the Nsp1 of SARS-CoV-2 and other β -coronaviruses by simulations and crystallography. <i>ELife</i> , 0, 11, .	2.8	12

#	ARTICLE	IF	CITATIONS
1594	Phylogenetic Relationships in Earthworm Megascolex Species (Oligochaeta: Megascolecidae) with Addition of Two New Species. <i>Diversity</i> , 2022, 14, 1006.	0.7	3
1595	Genome-Wide Identification and Expression Analysis of BraGLRs Reveal Their Potential Roles in Abiotic Stress Tolerance and Sexual Reproduction. <i>Cells</i> , 2022, 11, 3729.	1.8	6
1596	Evolutionary Diversity of Dus2 Enzymes Reveals Novel Structural and Functional Features among Members of the RNA Dihydrouridine Synthases Family. <i>Biomolecules</i> , 2022, 12, 1760.	1.8	0
1597	Identification and Functional Analysis of bZIP Genes in Cotton Response to Drought Stress. <i>International Journal of Molecular Sciences</i> , 2022, 23, 14894.	1.8	6
1598	Cell type diversity in a developing octopus brain. <i>Nature Communications</i> , 2022, 13, .	5.8	29
1599	An open source plant kinase chemogenomics set. <i>Plant Direct</i> , 2022, 6, .	0.8	1
1601	Tyroviruses are a new group of temperate phages that infect <i>Bacillus</i> species in soil environments worldwide. <i>BMC Genomics</i> , 2022, 23, .	1.2	5
1602	Differences in gut microbial fructoselysine degradation activity between breast-fed and formula-fed infants. <i>FEMS Microbiology Ecology</i> , 2022, 99, .	1.3	2
1603	NPASS database update 2023: quantitative natural product activity and species source database for biomedical research. <i>Nucleic Acids Research</i> , 2023, 51, D621-D628.	6.5	9
1604	A Practical Bioinformatics Workflow for Routine Analysis of Bacterial WGS Data. <i>Microorganisms</i> , 2022, 10, 2364.	1.6	6
1605	Evolutionary Impacts of Pattern Recognition Receptor Genes on Carnivora Complex Habitat Stress Adaptation. <i>Animals</i> , 2022, 12, 3331.	1.0	2
1606	Comparative Genomics Reveal the Utilization Ability of Variable Carbohydrates as Key Genetic Features of <i>Listeria</i> Pathogens in Their Pathogenic Lifestyles. <i>Pathogens</i> , 2022, 11, 1430.	1.2	1
1607	The L-Rhamnose Biosynthetic Pathway in <i>Trichomonas vaginalis</i> : Identification and Characterization of UDP-D-Glucose 4,6-dehydratase. <i>International Journal of Molecular Sciences</i> , 2022, 23, 14587.	1.8	1
1608	<i>Zunongwangia pacifica</i> sp. nov., isolated from surface seawater of the Western Pacific Ocean. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	0
1609	Multi-Omics of <i>Corynebacterium Pseudotuberculosis</i> 12CS0282 and an In Silico Reverse Vaccinology Approach Reveal Novel Vaccine and Drug Targets. <i>Proteomes</i> , 2022, 10, 39.	1.7	2
1610	Functional Diversification of Oyster Big Defensins Generates Antimicrobial Specificity and Synergy against Members of the Microbiota. <i>Marine Drugs</i> , 2022, 20, 745.	2.2	5
1611	<i>Lactobacillus reuteri</i> tryptophan metabolism promotes host susceptibility to CNS autoimmunity. <i>Microbiome</i> , 2022, 10, .	4.9	27
1613	Complete Mitogenome and Phylogenetic Analyses of <i>Galerita orientalis</i> Schmidt-Goebel, 1846 (Insecta: Tj ETQq1 1.0.784314 rgBT /Ove	1.0	1

#	ARTICLE	IF	CITATIONS
1614	Argopistes sexvittatus and Argopistes capensis (Chrysomelidae: Alticini): Mitogenomics and Phylogeny of Two Flea Beetles Affecting Olive Trees. <i>Genes</i> , 2022, 13, 2195.	1.0	1
1618	Whole-genome scanning reveals environmental selection mechanisms that shape diversity in populations of the epipelagic diatom <i>Chaetoceros</i> . <i>PLoS Biology</i> , 2022, 20, e3001893.	2.6	7
1619	NDM-1 and OXA-48-Like Carbapenemases (OXA-48, OXA-181 and OXA-252) Co-Producing <i>Shewanella xiamenensis</i> from Hospital Wastewater, China. <i>Infection and Drug Resistance</i> , 0, Volume 15, 6927-6938.	1.1	4
1621	Comparative Genomic Analysis of a Multidrug-Resistant <i>Staphylococcus hominis</i> ShoR14 Clinical Isolate from Terengganu, Malaysia, Led to the Discovery of Novel Mobile Genetic Elements. <i>Pathogens</i> , 2022, 11, 1406.	1.2	2
1623	Clostridia isolated from helminth-colonized humans promote the life cycle of <i>Trichuris</i> species. <i>Cell Reports</i> , 2022, 41, 111725.	2.9	7
1624	Genome-Scale Investigation of GARP Family Genes Reveals Their Pivotal Roles in Nutrient Stress Resistance in Allotetraploid Rapeseed. <i>International Journal of Molecular Sciences</i> , 2022, 23, 14484.	1.8	3
1625	Identification and expression profiles of xylogen-like arabinogalactan protein (XYLP) gene family in <i>Phyllostachys edulis</i> in different developmental tissues and under various abiotic stresses. <i>International Journal of Biological Macromolecules</i> , 2023, 227, 1098-1118.	3.6	1
1627	BAHD Company: The Ever-Expanding Roles of the BAHD Acyltransferase Gene Family in Plants. <i>Annual Review of Plant Biology</i> , 2023, 74, 165-194.	8.6	10
1628	<sc>CIPK</sc> is essential for salt stress signalling in <i>Marchantia polymorpha</i>. <i>New Phytologist</i> , 0, , .	3.5	0
1629	Renewal of planktonic foraminifera diversity after the Cretaceous Paleogene mass extinction by benthic colonizers. <i>Nature Communications</i> , 2022, 13, .	5.8	5
1630	Whole genome SNPs among 8 chicken breeds enable identification of genetic signatures that underlie breed features. <i>Journal of Integrative Agriculture</i> , 2023, 22, 2200-2212.	1.7	3
1632	Polyenic Antibiotics and Other Antifungal Compounds Produced by Hemolytic <i>Streptomyces</i> Species. <i>International Journal of Molecular Sciences</i> , 2022, 23, 15045.	1.8	1
1633	Diversity of resistant determinants, virulence factors, and mobile genetic elements in <i>Acinetobacter baumannii</i> from India: A comprehensive in silico genome analysis. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	2
1634	Characterization of the VP2 and NS1 genes from canine parvovirus type 2 (CPV-2) and feline panleukopenia virus (FPV) in Northern China. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	6
1638	Nutrient niche specificity for glycosaminoglycans is reflected in polysaccharide utilization locus architecture of gut <i>Bacteroides</i> species. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
1640	Non-cyanobacterial diazotrophs: global diversity, distribution, ecophysiology, and activity in marine waters. <i>FEMS Microbiology Reviews</i> , 2023, 47, .	3.9	11
1641	First report of ectomycorrhizae in <i>Prunus serotina</i> in the exotic range. <i>Plant and Soil</i> , 2023, 484, 171-181.	1.8	2
1643	Identification, evolution, and expression analysis of OsBSK gene family in <i>Oryza sativa</i> Japonica. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	2

#	ARTICLE	IF	CITATIONS
1644	Epigenetic Stress and Long-Read cDNA Sequencing of Sunflower (<i>Helianthus annuus</i> L.) Revealed the Origin of the Plant Retrotranscriptome. <i>Plants</i> , 2022, 11, 3579.	1.6	2
1645	Hybridization and diversity of aquatic macrophyte <i>Sparganium</i> L. (Typhaceae) as revealed by high-throughput nrDNA sequencing. <i>Scientific Reports</i> , 2022, 12, .	1.6	4
1646	Potential of bioaugmentation of heavy metal contaminated soils in the Zambian Copperbelt using autochthonous filamentous fungi. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
1647	Bioactivity Profiling of In Silico Predicted Linear Toxins from the Ants <i>Myrmica rubra</i> and <i>Myrmica ruginodis</i> . <i>Toxins</i> , 2022, 14, 846.	1.5	4
1648	Population structure and genetic diversity in wild dotted gizzard shad (<i>Konosirus punctatus</i>) revealed by microsatellite markers. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	1
1649	Analyses of Cullin1 homologs reveal functional redundancy in S-RNase-based self-incompatibility and evolutionary relationships in eudicots. <i>Plant Cell</i> , 2023, 35, 673-699.	3.1	2
1650	Reconstruction of the Major Maternal and Paternal Lineages in the Feral New Zealand Kaimanawa Horses. <i>Animals</i> , 2022, 12, 3508.	1.0	1
1651	A broad specificity \hat{I}^2 -propeller enzyme from <i>Rhodopseudomonas palustris</i> that hydrolyzes many lactones including \hat{I}^3 -valerolactone. <i>Journal of Biological Chemistry</i> , 2022, , 102782.	1.6	0
1652	Investigation and Expression Analysis of R2R3-MYBs and Anthocyanin Biosynthesis-Related Genes during Seed Color Development of Common Bean (<i>Phaseolus vulgaris</i>). <i>Plants</i> , 2022, 11, 3386.	1.6	4
1654	Genome-resolved insight into the reservoir of antibiotic resistance genes in aquatic microbial community. <i>Scientific Reports</i> , 2022, 12, .	1.6	0
1655	Comparison of prokaryotes between Mount Everest and the Mariana Trench. <i>Microbiome</i> , 2022, 10, .	4.9	2
1656	Genome-Wide Identification of AP2/ERF Superfamily Genes in <i>Juglans mandshurica</i> and Expression Analysis under Cold Stress. <i>International Journal of Molecular Sciences</i> , 2022, 23, 15225.	1.8	3
1657	Calcium-permeable channelrhodopsins for the photocontrol of calcium signalling. <i>Nature Communications</i> , 2022, 13, .	5.8	4
1658	Time-scale analysis of the long-term variability of human gut microbiota characteristics in Chinese individuals. <i>Communications Biology</i> , 2022, 5, .	2.0	3
1659	The endocytic TPLATE complex internalizes ubiquitinated plasma membrane cargo. <i>Nature Plants</i> , 2022, 8, 1467-1483.	4.7	6
1660	Cloning and Functional Characterization of SpZIP2. <i>Genes</i> , 2022, 13, 2395.	1.0	2
1662	Discovery of \hat{I}^{\pm} -Glucosidase Raises the Possibility of \hat{I}^{\pm} -Glucosides in Nature. <i>ACS Omega</i> , 2022, 7, 47411-47423.	1.6	2
1663	Identification and Functional Analysis of CAD Gene Family in Pomegranate (<i>Punica granatum</i>). <i>Genes</i> , 2023, 14, 26.	1.0	4

#	ARTICLE	IF	CITATIONS
1664	Genomic landscape of the SARS-CoV-2 pandemic in Brazil suggests an external P.1 variant origin. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
1665	Identification, Characterization and Expression Profiling of the RS Gene Family during the Withering Process of White Tea in the Tea Plant (<i>Camellia sinensis</i>) Reveal the Transcriptional Regulation of CsRS8. <i>International Journal of Molecular Sciences</i> , 2023, 24, 202.	1.8	2
1667	Duplicate genes as sources for rapid adaptive evolution of sperm under environmental pollution in tree sparrow. <i>Molecular Ecology</i> , 2023, 32, 1673-1684.	2.0	3
1668	How elevated nitrogen load affects bacterial community structure and nitrogen cycling services in coastal water. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
1669	Decoupling of respiration rates and abundance in marine prokaryoplankton. <i>Nature</i> , 2022, 612, 764-770.	13.7	19
1672	Genome-Wide Identification of the SUN Gene Family in Melon (<i>Cucumis melo</i>) and Functional Characterization of Two CmSUN Genes in Regulating Fruit Shape Variation. <i>International Journal of Molecular Sciences</i> , 2022, 23, 16047.	1.8	4
1673	Genome-Based Analysis of Virulence Factors and Biofilm Formation in Novel <i>P. aeruginosa</i> Strains Isolated from Household Appliances. <i>Microorganisms</i> , 2022, 10, 2508.	1.6	1
1674	Characterization and phylogenetic implications of newly sequenced mitogenomes of Five Mileewa and Processina species from China (Hemiptera: Cicadellidae: Mileewinae). <i>Scientific Reports</i> , 2022, 12, .	1.6	2
1675	Peptidoglycan recycling mediated by an ABC transporter in the plant pathogen <i>Agrobacterium tumefaciens</i> . <i>Nature Communications</i> , 2022, 13, .	5.8	6
1676	Diversity dynamics of aerobic anoxygenic phototrophic bacteria in a freshwater lake. <i>Environmental Microbiology Reports</i> , 2023, 15, 60-71.	1.0	8
1677	Chloroplast genome assemblies and comparative analyses of commercially important <i>Vaccinium</i> berry crops. <i>Scientific Reports</i> , 2022, 12, .	1.6	12
1679	NGS-based genome wide association study helps to develop co-dominant marker for the physical map-based locus of PFRU controlling flowering in cultivated octoploid strawberry. <i>Euphytica</i> , 2023, 219, .	0.6	0
1680	Conservation of an <i>Agrobacterium</i> cT-DNA insert in <i>Camellia</i> section <i>Thea</i> reveals the ancient origin of tea plants from a genetically modified ancestor. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	5
1682	Resistome and virulome diversity of foodborne pathogens isolated from artisanal food production chain of animal origin in the Mediterranean region. <i>Italian Journal of Food Safety</i> , 2022, 11, .	0.5	0
1684	Gut colonization by <i>Bacteroides</i> requires translation by an <i>EFa</i> paralog lacking <i>GTPase</i> activity. <i>EMBO Journal</i> , 2023, 42, .	3.5	7
1685	First report of tomato chlorosis virus (ToCV) and detection of other viruses in field-grown tomatoes in North-Western region of India. <i>VirusDisease</i> , 0, , .	1.0	0
1686	Cyanobacterial Blooms Are Not a Result of Positive Selection by Freshwater Eutrophication. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	2
1687	Genetic Features of <i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> Strains Circulating in the West of France Deciphered by Whole-Genome Sequencing. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	6

#	ARTICLE	IF	CITATIONS
1688	Virome Analysis of Normal and Growth Retardation Disease-Affected <i>Macrobrachium rosenbergii</i> . <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	7
1689	Deep Diversity: Extensive Variation in the Components of Complex Visual Systems across Animals. <i>Cells</i> , 2022, 11, 3966.	1.8	7
1691	Farming Practice Influences Antimicrobial Resistance Burden of Non-Aureus Staphylococci in Pig Husbandries. <i>Microorganisms</i> , 2023, 11, 31.	1.6	2
1692	The complete chloroplast genome of <i>Thermopsis lanceolata</i> : genome structure and its phylogenetic relationships within the family Fabaceae. <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 2076-2080.	0.2	0
1693	Widespread formation of intracellular calcium carbonates by the bloom-forming cyanobacterium <i>Microcystis</i> . <i>Environmental Microbiology</i> , 2023, 25, 751-765.	1.8	1
1695	Genome-based analyses of the genus <i>Acidovorax</i> : proposal of the two novel genera <i>Paracidovorax</i> gen. nov., <i>Paenacidovorax</i> gen. nov. and the reclassification of <i>Acidovorax antarcticus</i> as <i>Comamonas antarctica</i> comb. nov. and emended description of the genus <i>Acidovorax</i> . <i>Archives of Microbiology</i> , 2023, 205, .	1.0	4
1696	Pan-kinome of <i>Legionella</i> expanded by a bioinformatics survey. <i>Scientific Reports</i> , 2022, 12, .	1.6	3
1697	To be or not to be: Integrative taxonomy and species delimitation in the daddy long-legs spiders of the genus <i>Physocyclus</i> (Araneae, Pholcidae) using DNA barcoding and morphology. <i>ZooKeys</i> , 0, 1135, 93-118.	0.5	7
1699	Genome-Wide Analysis of AP2/ERF Gene Superfamily in Ramie (<i>Boehmeria nivea</i> L.) Revealed Their Synergistic Roles in Regulating Abiotic Stress Resistance and Ramet Development. <i>International Journal of Molecular Sciences</i> , 2022, 23, 15117.	1.8	3
1700	Virulence Profile, Antibiotic Resistance, and Phylogenetic Relationships among <i>Escherichia coli</i> Strains Isolated from the Feces and Urine of Hospitalized Patients. <i>Pathogens</i> , 2022, 11, 1528.	1.2	4
1701	<i>Vulcanimicrobium alpinus</i> gen. nov. sp. nov., the first cultivated representative of the candidate phylum "Eremiobacterota", is a metabolically versatile aerobic anoxygenic phototroph. <i>ISME Communications</i> , 2022, 2, .	1.7	8
1702	Sourcing thermotolerant poly(ethylene terephthalate) hydrolase scaffolds from natural diversity. <i>Nature Communications</i> , 2022, 13, .	5.8	51
1703	Characterization of the immunoglobulin lambda chain locus from diverse populations reveals extensive genetic variation. <i>Genes and Immunity</i> , 2023, 24, 21-31.	2.2	11
1704	Assessment of biodiversity, global distribution, and putative ecological niches of suessiacean dinoflagellates by DNA metabarcoding. <i>Frontiers in Ecology and Evolution</i> , 0, 10, .	1.1	2
1706	Diversity Analysis Using Agricultural Traits and SSR Markers of Wheat Germplasms. <i>Han'guk Yukchong Hakhoe Chi</i> , 2022, 54, 345-357.	0.2	1
1707	Genomic characterization of Japanese meningococcal strains isolated over a 17-year period between 2003 and 2020 in Japan. <i>Vaccine</i> , 2023, 41, 416-426.	1.7	3
1709	A Hepatocyte Nuclear Factor <i>HNF4</i> Mediates Desiccation Tolerance and Fecundity in Whitefly (<i>Bemisia tabaci</i>). <i>Environmental Entomology</i> , 0, , .	0.7	3
1711	Genome Evolution and Early Introductions of the SARS-CoV-2 Omicron Variant in Mexico. <i>Virus Evolution</i> , 2022, 8, .	2.2	3

#	ARTICLE	IF	CITATIONS
1712	Characterization of unconventional pathogenic <i>Escherichia coli</i> isolated from bloodstream infection: virulence beyond the opportunism. <i>Brazilian Journal of Microbiology</i> , 2023, 54, 15-28.	0.8	1
1713	<i>Bactrocera dorsalis</i> in the Indian Ocean: A tale of two invasions. <i>Evolutionary Applications</i> , 2023, 16, 48-61.	1.5	4
1714	Population dynamics and antimicrobial resistance of <i>Salmonella</i> Derby ST40 from Shenzhen, China. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
1715	Metagenomics and metatranscriptomics reveal broadly distributed, active, novel methanotrophs in the Gulf of Mexico hypoxic zone and in the marine water column. <i>FEMS Microbiology Ecology</i> , 2023, 99, .	1.3	5
1716	Detection and sequence analysis of Canine morbillivirus in multiple species of the Mustelidae family. <i>BMC Veterinary Research</i> , 2022, 18, .	0.7	1
1717	Genome-wide investigation and expression pattern of <i>PHR</i> family genes in cotton under low phosphorus stress. <i>PeerJ</i> , 0, 10, e14584.	0.9	0
1718	Genome-Wide Characterization of Trehalose-6-Phosphate Synthase Gene Family of <i>Brassica napus</i> and Potential Links with Agronomic Traits. <i>International Journal of Molecular Sciences</i> , 2022, 23, 15714.	1.8	2
1719	Telomeres are shorter in wild <i>Saccharomyces cerevisiae</i> isolates than in domesticated ones. <i>Genetics</i> , 2023, 223, .	1.2	4
1720	Farnesyl/geranylgeranyl diphosphate synthases regulate the biosynthesis of alarm pheromone in a unique manner in the vetch aphid <i>Megoura viciae</i> . <i>Insect Molecular Biology</i> , 2023, 32, 229-239.	1.0	3
1722	Genome-Wide Identification and Phylogenetic Analysis of TRP Gene Family Members in Saurian. <i>Animals</i> , 2022, 12, 3593.	1.0	1
1723	Distribution of Extremely Heat-Resistant <i>Escherichia coli</i> in the Beef Production and Processing Continuum. <i>Journal of Food Protection</i> , 2023, 86, 100031.	0.8	2
1724	Genetic Diversity Analysis and Core Collection Construction of the <i>Actinidia chinensis</i> Complex (Kiwifruit) Based on SSR Markers. <i>Agronomy</i> , 2022, 12, 3078.	1.3	2
1725	Increase in NDM-1 and NDM-1/OXA-48-producing <i>Klebsiella pneumoniae</i> in Germany associated with the war in Ukraine, 2022. <i>Eurosurveillance</i> , 2022, 27, .	3.9	17
1726	Environmental predictors of electroactive bacterioplankton in small boreal lakes. <i>Environmental Microbiology</i> , 2023, 25, 705-720.	1.8	3
1727	Geographically Disperse, Culturable Seed-Associated Microbiota in Forage Plants of Alfalfa (<i>Medicago</i>) as Plant Stress-Tolerance Enhancers. <i>Biology</i> , 2022, 11, 1838.	1.3	2
1728	Discovery and characterization of novel type I-D CRISPR-guided transposons identified among diverse Tn7-like elements in cyanobacteria. <i>Nucleic Acids Research</i> , 2023, 51, 765-782.	6.5	16
1729	Functional Characterization of the Ryanodine Receptor Gene in <i>Diaphorina citri</i> . <i>Life</i> , 2022, 12, 2005.	1.1	1
1730	The methanogen core and pangenome: conservation and variability across biology's growth temperature extremes. <i>DNA Research</i> , 2023, 30, .	1.5	3

#	ARTICLE	IF	CITATIONS
1733	Plastome Characterization, Phylogenetic Relationships, and Regional Conservation Status of <i>Ficus populifolia</i> Vahl. (Moraceae), a Peripherally Isolated Plant Population in the Arabian Peninsula. <i>Forests</i> , 2022, 13, 2063.	0.9	1
1734	Marker gene analysis reveals novel viral genetic diversity in unsaturated soils. <i>Biology and Fertility of Soils</i> , 0, , .	2.3	0
1735	Intestinal gluconeogenesis: metabolic benefits make sense in the light of evolution. <i>Nature Reviews Gastroenterology and Hepatology</i> , 2023, 20, 183-194.	8.2	8
1736	How Do Gene Expression Patterns Change in Response to Osmotic Stresses in Kuruma Shrimp (<i>Marsupenaeus japonicus</i>)?. <i>Journal of Marine Science and Engineering</i> , 2022, 10, 1870.	1.2	2
1737	Success factors of great oceanic dispersers: Case of Squamata in the Pacific Ocean. <i>Journal of Zoology</i> , 0, , .	0.8	0
1738	Mining of novel secondary metabolite biosynthetic gene clusters from acid mine drainage. <i>Scientific Data</i> , 2022, 9, .	2.4	3
1740	Evolution of monkeypox virus from 2017 to 2022: In the light of point mutations. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	13
1741	Groups of Geomicrobiological Indicators Are Spread across Gas-Hydrate and Non-Gas-Hydrate Areas in the Northern Part of the Sea of Japan. <i>Biology</i> , 2022, 11, 1802.	1.3	2
1742	Saponin Biosynthesis in Pulses. <i>Plants</i> , 2022, 11, 3505.	1.6	6
1743	Comprehensive Genome Analysis of <i>Neisseria meningitidis</i> from South America Reveals a Distinctive Pathogenicity-Related Prophage Repertoire. <i>International Journal of Molecular Sciences</i> , 2022, 23, 15731.	1.8	0
1744	<i>Actinomyces ruminis</i> sp. nov., an obligately anaerobic bacterium isolated from the rumen of cattle. <i>Archives of Microbiology</i> , 2023, 205, .	1.0	4
1745	Cannabinoid receptor 2 evolutionary gene loss makes parrots more susceptible to neuroinflammation. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2022, 289, .	1.2	3
1746	Global patterns of diversity and metabolism of microbial communities in deep-sea hydrothermal vent deposits. <i>Microbiome</i> , 2022, 10, .	4.9	23
1747	Genetic Diversity and Maternal Lineage of Indo-Pacific Bottlenose Dolphin (<i>Tursiops aduncus</i>) in the Andaman Sea of Thailand. <i>Diversity</i> , 2022, 14, 1093.	0.7	0
1748	Microcalorimetry: A Novel Application to Measure In Vitro Phage Susceptibility of <i>Staphylococcus aureus</i> in Human Serum. <i>Viruses</i> , 2023, 15, 14.	1.5	2
1749	Molecular epidemiological study of animal rabies in Kazakhstan. <i>Journal of Integrative Agriculture</i> , 2023, 22, 1266-1275.	1.7	1
1750	Induction of Multiple Immune Signaling Pathways in <i>Gryllodes sigillatus</i> Crickets during Overt Viral Infections. <i>Viruses</i> , 2022, 14, 2712.	1.5	0
1751	Comparative Genomics of <i>Lentilactobacillus parabuchneri</i> isolated from dairy, KEM complex, Makgeolli, and Saliva Microbiomes. <i>BMC Genomics</i> , 2022, 23, .	1.2	2

#	ARTICLE	IF	CITATIONS
1752	Molecular epidemiology of <i>Streptococcus pneumoniae</i> isolated from children with community-acquired pneumonia under 5 years in Chengdu, China. <i>Epidemiology and Infection</i> , 2023, 151, .	1.0	1
1754	First record of the human infection of <i>Brucella melitensis</i> in Kyrgyzstan: evidence from whole-genome sequencing-based analysis. <i>Infectious Diseases of Poverty</i> , 2022, 11, .	1.5	2
1755	Discovery of Highly Trimethoprim-Resistant DfrB Dihydrofolate Reductases in Diverse Environmental Settings Suggests an Evolutionary Advantage Unrelated to Antibiotic Resistance. <i>Antibiotics</i> , 2022, 11, 1768.	1.5	2
1756	The genomic analysis of a wide peach germplasm collection revealed genetic relationships between European landraces and American ferals and landraces. <i>Acta Horticulturae</i> , 2022, , 81-88.	0.1	0
1758	Crystal structure of the feruloyl esterase from <i>Lentilactobacillus buchneri</i> reveals a novel homodimeric state. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
1760	Revealing oxidative pentose metabolism in new <i>Pseudomonas putida</i> isolates. <i>Environmental Microbiology</i> , 0, , .	1.8	4
1762	Exploring the role and expression pattern of WRKY transcription factor in the growth and development of <i>Bletilla striata</i> based on transcriptome. <i>Gene Reports</i> , 2022, , 101730.	0.4	0
1764	Genomics, Origin and Selection Signals of Loudi Cattle in Central Hunan. <i>Biology</i> , 2022, 11, 1775.	1.3	0
1765	Diversity and Prevalence of <i>Clostridium innocuum</i> in the Human Gut Microbiota. <i>MSphere</i> , 2023, 8, .	1.3	6
1766	Evolutionary reconstruction, nomenclature and functional meta-analysis of the Kiwellin protein family. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
1767	Population Genetics and Anastomosis Group's Geographical Distribution of <i>Rhizoctonia solani</i> Associated with Soybean. <i>Genes</i> , 2022, 13, 2417.	1.0	2
1768	First Case of Monkeypox in Venezuela: Partial Complete Genome Sequence Allowed Its Grouping into the West African Clade II. <i>Tropical Medicine and Infectious Disease</i> , 2023, 8, 2.	0.9	0
1769	An Emerging Lineage of Uropathogenic Extended Spectrum β -Lactamase <i>Escherichia coli</i> ST127. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	1
1770	The electronic tree of life (eToL): a net of long probes to characterize the microbiome from RNA-seq data. <i>BMC Microbiology</i> , 2022, 22, .	1.3	10
1771	Within-Host Genotypic and Phenotypic Diversity of Contemporaneous Carbapenem-Resistant <i>Klebsiella pneumoniae</i> from Blood Cultures of Patients with Bacteremia. <i>MBio</i> , 2022, 13, .	1.8	7
1772	Scanning aldoxime dehydratase sequence space and characterization of a new aldoxime dehydratase from <i>Fusarium vanettenii</i> . <i>Enzyme and Microbial Technology</i> , 2023, 164, 110187.	1.6	8
1775	Plastid phylogenomics uncovers multiple species in <i>Medicago truncatula</i> (Fabaceae) germplasm accessions. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
1776	A proof-of-concept study on the genomic evolution of Sars-Cov-2 in molnupiravir-treated, paxlovid-treated and drug-naïve patients. <i>Communications Biology</i> , 2022, 5, .	2.0	13

#	ARTICLE	IF	CITATIONS
1777	Extended-spectrum β -lactamase- and AmpC β -lactamase-producing Enterobacterales associated with urinary tract infections in the New Zealand community: a case-control study. <i>International Journal of Infectious Diseases</i> , 2023, 128, 325-334.	1.5	3
1778	<i>Canibacter zhuwentaonis</i> sp. nov. and <i>Canibacter zhoujuaniae</i> sp. nov., isolated from <i>Marmota himalayana</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	1
1780	Spatiotemporal and ontogenetic variation, microbial selection, and predicted Bd-inhibitory function in the skin-associated microbiome of a Rocky Mountain amphibian. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
1781	Metabolic reconstruction of the near complete microbiome of the model sponge <i>Lanthella basta</i> . <i>Environmental Microbiology</i> , 2023, 25, 646-660.	1.8	4
1782	The transcription factor <i>Zic4</i> promotes tentacle formation and prevents epithelial transdifferentiation in <i>Hydra</i> . <i>Science Advances</i> , 2022, 8, .	4.7	5
1783	Sequence and structure-guided discovery of a novel NADH-dependent 7β -hydroxysteroid dehydrogenase for efficient biosynthesis of ursodeoxycholic acid. <i>Bioorganic Chemistry</i> , 2023, 131, 106340.	2.0	4
1784	Identification of an α -(1 \rightarrow 6)-Mannosyltransferase Contributing To Biosynthesis of the Fungal-Type Galactomannan α -Core-Mannan Structure in <i>Aspergillus fumigatus</i> . <i>MSphere</i> , 2022, 7, .	1.3	6
1785	Functional analysis of <i>CqPORB</i> in the regulation of chlorophyll biosynthesis in <i>Chenopodium quinoa</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	0
1786	Reekeek- and roodoooviruses, two different <i>Microviridae</i> clades constituted by the smallest DNA phages. <i>Virus Evolution</i> , 2023, 9, .	2.2	5
1787	Chromosome-scale genome assembly of a Japanese chili pepper landrace, <i>Capsicum annuum</i> 'Takanotsume'. <i>DNA Research</i> , 2023, 30, .	1.5	7
1790	An ST131 clade and a phylogroup A clade bearing an O101-like O-antigen cluster predominate among bloodstream <i>Escherichia coli</i> isolates from South-West Nigeria hospitals. <i>Microbial Genomics</i> , 2022, 8, .	1.0	4
1791	Patterns of abundance, chromosomal localization, and domain organization among c-di-GMP-metabolizing genes revealed by comparative genomics of five alphaproteobacterial orders. <i>BMC Genomics</i> , 2022, 23, .	1.2	1
1793	Use of an Integrated Approach Involving AlphaFold Predictions for the Evolutionary Taxonomy of Duplodnaviria Viruses. <i>Biomolecules</i> , 2023, 13, 110.	1.8	4
1794	A clinical KPC-producing <i>Klebsiella michiganensis</i> strain carrying <i>IncFII/IncFIA (HI1)/IncFIB (K)</i> multiple replicon plasmid. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
1795	Phylogenomics of five <i>Pseudanabaena</i> cyanophages and evolutionary traces of horizontal gene transfer. <i>Environmental Microbiomes</i> , 2023, 18, .	2.2	1
1796	Distinct traces of mixed ancestry in western commercial pig genomes following gene flow from Chinese indigenous breeds. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	3
1798	The probiotic and immunomodulation effects of <i>Limosilactobacillus reuteri</i> RGW1 isolated from calf feces. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	6
1800	Antimicrobial Resistance of and Genomic Insights into <i>Pasteurella multocida</i> Strains Isolated from Australian Pigs. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	5

#	ARTICLE	IF	CITATIONS
1801	Antimicrobial Susceptibility and Molecular Features of Colonizing Isolates of <i>Pseudomonas aeruginosa</i> and the Report of a Novel Sequence Type (ST) 3910 from Thailand. <i>Antibiotics</i> , 2023, 12, 165.	1.5	0
1802	<i>Acanthopharynx</i> Marine Nematodes (Nematoda, Chromadoria, Desmodoridae) Dwelling in Tropical Demosponges: Integrative Taxonomy with Description of a New Species. <i>Diversity</i> , 2023, 15, 48.	0.7	2
1803	Commensal Lactobacilli Metabolically Contribute to Cervical Epithelial Homeostasis in a Species-Specific Manner. <i>MSphere</i> , 2023, 8, .	1.3	3
1804	Features of <i>Mycobacterium bovis</i> Complete Genomes Belonging to 5 Different Lineages. <i>Microorganisms</i> , 2023, 11, 177.	1.6	2
1806	Comparative phylogenomics of <i>Trueperella pyogenes</i> reveals host-based distinction of strains. <i>Antonie Van Leeuwenhoek</i> , 0, , .	0.7	0
1807	Prediction of growth/no growth status of previously unseen bacterial strain using Raman spectroscopy and machine learning. <i>LWT - Food Science and Technology</i> , 2023, 174, 114449.	2.5	2
1808	Predictive Power of Long-Read Whole-Genome Sequencing for Rapid Diagnostics of Multidrug-Resistant <i>Brachyspira hyodysenteriae</i> Strains. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	5
1809	Detection of West Nile Virus Lineage 2 in Eastern Romania and First Identification of Sindbis Virus RNA in Mosquitoes Analyzed using High-Throughput Microfluidic Real-Time PCR. <i>Viruses</i> , 2023, 15, 186.	1.5	6
1810	Molecular evidence of <i>Borrelia</i> spp. in bats from C�rdoba Department, northwest Colombia. <i>Parasites and Vectors</i> , 2023, 16, .	1.0	3
1811	A Nuclear Export Signal in KHNYN Required for Its Antiviral Activity Evolved as ZAP Emerged in Tetrapods. <i>Journal of Virology</i> , 0, , .	1.5	0
1812	Longitudinal, Multi-Platform Metagenomics Yields a High-Quality Genomic Catalog and Guides an <i>In Vitro</i> Model for Cheese Communities. <i>MSystems</i> , 2023, 8, .	1.7	4
1813	Overexpression of the <i>Liriodendron chinense</i> CONSTANS gene in <i>Arabidopsis</i> causes earlier flowering under long-day conditions. <i>Plant Growth Regulation</i> , 0, , .	1.8	0
1814	Isolation and Characterization of Distinct Rotavirus A in Bat and Rodent Hosts. <i>Journal of Virology</i> , 0, , .	1.5	1
1815	First molecular characterization of <i>Escherichia coli</i> O157:H7 isolates from clinical samples in Paraguay using whole-genome sequencing. <i>Revista Argentina De Microbiologia</i> , 2023, 55, 111-119.	0.4	2
1816	A widespread family of phage-inducible chromosomal islands only steals bacteriophage tails to spread in nature. <i>Cell Host and Microbe</i> , 2023, 31, 69-82.e5.	5.1	9
1817	Phyllosphere Exudates Select for Distinct Microbiome Members in Sorghum Epicuticular Wax and Aerial Root Mucilage. <i>Phytobiomes Journal</i> , 2023, 7, 184-197.	1.4	5
1818	A calf with hind limb paralysis and dysstasia and a genome sequence analysis of an isolated <i>Clostridium perfringens</i> toxinotype E strain. <i>Journal of Veterinary Medical Science</i> , 2023, , .	0.3	0
1819	In silico analysis of NAC gene family in the mangrove plant <i>Avicennia marina</i> provides clues for adaptation to intertidal habitats. <i>Plant Molecular Biology</i> , 2023, 111, 393-413.	2.0	2

#	ARTICLE	IF	CITATIONS
1822	Evaluating the transmission feasibility of SARS-CoV-2 Omicron (B.1.1.529) variant to 143 mammalian hosts: insights from S protein RBD and host ACE2 interaction studies. <i>Functional and Integrative Genomics</i> , 2023, 23, .	1.4	5
1823	Emergence of plasmid-mediated colistin resistance <i>mcr-3.5</i> gene in <i>Citrobacter amalonaticus</i> and <i>Citrobacter sedlakii</i> isolated from healthy individual in Thailand. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	2
1824	Genomic study and lipidomic bioassay of <i>Leeuwenhoekiiella parthenopeia</i> : A novel rare biosphere marine bacterium that inhibits tumor cell viability. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
1825	Analyzing the genetic diversity and biotechnological potential of <i>Leuconostoc pseudomesenteroides</i> by comparative genomics. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
1826	Phylogenetic analysis and virulence characteristics of methicillin-resistant <i>Staphylococcus aureus</i> ST764-SCC <i>mec</i> II: an emerging hypervirulent clone ST764-t1084 in China. <i>Emerging Microbes and Infections</i> , 2023, 12, .	3.0	5
1827	Systematic characterization of <i>Brassica napus</i> UBC13 genes involved in DNA-damage response and K63-linked polyubiquitination. <i>BMC Plant Biology</i> , 2023, 23, .	1.6	1
1828	Comprehensive Analysis of Major Latex-Like Protein Family Genes in Cucumber (<i>Cucumis sativus</i> L.) and Their Potential Roles in Phytophthora Blight Resistance. <i>International Journal of Molecular Sciences</i> , 2023, 24, 784.	1.8	5
1829	Multiplex MinION sequencing suggests enteric adenovirus F41 genetic diversity comparable to pre-COVID-19 era. <i>Microbial Genomics</i> , 2023, 9, .	1.0	1
1830	The Histone Chaperone Network Is Highly Conserved in <i>Physarum polycephalum</i> . <i>International Journal of Molecular Sciences</i> , 2023, 24, 1051.	1.8	0
1831	Identification and taxonomy of <i>Streptomyces justiciae</i> strain RA-WS2: a novel setomimycin producing actinobacterium. <i>3 Biotech</i> , 2023, 13, .	1.1	1
1833	Adaptive Evolution of the OAS Gene Family Provides New Insights into the Antiviral Ability of Laurasiatherian Mammals. <i>Animals</i> , 2023, 13, 209.	1.0	2
1836	A chromosome-level genome assembly reveals that a bipartite gene cluster formed via an inverted duplication controls monoterpenoid biosynthesis in <i>Schizonepeta tenuifolia</i> . <i>Molecular Plant</i> , 2023, 16, 533-548.	3.9	7
1837	Whole-genome sequencing reveals genomic characterization of <i>Listeria monocytogenes</i> from food in China. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	10
1838	Prophage-Derived Regions in <i>Curtobacterium</i> Genomes: Good Things, Small Packages. <i>International Journal of Molecular Sciences</i> , 2023, 24, 1586.	1.8	2
1839	<i>Limosilactobacillus walteri</i> sp. nov., a novel probiotic antimicrobial lipopeptide-producing bacterium. <i>FEMS Microbiology Letters</i> , 2023, 370, .	0.7	4
1841	<i>Escherichia coli</i> O80 in Healthy Cattle: Absence of Shigatoxigenic and Enteropathogenic <i>E. coli</i> O80:H2 and (Phylo) Genomics of Non-Clonal Complex 165 <i>E. coli</i> O80. <i>Microorganisms</i> , 2023, 11, 230.	1.6	1
1842	Whole-genome sequencing of SARS-CoV-2 isolates from symptomatic and asymptomatic individuals in Tanzania. <i>Frontiers in Medicine</i> , 0, 9, .	1.2	1
1843	Genome-Wide Analysis of the Mads-Box Transcription Factor Family in <i>Solanum melongena</i> . <i>International Journal of Molecular Sciences</i> , 2023, 24, 826.	1.8	2

#	ARTICLE	IF	CITATIONS
1844	Diversity and prevalence of type VI secretion system effectors in clinical <i>Pseudomonas aeruginosa</i> isolates. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
1845	Enrichment of keystone fungal taxa after flue gas desulphurization gypsum application drives reclamation of the saline-sodic soil. <i>Land Degradation and Development</i> , 2023, 34, 2276-2287.	1.8	3
1846	Whole-Genome and Plasmid Comparative Analysis of <i>Campylobacter jejuni</i> from Human Patients in Toyama, Japan, from 2015 to 2019. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	5
1847	Genome-wide identification of HD-ZIP gene family and screening of genes related to prickly development in <i>Zanthoxylum armatum</i> . <i>Plant Genome</i> , 2023, 16, .	1.6	3
1848	Novel CaLB-like Lipase Found Using ProspectBIO, a Software for Genome-Based Bioprospection. <i>BioTech</i> , 2023, 12, 6.	1.3	0
1849	Phylogenomic Analysis Supports the Transfer of 20 Pathovars from <i>Xanthomonas campestris</i> into <i>Xanthomonas euvesicatoria</i> . <i>Taxonomy</i> , 2023, 3, 29-45.	0.4	3
1851	Genome-Wide Identification and Analysis of the Heat-Shock Protein Gene in <i>L. edodes</i> and Expression Pattern Analysis under Heat Shock. <i>Current Issues in Molecular Biology</i> , 2023, 45, 614-627.	1.0	4
1852	Characterization and biofouling potential analysis of two cyanobacterial strains isolated from Cape Verde and Morocco. <i>FEMS Microbiology Ecology</i> , 2023, 99, .	1.3	2
1853	CanB is a metabolic mediator of antibiotic resistance in <i>Neisseria gonorrhoeae</i> . <i>Nature Microbiology</i> , 2023, 8, 28-39.	5.9	3
1854	Identification of Kazal Inhibitor Scaffolds with Identical Canonical Binding Loops and Their Effects on Binding Properties. <i>Biochemistry</i> , 2023, 62, 535-542.	1.2	0
1855	The Mitochondrial Genome of the Globally Invasive Barnacle <i>Megabalanus coccopoma</i> Darwin 1854 (Crustacea: Balanomorpha): Rearrangement and Phylogenetic Consideration within Balanomorpha. <i>Diversity</i> , 2023, 15, 117.	0.7	1
1856	Genomic insights of mcr-1 harboring <i>Escherichia coli</i> by geographical region and a One-Health perspective. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
1857	Chloroplast inner envelope protein FtsH11 is involved in the adjustment of assembly of chloroplast ATP synthase under heat stress. <i>Plant, Cell and Environment</i> , 0, , .	2.8	4
1858	The compact Cas Φ (Cas12l) Φ -bracelet Φ ™ provides a unique structural platform for DNA manipulation. <i>Cell Research</i> , 2023, 33, 229-244.	5.7	15
1859	A high-quality genome compendium of the human gut microbiome of Inner Mongolians. <i>Nature Microbiology</i> , 2023, 8, 150-161.	5.9	11
1860	Genomic Diversity of the Rarely Observed Genotype of the <i>Mycobacterium tuberculosis</i> Central Asian (CAS) Lineage 3 from North Brazil. <i>Microorganisms</i> , 2023, 11, 132.	1.6	0
1861	Ammonium Uptake, Mediated by Ammonium Transporters, Mitigates Manganese Toxicity in Duckweed, <i>Spirodela polyrhiza</i> . <i>Plants</i> , 2023, 12, 208.	1.6	6
1863	<i>Aeromonas</i> spp. from hospital sewage act as a reservoir of genes resistant to last-line antibiotics. <i>Drug Resistance Updates</i> , 2023, 67, 100925.	6.5	6

#	ARTICLE	IF	CITATIONS
1864	The chromosome-scale genome assembly of the yellowtail clownfish <i>Amphiprion clarkii</i> provides insights into the melanistic pigmentation of anemonefish. <i>G3: Genes, Genomes, Genetics</i> , 2023, 13, .	0.8	4
1865	Machine learning enables prediction of metabolic system evolution in bacteria. <i>Science Advances</i> , 2023, 9, .	4.7	6
1866	Genomics of <i>Tenacibaculum</i> Species in British Columbia, Canada. <i>Pathogens</i> , 2023, 12, 101.	1.2	4
1867	Draft genome sequence of <i>Streptomyces</i> sp. KD18, isolated from industrial soil. <i>3 Biotech</i> , 2023, 13, .	1.1	1
1868	Genome-Wide Analysis of Aquaporin Gene Family in <i>Triticum turgidum</i> and Its Expression Profile in Response to Salt Stress. <i>Genes</i> , 2023, 14, 202.	1.0	24
1869	Molecular analyses of pseudoscorpions in a subterranean biodiversity hotspot reveal cryptic diversity and microendemism. <i>Scientific Reports</i> , 2023, 13, .	1.6	13
1871	Comparative genomics and molecular epidemiology of colistin-resistant <i>Acinetobacter baumannii</i> . <i>Computational and Structural Biotechnology Journal</i> , 2023, 21, 574-585.	1.9	10
1872	Exploring Evolutionary Relationships within Neodermata Using Putative Orthologous Groups of Proteins, with Emphasis on Peptidases. <i>Tropical Medicine and Infectious Disease</i> , 2023, 8, 59.	0.9	2
1873	A new and efficient enrichment method for metagenomic sequencing of Monkeypox virus. <i>BMC Genomics</i> , 2023, 24, .	1.2	2
1874	Nuclear Genome Sequence and Gene Expression of an Intracellular Fungal Endophyte Stimulating the Growth of Cranberry Plants. <i>Journal of Fungi (Basel, Switzerland)</i> , 2023, 9, 126.	1.5	2
1875	Anticodon table of the chloroplast genome and identification of putative quadruplet anticodons in chloroplast tRNAs. <i>Scientific Reports</i> , 2023, 13, .	1.6	0
1877	Resistance of QYm.nau-2D to wheat yellow mosaic virus was derived from an alien introgression into common wheat. <i>Theoretical and Applied Genetics</i> , 2023, 136, 1-16.	1.8	0
1878	<i>Terrisporobacter hibernicus</i> sp. nov., isolated from bovine faeces in Northern Ireland. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2023, 73, .	0.8	1
1879	HLA Class I Supertype Classification Based on Structural Similarity. <i>Journal of Immunology</i> , 2023, 210, 103-114.	0.4	3
1880	New fossils of Sphaeriusidae from mid-Cretaceous Burmese amber revealed by confocal microscopy (Coleoptera: Myxophaga). <i>Frontiers in Earth Science</i> , 0, 10, .	0.8	6
1881	Genetic diversity in early maturity Chinese and European elite soybeans: A comparative analysis. <i>Euphytica</i> , 2023, 219, .	0.6	5
1883	Gene loss and symbiont switching during adaptation to the deep sea in a globally distributed symbiosis. <i>ISME Journal</i> , 2023, 17, 453-466.	4.4	6
1884	Reconstruction of Plastid Proteomes of Apicomplexans and Close Relatives Reveals the Major Evolutionary Outcomes of Cryptic Plastids. <i>Molecular Biology and Evolution</i> , 2023, 40, .	3.5	11

#	ARTICLE	IF	CITATIONS
1885	Impacts of organic loading rate and hydraulic retention time on organics degradation, interspecies interactions and functional traits in thermophilic anaerobic co-digestion of food waste and sewage sludge. <i>Bioresource Technology</i> , 2023, 370, 128578.	4.8	3
1886	Identification of Portuguese traditional grapevines using molecular marker-based strategies. <i>Scientia Horticulturae</i> , 2023, 311, 111826.	1.7	6
1887	Genetic mapping and regional association analysis revealed a CYTOKININ RESPONSE FACTOR 10 gene controlling flowering time in <i>Brassica napus</i> L.. <i>Industrial Crops and Products</i> , 2023, 193, 116239.	2.5	3
1888	Squalene synthase in plants â€“ Functional intricacy and evolutionary divergence while retaining a core catalytic structure. <i>Plant Gene</i> , 2023, 33, 100403.	1.4	2
1889	Genomic survey of NPF and NRT2 transporter gene families in five inbred maize lines and their responses to pathogens infection. <i>Genomics</i> , 2023, 115, 110555.	1.3	1
1890	Molecular characterization of a chalcone synthase gene RhCHS from <i>Rhododendron</i> — <i>Hybridum</i> Hort. <i>Gene</i> , 2023, 857, 147176.	1.0	2
1891	Persistence and molecular epidemiology of blaNDM-positive Gram-negative bacteria in three broiler farms: A longitudinal study (2015â€“2021). <i>Journal of Hazardous Materials</i> , 2023, 446, 130725.	6.5	5
1892	Mitochondrial characteristics of the powdery mildew genus <i>Erysiphe</i> revealed an extraordinary evolution in protein-coding genes. <i>International Journal of Biological Macromolecules</i> , 2023, 230, 123153.	3.6	2
1893	Ultraconserved elements-based phylogenomic systematics of the snake superfamily Elapoidea, with the description of a new Afro-Asian family. <i>Molecular Phylogenetics and Evolution</i> , 2023, 180, 107700.	1.2	3
1894	Genome-resolved metagenomics reveals depth-related patterns of microbial community structure and functions in a highly stratified, AMD overlaying mine tailings. <i>Journal of Hazardous Materials</i> , 2023, 447, 130774.	6.5	4
1895	Identification of diverse papillomaviruses in captive black-and-white ruffed lemurs (<i>Varecia variegata</i>). <i>Archives of Virology</i> , 2023, 168, .	0.9	1
1896	The Fate of Duplicated Enzymes in Prokaryotes: The Case of Isomerases. <i>Journal of Molecular Evolution</i> , 2023, 91, 76-92.	0.8	1
1897	High-efficiency production of 5-hydroxyectoine using metabolically engineered <i>Corynebacterium glutamicum</i> . <i>Microbial Cell Factories</i> , 2022, 21, .	1.9	4
1898	Significant Differences in Planktonic Virus Communities Between â€œCellular Fractionâ€•(0.22â€“~â€“3.0â€“ μ m), and â€œViral Fractionâ€•(<â€“0.22â€“ μ m) in the Ocean. <i>Microbial Ecology</i> , 2023, 86, 825-842.	1.4	3
1899	Metagenomic analysis reveals unexplored diversity of archaeal virome in the human gut. <i>Nature Communications</i> , 2022, 13, .	5.8	14
1900	Marine Sponge and Octocoral-Associated Bacteria Show Versatile Secondary Metabolite Biosynthesis Potential and Antimicrobial Activities against Human Pathogens. <i>Marine Drugs</i> , 2023, 21, 34.	2.2	5
1901	Diversity of Bacterial Secondary Metabolite Biosynthetic Gene Clusters in Three Vietnamese Sponges. <i>Marine Drugs</i> , 2023, 21, 29.	2.2	2
1902	Antimicrobial Resistance and Genetic Diversity of <i>Pseudomonas aeruginosa</i> Strains Isolated from Equine and Other Veterinary Samples. <i>Pathogens</i> , 2023, 12, 64.	1.2	4

#	ARTICLE	IF	CITATIONS
1904	Immunogenetic basis of chicken's heterophil to lymphocyte ratio revealed by genome-wide indel variants analysis. <i>Journal of Integrative Agriculture</i> , 2023, 22, 2810-2823.	1.7	1
1905	Identification and analysis of odorant receptors expressed in the two main olfactory organs, antennae and palps, of <i>Schistocerca americana</i> . <i>Scientific Reports</i> , 2022, 12, .	1.6	1
1906	Ancient multiplicity in cyclic nucleotide-gated (CNG) cation channel repertoire was reduced in the ancestor of Olfactores before re-expansion by whole genome duplications in vertebrates. <i>PLoS ONE</i> , 2022, 17, e0279548.	1.1	0
1908	Diversity of Filamentous Fungi Associated with Dairy Processing Environments and Spoiled Products in Brazil. <i>Foods</i> , 2023, 12, 153.	1.9	1
1909	Functional Characterization of the Cystine-Rich-Receptor-like Kinases (CRKs) and Their Expression Response to <i>Sclerotinia sclerotiorum</i> and Abiotic Stresses in <i>Brassica napus</i> . <i>International Journal of Molecular Sciences</i> , 2023, 24, 511.	1.8	2
1910	A choline-releasing glycerophosphodiesterase essential for phosphatidylcholine biosynthesis and blood stage development in the malaria parasite. <i>ELife</i> , 0, 11, .	2.8	8
1911	213. Following the hidden footsteps of past human migrations via the goat genome. , 2022, , .		0
1912	Multiple variation patterns of terpene synthases in 26 maize genomes. <i>BMC Genomics</i> , 2023, 24, .	1.2	1
1913	A Maverick-like cluster in the genome of a pathogenic, moderately virulent strain of <i>Gallibacterium anatis</i> , ESV200, a transient biofilm producer. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	0
1914	Genome-wide identification of germin-like proteins in peanut (<i>Arachis hypogea</i> L.) and expression analysis under different abiotic stresses. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
1915	Mutational characterization of Omicron SARS-CoV-2 lineages circulating in Chhattisgarh, a central state of India. <i>Frontiers in Medicine</i> , 0, 9, .	1.2	4
1916	Enhancer-instructed epigenetic landscape and chromatin compartmentalization dictate a primary antibody repertoire protective against specific bacterial pathogens. <i>Nature Immunology</i> , 2023, 24, 320-336.	7.0	8
1917	A Molecular and Epidemiological Investigation of a Large SARS-CoV-2 Outbreak in a Long-Term Care Facility in Luxembourg, 2021. <i>Geriatrics (Switzerland)</i> , 2023, 8, 19.	0.6	1
1919	Evolutionary and genomic perspectives of brain aging and neurodegenerative diseases. <i>Progress in Brain Research</i> , 2023, , 165-215.	0.9	4
1920	EasyAmplicon: An easy-to-use, open-source, reproducible, and community-based pipeline for amplicon data analysis in microbiome research. , 2023, 2, .		36
1921	Biotin pathway in novel <i>Fodinibius salsisoli</i> sp. nov., isolated from hypersaline soils and reclassification of the genus <i>Aliifodinibius</i> as <i>Fodinibius</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	7
1922	Using a combination of short- and long-read sequencing to investigate the diversity in plasmid- and chromosomally encoded extended-spectrum beta-lactamases (ESBLs) in clinical <i>Shigella</i> and <i>Salmonella</i> isolates in Belgium. <i>Microbial Genomics</i> , 2023, 9, .	1.0	1
1923	Identification and transfer of a new Pm21 haplotype with high genetic diversity and a special molecular resistance mechanism. <i>Theoretical and Applied Genetics</i> , 2023, 136, .	1.8	1

#	ARTICLE	IF	CITATIONS
1924	A Diverged Transcriptional Network for Usage of Two Fe-S Cluster Biogenesis Machineries in the Delta-Proteobacterium <i>Myxococcus xanthus</i> . <i>MBio</i> , 2023, 14, .	1.8	1
1926	Genome-wide identification of the class III peroxidase gene family of sugarcane and its expression profiles under stresses. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	4
1927	Genome-wide identification and transcriptome-based expression pattern of chemosensory genes in two wild silkmoths, <i>Antheraea pernyi</i> and <i>Antheraea yamamai</i> . <i>Journal of Insects As Food and Feed</i> , 2023, 9, 823-840.	2.1	0
1928	Establishment of Tibetan-Sheep-Specific SNP Genetic Markers. <i>Agriculture (Switzerland)</i> , 2023, 13, 322.	1.4	0
1929	Split k-mer analysis compared to cgMLST and SNP-based core genome analysis for detecting transmission of vancomycin-resistant enterococci: results from routine outbreak analyses across different hospitals and hospitals networks in Berlin, Germany. <i>Microbial Genomics</i> , 2023, 9, .	1.0	1
1930	Hypersaline Lake Urmia: a potential hotspot for microbial genomic variation. <i>Scientific Reports</i> , 2023, 13, .	1.6	5
1931	Cryptic diversity in Zoraptera: <i>Latinozoros barberi</i> (Gurney, 1938) is a complex of at least three species (Zoraptera: Spiralizoridae). <i>PLoS ONE</i> , 2023, 18, e0280113.	1.1	1
1932	PyuARF16/33 Are Involved in the Regulation of Lignin Synthesis and Rapid Growth in <i>Populus yunnanensis</i> . <i>Genes</i> , 2023, 14, 278.	1.0	3
1933	Decoupling peptide binding from T cell receptor recognition with engineered chimeric MHC-I molecules. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	3
1935	ViralCC retrieves complete viral genomes and virus-host pairs from metagenomic Hi-C data. <i>Nature Communications</i> , 2023, 14, .	5.8	4
1936	Genome-Wide Identification and Expression Analysis of UBiA Family Genes Associated with Abiotic Stress in Sunflowers (<i>Helianthus annuus</i> L.). <i>International Journal of Molecular Sciences</i> , 2023, 24, 1883.	1.8	1
1937	Genomic epidemiology of <i>Campylobacter fetus</i> subsp. <i>venerealis</i> from Germany. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	2
1939	Antimicrobial resistance characteristics and phylogenetic relationships of pleuromutilin-resistant <i>Enterococcus</i> isolates from different environmental samples along a laying hen production chain. <i>Journal of Environmental Sciences</i> , 2024, 137, 195-205.	3.2	2
1941	Mpox, Caused by the MPXV of the Clade IIb Lineage, Goes Global. <i>Tropical Medicine and Infectious Disease</i> , 2023, 8, 76.	0.9	13
1942	Rare ribosomal RNA sequences from archaea stabilize the bacterial ribosome. <i>Nucleic Acids Research</i> , 2023, 51, 1880-1894.	6.5	5
1943	Parallel duplication and loss of aquaporin-encoding genes during the "out of the sea" transition as potential key drivers of animal terrestrialization. <i>Molecular Ecology</i> , 2023, 32, 2022-2040.	2.0	2
1944	Draft Genome Sequence of Seven Pigmented Strains of <i>Xanthomonas citri</i> pv. <i>anacardii</i> , the Causal Agent of Cashew Angular Spot. <i>Phytopathology</i> , 0, .	1.1	0
1945	Contribution of photic and aphotic N_2 fixation to production in an oligotrophic sea. <i>Limnology and Oceanography</i> , 2023, 68, 692-708.	1.6	2

#	ARTICLE	IF	CITATIONS
1946	Sphingomonas sediminicola Is an Endosymbiotic Bacterium Able to Induce the Formation of Root Nodules in Pea (<i>Pisum sativum</i> L.) and to Enhance Plant Biomass Production. <i>Microorganisms</i> , 2023, 11, 199.	1.6	9
1947	Uncovering a miltiradiene biosynthetic gene cluster in the Lamiaceae reveals a dynamic evolutionary trajectory. <i>Nature Communications</i> , 2023, 14, .	5.8	13
1948	Phylogeny and cross-regulation of the YjjM and LeuO transcription factors translated as multiple protein forms from one gene in <i>Escherichia coli</i> . <i>Mathematical Biology and Bioinformatics</i> , 2023, 18, 1-14.	0.1	0
1949	Genome-centered metagenomics illuminates adaptations of core members to a partial Nitritationâ€“Anammox bioreactor under periodic microaeration. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	2
1950	A Global Lexical Database (GLED) for Computational Historical Linguistics. <i>Journal of Open Humanities Data</i> , 2023, 9, .	0.1	0
1951	Prevalence and genetic characteristics of <i>fosB</i> -positive <i>Staphylococcus aureus</i> in duck farms in Guangdong, China in 2020. <i>Journal of Antimicrobial Chemotherapy</i> , 2023, 78, 802-809.	1.3	2
1952	Stabilization of membrane topologies by proteinaceous remorin scaffolds. <i>Nature Communications</i> , 2023, 14, .	5.8	6
1953	<i>Methanocaldococcus lauensis</i> sp. nov., a novel deep-sea hydrothermal vent hyperthermophilic methanogen. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2023, 73, .	0.8	0
1954	<i>Solicola gregarius</i> gen. nov., sp. nov., a soil actinobacterium isolated after enhanced cultivation with <i>Micrococcus luteus</i> culture supernatant. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2023, 73, .	0.8	2
1955	Whole-Genome Sequence of <i>Aeromonas</i> spp. Isolated from a Dairy Farm in Central Texas. <i>Microbiology Research</i> , 2023, 14, 161-176.	0.8	0
1956	Draft genome of <i>Raoultella planticola</i> , a high lead resistance bacterium from industrial wastewater. <i>AMB Express</i> , 2023, 13, .	1.4	3
1957	Genetic and Structural Diversity of Prokaryotic Ice-Binding Proteins from the Central Arctic Ocean. <i>Genes</i> , 2023, 14, 363.	1.0	5
1958	Importance of timely metadata curation to the global surveillance of genetic diversity. <i>Conservation Biology</i> , 2023, 37, .	2.4	7
1960	Evolution and emergence of primateâ€“specific interferon regulatory factor 9. <i>Journal of Medical Virology</i> , 2023, 95, .	2.5	3
1961	Population structure of the fireworm <i>Hermodice carunculata</i> in the wider Caribbean, Atlantic and Mediterranean Sea. <i>Journal of the Marine Biological Association of the United Kingdom</i> , 2023, 103, .	0.4	1
1962	Microbial Contributions to Iodide Enrichment in Deep Groundwater in the North China Plain. <i>Environmental Science & Technology</i> , 2023, 57, 2625-2635.	4.6	2
1963	The FANCCâ€“FANCEâ€“FANCF complex is evolutionarily conserved and regulates meiotic recombination. <i>Nucleic Acids Research</i> , 2023, 51, 2516-2528.	6.5	5
1964	Genomeâ€“wide diversity analysis suggests divergence among Upper Guinea and the Dahomey Gap populations of the <i>Sisr</i> berry (<i>Syn: miracle fruit</i>) plant (<i>Synsepalum dulcificum</i>) [Schumach.] Tj ETQq1 1 0.7&4314 rgBT /Over		

#	ARTICLE	IF	CITATIONS
1966	Pneumococcal capsule expression is controlled through a conserved, distal cis-regulatory element during infection. <i>PLoS Pathogens</i> , 2023, 19, e1011035.	2.1	4
1967	Genomic diversity and ecological distribution of marine <i>Pseudoalteromonas</i> phages. <i>Marine Life Science and Technology</i> , 2023, 5, 271-285.	1.8	4
1968	Pre-epidemic evolution of the MRSA USA300 clade and a molecular key for classification. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 13, .	1.8	1
1969	Exploring the Potential Molecular Mechanisms of Interactions between a Probiotic Consortium and Its Coral Host. <i>MSystems</i> , 2023, 8, .	1.7	4
1972	The genome of sheep ked (<i>Melophagus ovinus</i>) reveals potential mechanisms underlying reproduction and narrower ecological niches. <i>BMC Genomics</i> , 2023, 24, .	1.2	14
1973	Genome-Wide Identification of BTB Domain-Containing Gene Family in Grapevine (<i>Vitis vinifera</i> L.). <i>Agriculture (Switzerland)</i> , 2023, 13, 252.	1.4	1
1974	Canonical or noncanonical? Structural plasticity of serine protease-binding loops in <sc>Kunitz</sc> protease inhibitors. <i>Protein Science</i> , 2023, 32, .	3.1	2
1975	A global synthesis of microplastic contamination in wild fish species: Challenges for conservation, implications for sustainability of wild fish stocks and future directions. <i>Advances in Marine Biology</i> , 2023, , 159-200.	0.7	3
1976	Forensic characteristics and genetic substructure analysis of the Handan Han population, Northern China. <i>Annals of Human Biology</i> , 2023, 50, 123-125.	0.4	0
1977	Improvement and Validation of a Multi-Locus Variable Number of Tandem Repeats Analysis (MLVA8+) for <i>Klebsiella pneumoniae</i> , <i>Klebsiella variicola</i> , and <i>Klebsiella quasipneumoniae</i> . <i>Microorganisms</i> , 2023, 11, 444.	1.6	0
1978	Gene Structural Specificity and Expression of MADS-Box Gene Family in <i>Camellia chekiangoleosa</i> . <i>International Journal of Molecular Sciences</i> , 2023, 24, 3434.	1.8	4
1979	Berry species and crop management approaches affect species diversity and abundance of predatory mites (Acari: Phytoseiidae). <i>Experimental and Applied Acarology</i> , 2023, 89, 215-230.	0.7	0
1981	The Genus <i>Spinopygina</i> gen. nov. (Diptera, Sciaridae) from Western North America: Preliminary Molecular Phylogeny and Description of Seven New Species. <i>Insects</i> , 2023, 14, 173.	1.0	1
1982	Genetic monitoring on the world's first MSC eco-labeled common octopus (<i>O. vulgaris</i>) fishery in western Asturias, Spain. <i>Scientific Reports</i> , 2023, 13, .	1.6	1
1983	Comparative functional analysis of macrophage phagocytosis in Dagu chickens and Wenchang chickens. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	0
1984	Phylogenomic analyses across land plants reveals motifs and coexpression patterns useful for functional prediction in the BAHD acyltransferase family. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	1
1985	Genomic Insights into the Origin of a Thermotolerant Tomato Line and Identification of Candidate Genes for Heat Stress. <i>Genes</i> , 2023, 14, 535.	1.0	1
1987	Characterisation of the complete mitochondrial genome of <i>Taraxacum mongolicum</i> revealed five repeat-mediated recombinations. <i>Plant Cell Reports</i> , 2023, 42, 775-789.	2.8	13

#	ARTICLE	IF	CITATIONS
1989	1700029115Rik orchestrates the biosynthesis of acrosomal membrane proteins required for sperm-egg interaction. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	3.3	3
1990	Clonal relatedness of coagulase-positive staphylococci among healthy dogs and dog-owners in Spain. Detection of multidrug-resistant-MSSA-CC398 and novel linezolid-resistant-MRSA-CC5. Frontiers in Microbiology, 0, 14, .	1.5	6
1991	Discovery of the Streamlined Haloarchaeon <i>Haloarutilus salinus</i> , Comprising a New Order Widespread in Hypersaline Environments across the World. MSystems, 2023, 8, .	1.7	5
1992	A new species of Sedum (Crassulaceae) from Mount Danxia in Guangdong, China. PhytoKeys, 0, 221, 117-129.	0.4	1
1993	Genome-wide analysis of the GLP gene family and overexpression of GLP1-5 to promote lignin accumulation during early somatic embryo development in <i>Dimocarpus longan</i> . BMC Genomics, 2023, 24, .	1.2	5
1994	Those Nematode-Trapping Fungi That are not Everywhere: Hints Towards Soil Microbial Biogeography. Journal of Microbiology, 0, , .	1.3	1
1996	Genome-wide identification and expression profiling reveal the regulatory role of U-box E3 ubiquitin ligase genes in strawberry fruit ripening and abiotic stresses resistance. Frontiers in Plant Science, 0, 14, .	1.7	2
1998	Genomic insights into the genetic basis of cotton breeding in China. Molecular Plant, 2023, 16, 662-677.	3.9	8
2000	Enterococcal bacteriophage: A survey of the tail associated lysin landscape. Virus Research, 2023, 327, 199073.	1.1	0
2001	Novel Clinical mNGS-Based Machine Learning Model for Rapid Antimicrobial Susceptibility Testing of <i>Acinetobacter baumannii</i> . Journal of Clinical Microbiology, 2023, 61, .	1.8	4
2004	<i>arfA</i> antisense RNA regulates MscL excretory activity. Life Science Alliance, 2023, 6, e202301954.	1.3	0
2005	Structural variation (SV)-based pan-genome and GWAS reveal the impacts of SVs on the speciation and diversification of allotetraploid cottons. Molecular Plant, 2023, 16, 678-693.	3.9	14
2006	Genomes of the human filarial parasites <i>Mansonella perstans</i> and <i>Mansonella ozzardi</i> . Frontiers in Tropical Diseases, 0, 4, .	0.5	8
2007	Large Multicountry Outbreak of Invasive Listeriosis by a <i>Listeria monocytogenes</i> ST394 Clone Linked to Smoked Rainbow Trout, 2020 to 2021. Microbiology Spectrum, 2023, 11, .	1.2	1
2008	Interactions of TonB-dependent transporter FoxA with siderophores and antibiotics that affect binding, uptake, and signal transduction. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	3.3	2
2009	Maternal Rumen Bacteriota Shapes the Offspring Rumen Bacteriota, Affecting the Development of Young Ruminants. Microbiology Spectrum, 2023, 11, .	1.2	1
2012	COVID-19-Associated Pulmonary Aspergillosis Isolates Are Genomically Diverse but Similar to Each Other in Their Responses to Infection-Relevant Stresses. Microbiology Spectrum, 2023, 11, .	1.2	4
2013	Identification of two insecticide resistance markers in Ethiopian <i>Anopheles stephensi</i> mosquitoes using a multiplex amplicon sequencing assay. Scientific Reports, 2023, 13, .	1.6	4

#	ARTICLE	IF	CITATIONS
2014	Substrate specificity and transglycosylation capacity of α -L-fucosidases across GH29 assessed by bioinformatics-assisted selection of functional diversity. <i>Glycobiology</i> , 2023, 33, 396-410.	1.3	3
2015	Coevolutionary signals in metabotropic glutamate receptors capture residue contacts and long-range functional interactions. <i>Journal of Biological Chemistry</i> , 2023, 299, 103030.	1.6	2
2016	Global population structure and genomic surveillance framework of carbapenem-resistant <i>Salmonella enterica</i> . <i>Drug Resistance Updates</i> , 2023, 68, 100953.	6.5	9
2017	Small Auxin Up RNA (SAUR) gene family identification and functional genes exploration during the floral organ and fruit developmental stages in pineapple (<i>Ananas comosus</i> L.) and its response to salinity and drought stresses. <i>International Journal of Biological Macromolecules</i> , 2023, 237, 124061.	3.6	4
2018	Delineation of the complex microbial nitrogen-transformation network in an anammox-driven full-scale wastewater treatment plant. <i>Water Research</i> , 2023, 235, 119799.	5.3	9
2019	Foremost report of the whole genome of <i>Spirabilibacterium mucosae</i> from India and comparative genomics of the novel genus <i>Spirabilibacterium</i> . <i>Gene</i> , 2023, 867, 147359.	1.0	0
2020	A novel lytic bacteriophage against colistin-resistant <i>Escherichia coli</i> isolated from different animals. <i>Virus Research</i> , 2023, 329, 199090.	1.1	0
2021	Phylogenomics reveals insights into the functional evolution of the genus <i>Agrobacterium</i> and enables the description of <i>Agrobacterium divergens</i> sp. nov. <i>Systematic and Applied Microbiology</i> , 2023, 46, 126420.	1.2	2
2022	Seed treatment with plant-defense elicitors decreases the abundance of ammonia oxidizers associated with winter wheat roots. <i>Soil Biology and Biochemistry</i> , 2023, 180, 109016.	4.2	1
2023	Characterization of chitinases from the GH18 gene family in the myxomycete <i>Physarum polycephalum</i> . <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2023, 1867, 130343.	1.1	2
2024	Determination of <i>Shigella</i> spp. via label-free SERS spectra coupled with deep learning. <i>Microchemical Journal</i> , 2023, 189, 108539.	2.3	6
2025	QSP: An open sequence database for quorum sensing related gene analysis with an automatic annotation pipeline. <i>Water Research</i> , 2023, 235, 119814.	5.3	6
2026	CRISPR-Cas phage defense systems and prophages in <i>Candidatus Accumulibacter</i> . <i>Water Research</i> , 2023, 235, 119906.	5.3	6
2027	First report of enterotoxigenic <i>Staphylococcus argenteus</i> as a foodborne pathogen. <i>International Journal of Food Microbiology</i> , 2023, 394, 110182.	2.1	0
2028	The first evidence of blaCTX-M-55, QnrVC5, and novel insight into the genome of MDR <i>Vibrio vulnificus</i> isolated from Asian sea bass (<i>Lateolabrax niloticus</i>) identified by resistome analysis. <i>Aquaculture</i> , 2023, 571, 739500.	1.7	7
2029	One global disseminated 193 kb high-risk hybrid plasmid harboring tet(X4), mcr or blaNDM threatening public health. <i>Science of the Total Environment</i> , 2023, 876, 162807.	3.9	5
2030	Isolation and characterization of the new isolated bacteriophage YZU-L1 against <i>Citrobacter freundii</i> from a package-swelling of meat product. <i>Microbial Pathogenesis</i> , 2023, 179, 106098.	1.3	1
2031	Whole genome analysis of Gram-negative bacteria using the EPISEQ CS application and other bioinformatic platforms. <i>Journal of Global Antimicrobial Resistance</i> , 2023, 33, 61-71.	0.9	0

#	ARTICLE	IF	CITATIONS
2032	Cost-effective hybrid long-short read assembly delineates alternative GC-rich <i>Streptomyces</i> hosts for natural product discovery. <i>Synthetic and Systems Biotechnology</i> , 2023, 8, 253-261.	1.8	0
2033	Association of resistance to quaternary ammonium compounds and organic acids with genetic markers and their relationship to <i>Escherichia coli</i> serogroup. <i>Food Microbiology</i> , 2023, 113, 104267.	2.1	4
2034	A new deep-sea water conger eel of the genus <i>Rhynchoconger</i> (<i>Anguilliformes</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 667 Td 2023, 102, 1245-1252.	0.7	0
2035	Emergence of terpene chemical communication in insects: Evolutionary recruitment of isoprenoid metabolism. <i>Protein Science</i> , 2023, 32, .	3.1	4
2036	Genomic characterization of endemic diarrheagenic <i>Escherichia coli</i> and <i>Escherichia albertii</i> from infants with diarrhea in Vietnam. <i>PLoS Neglected Tropical Diseases</i> , 2023, 17, e0011259.	1.3	1
2037	Dynamic change of the carotenoid metabolic pathway profile during oolong tea processing with supplementary LED light. <i>Food Research International</i> , 2023, 169, 112839.	2.9	4
2040	Genomic characterization of Lumpy Skin Disease virus (LSDV) from India: Circulation of Kenyan-like LSDV strains with unique kelch-like proteins. <i>Acta Tropica</i> , 2023, 241, 106838.	0.9	4
2041	Chromosome-level genome assembly and population genomic resource to accelerate orphan crop lablab breeding. <i>Nature Communications</i> , 2023, 14, .	5.8	10
2042	Shisa reduces the sensitivity of homomeric RDL channel to GABA in the two-spotted spider mite, <i>Tetranychus urticae</i> Koch. <i>Pesticide Biochemistry and Physiology</i> , 2023, 192, 105414.	1.6	0
2043	Tracking the Source of Human Q Fever from a Southern French Village: Sentinel Animals and Environmental Reservoir. <i>Microorganisms</i> , 2023, 11, 1016.	1.6	1
2044	Metagenomic surveillance of antibiotic resistome in influent and effluent of wastewater treatment plants located on the Qinghai-Tibetan Plateau. <i>Science of the Total Environment</i> , 2023, 870, 162031.	3.9	8
2045	WGS analysis of two <i>Staphylococcus aureus</i> bacteriophages from sewage in China provides insights into the genetic feature of highly efficient lytic phages. <i>Microbiological Research</i> , 2023, 271, 127369.	2.5	4
2046	Identification and characterization of ABC proteins in an important rice insect pest, <i>Cnaphalocrocis medinalis</i> unveil their response to Cry1C toxin. <i>International Journal of Biological Macromolecules</i> , 2023, 237, 123949.	3.6	1
2047	The distinct plastisphere microbiome in the terrestrial-marine ecotone is a reservoir for putative degraders of petroleum-based polymers. <i>Journal of Hazardous Materials</i> , 2023, 453, 131399.	6.5	8
2054	Identification and Characterization of the HERV-K (HML-8) Group of Human Endogenous Retroviruses in the Genome. <i>AIDS Research and Human Retroviruses</i> , 2023, 39, 176-194.	0.5	1
2055	Epidemiology of Infectious Bursal Disease Virus in Poland during 2016–2022. <i>Viruses</i> , 2023, 15, 289.	1.5	0
2056	Unintended consequences: Renaming botulinum neurotoxin-producing species of clostridium and related species. <i>Toxicon</i> , 2023, 224, 107036.	0.8	0
2057	Emergence of <i>Vibrio parahaemolyticus</i> serotype O10:K4 in Thailand. <i>Microbiology and Immunology</i> , 2023, 67, 201-203.	0.7	3

#	ARTICLE	IF	CITATIONS
2058	Genome-Wide Analyses of Thaumatin-like Protein Family Genes Reveal the Involvement in the Response to Low-Temperature Stress in <i>Ammopiptanthus nanus</i> . <i>International Journal of Molecular Sciences</i> , 2023, 24, 2209.	1.8	8
2059	Evaluating the hologenome concept by analyzing the root-endosphere microbiota of chimeric plants. <i>IScience</i> , 2023, 26, 106031.	1.9	2
2060	Genome-wide characterization, phylogenetic and expression analysis of Histone gene family in cucumber (<i>Cucumis sativus</i> L.). <i>International Journal of Biological Macromolecules</i> , 2023, 230, 123401.	3.6	3
2061	Mining metatranscriptomes reveals a vast world of viroid-like circular RNAs. <i>Cell</i> , 2023, 186, 646-661.e4.	13.5	23
2062	Phylogenetic analysis of the MCL1 BH3 binding groove and rBH3 sequence motifs in the p53 and INK4 protein families. <i>PLoS ONE</i> , 2023, 18, e0277726.	1.1	1
2064	Mechanistic and evolutionary insights into alkaline phosphatase superfamily through structure-function studies on <i>Sphingomonas</i> alkaline phosphatase. <i>Archives of Biochemistry and Biophysics</i> , 2023, 736, 109524.	1.4	0
2066	Rapid emergence of extensively drug-resistant <i>Shigella sonnei</i> in France. <i>Nature Communications</i> , 2023, 14, .	5.8	14
2068	Impact of Starch Binding Domain Fusion on Activities and Starch Product Structure of 4- α -Glucanotransferase. <i>Molecules</i> , 2023, 28, 1320.	1.7	5
2069	High abundance of hydrocarbon-degrading <i>Alcanivorax</i> in plumes of hydrothermally active volcanoes in the South Pacific Ocean. <i>ISME Journal</i> , 2023, 17, 600-610.	4.4	5
2070	Genomic Analysis of the Rare Slightly Halophilic Myxobacterium <i>Paraliomyxa miuraensis</i> SMH-27-4, the Producer of the Antibiotic Miuraenamides. <i>Microorganisms</i> , 2023, 11, 371.	1.6	3
2072	Presence and Persistence of <i>Listeria monocytogenes</i> in the Danish Ready-to-Eat Food Production Environment. <i>Hygiene</i> , 2023, 3, 18-32.	0.5	3
2073	<i>Naegleria</i> genus pangenome reveals new structural and functional insights into the versatility of these free-living amoebae. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
2075	Comparative Genomic Analysis Reveals the Functional Traits and Safety Status of Lactic Acid Bacteria Retrieved from Artisanal Cheeses and Raw Sheep Milk. <i>Foods</i> , 2023, 12, 599.	1.9	5
2076	Phylogeny and adaptive evolution of subgenus <i>Rhizirideum</i> (Amaryllidaceae, <i>Allium</i>) based on plastid genomes. <i>BMC Plant Biology</i> , 2023, 23, .	1.6	5
2077	Comparative genomic study of the <i>Penicillium</i> genus elucidates a diverse pangenome and 15 lateral gene transfer events. <i>IMA Fungus</i> , 2023, 14, .	1.7	7
2080	<i>Cupriavidus pinatubonensis</i> JMP134 Alleviates Sulfane Sulfur Toxicity after the Loss of Sulfane Dehydrogenase through Oxidation by Persulfide Dioxygenase and Hydrogen Sulfide Release. <i>Metabolites</i> , 2023, 13, 218.	1.3	0
2081	Diversity of Surface Fibril Patterns in Mimivirus Isolates. <i>Journal of Virology</i> , 2023, 97, .	1.5	2
2082	Two genes, ANS and UFGT2, from <i>Vaccinium</i> spp. are key steps for modulating anthocyanin production. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	8

#	ARTICLE	IF	CITATIONS
2084	Genomic epidemiology of <i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> isolates from Canadian dairy herds provides evidence for multiple infection events. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	6
2085	Ribosomes lacking bS21 gain function to regulate protein synthesis in <i>Flavobacterium johnsoniae</i> . <i>Nucleic Acids Research</i> , 2023, 51, 1927-1942.	6.5	5
2087	Pyridoxal 5-phosphate synthesis and salvage in Bacteria and Archaea: predicting pathway variant distributions and holes. <i>Microbial Genomics</i> , 2023, 9, .	1.0	2
2088	The Complete Mitochondrial Genome of <i>Torix tukubana</i> (Annelida: Hirudinea: Glossiphoniidae). <i>Genes</i> , 2023, 14, 388.	1.0	2
2089	An immune-suppressing protein in human endogenous retroviruses. <i>Bioinformatics Advances</i> , 2023, 3, .	0.9	0
2090	CD99 and the Chicken Alloantigen D Blood System. <i>Genes</i> , 2023, 14, 402.	1.0	1
2091	Centromere repositioning and shifts in wheat evolution. <i>Plant Communications</i> , 2023, 4, 100556.	3.6	16
2092	Mycological research and citizen science: morphological features and DNA sequencing reveal seven new species records for the Greek mycobiota. <i>Plant Biosystems</i> , 2023, 157, 640-657.	0.8	1
2095	Aim18p and Aim46p are chalcone isomerase domain-containing mitochondrial hemoproteins in <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2023, 299, 102981.	1.6	1
2096	Molecular phylogeny reveals distinct evolutionary lineages of the banded krait, <i>Bungarus fasciatus</i> (Squamata, Elapidae) in Asia. <i>Scientific Reports</i> , 2023, 13, .	1.6	3
2098	CrAssphage May Be Viable Markers of Contamination in Pristine and Contaminated River Water. <i>MSystems</i> , 2023, 8, .	1.7	2
2099	Comparative Genomic Study of <i>Streptococcus anginosus</i> Reveals Distinct Group of Urinary Strains. <i>MSphere</i> , 2023, 8, .	1.3	2
2100	Successful Whole Genome Nanopore Sequencing of Swine Influenza A Virus (swIAV) Directly from Oral Fluids Collected in Polish Pig Herds. <i>Viruses</i> , 2023, 15, 435.	1.5	2
2101	Plastome Phylogeny and Taxonomy of <i>Cinnamomum guizhouense</i> (Lauraceae). <i>Forests</i> , 2023, 14, 310.	0.9	0
2102	Multifaceted Target Specificity Analysis as a Tool in Antimicrobial Drug Development: Type III Pantothenate Kinases as a Case Study. <i>ChemMedChem</i> , 2023, 18, .	1.6	1
2104	A Genomic Survey of the Natural Product Biosynthetic Potential of Actinomycetes Isolated from New Zealand Lichens. <i>MSystems</i> , 2023, 8, .	1.7	2
2106	Prevalence of Potential Pathogenic and Antimicrobial Resistant <i>Escherichia coli</i> in Danish Broilers. <i>Antibiotics</i> , 2023, 12, 344.	1.5	1
2107	<i>Corynebacterium megadyptis</i> sp. nov. with two subspecies, <i>Corynebacterium megadyptis</i> subsp. <i>megadyptis</i> subsp. nov. and <i>Corynebacterium megadyptis</i> subsp. <i>dunedinense</i> subsp. nov. isolated from yellow-eyed penguins. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2023, 73, .	0.8	3

#	ARTICLE	IF	CITATIONS
2108	Distinct Molecular Patterns of Two-Component Signal Transduction Systems in Thermophilic Cyanobacteria as Revealed by Genomic Identification. <i>Biology</i> , 2023, 12, 271.	1.3	3
2109	HGTphlyoDetect: facilitating the identification and phylogenetic analysis of horizontal gene transfer. <i>Briefings in Bioinformatics</i> , 2023, 24, .	3.2	2
2111	Flux regulation through glycolysis and respiration is balanced by inositol pyrophosphates in yeast. <i>Cell</i> , 2023, 186, 748-763.e15.	13.5	14
2114	Bacterial volatile organic compounds (VOCs) promote growth and induce metabolic changes in rice. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	10
2115	Population genomic analysis reveals the emergence of high-risk carbapenem-resistant <i>Escherichia coli</i> among ICU patients in China. <i>Journal of Infection</i> , 2023, 86, 316-328.	1.7	7
2117	A new species of <i>Caulophacus</i> (Hexactinellida: Lyssacinosida: Rossellidae) from the western Pacific Ocean, with new insights into the mitochondrial genome characteristics of hexactinellid sponges. <i>Frontiers in Marine Science</i> , 0, 10, .	1.2	1
2118	Uncovering a Complex Virome Associated with the Cacao Pathogens <i>Ceratocystis cacaofunesta</i> and <i>Ceratocystis fimbriata</i> . <i>Pathogens</i> , 2023, 12, 287.	1.2	3
2120	Molecular phylogenetics of the sucking louse genus <i>Lemurpediculus</i> (Insecta: Phthiraptera), ectoparasites of lemurs, with descriptions of three new species. <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2023, 20, 138-152.	0.6	2
2121	Genome and haplotype provide insights into the population differentiation and breeding improvement of <i>Gossypium barbadense</i> . <i>Journal of Advanced Research</i> , 2023, 54, 15-27.	4.4	2
2122	Odorant-Binding and Chemosensory Proteins in <i>Anthonomus eugenii</i> (Coleoptera: Curculionidae) and Their Tissue Expression. <i>International Journal of Molecular Sciences</i> , 2023, 24, 3406.	1.8	0
2124	Molecular mechanism of Rubisco activase: Dynamic assembly and Rubisco remodeling. <i>Frontiers in Molecular Biosciences</i> , 0, 10, .	1.6	4
2125	The RNase III enzyme <i>Dicer1</i> is essential for larval development in <i>Bombyx mori</i> . <i>Insect Science</i> , 2023, 30, 1309-1324.	1.5	5
2127	Shuffled ATG8 interacting motifs form an ancestral bridge between UFMylation and autophagy. <i>EMBO Journal</i> , 2023, 42, .	3.5	11
2128	On the mysterious Seychellois endemic spider genus <i>Cenemus</i> (Araneae, Pholcidae). <i>Arthropod Systematics and Phylogeny</i> , 0, 81, 179-200.	5.5	3
2129	DNA signaturing derived from the internal transcribed spacer 2 (ITS2): a novel tool for identifying <i>Desmodesmus</i> species (Scenedesmaceae, Chlorophyta). <i>Fottea</i> , 2023, 23, 1-7.	0.4	1
2131	Diverse DNA virus genomes identified in fecal samples of Mexican free-tailed bats (<i>Tadarida</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 TFS	1.1	2
2133	Genome-wide identification and analysis of the evolution and expression pattern of the <i>HVA22</i> gene family in three wild species of tomatoes. <i>PeerJ</i> , 0, 11, e14844.	0.9	1
2134	Genomic analysis of the international high-risk clonal lineage <i>Klebsiella pneumoniae</i> sequence type 395. <i>Genome Medicine</i> , 2023, 15, .	3.6	13

#	ARTICLE	IF	CITATIONS
2135	Complete Genome Sequence of the Ice-Nucleation-Active <i>Pseudomonas syringae</i> Strain MUP17, Isolated from the Frost-Damaged Barley Cultivar <i>Hordeum vulgare</i> cv. La Trobe. <i>Microbiology Resource Announcements</i> , 2023, 12, .	0.3	0
2136	Antioxidant enzymes that target hydrogen peroxide are conserved across the animal kingdom, from sponges to mammals. <i>Scientific Reports</i> , 2023, 13, .	1.6	2
2137	Whole-genome sequencing-based analyses of drug-resistant <i>Mycobacterium tuberculosis</i> from Taiwan. <i>Scientific Reports</i> , 2023, 13, .	1.6	5
2138	Complete Genome Sequence of the Ice-Nucleation-Active <i>Pseudomonas syringae</i> Strain MUP20, Isolated from Frost-Damaged Wheat (<i>Triticum aestivum</i> cv. Scepter) in Western Australia. <i>Microbiology Resource Announcements</i> , 2023, 12, .	0.3	0
2140	Complete Genome Sequence of the Ice-Nucleation-Active <i>Pseudomonas syringae</i> pv. <i>lisi</i> Isolate MUP32, Isolated from Frost-Damaged Pea (<i>Pisum sativum</i> subsp. <i>arvense</i> cv. Dundale) in New South Wales. <i>Microbiology Resource Announcements</i> , 2023, 12, .	0.3	0
2141	Expansion of Kuravirus-like Phage Sequences within the Past Decade, including <i>Escherichia</i> Phage YF01 from Japan, Prompt the Creation of Three New Genera. <i>Viruses</i> , 2023, 15, 506.	1.5	4
2142	A 10-year microbiological study of <i>Pseudomonas aeruginosa</i> strains revealed the circulation of populations resistant to both carbapenems and quaternary ammonium compounds. <i>Scientific Reports</i> , 2023, 13, .	1.6	7
2143	A conserved zinc-binding site in <i>Acinetobacter baumannii</i> PBP2 required for elongasome-directed bacterial cell shape. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	3.3	3
2144	Morphological and genomic characteristics of two novel actinomycetes, <i>Ornithinimicrobium sufpigmenti</i> sp. nov. and <i>Ornithinimicrobium faecis</i> sp. nov. isolated from bat faeces (<i>Rousettus</i>) Tj ETQq0 0 0 rgBTi/Overlock010 Tf 50 4		
2145	<i>Streptococcus suis</i> outbreak caused by an emerging zoonotic strain with acquired multi-drug resistance in Thailand. <i>Microbial Genomics</i> , 2023, 9, .	1.0	7
2146	Monthly dynamics of microbial communities and variation of nitrogen-cycling genes in an industrial-scale expanded granular sludge bed reactor. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
2150	Genome-Wide Identification and Expression Analysis of the Ammonium Transporter Family Genes in Soybean. <i>International Journal of Molecular Sciences</i> , 2023, 24, 3991.	1.8	3
2151	Emergence and Evolution of OXA-23-Producing ST46Pas-ST462Oxf-KL28-OCL1 Carbapenem-Resistant <i>Acinetobacter baumannii</i> Mediated by a Novel ISAbal-Based Tn7534 Transposon. <i>Antibiotics</i> , 2023, 12, 396.	1.5	0
2152	The genetic diversity, replication, and transmission of 2009 pandemic H1N1 viruses in China. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	0
2153	Using PhyloSuite for molecular phylogeny and tree-based analyses. , 2023, 2, .		46
2154	Transcriptome Identification of R2R3-MYB Gene Family Members in <i>Pinus massoniana</i> and PmMYB4 Response to Drought Stress. <i>Forests</i> , 2023, 14, 410.	0.9	6
2155	Humpback spiders from Ecuador: relationships, prosoma inflation and genital asymmetry (Araneae:) Tj ETQq0 0 0 rgBTi/Overlock0	0.5	0
2156	Emergence, phylogeography, and adaptive evolution of mpox virus. <i>New Microbes and New Infections</i> , 2023, 52, 101102.	0.8	7

#	ARTICLE	IF	CITATIONS
2157	Identification and Genetic Characterization of MERS-Related Coronavirus Isolated from <i>Nathusiusâ€™™</i> Pipistrelle (<i>Pipistrellus nathusii</i>) near Zvenigorod (Moscow Region, Russia). <i>International Journal of Environmental Research and Public Health</i> , 2023, 20, 3702.	1.2	5
2158	Comparison of in vitro activities of newer triazoles and classic antifungal agents against dermatophyte species isolated from Iranian University Hospitals: a multi-central study. <i>Annals of Clinical Microbiology and Antimicrobials</i> , 2023, 22, .	1.7	1
2159	Polymorphism of Avirulence Genes and Adaptation to <i>Brassica</i> Resistance Genes Is Gene-Dependent in the Phytopathogenic Fungus <i>Leptosphaeria maculans</i> . <i>Phytopathology</i> , 2023, 113, 1222-1232.	1.1	4
2160	Whole-Genome Comparison Reveals Structural Variations behind Heading Leaf Trait in <i>Brassica oleracea</i> . <i>International Journal of Molecular Sciences</i> , 2023, 24, 4063.	1.8	3
2161	Global Analyses of Multi-Locus Sequence Typing Data Reveal Geographic Differentiation, Hybridization, and Recombination in the <i>Cryptococcus Agattii</i> Species Complex. <i>Journal of Fungi (Basel, Switzerland)</i> , 2023, 9, 276.	1.5	3
2162	Genomic Evidence for Direct Transmission of mecC-MRSA between a Horse and Its Veterinarian. <i>Antibiotics</i> , 2023, 12, 408.	1.5	5
2163	Digestive enzymes and sphingomyelinase D in spiders without venom (Uloboridae). <i>Scientific Reports</i> , 2023, 13, .	1.6	5
2164	Gene based markers improve precision of genome-wide association studies and accuracy of genomic predictions in rice breeding. <i>Heredity</i> , 2023, 130, 335-345.	1.2	4
2165	MitoSNARE Assembly and Disassembly Factors Regulate Basal Autophagy and Aging in <i>C. elegans</i> . <i>International Journal of Molecular Sciences</i> , 2023, 24, 4230.	1.8	0
2166	High Prevalence of Livestock-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> in Hungarian Pig Farms and Genomic Evidence for the Spillover of the Pathogen to Humans. <i>Transboundary and Emerging Diseases</i> , 2023, 2023, 1-13.	1.3	1
2167	Genomic Epidemiological Analysis of Antimicrobial-Resistant Bacteria with Nanopore Sequencing. <i>Methods in Molecular Biology</i> , 2023, , 227-246.	0.4	0
2168	Genomic and clinical characteristics of carbapenem-resistant <i>Enterobacter cloacae</i> complex isolates collected in a Chinese tertiary hospital during 2013â€™2021. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	3
2169	Phylogeography of <i>Ramalina</i> (Lichenized Fungi, Ascomycota) in the Mediterranean Basin, Europe, and Macaronesia. <i>Diversity</i> , 2023, 15, 310.	0.7	1
2170	Whole-genome-based characterization of <i>Campylobacter jejuni</i> from human patients with gastroenteritis collected over an 18 year period reveals increasing prevalence of antimicrobial resistance. <i>Microbial Genomics</i> , 2023, 9, .	1.0	1
2171	Bacterial origins of thymidylate metabolism in Asgard archaea and Eukarya. <i>Nature Communications</i> , 2023, 14, .	5.8	1
2172	Conservation of land plant-specific receptor-like cytoplasmic kinase subfamily XI possessing a unique kinase insert domain. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	0
2173	Whole-Genome Sequences of a <i>Lactobacillus melliventris</i> Strain and Its <i>Myovirus</i> Temperate Phage, phiBH004, Isolated from the Digestive Tract of <i>Apis mellifera</i> in Switzerland. <i>Microbiology Resource Announcements</i> , 2023, 12, .	0.3	0
2174	Effectiveness of BNT162b2 and ChAdOx1 against SARS-CoV-2 household transmission: a prospective cohort study in England. <i>Wellcome Open Research</i> , 0, 8, 96.	0.9	0

#	ARTICLE	IF	CITATIONS
2175	Giant proteins in a giant cell: Molecular basis of ultrafast Ca ²⁺ -dependent cell contraction. <i>Science Advances</i> , 2023, 9, .	4.7	4
2176	Importance of mobile genetic element immunity in numerically abundant <i>Trichodesmium</i> clades. <i>ISME Communications</i> , 2023, 3, .	1.7	4
2177	Monkeypox virus (MPXV) genomics: A mutational and phylogenomic analyses of B.1 lineages. <i>Travel Medicine and Infectious Disease</i> , 2023, 52, 102551.	1.5	18
2179	<i>Gastrodia bawanglingensis</i> (Orchidaceae, Epidendroideae), a new species from Hainan Island, China. <i>PhytoKeys</i> , 0, 220, 39-50.	0.4	0
2180	DNA Barcoding of Moon Jellyfish (Cnidaria, Scyphozoa, Ulmaridae, Aurelia): Two Cryptic Species from the Azores (NE Atlantic, Macaronesia), and Evaluation of the Non-Indigenous Species (NIS). <i>Diversity</i> , 2023, 15, 323.	0.7	1
2182	A Global Survey of Hypervirulent <i>Aeromonas hydrophila</i> (vAh) Identified vAh Strains in the Lower Mekong River Basin and Diverse Opportunistic Pathogens from Farmed Fish and Other Environmental Sources. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	2
2183	Metagenomic analysis reveals patterns and hosts of antibiotic resistance in different pig farms. <i>Environmental Science and Pollution Research</i> , 2023, 30, 52087-52106.	2.7	3
2184	Epizoans on Floating Golden Tide Macroalgae in the Southern Yellow Sea. <i>Journal of Marine Science and Engineering</i> , 2023, 11, 479.	1.2	0
2185	Roadmap to the study of gene and protein phylogeny and evolution—A practical guide. <i>PLoS ONE</i> , 2023, 18, e0279597.	1.1	4
2186	Revealing within-species diversity in uncultured human gut bacteria with single-cell long-read sequencing. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	5
2188	Ubiquitin-like conjugation by bacterial cGAS enhances anti-phage defence. <i>Nature</i> , 2023, 616, 326-331.	13.7	37
2189	Validation by SSRs of Morphometric Markers for Genetic Variability in <i>Araucaria araucana</i> (Molina) K. Koch. <i>Forests</i> , 2023, 14, 466.	0.9	2
2190	Genome-Wide Investigation of the NAC Transcription Factor Family in <i>Apocynum venetum</i> Revealed Their Synergistic Roles in Abiotic Stress Response and Trehalose Metabolism. <i>International Journal of Molecular Sciences</i> , 2023, 24, 4578.	1.8	2
2191	A parasitic fungus employs mutated eIF4A to survive on rocaglate-synthesizing <i>Aglaia</i> plants. <i>ELife</i> , 0, 12, .	2.8	6
2192	Genomic Analysis of Two Novel Bacteriophages Infecting <i>Acinetobacter beijerinckii</i> and halotolerans Species. <i>Viruses</i> , 2023, 15, 643.	1.5	0
2193	The Prevalence of Plasmid-Mediated Colistin Resistance Gene <i>mcr-1</i> and Different Transferability and Fitness of <i>mcr-1</i> -Bearing IncX4 Plasmids in <i>Escherichia coli</i> from Pigeons. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	2
2194	Clonal Expansion of Multidrug-Resistant <i>Streptococcus dysgalactiae</i> Subspecies <i>equisimilis</i> Causing Bacteremia, Japan, 2005–2021. <i>Emerging Infectious Diseases</i> , 2023, 29, 528-539.	2.0	6
2195	Mitochondrial phylogenomics provides conclusive evidence that the family Ancyrocephalidae is deeply paraphyletic. <i>Parasites and Vectors</i> , 2023, 16, .	1.0	1

#	ARTICLE	IF	CITATIONS
2196	Coordination of bacterial cell wall and outer membrane biosynthesis. <i>Nature</i> , 2023, 615, 300-304.	13.7	20
2197	Unveiling the evolutionary relationships and the high cryptic diversity in Andean rainfrogs (<i>Craugastoridae</i> : <i>Pristimantis myersi</i> group). <i>PeerJ</i> , 0, 11, e14715.	0.9	2
2198	Tongue sole creatine kinases function as DAMP and activate antimicrobial immunity via TLR2. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	0
2199	Recent Progress in the Production of Cyanide-Converting Nitrilases—Comparison with Nitrile-Hydrolyzing Enzymes. <i>Catalysts</i> , 2023, 13, 500.	1.6	1
2200	Comparative-genomic analysis reveals dynamic NLR gene loss and gain across Apiaceae species. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	1
2201	Analysis of CRISPR-Cas Loci and their Targets in <i>Levilactobacillus brevis</i> . <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 0, , .	2.2	1
2202	Sticky decisions: The multilayered regulation of adhesin production by bacteria. <i>PLoS Genetics</i> , 2023, 19, e1010648.	1.5	2
2203	The mitochondrial genome of <i>Heterosentis pseudobagri</i> (Wang & Zhang, 1987) Pichelin & Cribb, 1999 reveals novel aspects of tRNA genes evolution in <i>Acanthocephala</i> . <i>BMC Genomics</i> , 2023, 24, .	1.2	2
2204	Genome-Wide Identification and Expression Characteristics of Cytokinin Response Factors in Soybean. <i>Journal of Plant Growth Regulation</i> , 2023, 42, 4484-4496.	2.8	1
2205	Evolutionary ecology of microbial populations inhabiting deep sea sediments associated with cold seeps. <i>Nature Communications</i> , 2023, 14, .	5.8	9
2206	Structure of the <i>T. brucei</i> kinetoplastid RNA editing substrate-binding complex core component, RESC5. <i>PLoS ONE</i> , 2023, 18, e0282155.	1.1	2
2207	The enormous repetitive Antarctic krill genome reveals environmental adaptations and population insights. <i>Cell</i> , 2023, 186, 1279-1294.e19.	13.5	23
2208	Heritability and gene functions associated with sclerotia formation of <i>Rhizoctonia solani</i> AG-7 using whole genome sequencing and genome-wide association study. <i>Microbial Genomics</i> , 2023, 9, .	1.0	0
2209	Analysis of genetic diversity and selection signals in Chaling cattle of southern China using whole-genome scan. <i>Animal Genetics</i> , 2023, 54, 284-294.	0.6	1
2210	On New Species of Three Genera of Zosimeidae Seifried, 2003 (Copepoda: Harpacticoida) from the Deep Sea of the Gulf of California and Gulf of Mexico, with Notes on the Phylogeny of the Family and on the Species Groups of Zosime Boeck, 1873. <i>Diversity</i> , 2023, 15, 363.	0.7	0
2211	Structural Characterization of the Chlorophyllide a Oxygenase (CAO) Enzyme Through an In Silico Approach. <i>Journal of Molecular Evolution</i> , 2023, 91, 225-235.	0.8	0
2212	Evolutionary and phylogenetic analyses of 11 <i>Cerasus</i> species based on the complete chloroplast genome. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	10
2214	Immunogenic Properties and Antigenic Similarity of Virus-like Particles Derived from Human Polyomaviruses. <i>International Journal of Molecular Sciences</i> , 2023, 24, 4907.	1.8	0

#	ARTICLE	IF	CITATIONS
2216	Limited Song Mixing Without Genomic Gene Flow in a Contact Zone Between Two Songbird Species. <i>Molecular Biology and Evolution</i> , 2023, 40, .	3.5	2
2218	Identification and characterization of thousands of bacteriophage satellites across bacteria. <i>Nucleic Acids Research</i> , 2023, 51, 2759-2777.	6.5	19
2219	Isolation and characterization of a novel <i>Tenacibaculum</i> species and a corresponding bacteriophage from a Mediterranean fish hatchery: Description of <i>Tenacibaculum larymnensis</i> sp. nov. and <i>Tenacibaculum</i> phage Larrie. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
2220	Sequence-structural features and evolution of the Î±-amylase family GH119 revealed by the in silico analysis of its relatedness to the family GH57. , 2023, 78, 1847-1860.		2
2221	Integrating Multi-Omics Analysis Reveals the Regulatory Mechanisms of Whiteâ€™Violet Mutant Flowers in Grape Hyacinth (<i>Muscari latifolium</i>). <i>International Journal of Molecular Sciences</i> , 2023, 24, 5044.	1.8	1
2222	Assessment of the Diversity, Distinctiveness and Conservation of Australiaâ€™s Central Queensland Coastal Rainforests Using DNA Barcoding. <i>Diversity</i> , 2023, 15, 378.	0.7	0
2223	Class 1 integrons and multiple mobile genetic elements in clinical isolates of the <i>Klebsiella pneumoniae</i> complex from a tertiary hospital in eastern China. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	4
2224	Genome-Wide Identification and Expression Analysis of the HSF Gene Family in Poplar. <i>Forests</i> , 2023, 14, 510.	0.9	4
2225	Phylogenetic Analysis and Virulence Characteristics of Methicillin-Resistant <i>Staphylococcus aureus</i> ST45 in China: a Hyper-Virulent Clone Associated with Bloodstream Infections. <i>MSystems</i> , 0, , .	1.7	0
2227	Human and bacterial TatD enzymes exhibit apurinic/aprimidinic (AP) endonuclease activity. <i>Nucleic Acids Research</i> , 2023, 51, 2838-2849.	6.5	3
2228	Genetic Structure Analysis of 155 Transboundary and Local Populations of Cattle (<i>Bos taurus</i> , <i>Bos</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 24, 5061.	1.8	1
2229	Novel rubble-dwelling predators of herbivorous juvenile crown-of-thorns starfish (<i>Acanthaster</i> sp.). <i>Coral Reefs</i> , 2023, 42, 579-591.	0.9	5
2231	ProFeatMap: a highly customizable tool for 2D feature representation of protein sets. <i>Bioinformatics Advances</i> , 2023, 3, .	0.9	2
2232	The terrestrial isopod symbiont <i>Candidatus</i> <i>Hepaticola porcellionum</i> â€™ is a potential nutrient scavenger related to <i>Holosporales</i> symbionts of protists. <i>ISME Communications</i> , 2023, 3, .	1.7	2
2234	Development of Multiple Nucleotide Polymorphism Molecular Markers for Enoki Mushroom (<i>Flammulina filiformis</i>) Cultivars Identification. <i>Journal of Fungi (Basel, Switzerland)</i> , 2023, 9, 330.	1.5	3
2235	Characterization of the complete mitochondrial genomes of two Critically Endangered wedgefishes: <i>Rhynchobatus djiddensis</i> and <i>Rhynchobatus australiae</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2023, 8, 352-358.	0.2	2
2237	Core genome multilocus sequence typing scheme for <i>Bacillus cereus</i> group bacteria. <i>Research in Microbiology</i> , 2023, 174, 104050.	1.0	5
2239	UBC gene family and their potential functions on the cellular homeostasis under the elevated pCO ₂ stress in the diatom <i>Phaeodactylum tricornutum</i> . <i>Ecological Indicators</i> , 2023, 148, 110106.	2.6	0

#	ARTICLE	IF	CITATIONS
2241	Genetic Diversity and Population Structure of <i>Anopheles funestus</i> in Western Kenya Based on Mitochondrial DNA Marker COII. <i>Insects</i> , 2023, 14, 273.	1.0	2
2243	Development of the oral resistome during the first decade of life. <i>Nature Communications</i> , 2023, 14, .	5.8	7
2245	Fern cell walls and the evolution of arabinogalactan proteins in streptophytes. <i>Plant Journal</i> , 2023, 114, 875-894.	2.8	3
2246	Phenotypic and genotypic survey of antibiotic resistance in <i>Salmonella enterica</i> isolates from dairy farms in Uruguay. <i>Frontiers in Veterinary Science</i> , 0, 10, .	0.9	2
2247	Characterization of Unexpected Self-Acylation Activity of Acyl Carrier Proteins in a Modular Type I Apicomplexan Polyketide Synthase. <i>ACS Chemical Biology</i> , 2023, 18, 785-793.	1.6	3
2248	Evolution of Restriction Modification Systems Consisting of One Restriction Endonuclease and Two DNA Methyltransferases. <i>Biochemistry (Moscow)</i> , 2023, 88, 253-261.	0.7	0
2250	Molecular surveillance reveals the emergence and dissemination of NDM-5-producing <i>Escherichia coli</i> high-risk clones in Germany, 2013 to 2019. <i>Eurosurveillance</i> , 2023, 28, .	3.9	7
2255	Whole-genome analysis showed the promotion of genetic diversity and coevolution in <i>Staphylococcus aureus</i> lytic bacteriophages and their hosts mediated by prophages via worldwide recombination events. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
2256	ORGANIZATION AND POLYMORPHISM OF THE CHLOROPLAST GENOME REGION <i>psbA-trnH</i> IN REPRESENTATIVES OF THE GONIOLIMON BOISS.. <i>Biologichni Systemy</i> , 2022, 14, 137-142.	0.0	0
2258	PHYLOGENETIC RELATIONSHIPS OF UKRAINIAN ACCESSIONS OF <i>LATHYRUS VENETUS</i> (MILL.) WOHLF. AND <i>L. VERNUS</i> (L.) BERNH. BASED ON THE ANALYSIS OF THE <i>psbA-trnH</i> REGION OF THE CHLOROPLAST GENOME. <i>Biologichni Systemy</i> , 2022, 14, 39-44.	0.0	3
2259	Genome-Wide Identification and Expression Analysis of NPF Genes in Cucumber (<i>Cucumis sativus</i> L.). <i>Plants</i> , 2023, 12, 1252.	1.6	3
2260	A cryptic natural variant allele of <i>BYPASS2</i> suppresses the <i>bypass1</i> mutant phenotype. <i>Plant Physiology</i> , 0, , .	2.3	0
2263	Comparative Genomic Analysis of Enterococci across Sectors of the One Health Continuum. <i>Microorganisms</i> , 2023, 11, 727.	1.6	3
2264	A phylogenomic analysis of <i>Limosilactobacillus reuteri</i> reveals ancient and stable evolutionary relationships with rodents and birds and zoonotic transmission to humans. <i>BMC Biology</i> , 2023, 21, .	1.7	8
2265	Co-Surveillance of Rotaviruses in Humans and Domestic Animals in Central Uganda Reveals Circulation of Wide Genotype Diversity in the Animals. <i>Viruses</i> , 2023, 15, 738.	1.5	2
2266	Passing the post: roles of posttranslational modifications in the form and function of extracellular matrix. <i>American Journal of Physiology - Cell Physiology</i> , 2023, 324, C1179-C1197.	2.1	3
2267	Uncovering the specificity and predictability of tryptophan metabolism in lactic acid bacteria with genomics and metabolomics. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 13, .	1.8	11
2268	Population Structure, Genetic Diversity and Candidate Genes for the Adaptation to Environmental Stress in <i>Picea koraiensis</i> . <i>Plants</i> , 2023, 12, 1266.	1.6	1

#	ARTICLE	IF	CITATIONS
2269	Lipid extract derived from newly isolated <i>Rhodotorula toruloides</i> LAB-07 for cosmetic applications. <i>Computational and Structural Biotechnology Journal</i> , 2023, 21, 2009-2017.	1.9	3
2271	The Lichen Flavin-Dependent Halogenase, DnHal: Identification, Heterologous Expression and Functional Characterization. <i>Applied Biochemistry and Biotechnology</i> , 0, , .	1.4	0
2272	Co-Occurrence and Cooperation between Comammox and Anammox Bacteria in a Full-Scale Attached Growth Municipal Wastewater Treatment Process. <i>Environmental Science & Technology</i> , 2023, 57, 5013-5023.	4.6	10
2273	<i>Nitzschia captiva</i> sp. nov. (Bacillariophyta), the essential prey diatom of the kleptoplastic dinoflagellate <i>Durinskia capensis</i> , compared with <i>N. agnita</i> , <i>N. kuetingioides</i> and other species. <i>Phycologia</i> , 2023, 62, 136-151.	0.6	2
2275	In silico Analysis of Diverse Endo- β -1,4-glucanases Reveals Their Molecular Evolution. <i>Journal of Evolutionary Biochemistry and Physiology</i> , 2023, 59, 94-106.	0.2	0
2276	The Complete Mitochondrial Genome of Box Tree Moth <i>Cydalima perspectalis</i> and Insights into Phylogenetics in Pyraloidea. <i>Animals</i> , 2023, 13, 1045.	1.0	4
2277	Genome Characterisation of the CGMMV Virus Population in Australiaâ€”Informing Plant Biosecurity Policy. <i>Viruses</i> , 2023, 15, 743.	1.5	0
2281	Eurypsychrophilic acidophiles: From (meta)genomes to low-temperature biotechnologies. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	2
2282	IFN-Induced PARPsâ€™ Sensors of Foreign Nucleic Acids?. <i>Pathogens</i> , 2023, 12, 457.	1.2	1
2283	The first detection of two <i>Aeromonas</i> strains in mice of the genus <i>Apodemus</i> . <i>Scientific Reports</i> , 2023, 13, .	1.6	0
2284	Conservation and Expansion of Transcriptional Factor Repertoire in the <i>Fusarium oxysporum</i> Species Complex. <i>Journal of Fungi (Basel, Switzerland)</i> , 2023, 9, 359.	1.5	1
2285	Unlocking the microbial studies through computational approaches: how far have we reached?. <i>Environmental Science and Pollution Research</i> , 2023, 30, 48929-48947.	2.7	4
2287	Genomic Characterization of <i>Staphylococcus aureus</i> in Wildlife. <i>Animals</i> , 2023, 13, 1064.	1.0	6
2288	Phylogeny and Evolutionary Timescale of Muscidae (Diptera: Calyptratae) Inferred from Mitochondrial Genomes. <i>Insects</i> , 2023, 14, 286.	1.0	2
2289	Transcription factor bHLH121 regulates root cortical aerenchyma formation in maize. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	3.3	10
2290	Cervicovaginal Human Papillomavirus Genomes, Microbiota Composition and Cytokine Concentrations in South African Adolescents. <i>Viruses</i> , 2023, 15, 758.	1.5	0
2292	Genomic Insights into Niche Partitioning across Sediment Depth among Anaerobic Methane-Oxidizing Archaea in Global Methane Seeps. <i>MSystems</i> , 2023, 8, .	1.7	4
2293	SPOC domain proteins in health and disease. <i>Genes and Development</i> , 2023, 37, 140-170.	2.7	2

#	ARTICLE	IF	CITATIONS
2294	Characterization and Comparative Genomic Analysis of Three Virulent <i>E. coli</i> Bacteriophages with the Potential to Reduce Antibiotic-Resistant Bacteria in the Environment. <i>International Journal of Molecular Sciences</i> , 2023, 24, 5696.	1.8	5
2295	Avian influenza H5N1 in a great white pelican (<i>Pelecanus onocrotalus</i>), Mauritania 2022. <i>Veterinary Research Communications</i> , 0, , .	0.6	3
2296	In the light of evolution: keratins as exceptional tumor biomarkers. <i>PeerJ</i> , 0, 11, e15099.	0.9	5
2297	Chlorine Dioxide Reprograms Rhizosphere Microbial Communities to Enrich Interactions with Tobacco (<i>Nicotiana tabacum</i>). <i>Polish Journal of Microbiology</i> , 2023, 72, 47-60.	0.6	0
2298	Analysis of Genome Structure and Its Variations in Potato Cultivars Grown in Russia. <i>International Journal of Molecular Sciences</i> , 2023, 24, 5713.	1.8	2
2299	ABC transporters linked to multiple herbicide resistance in blackgrass (<i>Alopecurus myosuroides</i>). <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	4
2300	Neofunctionalization of tandem duplicate genes encoding putative β -arabinofuranosidases in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 0, , .	2.3	1
2304	Phylogenetic trees, conserved motifs and predicted subcellular localization for transcription factor families in pearl millet. <i>BMC Research Notes</i> , 2023, 16, .	0.6	0
2305	High Andean Steppes of Southern Chile Contain Little-Explored <i>Peltigera</i> Lichen Symbionts. <i>Journal of Fungi</i> (Basel, Switzerland), 2023, 9, 372.	1.5	0
2306	Soil microbial communities regulate the threshold effect of salinity stress on SOM decomposition in coastal salt marshes. <i>Fundamental Research</i> , 2023, 3, 868-879.	1.6	4
2307	A Representative Collection of Commensal Extended-Spectrum- and AmpC- β -Lactamase-Producing <i>Escherichia coli</i> of Animal Origin for Phage Sensitivity Studies. <i>Phage</i> , 2023, 4, 35-45.	0.8	4
2308	Structure and dynamics of the <i>Arabidopsis</i> O-fucosyltransferase SPINDLY. <i>Nature Communications</i> , 2023, 14, .	5.8	5
2309	Draft genome sequences of rare <i>Lelliottia nimipressuralis</i> strain MEZLN61 and two <i>Enterobacter kobei</i> strains MEZEK193 and MEZEK194 carrying mobile colistin resistance gene <i>mcr-9</i> isolated from wastewater in South Africa. <i>Journal of Global Antimicrobial Resistance</i> , 2023, 33, 231-237.	0.9	4
2310	Genomic Analysis of the Deep-Sea Bacterium <i>Shewanella</i> sp. MTB7 Reveals Backgrounds Related to Its Deep-Sea Environment Adaptation. <i>Microorganisms</i> , 2023, 11, 798.	1.6	1
2311	Development and Clinical Application of a Multilocus Sequence Typing Scheme for <i>Bacteroides fragilis</i> Based on Whole-Genome Sequencing Data. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	1
2312	Extensive Cryptic Diversity and Ecological Associations Uncovered among Mexican and Global Collections of <i>Naegleria</i> and <i>Vermamoeba</i> Species by 18S Ribosomal DNA, Internal Transcribed Spacer, and Cytochrome Oxidase Subunit I Sequence Analysis. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	1
2313	Food odors alter behavioral responses and olfactory receptors expression in grass carp (<i>Ctenopharyngodon idellus</i>). <i>Aquaculture and Fisheries</i> , 2023, , .	1.2	1
2314	Critical Assessment of the Biomarker Discovery and Classification Methods for Multiclass Metabolomics. <i>Analytical Chemistry</i> , 2023, 95, 5542-5552.	3.2	11

#	ARTICLE	IF	CITATIONS
2315	Phylogroup-specific variation shapes the clustering of antimicrobial resistance genes and defence systems across regions of genome plasticity in <i>Pseudomonas aeruginosa</i> . <i>EBioMedicine</i> , 2023, 90, 104532.	2.7	11
2316	Transposable Element Interactions Shape the Ecology of the Deer Mouse Genome. <i>Molecular Biology and Evolution</i> , 2023, 40, .	3.5	6
2317	Complete Genome Sequence and Analysis of a ST573 Multidrug-Resistant Methicillin-Resistant <i>Staphylococcus aureus</i> SauR3 Clinical Isolate from Terengganu, Malaysia. <i>Pathogens</i> , 2023, 12, 502.	1.2	2
2318	Revisiting Microbial Diversity in Hypersaline Microbial Mats from Guerrero Negro for a Better Understanding of Methanogenic Archaeal Communities. <i>Microorganisms</i> , 2023, 11, 812.	1.6	2
2319	The persistence and stabilization of auxiliary genes in the human skin virome. <i>Virology Journal</i> , 2023, 20, .	1.4	0
2320	Genome-Wide Identification and Expression Analysis of TPS Gene Family in <i>Liriodendron chinense</i> . <i>Genes</i> , 2023, 14, 770.	1.0	2
2321	Molecular evolutionary model based on phylogenetic and mutation analysis of SARS-CoV-2 spike protein sequences from Asian countries: A phylogenomic approach. <i>Informatics in Medicine Unlocked</i> , 2023, 38, 101221.	1.9	2
2322	<i>Sida chlorotic leaf virus</i> : a new recombinant begomovirus found in non-cultivated plants and <i>Cucumis sativus</i> L. <i>PeerJ</i> , 0, 11, e15047.	0.9	0
2323	Phylogenetic diversity of core rumen microbiota as described by cryo-ET. <i>MicroLife</i> , 2023, 4, .	1.0	1
2324	The phylogeny and metabolic potentials of an n-alkane-degrading <i>Venatorbacter</i> bacterium isolated from deep-sea sediment of the Mariana Trench. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	2
2325	Bacteriophage antidefense genes that neutralize TIR and STING immune responses. <i>Cell Reports</i> , 2023, 42, 112305.	2.9	9
2326	On the Origin and Evolution of Microbial Mercury Methylation. <i>Genome Biology and Evolution</i> , 2023, 15, .	1.1	3
2327	Protein Homology Modeling for Effective Drug Design. <i>Methods in Molecular Biology</i> , 2023, , 329-337.	0.4	0
2328	The identification and phylogenetic analysis of <i>SARS-CoV-2</i> delta variants in Taiwan. <i>Kaohsiung Journal of Medical Sciences</i> , 0, , .	0.8	3
2329	Genome-Wide Identification and Analysis of the MADS-Box Transcription Factor Genes in Blueberry (<i>Vaccinium</i> spp.) and Their Expression Pattern during Fruit Ripening. <i>Plants</i> , 2023, 12, 1424.	1.6	5
2330	Isolation and characterization of bioactive metabolites of <i>Bacillus enclensis</i> CARE-V7 strain from southeast coast of India. <i>Biomass Conversion and Biorefinery</i> , 0, , .	2.9	0
2331	Genomic analysis of chromosomal cointegrated bla _{NDM-1} -carrying ICE and bla _{RSA-1} -carrying IME from clinical multidrug resistant <i>Aeromonas caviae</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 13, .	1.8	0
2332	Global population structure, genomic diversity and carbohydrate fermentation characteristics of clonal complex 119 (CC119), an understudied Shiga toxin-producing <i>E. coli</i> (STEC) lineage including O165:H25 and O172:H25. <i>Microbial Genomics</i> , 2023, 9, .	1.0	0

#	ARTICLE	IF	CITATIONS
2333	Alterations of gut microbes and their correlation with clinical features in middle and end-stages chronic kidney disease. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 13, .	1.8	1
2334	Phylogenomic investigation of an outbreak of fluoroquinolone-resistant <i>Salmonella enterica</i> subsp. <i>enterica</i> serovar Paratyphi A in Phnom Penh, Cambodia. <i>Microbial Genomics</i> , 2023, 9, .	1.0	1
2335	Genome-wide identification, expression analysis, and transcriptome analysis of the IAA gene family in <i>Zoysia japonica</i> . <i>Molecular Biology Reports</i> , 0, , .	1.0	0
2336	Genome-wide characterization and expression analysis of the MLO gene family sheds light on powdery mildew resistance in <i>Lagenaria siceraria</i> . <i>Heliyon</i> , 2023, 9, e14624.	1.4	4
2340	Diversity of Gracilariaceae (Rhodophyta) in China: An integrative morphological and molecular assessment including a description of <i>Gracilaria tsengii</i> sp. nov.. <i>Algal Research</i> , 2023, 71, 103074.	2.4	1
2341	Characterization and metabolomic profiling of two pigment producing fungi from infected fruits of Indian Gooseberry. <i>Archives of Microbiology</i> , 2023, 205, .	1.0	4
2342	Microbial composition of tumorous and adjacent gastric tissue is associated with prognosis of gastric cancer. <i>Scientific Reports</i> , 2023, 13, .	1.6	8
2343	Bioprospecting of desert actinobacteria with special emphases on griseoviridin, mitomycin C and a new bacterial metabolite producing <i>Streptomyces</i> sp. PU-KB10â€“4. <i>BMC Microbiology</i> , 2023, 23, .	1.3	3
2344	Draft genome sequence of <i>Enterobacter chengduensis</i> ECC445, isolated from fresh water in the West Indies. <i>BMC Genomic Data</i> , 2023, 24, .	0.7	1
2345	Integration of Selection Signatures and Protein Interactions Reveals NR6A1, PAPP2, and PIK3C2B as the Promising Candidate Genes Underlying the Characteristics of Licha Black Pig. <i>Biology</i> , 2023, 12, 500.	1.3	2
2346	Genomic Characterization and Pathogenicity of BJEU06-1-Like PRRSV-1 ZD-1 Isolated in China. <i>Transboundary and Emerging Diseases</i> , 2023, 2023, 1-12.	1.3	5
2347	A Novel Dependoparvovirus Identified in Cloacal Swabs of Monk Parakeet (<i>Myiopsitta monachus</i>) from Urban Areas of Spain. <i>Viruses</i> , 2023, 15, 850.	1.5	1
2348	Elucidating SNP-Based Population Structure and Genetic Diversity of <i>Bruguiera gymnorhiza</i> (L.) Savigny in Thailand. <i>Forests</i> , 2023, 14, 693.	0.9	1
2349	A new cryptic species of <i>Brazilozoros</i> Kukulova-Peck & Peck, 1993 from French Guiana (Zoraptera), Tj ETQq1 1.0,784314 1 rgBT /Ove 0.2	1.0	1
2350	In-depth study of tomato and weed viromes reveals undiscovered plant virus diversity in an agroecosystem. <i>Microbiome</i> , 2023, 11, .	4.9	21
2351	Functional characterization of the <i>GhNRT2.1e</i> gene reveals its significant role in improving nitrogen use efficiency in <i>Gossypium hirsutum</i> . <i>PeerJ</i> , 0, 11, e15152.	0.9	0
2352	Discovery of an Abundant Viral Genus in Polar Regions through the Isolation and Genomic Characterization of a New Virus against <i>Oceanospirillaceae</i> . <i>Applied and Environmental Microbiology</i> , 2023, 89, .	1.4	4
2354	The genome of <i>Lactuca saligna</i> , a wild relative of lettuce, provides insight into non-host resistance to the downy mildew <i>Bremia lactucae</i> . <i>Plant Journal</i> , 2023, 115, 108-126.	2.8	2

#	ARTICLE	IF	CITATIONS
2355	Niche Modification by Sulfate-Reducing Bacteria Drives Microbial Community Assembly in Anoxic Marine Sediments. <i>MBio</i> , 0, , .	1.8	1
2356	Characterization of resistance genes and plasmids from sick children caused by <i>Salmonella enterica</i> resistance to azithromycin in Shenzhen, China. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 13, .	1.8	2
2357	Polymorphism analysis of major histocompatibility complex (MHC) DQB gene in the Asiatic black bear (<i>Ursus thibetanus</i>). <i>Mammal Research</i> , 0, , .	0.6	0
2360	Genomic characterization and identification of virulence-related genes in <i>Vibrio nigripulchritudo</i> isolated from white leg shrimp <i>Penaeus vannamei</i> . <i>Journal of Fish Diseases</i> , 2023, 46, 779-790.	0.9	1
2363	RND pumps across the genus <i>Acinetobacter</i> : AdellK is the universal efflux pump. <i>Microbial Genomics</i> , 2023, 9, .	1.0	4
2364	Prevalence and Molecular Characterization of Methicillin-Resistant Staphylococci (MRS) and Mammaliococci (MRM) in Dromedary Camels from Algeria: First Detection of SCCmec-mecC Hybrid in Methicillin-Resistant <i>Mammaliococcus lentus</i> . <i>Antibiotics</i> , 2023, 12, 674.	1.5	3
2365	Genomic Characterization and Genetic Profiles of <i>Salmonella Gallinarum</i> Strains Isolated from Layers with Fowl Typhoid in Colombia. <i>Genes</i> , 2023, 14, 823.	1.0	1
2366	Genome-wide analysis emancipates genomic diversity and signature of selection in Altay white-headed cattle of Xinjiang, China. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	1
2367	Enrichment Culture but Not Metagenomic Sequencing Identified a Highly Prevalent Phage Infecting <i>Lactiplantibacillus plantarum</i> in Human Feces. <i>Microbiology Spectrum</i> , 0, , .	1.2	0
2368	Population structure and selective signature of sheep around Tarim Basin. <i>Frontiers in Ecology and Evolution</i> , 0, 11, .	1.1	0
2369	Genomic diversity of aquaporins across genus <i>Oryza</i> provides a rich genetic resource for development of climate resilient rice cultivars. <i>BMC Plant Biology</i> , 2023, 23, .	1.6	3
2370	Identification of the NAC Transcription Factor Family during Early Seed Development in <i>Akebia trifoliata</i> (Thunb.) Koidz. <i>Plants</i> , 2023, 12, 1518.	1.6	5
2371	Phylogenetic and Spatiotemporal Analyses of Porcine Epidemic Diarrhea Virus in Guangxi, China during 2017–2022. <i>Animals</i> , 2023, 13, 1215.	1.0	0
2372	Genomic surveillance identifies SARS-CoV-2 transmission patterns in local university populations, Wisconsin, USA, 2020–2022. <i>Microbial Genomics</i> , 2023, 9, .	1.0	2
2373	RNA-binding proteins that lack canonical RNA-binding domains are rarely sequence-specific. <i>Scientific Reports</i> , 2023, 13, .	1.6	6
2374	CRISPR-Cas9 enrichment, a new strategy in microbial metagenomics to investigate complex genomic regions: The case of an environmental integron. <i>Molecular Ecology Resources</i> , 2023, 23, 1288-1298.	2.2	3
2375	Receptor Elimination by E3 Ubiquitin Ligase Recruitment (REULR): A Targeted Protein Degradation Toolbox. <i>ACS Synthetic Biology</i> , 2023, 12, 1081-1093.	1.9	9
2376	Whole-genome sequences from wild-type and laboratory-evolved strains define the allelome and establish its hallmarks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	3.3	6

#	ARTICLE	IF	CITATIONS
2377	First insight into the phylogeny of fine-leaved <i>Festuca</i> in the Altai Mountain Country based on genome-wide genotyping. <i>Ecology and Evolution</i> , 2023, 13, .	0.8	1
2378	Insight into the genomes of dominant yeast symbionts of European spruce bark beetle, <i>Ips typographus</i> . <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	4
2379	Sterol methyltransferases in uncultured bacteria complicate eukaryotic biomarker interpretations. <i>Nature Communications</i> , 2023, 14, .	5.8	3
2381	The Snapdragon Genomes Reveal the Evolutionary Dynamics of the <i>S</i> -Locus Supergene. <i>Molecular Biology and Evolution</i> , 2023, 40, .	3.5	4
2382	Loss-of-Function of <i>xpc</i> Sensitizes Zebrafish to Ultraviolet Irradiation. <i>Fishes</i> , 2023, 8, 191.	0.7	2
2383	Assessment of plasmids for relating the 2020 <i>Salmonella enterica</i> serovar Newport onion outbreak to farms implicated by the outbreak investigation. <i>BMC Genomics</i> , 2023, 24, .	1.2	0
2384	Guess who? Evaluating individual acoustic monitoring for males and females of the Tawny Pipit, a migratory passerine bird with a simple song. <i>Journal of Ornithology</i> , 0, , .	0.5	1
2385	Expression of the primate-specific LINC00473 RNA in mouse neurons promotes excitability and CREB-regulated transcription. <i>Journal of Biological Chemistry</i> , 2023, 299, 104671.	1.6	4
2386	The complete reference genome for grapevine (<i>Vitis vinifera</i> L.) genetics and breeding. <i>Horticulture Research</i> , 2023, 10, .	2.9	38
2388	Expansion and collapse of VEGF diversity in major clades of the animal kingdom. <i>Angiogenesis</i> , 0, , .	3.7	1
2389	Insight into the evolutionary and domesticated history of the most widely cultivated mushroom <i>Agaricus bisporus</i> via mitogenome sequences of 361 global strains. <i>BMC Genomics</i> , 2023, 24, .	1.2	0
2390	Molecular characterization and comparative genomic analysis of <i>Acinetobacter baumannii</i> isolated from the community and the hospital: an epidemiological study in Segamat, Malaysia. <i>Microbial Genomics</i> , 2023, 9, .	1.0	1
2391	Phylomitogenomic Analyses Provided Further Evidence for the Resurrection of the Family Pseudoacanthocephalidae (Acanthocephala: Echinorhynchida). <i>Animals</i> , 2023, 13, 1256.	1.0	6
2392	ADAR1 Biology Can Hinder Effective Antiviral RNA Interference. <i>Journal of Virology</i> , 2023, 97, .	1.5	4
2394	<i>Nocardia pulmonis</i> sp. nov., an actinomycete isolated from a patient with pulmonary infection. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2023, 73, .	0.8	0
2395	Quantification of diversity sampling bias resulting from rice root bacterial isolation on popular and nitrogen-free culture media using 16S amplicon barcoding. <i>PLoS ONE</i> , 2023, 18, e0279049.	1.1	2
2396	The Spread of Peste Des Petits Ruminants Virus Lineage IV in West Africa. <i>Animals</i> , 2023, 13, 1268.	1.0	3
2397	Whole-genome sequencing of <i>Shigella</i> for surveillance purposes shows (inter)national relatedness and multidrug resistance in isolates from men who have sex with men. <i>Microbial Genomics</i> , 2023, 9, .	1.0	0

#	ARTICLE	IF	CITATIONS
2398	Characterization and Association of Rips Repertoire to Host Range of Novel <i>Ralstonia solanacearum</i> Strains by In Silico Approaches. <i>Microorganisms</i> , 2023, 11, 954.	1.6	0
2399	The terpene synthase genes of <i>Melaleuca alternifolia</i> (tea tree) and comparative gene family analysis among Myrtaceae essential oil crops. <i>Plant Systematics and Evolution</i> , 2023, 309, .	0.3	4
2401	Metagenomic insights into the composition and function of the gut microbiota of mice infected with <i>Toxoplasma gondii</i> . <i>Frontiers in Immunology</i> , 0, 14, .	2.2	2
2402	Genetic characterization of ESBL-producing and ciprofloxacin-resistant <i>Escherichia coli</i> from Belgian broilers and pigs. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	3
2404	Ancient origin of Jingchuvirales derived glycoproteins integrated in arthropod genomes. <i>Genetics and Molecular Biology</i> , 2023, 46, .	0.6	1
2406	Integrative taxonomy using the plant core <sc>DNA</sc> barcodes in Sumatra's Burseraceae. <i>Ecology and Evolution</i> , 2023, 13, .	0.8	1
2407	The photicâ€aphotic divide is a strong ecological and evolutionary force determining the distribution of ciliates (<i>Alveolata</i> , <i>Ciliophora</i>) in the ocean. <i>Journal of Eukaryotic Microbiology</i> , 2023, 70, .	0.8	2
2408	The evolution and international spread of extensively drug resistant <i>Shigella sonnei</i> . <i>Nature Communications</i> , 2023, 14, .	5.8	11
2409	A paleogenome from a Holocene individual supports genetic continuity in Southeast Alaska. <i>IScience</i> , 2023, 26, 106581.	1.9	3
2412	Distribution and abundance of tetraether lipid cyclization genes in terrestrial hot springs reflect <sc>pH</sc>. <i>Environmental Microbiology</i> , 2023, 25, 1644-1658.	1.8	2
2413	Genome-Wide Identification and Transcriptome-Based Expression Profile of Cuticular Protein Genes in <i>Antheraea pernyi</i> . <i>International Journal of Molecular Sciences</i> , 2023, 24, 6991.	1.8	3
2414	An Integrative Analysis of Metabolome and Transcriptome Reveals the Molecular Regulatory Mechanism of the Accumulation of Flavonoid Glycosides in Different <i>Cyclocarya paliurus</i> Ploidies. <i>Forests</i> , 2023, 14, 770.	0.9	2
2415	Heat-Induced Transcriptome and Genome-Wide Analysis of NHL Genes in Maize (<i>Zea mays</i> L.) Suggest a Role of ZmNHLs Under Heat Stress. <i>Journal of Plant Growth Regulation</i> , 0, , .	2.8	0
2416	Draft Genomes of Halophilic <i>Chromohalobacter</i> and <i>Halomonas</i> Strains Isolated from Brines of The Carpathian Foreland, Poland. <i>Journal of Genomics</i> , 2023, 11, 14-19.	0.6	1
2417	Symbiosis preservation: Putative regulation of fatty acyl-CoA reductase by miR-31a within the symbiont harboring bacteriome through tsetse evolution. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	0
2418	Cotton leafroll dwarf disease: An enigmatic viral disease in cotton. <i>Molecular Plant Pathology</i> , 2023, 24, 513-526.	2.0	8
2419	Monkeypox virus: phylogenomics, hostâ€pathogen interactome and mutational cascade. <i>Microbial Genomics</i> , 2023, 9, .	1.0	2
2420	On-person adaptive evolution of <i>Staphylococcus aureus</i> during treatment for atopic dermatitis. <i>Cell Host and Microbe</i> , 2023, 31, 593-603.e7.	5.1	14

#	ARTICLE	IF	CITATIONS
2422	Role of horizontal gene transfers and microbial ecology in the evolution of fluxes through the tricarboxylic acid cycle. <i>International Journal of Astrobiology</i> , 0, , 1-15.	0.9	0
2423	A tRNA modification in <i>Mycobacterium tuberculosis</i> facilitates optimal intracellular growth. <i>ELife</i> , 0, 12, .	2.8	3
2424	Parapatric speciation of <i>Meiothermus</i> in serpentinite-hosted aquifers in Oman. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
2426	Micro-photoautotroph predation as a driver for trophic niche specialization in 12 syntopic Indo-Pacific parrotfish species. <i>Biological Journal of the Linnean Society</i> , 2023, 139, 91-114.	0.7	5
2427	Draft genomes of halophilic Archaea strains isolated from brines of the Carpathian Foreland, Poland. <i>Journal of Genomics</i> , 2023, 11, 20-25.	0.6	0
2428	Evolutionary history of Euteliidae (Lepidoptera, Noctuoidea). <i>Systematic Entomology</i> , 2023, 48, 445-462.	1.7	1
2429	Previously uncharacterized rectangular bacterial structures in the dolphin mouth. <i>Nature Communications</i> , 2023, 14, .	5.8	1
2430	Amino acids integrate behaviors in nerveless placozoans. <i>Frontiers in Neuroscience</i> , 0, 17, .	1.4	7
2432	<i>Babesia duncani</i> multi-omics identifies virulence factors and drug targets. <i>Nature Microbiology</i> , 2023, 8, 845-859.	5.9	7
2434	Exploring Genetic Diversity in an <i>Ilex crenata</i> Breeding Germplasm. <i>Horticulturae</i> , 2023, 9, 485.	1.2	2
2435	Conserved intramolecular networks in GDAP1 are closely connected to CMT-linked mutations and protein stability. <i>PLoS ONE</i> , 2023, 18, e0284532.	1.1	2
2436	Genomic and metabolic analyses reveal antagonistic lanthipeptides in archaea. <i>Microbiome</i> , 2023, 11, .	4.9	4
2437	Whole genome analysis of two sympatric human <i>Mansonella</i> : <i>Mansonella perstans</i> and <i>Mansonella</i> sp. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 13, .	1.8	1
2438	Genomic Surveillance of SARS-CoV-2 Variants in the Dominican Republic and Emergence of a Local Lineage. <i>International Journal of Environmental Research and Public Health</i> , 2023, 20, 5503.	1.2	2
2439	SARS-CoV-2 BW lineage, a fast-growing Omicron variant from southeast Mexico bearing relevant escape mutations. <i>Infection</i> , 2023, 51, 1549-1555.	2.3	3
2440	The structure of microbial communities in redoximorphic microsites of Gleysol. <i>European Journal of Soil Science</i> , 0, , .	1.8	0
2442	Genomic Surveillance of SARS-CoV-2 in Healthcare Workers: A Critical Sentinel Group for Monitoring the SARS-CoV-2 Variant Shift. <i>Viruses</i> , 2023, 15, 984.	1.5	0
2444	Species-Level Taxonomic Characterization of Uncultured Core Gut Microbiota of Plateau Pika. <i>Microbiology Spectrum</i> , 0, , .	1.2	1

#	ARTICLE	IF	CITATIONS
2445	<i>Pseudomonas</i> Acts as a Reservoir of Novel Tigecycline Resistance Efflux Pump <i>tmexC6D6-toprJ1b</i> and <i>tmexCD-toprJ</i> Variants. <i>Microbiology Spectrum</i> , 0, , .	1.2	2
2446	Core-Genome Multilocus Sequence Typing for Epidemiological and Evolutionary Analyses of Phytopathogenic <i>Xanthomonas citri</i> . <i>Applied and Environmental Microbiology</i> , 0, , .	1.4	0
2447	TcbHLH14 a Jasmonate Associated MYC2-like Transcription Factor Positively Regulates Pyrethrin Biosynthesis in <i>Tanacetum cinerariifolium</i> . <i>International Journal of Molecular Sciences</i> , 2023, 24, 7379.	1.8	0
2448	Investigating the Source of <i>Salmonella</i> Agona Contamination in Australian Feed Mills Using Core Genome Phylogenetic Analysis. <i>Foodborne Pathogens and Disease</i> , 2023, 20, 132-137.	0.8	0
2449	A comprehensive genomic analysis provides insights on the high environmental adaptability of <i>Acinetobacter</i> strains. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	3
2450	Genetic Mapping of Flavonoid Grain Pigments in Durum Wheat. <i>Plants</i> , 2023, 12, 1674.	1.6	2
2451	Defining the relationship between phylogeny, clinical manifestation, and phenotype for <i>Trichophyton mentagrophytes/interdigitale</i> complex; a literature review and taxonomic recommendations. <i>Medical Mycology</i> , 2023, 61, .	0.3	5
2454	Novel Sources of Biodiversity and Biomolecules from Bacteria Isolated from a High Middle Ages Soil Sample in Palermo (Sicily, Italy). <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	1
2455	Genome profiling of uropathogenic <i>E. coli</i> from strictly defined community-acquired UTI in paediatric patients: a multicentric study. <i>Antimicrobial Resistance and Infection Control</i> , 2023, 12, .	1.5	0
2456	Reclassification of family A DNA polymerases reveals novel functional subfamilies and distinctive structural features. <i>Nucleic Acids Research</i> , 2023, 51, 4488-4507.	6.5	3
2457	Prevalence and molecular characteristics of polymyxin-resistant Enterobacterales in a Chinese tertiary teaching hospital. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 13, .	1.8	0
2458	Virotyping and genetic antimicrobial susceptibility testing of porcine ETEC/STEC strains and associated plasmid types. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	5
2459	Genetic characterization of the zoonotic parasite <i>Ancylostoma caninum</i> in the central and eastern United States. <i>Journal of Helminthology</i> , 2023, 97, .	0.4	2
2460	Development of SSR Molecular Markers and Genetic Diversity Analysis of TPS Gene Family in <i>Chimonanthus praecox</i> . <i>Agriculture (Switzerland)</i> , 2023, 13, 893.	1.4	1
2461	Mpox Virus: Its Molecular Evolution and Potential Impact on Viral Epidemiology. <i>Viruses</i> , 2023, 15, 995.	1.5	4
2462	Export of defensive glucosinolates is key for their accumulation in seeds. <i>Nature</i> , 2023, 617, 132-138.	13.7	8
2463	Viruses of sulfur oxidizing phototrophs encode genes for pigment, carbon, and sulfur metabolisms. <i>Communications Earth & Environment</i> , 2023, 4, .	2.6	3
2464	Evolink: A Phylogenetic Approach for Rapid Identification of Genotype-Phenotype Associations in Large-scale Microbial Multi-Species Data. <i>Bioinformatics</i> , 0, , .	1.8	0

#	ARTICLE	IF	CITATIONS
2465	Identification and expression analysis of SQUAMOSA promoter-binding protein (SBP) genes in mungbean. <i>Plant Biotechnology Reports</i> , 0, , .	0.9	0
2466	Longitudinal Study of <i>Lactococcus</i> Phages in a Canadian Cheese Factory. <i>Applied and Environmental Microbiology</i> , 2023, 89, .	1.4	3
2467	Identification of d-arabinan-degrading enzymes in mycobacteria. <i>Nature Communications</i> , 2023, 14, .	5.8	5
2468	Human CEACAM1 is targeted by a <i>Streptococcus pyogenes</i> adhesin implicated in puerperal sepsis pathogenesis. <i>Nature Communications</i> , 2023, 14, .	5.8	4
2469	VirClust – A Tool for Hierarchical Clustering, Core Protein Detection and Annotation of (Prokaryotic) Viruses. <i>Viruses</i> , 2023, 15, 1007.	1.5	10
2470	Extensive genome analysis identifies novel plasmid families in <i>Clostridium perfringens</i> . <i>Microbial Genomics</i> , 2023, 9, .	1.0	0
2471	Thai Local Chicken Breeds, Chee Fah and Fah Luang, Originated from Chinese Black-Boned Chicken with Introgression of Red Junglefowl and Domestic Chicken Breeds. <i>Sustainability</i> , 2023, 15, 6878.	1.6	3
2474	Uncovering the biogeographic pattern of the widespread nematode-trapping fungi <i>Arthrobotrys oligospora</i> : watershed is the key. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
2475	Comprehensive analysis and expression profiles of the AP2/ERF gene family during spring bud break in tea plant (<i>Camellia sinensis</i>). <i>BMC Plant Biology</i> , 2023, 23, .	1.6	2
2476	<i>Arabidopsis</i> nicotianamine synthases comprise a common core-NAS domain fused to a variable autoinhibitory C-terminus. <i>Journal of Biological Chemistry</i> , 2023, 299, 104732.	1.6	0
2477	Host-Specific Diversity of Culturable Bacteria in the Gut Systems of Fungus-Growing Termites and Their Potential Functions towards Lignocellulose Bioconversion. <i>Insects</i> , 2023, 14, 403.	1.0	11
2478	Diversity, distribution, and functional potentials of magroviruses from marine and brackish waters. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
2480	Microbial Processes of Methane Oxidation at the Kara Sea Sites of Gas Prospecting. <i>Microbiology</i> , 2023, 92, 171-182.	0.5	1
2481	The adenomatous polyposis coli protein 30 years on. <i>Seminars in Cell and Developmental Biology</i> , 2023, 150-151, 28-34.	2.3	2
2495	Long-Read Metagenomics and CAZyme Discovery. <i>Methods in Molecular Biology</i> , 2023, , 253-284.	0.4	0
2514	Characterization of RNase J. <i>Methods in Enzymology</i> , 2023, , 177-215.	0.4	1
2623	New insights to diversity and enzyme-substrate interactions of fungal glucuronoyl esterases. <i>Applied Microbiology and Biotechnology</i> , 2023, 107, 4447-4457.	1.7	0
2783	Amplicon-Based Nanopore Sequencing of Patients Infected by the SARS-CoV-2 Omicron (B.1.1.529) Variant in India. <i>Advances in Experimental Medicine and Biology</i> , 2023, , 271-283.	0.8	0

#	ARTICLE	IF	CITATIONS
3319	Fungal carboxylate transporters: recent manipulations and applications. <i>Applied Microbiology and Biotechnology</i> , 2023, 107, 5909-5922.	1.7	0
3474	Entry and egress of human astroviruses. <i>Advances in Virus Research</i> , 2023, , 81-119.	0.9	0
3476	A Comparison Study of Medicinal Plants Used Against SARS-CoV-2 and Those Recommended Against Malaria in Africa. , 2023, , 549-573.		0
3506	BacWGSpipe: A Snakemake Workflow for a Complete Analysis of Bacterial Whole-Genome Sequencing Data. , 2023, , .		0
3636	Combining data mining with rigorous whole-genome phylogenetics enables detailed comparative genomics from over 2.3 million genomes across Coronaviridae. , 2023, , .		0
3714	Anelloviridae taxonomy update 2023. <i>Archives of Virology</i> , 2023, 168, .	0.9	3
3847	Phylogenomics of Life Kingdom's Deubiquitinases. , 2023, , .		0
3848	Exploring the Archaeal Virosphere by Metagenomics. <i>Methods in Molecular Biology</i> , 2024, , 1-22.	0.4	0
4024	Analysis of Curtobacterium Genomic Sequences Reveals the Basis for Further Taxonomic Refinements. , 2023, , .		0
4064	Bacteriophage Taxonomy: A Continually Evolving Discipline. <i>Methods in Molecular Biology</i> , 2024, , 27-45.	0.4	0
4276	MBD2 couples DNA methylation to transposable element silencing during male gametogenesis. <i>Nature Plants</i> , 2024, 10, 13-24.	4.7	1
4388	High-resolution tracking of unconfined zebrafish behavior reveals stimulatory and anxiolytic effects of psilocybin. <i>Molecular Psychiatry</i> , 0, , .	4.1	2
4393	Possible solutions for the conservation of benthic habitats and organisms. , 2024, , 191-236.		0
4464	Efficient Multi-purpose Video Annotation for Fast Labeling. , 2023, , .		1
4466	Bacterial polyynes uncovered: a journey through their bioactive properties, biosynthetic mechanisms, and sustainable production strategies. <i>Natural Product Reports</i> , 0, , .	5.2	0
4605	Genomics of the Thermophilic Bacterium <i>Thermosulfidibacter takaii</i> Reveals Novel Lineage of Deep-Branching Bacterial Phylum. <i>Indian Journal of Microbiology</i> , 0, , .	1.5	0