

# Assembling Single-Cell Genomes and Mini-Metagenomes

Journal of Computational Biology

20, 714-737

DOI: [10.1089/cmb.2013.0084](https://doi.org/10.1089/cmb.2013.0084)

Citation Report

#	ARTICLE	IF	CITATIONS
1	The role of memory for past test in the underconfidence with practice effect.. Journal of Experimental Psychology: Learning Memory and Cognition, 2007, 33, 238-244.	0.7	128
2	Advancements toward a systems level understanding of the human oral microbiome. Frontiers in Cellular and Infection Microbiology, 2014, 4, 98.	1.8	76
3	Draft Genome Sequence of Mycobacterium cosmeticum DSM 44829. Genome Announcements, 2014, 2, .	0.8	1
4	Draft Genome Sequence of Mycobacterium vulneris DSM 45247 <sup>T</sup>. Genome Announcements, 2014, 2, .	0.8	4
5	Draft Genome Sequence of Staphylococcus aureus subsp. <i>aureus</i> Strain HG003, an NCTC8325 Derivative. Genome Announcements, 2014, 2, .	0.8	11
6	Draft Genome Sequence of Leuconostoc mesenteroides P45 Isolated from Pulque, a Traditional Mexican Alcoholic Fermented Beverage. Genome Announcements, 2014, 2, .	0.8	7
7	Draft Genome Sequence of Thalassotalea sp. Strain ND16A Isolated from Eastern Mediterranean Sea Water Collected from a Depth of 1,055 Meters. Genome Announcements, 2014, 2, .	0.8	8
8	Genome Sequence of Legionella massiliensis, Isolated from a Cooling Tower Water Sample. Genome Announcements, 2014, 2, .	0.8	0
9	Draft Genome Sequence of Mycobacterium austroafricanum DSM 44191. Genome Announcements, 2014, 2, .	0.8	3
10	Draft Genome Sequence of Mycobacterium mageritense DSM 44476 <sup>T</sup>. Genome Announcements, 2014, 2, .	0.8	0
11	Draft Genome Sequence of Mycobacterium triplex DSM 44626. Genome Announcements, 2014, 2, .	0.8	0
12	Draft Genome Sequence of Mycobacterium neoaurum Strain DSM 44074 <sup>T</sup>. Genome Announcements, 2014, 2, .	0.8	2
13	ExSPAnDer: a universal repeat resolver for DNA fragment assembly. Bioinformatics, 2014, 30, i293-i301.	1.8	103
14	Single-Cell Genomics Reveals Hundreds of Coexisting Subpopulations in Wild <i>Prochlorococcus</i>. Science, 2014, 344, 416-420.	6.0	506
15	Impact of single-cell genomics and metagenomics on the emerging view of extremophile "microbial dark matter". Extremophiles, 2014, 18, 865-875.	0.9	133
16	Recent advances in genomic DNA sequencing of microbial species from single cells. Nature Reviews Genetics, 2014, 15, 577-584.	7.7	146
17	A case control study of environmental and occupational exposures associated with methicillin resistant Staphylococcus aureus nasal carriage in patients admitted to a rural tertiary care hospital in a high density swine region. Environmental Health, 2014, 13, 54.	1.7	19
18	Noncontiguous finished genome sequence and description of Virgibacillus massiliensis sp. nov., a moderately halophilic bacterium isolated from human gut. New Microbes and New Infections, 2015, 8, 78-88.	0.8	10

#	ARTICLE	IF	CITATIONS
19	Environmental marine pathogen isolation using mesocosm culture of sharpsnout seabream: striking genomic and morphological features of novel <i>Endozoicomonas</i> sp.. <i>Scientific Reports</i> , 2015, 5, 17609.	1.6	60
20	Complete Genome Sequence of <i>Corynebacterium pseudotuberculosis</i> Strain E19, Isolated from a Horse in Chile. <i>Genome Announcements</i> , 2015, 3, .	0.8	3
21	Draft Genome Sequence of <i>Mycobacterium tuberculosis</i> Strain MT43, a Representative of the Manu2 Genotype. <i>Genome Announcements</i> , 2015, 3, .	0.8	1
22	Draft Genome Sequence of <i>Ardenticatena maritima</i> 110S, a Thermophilic Nitrate- and Iron-Reducing Member of the <i>Chloroflexi</i> Class <i>Ardenticatena</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	31
23	Draft Genome Sequence of <i>Ornatilinea apprima</i> P3M-1, an Anaerobic Member of the <i>Chloroflexi</i> Class <i>Anaerolineae</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	20
24	Draft Genome of <i>Thermanaerotherix daxensis</i> GNS-1, a Thermophilic Facultative Anaerobe from the <i>Chloroflexi</i> Class <i>Anaerolineae</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	28
25	Draft Genome Sequence of <i>Mycobacterium mucogenicum</i> Strain CSUR P2099. <i>Genome Announcements</i> , 2015, 3, .	0.8	1
26	Genome sequence of <i>Oceanobacillus picturae</i> strain S1, an halophilic bacterium first isolated in human gut. <i>Standards in Genomic Sciences</i> , 2015, 10, 91.	1.5	16
27	High-quality draft genome sequence of a new phytase-producing microorganism <i>Pantoea</i> sp. 3.5.1. <i>Standards in Genomic Sciences</i> , 2015, 10, 95.	1.5	3
28	Draft Genome Sequence of <i>Gulbenkiania mobilis</i> Strain MB1, a Sulfur-Metabolizing Thermophile Isolated from a Hot Spring in Central India. <i>Genome Announcements</i> , 2015, 3, .	0.8	6
29	Draft Genome Sequence of <i>Mycobacterium neworleansense</i> Strain ATCC 49404 T. <i>Genome Announcements</i> , 2015, 3, .	0.8	0
30	Draft Genome Sequence of <i>Levilinea saccharolytica</i> KIBI-1, a Member of the <i>Chloroflexi</i> Class <i>Anaerolineae</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	28
31	Draft Genome Sequence of <i>Mycobacterium peregrinum</i> Strain CSUR P2098. <i>Genome Announcements</i> , 2015, 3, .	0.8	1
32	Draft Genome Sequence of <i>Herpetosiphon geysericola</i> GC-42, a Nonphototrophic Member of the <i>Chloroflexi</i> Class <i>Chloroflexia</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	27
33	Draft Genome Sequence of <i>Candidatus Bacteroides pericalifornicus</i> , a New Member of the Bacteroidetes Phylum Found within the Oral Microbiome of Periodontitis Patients. <i>Genome Announcements</i> , 2015, 3, .	0.8	11
34	Draft Genome Sequence of <i>Mycobacterium lentiflavum</i> CSUR P1491. <i>Genome Announcements</i> , 2015, 3, .	0.8	1
35	Draft Genome Sequence of <i>Bacillus ginsengihumi</i> Strain M2.11 with Phytase Activity. <i>Genome Announcements</i> , 2015, 3, .	0.8	1
36	Draft Genome Sequence of <i>Leptolinea tardivitalis</i> YMTK-2, a Mesophilic Anaerobe from the <i>Chloroflexi</i> Class <i>Anaerolineae</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	33

#	ARTICLE	IF	CITATIONS
37	Draft Genome Sequence of the Marine Pathogen <i>Vibrio coralliilyticus</i> RE22. <i>Genome Announcements</i> , 2015, 3, .	0.8	6
38	Comparison of a Real-Time Multiplex PCR and Sequotyping Assay for Pneumococcal Serotyping. <i>PLoS ONE</i> , 2015, 10, e0137349.	1.1	24
39	Systematic Characteristic Exploration of the Chimeras Generated in Multiple Displacement Amplification through Next Generation Sequencing Data Reanalysis. <i>PLoS ONE</i> , 2015, 10, e0139857.	1.1	24
40	Expanding the Described Metabolome of the Marine Cyanobacterium <i>Moorea producens</i> JHB through Orthogonal Natural Products Workflows. <i>PLoS ONE</i> , 2015, 10, e0133297.	1.1	40
41	Genome Sequence of the Electrogenic Petroleum-Degrading <i>Thalassospira</i> sp. Strain HJ. <i>Genome Announcements</i> , 2015, 3, .	0.8	5
42	Genome Sequences of Five Disinfectant-Resistant <i>Listeria monocytogenes</i> Strains from Two Iberian Pork-Processing Plants. <i>Genome Announcements</i> , 2015, 3, .	0.8	6
43	Draft Genome Sequences of Five <i>Legionella pneumophila</i> Strains Isolated from Environmental Water Samples. <i>Genome Announcements</i> , 2015, 3, .	0.8	2
44	Draft Genome Sequence of <i>Mycobacterium tuberculosis</i> Strain MT11, Which Represents a New Lineage. <i>Genome Announcements</i> , 2015, 3, .	0.8	1
45	Draft Genome Sequence of <i>Mycobacterium europaeum</i> Strain CSUR P1344. <i>Genome Announcements</i> , 2015, 3, .	0.8	0
46	Draft Genome Sequence of <i>Mycobacterium bohemicum</i> Strain DSM 44277 T. <i>Genome Announcements</i> , 2015, 3, .	0.8	0
47	Spongiosine Production by a <i>Vibrio harveyi</i> Strain Associated with the Sponge <i>Tectitethya crypta</i> . <i>Journal of Natural Products</i> , 2015, 78, 493-499.	1.5	28
48	DIME: A Novel Framework for De Novo Metagenomic Sequence Assembly. <i>Journal of Computational Biology</i> , 2015, 22, 159-177.	0.8	15
49	Genome Sequence Databases: Sequencing and Assembly. , 2015, , .		2
50	Genome Sequence of the Clinical Isolate <i>Staphylococcus aureus</i> subsp. <i>aureus</i> Strain UAMS-1. <i>Genome Announcements</i> , 2015, 3, .	0.8	29
51	Draft Genome Sequence of the <i>Lactobacillus mucosae</i> Strain Marseille. <i>Genome Announcements</i> , 2015, 3, .	0.8	4
52	Reconstructing each cell's genome within complex microbial communities—dream or reality?. <i>Frontiers in Microbiology</i> , 2014, 5, 771.	1.5	58
53	Combining Mass Spectrometric Metabolic Profiling with Genomic Analysis: A Powerful Approach for Discovering Natural Products from Cyanobacteria. <i>Journal of Natural Products</i> , 2015, 78, 1671-1682.	1.5	156
54	Single-cell genomics-based analysis of virus–host interactions in marine surface bacterioplankton. <i>ISME Journal</i> , 2015, 9, 2386-2399.	4.4	207

#	ARTICLE	IF	CITATIONS
55	High-Resolution Analysis by Whole-Genome Sequencing of an International Lineage (Sequence Type 111) of <i>Pseudomonas aeruginosa</i> Associated with Metallo-Carbapenemases in the United Kingdom. <i>Journal of Clinical Microbiology</i> , 2015, 53, 2622-2631.	1.8	50
56	Exploring the Limits for Reduction of Plastid Genomes: A Case Study of the Mycoheterotrophic Orchids <i>Epipogium aphyllum</i> and <i>Epipogium roseum</i> . <i>Genome Biology and Evolution</i> , 2015, 7, 1179-1191.	1.1	116
57	The use of evolutionary approaches to understand single cell genomes. <i>Frontiers in Microbiology</i> , 2015, 6, 174.	1.5	7
58	Assessing the performance of the Oxford Nanopore Technologies MinION. <i>Biomolecular Detection and Quantification</i> , 2015, 3, 1-8.	7.0	436
59	It's a dirty job â€” A robust method for the purification and de novo genome assembly of <i>Cryptosporidium</i> from clinical material. <i>Journal of Microbiological Methods</i> , 2015, 113, 10-12.	0.7	12
60	Faustovirus, an Asfarvirus-Related New Lineage of Giant Viruses Infecting Amoebae. <i>Journal of Virology</i> , 2015, 89, 6585-6594.	1.5	191
61	Single-cell genomics of a rare environmental alphaproteobacterium provides unique insights into Rickettsiaceae evolution. <i>ISME Journal</i> , 2015, 9, 2373-2385.	4.4	51
62	Draft genome sequence of <i>Acinetobacter</i> sp. neg1 capable of degrading ochratoxin A. <i>FEMS Microbiology Letters</i> , 2015, 362, .	0.7	12
63	Genetic variation and the de novo assembly of human genomes. <i>Nature Reviews Genetics</i> , 2015, 16, 627-640.	7.7	310
64	InteMAP: Integrated metagenomic assembly pipeline for NGS short reads. <i>BMC Bioinformatics</i> , 2015, 16, 244.	1.2	25
65	Macrotene chromosomes provide insights to a new mechanism of high-order gene amplification in eukaryotes. <i>Nature Communications</i> , 2015, 6, 6154.	5.8	13
66	Whole-Genome Sequence and Annotation of Octopine-Utilizing <i>Pseudomonas kilonensis</i> (Previously <i>P.</i> ) Tj ETQq1 1.0,784314 rgBT /Ove	0.8	12
67	Mitochondrial Genome of <i>Palpitomonas bilix</i> : Derived Genome Structure and Ancestral System for Cytochrome <i>c</i> Maturation. <i>Genome Biology and Evolution</i> , 2016, 8, 3090-3098.	1.1	24
68	Draft Genome Sequence of a Multidrug-Resistant <i>Klebsiella quasipneumoniae</i> subsp. <i>similipneumoniae</i> Isolate from a Clinical Source. <i>Genome Announcements</i> , 2016, 4, .	0.8	10
69	Draft Genome Sequences of 40 <i>Salmonella enterica</i> Serovar Typhimurium Strains Isolated from Humans and Food in Brazil. <i>Genome Announcements</i> , 2016, 4, .	0.8	5
70	Archive of bacterial community in anhydrite crystals from a deep-sea basin provides evidence of past oil-spilling in a benthic environment in the Red Sea. <i>Biogeosciences</i> , 2016, 13, 6405-6417.	1.3	1
71	Distribution of <i>Prochlorococcus</i> Ecotypes in the Red Sea Basin Based on Analyses of <i>rpoC1</i> Sequences. <i>Frontiers in Marine Science</i> , 2016, 3, .	1.2	17
72	Demethylase Inhibitor Fungicide Resistance in <i>Pyrenophora teres</i> f. sp. <i>teres</i> Associated with Target Site Modification and Inducible Overexpression of <i>Cyp51</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 1279.	1.5	74

#	ARTICLE	IF	CITATIONS
73	Comprehensive Phylogenetic Analysis of Bovine Non-aureus Staphylococci Species Based on Whole-Genome Sequencing. <i>Frontiers in Microbiology</i> , 2016, 7, 1990.	1.5	49
74	Phylogenomics and Plastome Evolution of Tropical Forest Grasses ( <i>Leptaspis</i> , <i>Streptochaeta</i> : Poaceae). <i>Frontiers in Plant Science</i> , 2016, 7, 1993.	1.7	49
75	Sequencing rare marine actinomycete genomes reveals high density of unique natural product biosynthetic gene clusters. <i>Microbiology (United Kingdom)</i> , 2016, 162, 2075-2086.	0.7	61
76	Genomic characterization of symbiotic mycoplasmas from the stomach of deep-sea isopod <i>Bathynomus</i> sp. <i>Environmental Microbiology</i> , 2016, 18, 2646-2659.	1.8	49
77	Draft Genome Sequence of <i>Vibrio toranzoniae</i> Strain CECT 7225 T. <i>Genome Announcements</i> , 2016, 4, .	0.8	1
78	Genome Sequence of <i>Kocuria palustris</i> Strain W4. <i>Genome Announcements</i> , 2016, 4, .	0.8	0
79	Massive Amplification at an Unselected Locus Accompanies Complex Chromosomal Rearrangements in Yeast. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 1201-1215.	0.8	6
80	Draft Genome Sequence of Low-Passage Clinical Isolate <i>Porphyromonas gingivalis</i> MP4-504. <i>Genome Announcements</i> , 2016, 4, .	0.8	8
81	Draft Genome Sequence of <i>Tepidimonas taiwanensis</i> Strain MB2, a Chemolithotrophic Thermophile Isolated from a Hot Spring in Central India. <i>Genome Announcements</i> , 2016, 4, .	0.8	8
82	Draft Genome Sequence of the New Pathogen for Bivalve Larvae <i>Vibrio bivalvicida</i> . <i>Genome Announcements</i> , 2016, 4, .	0.8	2
83	An updated view of plasmid conjugation and mobilization in <i>Staphylococcus</i> . <i>Mobile Genetic Elements</i> , 2016, 6, e1208317.	1.8	83
84	Draft Genome Sequence of <i>Actinomyces odontolyticus</i> subsp. <i>actinosynbacter</i> Strain XH001, the Basibiont of an Oral TM7 Epibiont. <i>Genome Announcements</i> , 2016, 4, .	0.8	32
85	Draft Genome Sequence of the <i>Bactrocera oleae</i> Symbiont <i>Candidatus</i> <i>Erwinia dacicola</i> . <i>Genome Announcements</i> , 2016, 4, .	0.8	30
86	Draft Genome Sequences of <i>Mycobacterium kansasii</i> Strains 1010001454, 1010001458, 1010001468, 1010001493, 1010001495, and 1010001469, Isolated from Environmental Sources. <i>Genome Announcements</i> , 2016, 4, .	0.8	6
87	Polyclonal emergence of vancomycin-resistant <i>Enterococcus faecium</i> in Australia. <i>Journal of Antimicrobial Chemotherapy</i> , 2016, 72, dkw539.	1.3	21
88	Genome Sequence and Analysis of a Stress-Tolerant, Wild-Derived Strain of <i>Saccharomyces cerevisiae</i> Used in Biofuels Research. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 1757-1766.	0.8	61
89	Complete Genome Sequence of <i>Mesorhizobium ciceri</i> bv. <i>biserrulae</i> Strain WSM1284, an Efficient Nitrogen-Fixing Microsymbiont of the Pasture Legume <i>Biserrula pelecinus</i> . <i>Genome Announcements</i> , 2016, 4, .	0.8	5
90	Substrate preference, uptake kinetics and bioenergetics in a facultatively autotrophic, thermoacidophilic crenarchaeote. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw069.	1.3	10

#	ARTICLE	IF	CITATIONS
91	Susceptibility to chlorhexidine amongst multidrug-resistant clinical isolates of <i>Staphylococcus epidermidis</i> from bloodstream infections. <i>International Journal of Antimicrobial Agents</i> , 2016, 48, 86-90.	1.1	38
92	rnaQUAST: a quality assessment tool for <i>de novo</i> transcriptome assemblies. <i>Bioinformatics</i> , 2016, 32, 2210-2212.	1.8	106
93	MeCorS: Metagenome-enabled error correction of single cell sequencing reads. <i>Bioinformatics</i> , 2016, 32, 2199-2201.	1.8	8
94	Identification and functional study of type III-A CRISPR-Cas systems in clinical isolates of <i>Staphylococcus aureus</i> . <i>International Journal of Medical Microbiology</i> , 2016, 306, 686-696.	1.5	50
95	Draft Genome Sequence of <i>Stenotrophomonas maltophilia</i> SBo1 Isolated from <i>Bactrocera oleae</i> . <i>Genome Announcements</i> , 2016, 4, .	0.8	9
96	Complete Genome Sequence of <i>Mesorhizobium ciceri</i> Strain CC1192, an Efficient Nitrogen-Fixing Microsymbiont of <i>Cicer arietinum</i> . <i>Genome Announcements</i> , 2016, 4, .	0.8	19
97	Draft Genome Sequence of the Emerging Bivalve Pathogen <i>Vibrio tubiashii</i> subsp. <i>europaeus</i> . <i>Genome Announcements</i> , 2016, 4, .	0.8	2
98	Short communication: Heat-resistant <i>Escherichia coli</i> as potential persistent reservoir of extended-spectrum $\beta$ -lactamases and Shiga toxin-encoding phages in dairy. <i>Journal of Dairy Science</i> , 2016, 99, 8622-8632.	1.4	30
99	Region-wide and ecotype-specific differences in demographic histories of threespine stickleback populations, estimated from whole genome sequences. <i>Molecular Ecology</i> , 2016, 25, 5187-5202.	2.0	34
100	Metagenomics and Bioinformatics in Microbial Ecology: Current Status and Beyond. <i>Microbes and Environments</i> , 2016, 31, 204-212.	0.7	76
101	Laser capture microdissection microscopy and genome sequencing of the avian malaria parasite, <i>Plasmodium relictum</i> . <i>Parasitology Research</i> , 2016, 115, 4503-4510.	0.6	20
102	Whole-genome comparative analysis of the pathogen <i>Piscirickettsia salmonis</i> . <i>Veterinary Microbiology</i> , 2016, 196, 36-43.	0.8	27
103	Translational Biomedical Informatics. <i>Advances in Experimental Medicine and Biology</i> , 2016, , .	0.8	1
104	Metagenomics and Single-Cell Omics Data Analysis for Human Microbiome Research. <i>Advances in Experimental Medicine and Biology</i> , 2016, 939, 117-137.	0.8	3
105	Complete Genome Sequence of <i>Streptomyces parvulus</i> 2297, Integrating Site-Specifically with Actinophage R4. <i>Genome Announcements</i> , 2016, 4, .	0.8	2
106	Draft Genome Sequence of <i>Mycobacterium acapulcensis</i> Strain CSURP1424. <i>Genome Announcements</i> , 2016, 4, .	0.8	1
107	Chromosomer: a reference-based genome arrangement tool for producing draft chromosome sequences. <i>GigaScience</i> , 2016, 5, 38.	3.3	68
108	Draft genome of <i>Prochlorothrix hollandica</i> CCAP 1490/1T (CALU1027), the chlorophyll a/b-containing filamentous cyanobacterium. <i>Standards in Genomic Sciences</i> , 2016, 11, 82.	1.5	0

#	ARTICLE	IF	CITATIONS
109	Draft Genome Sequence of <i>Cutaneotrichosporon curvatus</i> DSM 101032 (Formerly <i>Cryptococcus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 4, .	0.8	12
110	Microbial Culturomics to Map Halophilic Bacterium in Human Gut: Genome Sequence and Description of <i>Oceanobacillus jeddahense</i> sp. nov.. <i>OMICS A Journal of Integrative Biology</i> , 2016, 20, 248-258.	1.0	11
111	Complete genome sequence of <i>Peptoclostridium difficile</i> strain Z31. <i>Gut Pathogens</i> , 2016, 8, 11.	1.6	17
112	Host-Associated Genomic Features of the Novel Uncultured Intracellular Pathogen <i>Ca. Ichthyocystis</i> Revealed by Direct Sequencing of Epitheliocysts. <i>Genome Biology and Evolution</i> , 2016, 8, 1672-1689.	1.1	12
113	Complete genome of <i>Staphylococcus aureus</i> Tager 104 provides evidence of its relation to modern systemic hospital-acquired strains. <i>BMC Genomics</i> , 2016, 17, 179.	1.2	6
114	Comprehensive molecular characterization of <i>Methylobacterium extorquens</i> AM1 adapted for 1-butanol tolerance. <i>Biotechnology for Biofuels</i> , 2016, 9, 84.	6.2	42
115	Genome Sequence of <i>Arthrobacter antarcticus</i> Strain W2, Isolated from a Slaughterhouse. <i>Genome Announcements</i> , 2016, 4, .	0.8	1
116	The Phormidolide Biosynthetic Gene Cluster: A <i>trans</i> -AT PKS Pathway Encoding a Toxic Macrocytic Polyketide. <i>ChemBioChem</i> , 2016, 17, 164-173.	1.3	36
117	Molecular mechanisms underlying the close association between soil <i>Burkholderia</i> and fungi. <i>ISME Journal</i> , 2016, 10, 253-264.	4.4	118
118	Discovery of a Bacterial Glycoside Hydrolase Family 3 (GH3) $\beta$ -Glucosidase with Myrosinase Activity from a <i>Citrobacter</i> Strain Isolated from Soil. <i>Journal of Agricultural and Food Chemistry</i> , 2016, 64, 1520-1527.	2.4	57
119	Whole genome sequence of the emerging oomycete pathogen <i>Pythium insidiosum</i> strain CDC-B5653 isolated from an infected human in the USA. <i>Genomics Data</i> , 2016, 7, 60-61.	1.3	19
120	Development and Validation of a PCR Assay To Detect the Prairie Epidemic Strain of <i>Pseudomonas aeruginosa</i> from Patients with Cystic Fibrosis. <i>Journal of Clinical Microbiology</i> , 2016, 54, 489-491.	1.8	11
121	MEGAnnotator: a user-friendly pipeline for microbial genomes assembly and annotation. <i>FEMS Microbiology Letters</i> , 2016, 363, fnw049.	0.7	94
122	Whole-Genome Sequencing Reveals a New Genospecies of <i>Methylobacterium</i> sp. GX513, Isolated from <i>Vitis vinifera</i> L. Xylem Sap. <i>Genome Announcements</i> , 2016, 4, .	0.8	2
123	Carbapenem- and Colistin-Resistant <i>Enterobacter cloacae</i> from Delta, Colorado, in 2015. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 3141-3144.	1.4	29
124	Complete genome sequence and description of <i>Lactococcus garvieae</i> M14 isolated from Algerian fermented milk. <i>New Microbes and New Infections</i> , 2016, 10, 122-131.	0.8	9
125	Emerging pathogens of gilthead seabream: characterisation and genomic analysis of novel intracellular $\beta$ -proteobacteria. <i>ISME Journal</i> , 2016, 10, 1791-1803.	4.4	34
126	Global metagenomic survey reveals a new bacterial candidate phylum in geothermal springs. <i>Nature Communications</i> , 2016, 7, 10476.	5.8	189



#	ARTICLE	IF	CITATIONS
127	TruSPAdes: barcode assembly of TruSeq synthetic long reads. <i>Nature Methods</i> , 2016, 13, 248-250.	9.0	40
128	Draft Genome Sequence of a <i>Klebsiella pneumoniae</i> Carbapenemase-Positive Sequence Type 111 <i>Pseudomonas aeruginosa</i> Strain. <i>Genome Announcements</i> , 2016, 4, .	0.8	3
129	Functional Comparison of Molluscum Contagiosum Virus vFLIP MC159 with Murine Cytomegalovirus M36/vICA and M45/vIRA Proteins. <i>Journal of Virology</i> , 2016, 90, 2895-2905.	1.5	15
130	High-Quality Draft Genome Sequence of Low-pH-Active <i>Veillonella parvula</i> Strain SHI-1, Isolated from Human Saliva within an In Vitro Oral Biofilm Model. <i>Genome Announcements</i> , 2016, 4, .	0.8	1
131	<sc>hybrid</sc>SPA<sc>des</sc>: an algorithm for hybrid assembly of short and long reads. <i>Bioinformatics</i> , 2016, 32, 1009-1015.	1.8	463
132	Linear-time superbubble identification algorithm for genome assembly. <i>Theoretical Computer Science</i> , 2016, 609, 374-383.	0.5	16
133	The Connection between Persistent, Disinfectant-Resistant <i>Listeria monocytogenes</i> Strains from Two Geographically Separate Iberian Pork Processing Plants: Evidence from Comparative Genome Analysis. <i>Applied and Environmental Microbiology</i> , 2016, 82, 308-317.	1.4	95
134	Single-cell genomics of uncultivated deep-branching magnetotactic bacteria reveals a conserved set of magnetosome genes. <i>Environmental Microbiology</i> , 2016, 18, 21-37.	1.8	115
135	A <sc>i>R</i></sc><i>ickettsiales</i> symbiont of amoebae with ancient features. <i>Environmental Microbiology</i> , 2016, 18, 2326-2342.	1.8	73
136	The clinically approved antiviral drug sofosbuvir inhibits Zika virus replication. <i>Scientific Reports</i> , 2017, 7, 40920.	1.6	167
137	MetaSort untangles metagenome assembly by reducing microbial community complexity. <i>Nature Communications</i> , 2017, 8, 14306.	5.8	52
138	Discovery of anaerobic lithoheterotrophic haloarchaea, ubiquitous in hypersaline habitats. <i>ISME Journal</i> , 2017, 11, 1245-1260.	4.4	79
139	Transcriptomic responses of the olive fruit fly <i>Bactrocera oleae</i> and its symbiont <i>Candidatus Erwinia dacicola</i> to olive feeding. <i>Scientific Reports</i> , 2017, 7, 42633.	1.6	58
140	Comparative analysis of <i>Corynebacterium glutamicum</i> genomes: a new perspective for the industrial production of amino acids. <i>BMC Genomics</i> , 2017, 18, 940.	1.2	35
141	Draft Genome Sequence of <i>Pseudomonas hussainii</i> Strain MB3, a Denitrifying Aerobic Bacterium Isolated from the Rhizospheric Region of Mangrove Trees in the Andaman Islands, India. <i>Genome Announcements</i> , 2017, 5, .	0.8	4
142	Genome sequence of three <i>Psychrobacter</i> sp. strains with potential applications in bioremediation. <i>Genomics Data</i> , 2017, 12, 7-10.	1.3	21
143	Global Molecular Epidemiology of IMP-Producing Enterobacteriaceae. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	61
144	Draft Genome Sequence of the Acidophilic, Halotolerant, and Iron/Sulfur-Oxidizing Acidihalobacter <i>prosperus</i> DSM 14174 (Strain V6). <i>Genome Announcements</i> , 2017, 5, .	0.8	15

#	ARTICLE	IF	CITATIONS
145	Comparative genomics uncovers the prolific and distinctive metabolic potential of the cyanobacterial genus <i>Moorea</i> . Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 3198-3203.	3.3	77
146	Development of standard methods for Zika virus propagation, titration, and purification. Journal of Virological Methods, 2017, 246, 65-74.	1.0	58
147	Comparison of Whole-Genome Sequencing Methods for Analysis of Three Methicillin-Resistant <i>Staphylococcus aureus</i> Outbreaks. Journal of Clinical Microbiology, 2017, 55, 1946-1953.	1.8	58
148	Permanent Draft Genome Sequence of the French Bean Symbiont <i>Rhizobium</i> sp. Strain RSm-3 Isolated from the Eastern Himalayan Region of India. Genome Announcements, 2017, 5, .	0.8	2
149	Genetic and Epidemiologic Trends of Norovirus Outbreaks in the United States from 2013 to 2016 Demonstrated Emergence of Novel GII.4 Recombinant Viruses. Journal of Clinical Microbiology, 2017, 55, 2208-2221.	1.8	222
150	Colistin Resistance in Carbapenem-Resistant <i>Klebsiella pneumoniae</i> Mediated by Chromosomal Integration of Plasmid DNA. Antimicrobial Agents and Chemotherapy, 2017, 61, .	1.4	9
151	MCR-1 and OXA-48 <i>In Vivo</i> Acquisition in KPC-Producing <i>Escherichia coli</i> after Colistin Treatment. Antimicrobial Agents and Chemotherapy, 2017, 61, .	1.4	74
152	Draft Genome Sequence of <i>Tannerella forsythia</i> Clinical Isolate 9610. Genome Announcements, 2017, 5, .	0.8	4
153	Draft Genome Sequence of <i>Mycobacterium boenickei</i> CIP 107829. Genome Announcements, 2017, 5, .	0.8	3
154	Draft Genome Sequence of <i>Chryseobacterium</i> Strain CBo1 Isolated from <i>Bactrocera oleae</i> . Genome Announcements, 2017, 5, .	0.8	4
155	Efficacy of Sterile Fecal Filtrate Transfer for Treating Patients With <i>Clostridium difficile</i> Infection. Gastroenterology, 2017, 152, 799-811.e7.	0.6	498
156	Genomic epidemiology of global VIM-producing Enterobacteriaceae. Journal of Antimicrobial Chemotherapy, 2017, 72, 2249-2258.	1.3	47
157	<i>Kiloniella majae</i> sp. nov., isolated from spider crab ( <i>Maja brachydactyla</i> ) and pullet carpet shell clam ( <i>Venerupis pullastra</i> ). Systematic and Applied Microbiology, 2017, 40, 274-279.	1.2	13
158	Short-chain alkanes fuel mussel and sponge <i>Cycloclasticus</i> symbionts from deep-sea gas and oil seeps. Nature Microbiology, 2017, 2, 17093.	5.9	80
159	Draft Genome Sequences of <i>Mycobacterium kansasii</i> Clinical Strains. Genome Announcements, 2017, 5, .	0.8	6
160	<i>Mycobacterium massilipolynesiensis</i> sp. nov., a rapidly-growing mycobacterium of medical interest related to <i>Mycobacterium phlei</i> . Scientific Reports, 2017, 7, 40443.	1.6	6
161	Draft Genome Sequence of the Fish Strain <i>Edwardsiella tarda</i> NCIMB 2034. Genome Announcements, 2017, 5, .	0.8	1
162	Complete Genome Sequence of <i>Arcobacter</i> sp. Strain LFT 1.7 Isolated from Great Scallop ( <i>Tritidacna</i> ) Tj ETQq1 1 0.784314 rgBT <sub>2</sub> /Overlook	0.8	0

#	ARTICLE	IF	CITATIONS
163	Permanent Draft Genome Sequence of <i>Rhizobium</i> sp. Strain LCM 4573, a Salt-Tolerant, Nitrogen-Fixing Bacterium Isolated from Senegalese Soils. <i>Genome Announcements</i> , 2017, 5, .	0.8	7
164	Draft Genome Sequence of <i>Anoxybacillus mongoliensis</i> Strain MB4, a Sulfur-Utilizing Aerobic Thermophile Isolated from a Hot Spring in Tattapani, Central India. <i>Genome Announcements</i> , 2017, 5, .	0.8	7
165	Characterization of Human Cytomegalovirus Genome Diversity in Immunocompromised Hosts by Whole-Genome Sequencing Directly From Clinical Specimens. <i>Journal of Infectious Diseases</i> , 2017, 215, 1673-1683.	1.9	88
166	Giant viruses with an expanded complement of translation system components. <i>Science</i> , 2017, 356, 82-85.	6.0	234
167	metaSPAdes: a new versatile metagenomic assembler. <i>Genome Research</i> , 2017, 27, 824-834.	2.4	2,779
168	Multilocus sequence typing of <i>Salmonella Typhimurium</i> reveals the presence of the highly invasive ST313 in Brazil. <i>Infection, Genetics and Evolution</i> , 2017, 51, 41-44.	1.0	41
169	A novel group of IncQ1 plasmids conferring multidrug resistance. <i>Plasmid</i> , 2017, 89, 22-26.	0.4	52
170	High-Throughput Next-Generation Sequencing of Polioviruses. <i>Journal of Clinical Microbiology</i> , 2017, 55, 606-615.	1.8	59
171	Molecular characterization of <i>Salmonella Typhimurium</i> isolated in Brazil by CRISPR-MVLST. <i>Journal of Microbiological Methods</i> , 2017, 133, 55-61.	0.7	22
172	Draft Genome Sequence of <i>Hydrogenibacillus schlegelii</i> MA48, a Deep-Branching Member of the <i>Bacilli</i> Class of <i>Firmicutes</i> . <i>Genome Announcements</i> , 2017, 5, .	0.8	7
173	Permanent Draft Genome Sequences of Three <i>Frankia</i> sp. Strains That Are Atypical, Noninfective, Ineffective Isolates. <i>Genome Announcements</i> , 2017, 5, .	0.8	4
174	Genomic divergence within non-photosynthetic cyanobacterial endosymbionts in rhopalodiacean diatoms. <i>Scientific Reports</i> , 2017, 7, 13075.	1.6	17
175	Metagenomic analysis reveals a green sulfur bacterium as a potential coral symbiont. <i>Scientific Reports</i> , 2017, 7, 9320.	1.6	29
176	Complete Genome Sequence of <i>Mesorhizobium ciceri</i> bv. <i>biserrulae</i> WSM1497, an Efficient Nitrogen-Fixing Microsymbiont of the Forage Legume <i>Biserrula pelecinus</i> . <i>Genome Announcements</i> , 2017, 5, .	0.8	6
177	Emergence of a <i>Streptococcus dysgalactiae</i> subspecies <i>equisimilis</i> stG62647-lineage associated with severe clinical manifestations. <i>Scientific Reports</i> , 2017, 7, 7589.	1.6	30
178	Draft Whole-Genome Assemblies of Drug-Resistant Clinical Isolates of <i>Klebsiella pneumoniae</i> from the Philippines. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
179	A New Reference Genome Assembly for the Microcrustacean <i>Daphnia pulex</i> . <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1405-1416.	0.8	95
180	Draft Genome Sequence of <i>Mycobacterium colombiense</i> . <i>Genome Announcements</i> , 2017, 5, .	0.8	0

#	ARTICLE	IF	CITATIONS
181	Genome Sequence of <i>Brevibacillus laterosporus</i> UNISS 18, a Pathogen of Mosquitoes and Flies. <i>Genome Announcements</i> , 2017, 5, .	0.8	5
182	A gut bacterial pathway metabolizes aromatic amino acids into nine circulating metabolites. <i>Nature</i> , 2017, 551, 648-652.	13.7	805
183	The genome nucleotide sequence of herpes simplex virus 1 strain L2. <i>Russian Journal of Bioorganic Chemistry</i> , 2017, 43, 140-142.	0.3	4
184	Lost in plasmids: next generation sequencing and the complex genome of the tick-borne pathogen <i>Borrelia burgdorferi</i> . <i>BMC Genomics</i> , 2017, 18, 422.	1.2	83
185	Bacteriocins of Non-aureus Staphylococci Isolated from Bovine Milk. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	46
186	Structural Variation Detection with Read Pair Information: An Improved Null Hypothesis Reduces Bias. <i>Journal of Computational Biology</i> , 2017, 24, 581-589.	0.8	3
187	Complete Genome Sequence of Roe Deer Picobirnavirus Strain PBV/roe_deer/SLO/D38-14/2014. <i>Genome Announcements</i> , 2017, 5, .	0.8	6
188	Complete Genome Sequence of Frog virus 3 , Isolated from a Strawberry Poison Frog ( <i>Oophaga</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 1	0.8	5
189	<i>In silico</i> analysis of virulence associated genes in genomes of <i>Escherichia coli</i> strains causing colibacillosis in poultry. <i>Journal of Veterinary Research (Poland)</i> , 2017, 61, 421-426.	0.3	2
190	Draft Genome Sequence of a Community-Acquired Methicillin-Resistant <i>Staphylococcus aureus</i> USA300 Isolate from a River Sample. <i>Genome Announcements</i> , 2017, 5, .	0.8	11
191	Draft Genome Sequences of <i>Alloscardovia macacae</i> UMA81211 and UMA81212, Isolated from the Feces of a Rhesus Macaque ( <i>Macaca mulatta</i> ). <i>Genome Announcements</i> , 2017, 5, .	0.8	0
192	Bioinformatic Analyses of Whole-Genome Sequence Data in a Public Health Laboratory. <i>Emerging Infectious Diseases</i> , 2017, 23, 1441-1445.	2.0	40
193	Dynamics of genomic innovation in the unicellular ancestry of animals. <i>ELife</i> , 2017, 6, .	2.8	121
194	Metagenomic Binning Recovers a Transcriptionally Active Gammaproteobacterium Linking Methanotrophy to Partial Denitrification in an Anoxic Oxygen Minimum Zone. <i>Frontiers in Marine Science</i> , 2017, 4, .	1.2	44
195	Comparative Genomic Analysis of Two <i>Vibrio toranzoniae</i> Strains with Different Virulence Capacity Reveals Clues on Its Pathogenicity for Fish. <i>Frontiers in Microbiology</i> , 2017, 8, 86.	1.5	6
196	Genomic Characterization of Dairy Associated <i>Leuconostoc</i> Species and Diversity of <i>Leuconostocs</i> in Undefined Mixed Mesophilic Starter Cultures. <i>Frontiers in Microbiology</i> , 2017, 8, 132.	1.5	43
197	A Perspective Study of Koumiss Microbiome by Metagenomics Analysis Based on Single-Cell Amplification Technique. <i>Frontiers in Microbiology</i> , 2017, 8, 165.	1.5	50
198	Genome-Centric Analysis of a Thermophilic and Cellulolytic Bacterial Consortium Derived from Composting. <i>Frontiers in Microbiology</i> , 2017, 8, 644.	1.5	61

#	ARTICLE	IF	CITATIONS
199	Clostridium chauvoei, an Evolutionary Dead-End Pathogen. <i>Frontiers in Microbiology</i> , 2017, 8, 1054.	1.5	33
200	Use of MALDI-TOF Mass Spectrometry for the Fast Identification of Gram-Positive Fish Pathogens. <i>Frontiers in Microbiology</i> , 2017, 8, 1492.	1.5	52
201	Methicillin Resistant Staphylococcus aureus Transmission in a Ghanaian Burn Unit: The Importance of Active Surveillance in Resource-Limited Settings. <i>Frontiers in Microbiology</i> , 2017, 8, 1906.	1.5	11
202	Mitochondrial genomes reveal recombination in the presumed asexual Fusarium oxysporum species complex. <i>BMC Genomics</i> , 2017, 18, 735.	1.2	65
203	Reduction of reactive red 241 by oxygen insensitive azoreductase purified from a novel strain Staphylococcus KU898286. <i>PLoS ONE</i> , 2017, 12, e0175551.	1.1	9
204	Lokiarchaea are close relatives of Euryarchaeota, not bridging the gap between prokaryotes and eukaryotes. <i>PLoS Genetics</i> , 2017, 13, e1006810.	1.5	136
205	Comparing and Evaluating Metagenome Assembly Tools from a Microbiologist's Perspective - Not Only Size Matters!. <i>PLoS ONE</i> , 2017, 12, e0169662.	1.1	186
206	Permanent draft genome sequence of Frankia sp. NRRL B-16219 reveals the presence of canonical nod genes, which are highly homologous to those detected in Candidatus Frankia Dg1 genome. <i>Standards in Genomic Sciences</i> , 2017, 12, 51.	1.5	17
207	Draft Genome Sequence of Carbapenemase-Producing Serratia marcescens Isolated from a Patient with Chronic Obstructive Pulmonary Disease. <i>Genome Announcements</i> , 2017, 5, .	0.8	12
208	Permanent Draft Genome Sequence of <i>Ensifer</i> sp. Strain LCM 4579, a Salt-Tolerant, Nitrogen-Fixing Bacterium Isolated from Senegalese Soil. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
209	Genome Sequences of Two Listeria monocytogenes Strains from Nectarines Associated with Listeriosis in 2014. <i>Genome Announcements</i> , 2017, 5, .	0.8	0
210	Permanent Draft Genome sequence for Frankia sp. strain Ccl49, a Nitrogen-Fixing Bacterium Isolated from Casuarina cunninghamiana that Infects Elaeagnaceae. <i>Journal of Genomics</i> , 2017, 5, 119-123.	0.6	6
211	Permanent Draft Genome Sequences for Mesorhizobium sp. Strains LCM 4576, LCM 4577, and ORS3428, Salt-Tolerant, Nitrogen-Fixing Bacteria Isolated from Senegalese Soils. <i>Genome Announcements</i> , 2017, 5, .	0.8	0
212	Analysis of single-cell genome sequences of bacteria and archaea. <i>Emerging Topics in Life Sciences</i> , 2017, 1, 249-255.	1.1	10
213	Genomic characterisation of clinical and environmental Pseudomonas putida group strains and determination of their role in the transfer of antimicrobial resistance genes to Pseudomonas aeruginosa. <i>BMC Genomics</i> , 2017, 18, 859.	1.2	48
214	eRP arrangement: a strategy for assembled genomic contig rearrangement based on replication profiling in bacteria. <i>BMC Genomics</i> , 2017, 18, 784.	1.2	4
215	Genomic characterization of eight <i>Ensifer</i> strains isolated from pristine caves and a whole genome phylogeny of <i>Ensifer</i> (Sinorhizobium). <i>Journal of Genomics</i> , 2017, 5, 12-15.	0.6	7
216	Draft Genome Sequences of <i>Neptuniibacter</i> sp. Strains LFT 1.8 and ATR 1.1. <i>Genome Announcements</i> , 2017, 5, .	0.8	0

#	ARTICLE	IF	CITATIONS
217	Neonatal intestinal colonization with extended-spectrum $\beta$ -lactamase-producing Enterobacteriaceae—a 5-year follow-up study. <i>Clinical Microbiology and Infection</i> , 2018, 24, 1004-1009.	2.8	19
218	Strain <i>Serratia</i> sp. S119: A potential biofertilizer for peanut and maize and a model bacterium to study phosphate solubilization mechanisms. <i>Applied Soil Ecology</i> , 2018, 126, 107-112.	2.1	28
219	Survival of antibiotic resistant bacteria following artificial solar radiation of secondary wastewater effluent. <i>Science of the Total Environment</i> , 2018, 626, 1005-1011.	3.9	17
220	A 12.3-kb Duplication Within the <i>VWF</i> Gene in Pigs Affected by Von Willebrand Disease Type 3. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 577-585.	0.8	7
221	Draft Genome Sequence of <i>Lactobacillus paracasei</i> DUP 13076, Which Exhibits Potent Antipathogenic Effects against <i>Salmonella enterica</i> Serovars Enteritidis, Typhimurium, and Heidelberg. <i>Genome Announcements</i> , 2018, 6, .	0.8	1
222	Draft Genome Sequences of Four Clinical <i>Legionella pneumophila</i> Isolates from Ontario, Canada. <i>Genome Announcements</i> , 2018, 6, .	0.8	0
223	Mitochondrial Genome of <i>Vannella croatica</i> (Amoebozoa, Discosea, Vannellida). <i>Journal of Eukaryotic Microbiology</i> , 2018, 65, 820-827.	0.8	3
224	The Genome Sequence of <i>Candidatus Fokinia solitaria</i> : Insights on Reductive Evolution in Rickettsiales. <i>Genome Biology and Evolution</i> , 2018, 10, 1120-1126.	1.1	40
225	Hopanoid-producing bacteria in the Red Sea include the major marine nitrite oxidizers. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	8
226	Ranavirus genotypes in the Netherlands and their potential association with virulence in water frogs ( <i>Pelophylax</i> spp.). <i>Emerging Microbes and Infections</i> , 2018, 7, 1-14.	3.0	11
227	Draft Genome Sequence of <i>Bowmanella denitrificans</i> JL63, a Bacterium Isolated from Whiteleg Shrimp ( <i>Litopenaeus vannamei</i> ) That Can Inhibit the Growth of <i>Vibrio parahaemolyticus</i> . <i>Genome Announcements</i> , 2018, 6, .	0.8	0
228	A giant virus infecting green algae encodes key fermentation genes. <i>Virology</i> , 2018, 518, 423-433.	1.1	92
229	<i>Sediminibacillus massiliensis</i> sp. nov., a moderately halophilic, Gram-positive bacterium isolated from a stool sample of a young Senegalese man. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 1225-1236.	0.7	3
230	Fructose liquid and solid formulations differently affect gut integrity, microbiota composition and related liver toxicity: a comparative in vivo study. <i>Journal of Nutritional Biochemistry</i> , 2018, 55, 185-199.	1.9	53
231	Complete Genome Sequences of Three Fish-Associated <i>Streptococcus agalactiae</i> Isolates. <i>Genome Announcements</i> , 2018, 6, .	0.8	5
232	<i>Lactobacillus backii</i> and <i>Pediococcus damnosus</i> isolated from 170-year-old beer recovered from a shipwreck lack the metabolic activities required to grow in modern lager beer. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	8
233	Genome sequence and description of <i>Haloferax massiliense</i> sp. nov., a new halophilic archaeon isolated from the human gut. <i>Extremophiles</i> , 2018, 22, 485-498.	0.9	14
234	Draft Genome Sequence of <i>Coxiella burnetii</i> Historical Strain Leningrad-2, Isolated from Blood of a Patient with Acute Q Fever in Saint Petersburg, Russia. <i>Genome Announcements</i> , 2018, 6, .	0.8	1

#	ARTICLE	IF	CITATIONS
235	Patterns of Genomic Variation in the Opportunistic Pathogen <i>Candida glabrata</i> Suggest the Existence of Mating and a Secondary Association with Humans. <i>Current Biology</i> , 2018, 28, 15-27.e7.	1.8	114
236	Clinical and molecular features of MDR livestock-associated MRSA ST9 with staphylococcal cassette chromosome <i>mecXII</i> in humans. <i>Journal of Antimicrobial Chemotherapy</i> , 2018, 73, 33-40.	1.3	47
237	Unravelling the Identity, Metabolic Potential and Global Biogeography of the Atmospheric Methane-oxidizing Upland Soil Cluster $\hat{\iota}$ . <i>Environmental Microbiology</i> , 2018, 20, 1016-1029.	1.8	103
238	Complete Genome Sequences of Three <i>Streptococcus agalactiae</i> Serotype Ia Isolates Obtained from Disease Outbreaks in Nile Tilapia ( <i>Oreochromis niloticus</i> ). <i>Genome Announcements</i> , 2018, 6, .	0.8	2
239	<sc>GPS</sc>it: An automated method for evolutionary analysis of nonculturable ciliated microeukaryotes. <i>Molecular Ecology Resources</i> , 2018, 18, 700-713.	2.2	36
240	Exploring the arthritogenicity of <i>Streptococcus dysgalactiae</i> subspecies <i>equisimilis</i> . <i>BMC Microbiology</i> , 2018, 18, 17.	1.3	8
241	First report of the isolation of bla <sub>IMI-1</sub> -producing colistin-heteroresistant <i>Enterobacter cloacae</i> in Japan, September 2016. <i>Journal of Infection and Chemotherapy</i> , 2018, 24, 941-943.	0.8	5
242	Complete Genome Sequence of <i>Xanthomonas arboricola</i> pv. <i>juglandis</i> Strain DW3F3, Isolated from a <i>Juglans regia</i> L. Bacterial Blighted Fruitlet. <i>Genome Announcements</i> , 2018, 6, .	0.8	12
243	Human Memory B Cells Targeting <i>Staphylococcus aureus</i> Exotoxins Are Prevalent with Skin and Soft Tissue Infection. <i>MBio</i> , 2018, 9, .	1.8	27
244	Draft Genome Sequence of <i>Methylovulum psychrotolerans</i> Sph1 T, an Obligate Methanotroph from Low-Temperature Environments. <i>Genome Announcements</i> , 2018, 6, .	0.8	5
245	The Enigmatic Genome of an Obligate Ancient <i>Spiroplasma</i> Symbiont in a Hadal Holothurian. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	38
246	<i>Staphylococcus edaphicus</i> sp. nov., Isolated in Antarctica, Harbors the <i>mecC</i> Gene and Genomic Islands with a Suspected Role in Adaptation to Extreme Environments. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	60
247	<i>Lactococcus lactis</i> Diversity in Undefined Mixed Dairy Starter Cultures as Revealed by Comparative Genome Analyses and Targeted Amplicon Sequencing of <i>epsD</i> . <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	25
248	Genetic studies to re-affiliate <i>Edwardsiella tarda</i> fish isolates to <i>Edwardsiella piscicida</i> and <i>Edwardsiella anguillarum</i> species. <i>Systematic and Applied Microbiology</i> , 2018, 41, 30-37.	1.2	58
249	Genome sequencing of two <i>Bacillus anthracis</i> strains: a virulent strain and a vaccinal strain. <i>Brazilian Journal of Microbiology</i> , 2018, 49, 18-19.	0.8	3
250	Additives in Plasticised Polyvinyl Chloride Fuel Microbial Nitrate Reduction at High pH: Implications for Nuclear Waste Disposal. <i>Frontiers in Environmental Science</i> , 2018, 6, .	1.5	12
251	Draft Genome Sequence of the Industrially Significant Bacterium <i>Bacillus amyloliquefaciens</i> NRRL 942. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	3
252	Draft Genome Sequences of <i>Mycobacterium senuense</i> Isolate GF74 and <i>Mycobacterium colombiense</i> Isolates GF28 and GF76 from a Swine Farm in Japan. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	16

#	ARTICLE	IF	CITATIONS
253	Draft Genome Sequence of the Industrially Significant Bacterium <i>Pseudomonas fluorescens</i> ATCC 13525. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	5
254	Whole-Genome Sequences of Two <i>Pseudomonas fluorescens</i> Strains Isolated from Roots of Tomato and Cucumber Plants. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	0
255	Draft Whole-Genome Sequence of <i>Leishmania</i> ( <i>Viannia</i> ) <i>braziliensis</i> Presenting <i>Leishmania</i> RNA Virus 1, from Western Amazon, Brazil. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	0
256	Genome wide characterization of enterotoxigenic <i>Escherichia coli</i> serogroup O6 isolates from multiple outbreaks and sporadic infections from 1975-2016. <i>PLoS ONE</i> , 2018, 13, e0208735.	1.1	8
257	Nine draft genome sequences of <i>Claviceps purpurea</i> s.lat., including <i>C. arundinis</i> , <i>C. humidiphila</i> , and <i>C. cf. spartinae</i> , pseudomolecules for the pitch canker pathogen <i>Fusarium circinatum</i> , draft genome of <i>Davidsoniella eucalypti</i> , <i>Grosmannia galeiformis</i> , <i>Quambalaria eucalypti</i> , and <i>Teratosphaeria destructans</i> . <i>IMA Fungus</i> , 2018, 9, 401-418.	1.7	31
259	Metatranscriptomic Investigation of Adaptation in NO and N2O Production From a Lab-Scale Nitrification Process Upon Repeated Exposure to Anoxic Aerobic Cycling. <i>Frontiers in Microbiology</i> , 2018, 9, 3012.	1.5	10
260	Draft Genome Sequence of <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Enteritidis MS 501, a Potential Human Pathogen Isolated from Red Lettuce ( <i>Lactuca sativa</i> var. <i>capitata</i> ) in Karlsruhe, Germany. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	4
261	Viral diversity of <i>Rhipicephalus microplus</i> parasitizing cattle in southern Brazil. <i>Scientific Reports</i> , 2018, 8, 16315.	1.6	72
262	Transmission of <i>mcr-1</i> -Producing Multidrug-resistant Enterobacteriaceae in Public Transportation in Guangzhou, China. <i>Clinical Infectious Diseases</i> , 2018, 67, S217-S224.	2.9	33
263	Genome Sequences of <i>Acholeplasma laidlawii</i> Strains with Increased Resistance to Tetracycline and Melittin. <i>Genome Announcements</i> , 2018, 6, .	0.8	2
264	DNA Sequence Assembly and Annotation of Genes. <i>Learning Materials in Biosciences</i> , 2018, , 9-24.	0.2	0
265	High-Throughput Sequencing Facilitates Characterization of a "Forgotten" Plant Virus: The Case of a Henbane Mosaic Virus Infecting Tomato. <i>Frontiers in Microbiology</i> , 2018, 9, 2739.	1.5	9
266	Phenotypic and Genomic Properties of a Novel Deep-Lineage Haloalkaliphilic Member of the Phylum <i>Balneolaeota</i> From Soda Lakes Possessing Na <sup>+</sup> -Translocating Proteorhodopsin. <i>Frontiers in Microbiology</i> , 2018, 9, 2672.	1.5	29
267	Microfluidic and Paper-Based Devices for Disease Detection and Diagnostic Research. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2731.	1.8	49
268	Revisiting the Taxonomy of the Genus <i>Arcobacter</i> : Getting Order From the Chaos. <i>Frontiers in Microbiology</i> , 2018, 9, 2077.	1.5	245
269	A Fatal Bacteremia Caused by Hypermucousviscous KPC-2 Producing Extensively Drug-Resistant K64-ST11 <i>Klebsiella pneumoniae</i> in Brazil. <i>Frontiers in Medicine</i> , 2018, 5, 265.	1.2	30
270	Genome sequence of <i>Shigella sonnei</i> 4303. <i>Gut Pathogens</i> , 2018, 10, 47.	1.6	2
271	Firefly genomes illuminate parallel origins of bioluminescence in beetles. <i>ELife</i> , 2018, 7, .	2.8	108



#	ARTICLE	IF	CITATIONS
272	Draft Genome Sequences of Two <i>Bacillus</i> sp. Strains and Four <i>Cellulomonas</i> sp. Strains Isolated from Heavy-Metal-Contaminated Soil. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	2
273	The Tree of Life. <i>Grand Challenges in Biology and Biotechnology</i> , 2018, , 55-99.	2.4	8
274	Draft Genome Sequences of 10 Clinical K2-Type <i>Klebsiella pneumoniae</i> Strains Isolated in Russia. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	4
275	IS26 mediated antimicrobial resistance gene shuffling from the chromosome to a mosaic conjugative FII plasmid. <i>Plasmid</i> , 2018, 100, 22-30.	0.4	19
276	Response of bentonite microbial communities to stresses relevant to geodisposal of radioactive waste. <i>Chemical Geology</i> , 2018, 501, 58-67.	1.4	22
277	Identification and assessment of virulence of a natural reassortant of infectious bursal disease virus. <i>Veterinary Research</i> , 2018, 49, 89.	1.1	29
278	Single-cell genomics of co-sorted Nanoarchaeota suggests novel putative host associations and diversification of proteins involved in symbiosis. <i>Microbiome</i> , 2018, 6, 161.	4.9	44
279	Metagenomic Composition Analysis of an Ancient Sequenced Polar Bear Jawbone from Svalbard. <i>Genes</i> , 2018, 9, 445.	1.0	13
280	OXA-48 type carbapenemase in <i>Klebsiella pneumoniae</i> producing extended spectrum B-lactamases (ESBL) in Senegal. <i>African Journal of Microbiology Research</i> , 2018, 12, 413-418.	0.4	3
281	<i>Escherichia coli</i> ST131-22 as a Foodborne Uropathogen. <i>MBio</i> , 2018, 9, .	1.8	184
282	Co-production of MCR-1 and NDM-5 in <i>Escherichia coli</i> ; isolated from a colonization case of inpatient. <i>Infection and Drug Resistance</i> , 2018, Volume 11, 1157-1161.	1.1	15
283	Whole-Genome Sequencing and Bioinformatic Analysis of Isolates from Foodborne Illness Outbreaks of <i>Campylobacter jejuni</i> and <i>Salmonella enterica</i> . <i>Journal of Clinical Microbiology</i> , 2018, 56, .	1.8	29
284	Draft Genome Sequences of Two <i>Salmonella</i> Strains Isolated from Wild Animals on the Eastern Shore of Virginia. <i>Genome Announcements</i> , 2018, 6, .	0.8	1
285	Draft Genome Sequence of the First Documented Clinical <i>Siccibacter turicensis</i> Isolate in Austria. <i>Genome Announcements</i> , 2018, 6, .	0.8	3
286	Draft Genome Sequence of <i>Bifidobacterium longum</i> UMA026, Isolated from Holstein Dairy Cow Feces. <i>Genome Announcements</i> , 2018, 6, .	0.8	0
287	Introduction of Large Sequence Inserts by CRISPR-Cas9 To Create Pathogenicity Mutants in the Multinucleate Filamentous Pathogen <i>Sclerotinia sclerotiorum</i> . <i>MBio</i> , 2018, 9, .	1.8	89
288	Characterization of a community-acquired-MRSA USA300 isolate from a river sample in Austria and whole genome sequence based comparison to a diverse collection of USA300 isolates. <i>Scientific Reports</i> , 2018, 8, 9467.	1.6	22
289	Draft Whole-Genome Sequence of <i>Candidatus Liberibacter asiaticus</i> Strain TX1712 from Citrus in Texas. <i>Genome Announcements</i> , 2018, 6, .	0.8	5

#	ARTICLE	IF	CITATIONS
290	Cloning and Expression of the Organophosphate Pesticide-Degrading <i>phoA</i> Hydrolase Gene in Plasmid pMK-07 to Confer Cross-Resistance to Antibiotics. <i>BioMed Research International</i> , 2018, 2018, 1-13.	0.9	8
291	Core Genome Multilocus Sequence Typing and Single Nucleotide Polymorphism Analysis in the Epidemiology of <i>Brucella melitensis</i> Infections. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	1.8	58
292	Resilience of small intestinal beneficial bacteria to the toxicity of soybean oil fatty acids. <i>ELife</i> , 2018, 7, .	2.8	14
293	Multi-omic elucidation of aromatic catabolism in adaptively evolved <i>Rhodococcus opacus</i> . <i>Metabolic Engineering</i> , 2018, 49, 69-83.	3.6	50
294	Diversity of DHA-1-encoding plasmids in <i>Klebsiella pneumoniae</i> isolates from 16 French hospitals. <i>Journal of Antimicrobial Chemotherapy</i> , 2018, 73, 2981-2989.	1.3	10
295	Study of spontaneous mutations in the transmission of poplar chloroplast genomes from mother to offspring. <i>BMC Genomics</i> , 2018, 19, 411.	1.2	5
296	Colistin Resistance Mediated by <i>mcr-1</i> in ESBL-Producing, Multidrug Resistant <i>Salmonella</i> <i>Infantis</i> in Broiler Chicken Industry, Italy (2016-2017). <i>Frontiers in Microbiology</i> , 2018, 9, 1880.	1.5	42
297	A Novel Eukaryotic Denitrification Pathway in Foraminifera. <i>Current Biology</i> , 2018, 28, 2536-2543.e5.	1.8	75
298	Glucocorticoids Impair Phagocytosis and Inflammatory Response Against Crohn's Disease-Associated Adherent-Invasive <i>Escherichia coli</i> . <i>Frontiers in Immunology</i> , 2018, 9, 1026.	2.2	24
299	<i>Candidatus Nitrosocaldus cavascurensis</i> , an Ammonia Oxidizing, Extremely Thermophilic Archaeon with a Highly Mobile Genome. <i>Frontiers in Microbiology</i> , 2018, 9, 28.	1.5	86
300	Evolution of Phototrophy in the Chloroflexi Phylum Driven by Horizontal Gene Transfer. <i>Frontiers in Microbiology</i> , 2018, 9, 260.	1.5	143
301	A Polyphasic and Taxogenomic Evaluation Uncovers <i>Arcobacter cryaerophilus</i> as a Species Complex That Embraces Four Genomovars. <i>Frontiers in Microbiology</i> , 2018, 9, 805.	1.5	22
302	Vaccinia Virus Shuffling: deVV5, a Novel Chimeric Poxvirus with Improved Oncolytic Potency. <i>Cancers</i> , 2018, 10, 231.	1.7	15
303	Identification and genetic characterization of bovine enterovirus by combination of two next generation sequencing platforms. <i>Journal of Virological Methods</i> , 2018, 260, 21-25.	1.0	13
304	Convergent evolution of unusual complex I homologs with increased proton pumping capacity: energetic and ecological implications. <i>ISME Journal</i> , 2018, 12, 2668-2680.	4.4	33
305	Novel <i>Enterobacter</i> Lineage as Leading Cause of Nosocomial Outbreak Involving Carbapenemase-Producing Strains. <i>Emerging Infectious Diseases</i> , 2018, 24, 1505-1515.	2.0	45
306	The End of a 60-year Riddle: Identification and Genomic Characterization of an Iridovirus, the Causative Agent of White Fat Cell Disease in Zooplankton. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 1259-1272.	0.8	12
307	Short genome report of cellulose-producing commensal <i>Escherichia coli</i> 1094. <i>Standards in Genomic Sciences</i> , 2018, 13, 13.	1.5	2

#	ARTICLE	IF	CITATIONS
308	Genomic Epidemiology of Global Carbapenemase-Producing <i>Enterobacter</i> spp., 2008–2014. <i>Emerging Infectious Diseases</i> , 2018, 24, 1010-1019.	2.0	107
309	Phylogenetic and antimicrobial resistance gene analysis of <i>Salmonella</i> Typhimurium strains isolated in Brazil by whole genome sequencing. <i>PLoS ONE</i> , 2018, 13, e0201882.	1.1	48
310	Broad Phylogenetic Diversity Associated with Nitrogen Loss through Sulfur Oxidation in a Large Public Marine Aquarium. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	7
311	Typing and Species Identification of Clinical <i>Klebsiella</i> Isolates by Fourier Transform Infrared Spectroscopy and Matrix-Assisted Laser Desorption Ionization–Time of Flight Mass Spectrometry. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	1.8	56
312	Genomic Insights Into Energy Metabolism of <i>Carboxydocella therrautotrophica</i> Coupling Hydrogenogenic CO Oxidation With the Reduction of Fe(III) Minerals. <i>Frontiers in Microbiology</i> , 2018, 9, 1759.	1.5	23
313	Tracing mother-infant transmission of bacteriophages by means of a novel analytical tool for shotgun metagenomic datasets: METAnnotatorX. <i>Microbiome</i> , 2018, 6, 145.	4.9	54
315	Methanogens in the Antarctic Dry Valley permafrost. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	22
316	Draft Genome Sequence of the Intimin-Positive Enteropathogenic <i>Escherichia albertii</i> Strain MBT-EA1, Isolated from Lettuce. <i>Genome Announcements</i> , 2018, 6, .	0.8	3
317	<i>Ca. Endozoicomonas cretensis</i> : A Novel Fish Pathogen Characterized by Genome Plasticity. <i>Genome Biology and Evolution</i> , 2018, 10, 1363-1374.	1.1	10
318	Discovery of a Novel Periodontal Disease-Associated Bacterium. <i>Microbial Ecology</i> , 2019, 77, 267-276.	1.4	26
319	Genome sequence of the endophytic strain <i>Enterobacter</i> sp. J49, a potential biofertilizer for peanut and maize. <i>Genomics</i> , 2019, 111, 913-920.	1.3	30
320	Sequence Analysis. , 2019, , 292-322.		8
321	Metagenomic next-generation sequencing aids the diagnosis of viral infections in febrile returning travellers. <i>Journal of Infection</i> , 2019, 79, 383-388.	1.7	45
322	Recovery of FRI-5 carbapenemase at a Japanese hospital where FRI-4 carbapenemase was discovered. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 3390-3392.	1.3	7
323	Primer-free FISH probes from metagenomics/metatranscriptomics data permit the study of uncharacterised taxa in complex microbial communities. <i>Npj Biofilms and Microbiomes</i> , 2019, 5, 17.	2.9	11
324	A nemertean excitatory peptide/CCHamide regulates ciliary swimming in the larvae of <i>Lineus longissimus</i> . <i>Frontiers in Zoology</i> , 2019, 16, 28.	0.9	8
325	Identification of virulence and antibiotic resistance factors in <i>Arcobacter butzleri</i> isolated from bovine milk by Whole Genome Sequencing. <i>Italian Journal of Food Safety</i> , 2019, 8, 7840.	0.5	17
326	Tracking the environmental dissemination of carbapenem-resistant <i>Klebsiella pneumoniae</i> using whole genome sequencing. <i>Science of the Total Environment</i> , 2019, 691, 80-92.	3.9	26

#	ARTICLE	IF	CITATIONS
327	Genomic Diversity of Two Hydrocarbon-Degrading and Plant Growth-Promoting <i>Pseudomonas</i> Species Isolated from the Oil Field of BÅ³brka (Poland). <i>Genes</i> , 2019, 10, 443.	1.0	33
328	Molecular characteristics of oxazolidinone resistance in enterococci from a multicenter study in China. <i>BMC Microbiology</i> , 2019, 19, 162.	1.3	23
329	Draft Whole-Genome Sequences of 16 <i>Campylobacter jejuni</i> Isolates Obtained from Wild Birds. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	5
330	Draft Genome Sequences of Three Rhizospheric Plant Growth-Promoting Bacteria. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	5
331	Dictyochophyceae Plastid Genomes Reveal Unusual Variability in Their Organization. <i>Journal of Phycology</i> , 2019, 55, 1166-1180.	1.0	37
332	Whole-Genome Sequences of <i>Pantoea agglomerans</i> BL3, <i>Pseudomonas fluorescens</i> BL, and <i>Pseudomonas stutzeri</i> CM14, Isolated from Hops ( <i>Humulus lupulus</i> ). <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	5
333	Genetically diverse <i>Pseudomonas aeruginosa</i> populations display similar transcriptomic profiles in a cystic fibrosis explanted lung. <i>Nature Communications</i> , 2019, 10, 3397.	5.8	68
334	Human placenta has no microbiome but can contain potential pathogens. <i>Nature</i> , 2019, 572, 329-334.	13.7	513
335	Genome-wide sequencing and metabolic annotation of <i>Pythium irregulare</i> CBS 494.86: understanding Eicosapentaenoic acid production. <i>BMC Biotechnology</i> , 2019, 19, 41.	1.7	6
336	The Emergence of Chromosomally Located blaCTX-M-55 in <i>Salmonella</i> From Foodborne Animals in China. <i>Frontiers in Microbiology</i> , 2019, 10, 1268.	1.5	62
337	DNA extraction and amplicon production strategies deeply infâ€šluence the outcome of gut mycobiome studies. <i>Scientific Reports</i> , 2019, 9, 9328.	1.6	51
338	Probing the geological source and biological fate of hydrogen in Yellowstone hot springs. <i>Environmental Microbiology</i> , 2019, 21, 3816-3830.	1.8	22
339	Direct effects of organic pollutants on the growth and gene expression of the Baltic Sea model bacterium <i>Rheinheimerasp.</i> BAL341. <i>Microbial Biotechnology</i> , 2019, 12, 892-906.	2.0	19
340	Characterizing <i>Salmonella enterica</i> Serovar <i>Choleraesuis</i> , var. <i>Kunzensdorf</i> : A Comparative Case Study. <i>Frontiers in Veterinary Science</i> , 2019, 6, 316.	0.9	5
341	MetaMiner: A Scalable Peptidogenomics Approach for Discovery of Ribosomal Peptide Natural Products with Blind Modifications from Microbial Communities. <i>Cell Systems</i> , 2019, 9, 600-608.e4.	2.9	46
342	<i>Staphylococcus petrasii</i> diagnostics and its pathogenic potential enhanced by mobile genetic elements. <i>International Journal of Medical Microbiology</i> , 2019, 309, 151355.	1.5	2
343	Studying the gut virome in the metagenomic era: challenges and perspectives. <i>BMC Biology</i> , 2019, 17, 84.	1.7	113
344	Exfoliative toxin E, a new <i>Staphylococcus aureus</i> virulence factor with host-specific activity. <i>Scientific Reports</i> , 2019, 9, 16336.	1.6	20

#	ARTICLE	IF	CITATIONS
345	Evaluation of 16S rRNA gene sequencing for species and strain-level microbiome analysis. <i>Nature Communications</i> , 2019, 10, 5029.	5.8	1,007
346	Preventing dysbiosis of the neonatal mouse intestinal microbiome protects against late-onset sepsis. <i>Nature Medicine</i> , 2019, 25, 1772-1782.	15.2	91
347	Survey and genetic characterization of <i>Vibrio cholerae</i> in Apalachicola Bay, Florida (2012–2014). <i>Journal of Applied Microbiology</i> , 2019, 126, 1265-1277.	1.4	8
348	Plasmid Dissemination and Selection of a Multidrug-Resistant <i>Klebsiella pneumoniae</i> Strain during Transplant-Associated Antibiotic Therapy. <i>MBio</i> , 2019, 10, .	1.8	14
349	A Conserved Streptococcal Virulence Regulator Controls the Expression of a Distinct Class of M-Like Proteins. <i>MBio</i> , 2019, 10, .	1.8	8
350	Complete Genome Sequence of a Shiga Toxin-Converting Bacteriophage, Escherichia Phage Lys12581Vzw, Induced from an Outbreak Shiga Toxin-Producing <i>Escherichia coli</i> Strain. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	3
351	Neurological symptoms and mortality associated with <i>Streptococcus gallolyticus</i> subsp. <i>pasteurianus</i> in calves. <i>Veterinary Microbiology</i> , 2019, 236, 108369.	0.8	8
352	Assessing the viral content of uncultured picoeukaryotes in the global ocean by single cell genomics. <i>Molecular Ecology</i> , 2019, 28, 4272-4289.	2.0	25
353	Draft Genome Sequence of a <i>Chryseobacterium indologenes</i> Strain Isolated from a Blood Culture of a Hospitalized Child in Antananarivo, Madagascar. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	3
354	rnaSPAdes: a de novo transcriptome assembler and its application to RNA-Seq data. <i>GigaScience</i> , 2019, 8, .	3.3	428
355	Evolution of a 72-Kilobase Cointegrant, Conjugative Multiresistance Plasmid in Community-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> Isolates from the Early 1990s. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	1.4	12
356	Genetic Features of Antarctic <i>Acinetobacter radioresistens</i> Strain A154 Harboring Multiple Antibiotic-Resistance Genes. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 328.	1.8	9
357	Hospital outbreak caused by linezolid resistant <i>Enterococcus faecium</i> in Upper Austria. <i>Antimicrobial Resistance and Infection Control</i> , 2019, 8, 150.	1.5	13
358	A robust human norovirus replication model in zebrafish larvae. <i>PLoS Pathogens</i> , 2019, 15, e1008009.	2.1	112
359	Characterization of a Carbapenem-Resistant <i>Kluyvera cryocrescens</i> Isolate Carrying Blandm-1 from Hospital Sewage. <i>Antibiotics</i> , 2019, 8, 149.	1.5	19
360	Metagenomics and metatranscriptomics analyses reveal oxygen detoxification and mixotrophic potentials of an enriched anammox culture in a continuous stirred-tank reactor. <i>Water Research</i> , 2019, 166, 115039.	5.3	57
361	Intraspecific Variation in Protists: Clues for Microevolution from <i>Poteroispumella lacustris</i> (Chrysophyceae). <i>Genome Biology and Evolution</i> , 2019, 11, 2492-2504.	1.1	7
362	<i>Flavobacterium zhairuonensis</i> sp. nov., a gliding bacterium isolated from marine sediment of the East China Sea. <i>Journal of Microbiology</i> , 2019, 57, 1065-1072.	1.3	12

#	ARTICLE	IF	CITATIONS
363	Genomic Insights Into Five Strains of <i>Lactobacillus plantarum</i> With Biotechnological Potential Isolated From chicha, a Traditional Maize-Based Fermented Beverage From Northwestern Argentina. <i>Frontiers in Microbiology</i> , 2019, 10, 2232.	1.5	24
364	Combined cultivation and single-cell approaches to the phylogenomics of nuclearioid amoebae, close relatives of fungi. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20190094.	1.8	24
365	Molecular Characterization of Equine <i>Staphylococcus aureus</i> Isolates Exhibiting Reduced Oxacillin Susceptibility. <i>Toxins</i> , 2019, 11, 535.	1.5	24
366	Genomic polymorphism of <i>Mycoplasma flocculare</i> revealed by a newly developed multilocus sequence typing scheme. <i>Veterinary Microbiology</i> , 2019, 237, 108422.	0.8	1
367	Fueled by methane: deep-sea sponges from asphalt seeps gain their nutrition from methane-oxidizing symbionts. <i>ISME Journal</i> , 2019, 13, 1209-1225.	4.4	68
368	Isolation and molecular characterization of dengue virus clinical isolates from pediatric patients in New Delhi. <i>International Journal of Infectious Diseases</i> , 2019, 84, S25-S33.	1.5	19
369	Draft Genome Sequences for Dual-Toxin-Producing <i>Clostridium botulinum</i> Strains. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	2
370	Molecular Evolution of Human Adenovirus (HAdV) Species C. <i>Scientific Reports</i> , 2019, 9, 1039.	1.6	101
371	Dissecting the Evolutionary Development of the Species <i>Bifidobacterium animalis</i> through Comparative Genomics Analyses. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	11
372	First Isolation and Phylogenetic Analyses of Tick-Borne Encephalitis Virus in Lower Saxony, Germany. <i>Viruses</i> , 2019, 11, 462.	1.5	19
373	Multiple Lineages of Dengue Virus Serotype 2 Cosmopolitan Genotype Caused a Local Dengue Outbreak in Hangzhou, Zhejiang Province, China, in 2017. <i>Scientific Reports</i> , 2019, 9, 7345.	1.6	11
374	Identification and Characterization of a Novel Robigovirus Species from Sweet Cherry in Turkey. <i>Pathogens</i> , 2019, 8, 57.	1.2	11
375	Hybrid Genome Assembly of a Major Quantitative Disease Resistance Locus in Soybean Toward <i>Fusarium graminearum</i> . <i>Plant Genome</i> , 2019, 12, 180102.	1.6	8
376	New Microbial Lineages Capable of Carbon Fixation and Nutrient Cycling in Deep-Sea Sediments of the Northern South China Sea. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	36
377	Draft genome sequences of <i>Mycobacterium peregrinum</i> isolated from a pig with lymphadenitis and from soil on the same Japanese pig farm. <i>BMC Research Notes</i> , 2019, 12, 341.	0.6	4
378	Whole Genome Sequencing Based Surveillance of <i>L. monocytogenes</i> for Early Detection and Investigations of Listeriosis Outbreaks. <i>Frontiers in Public Health</i> , 2019, 7, 139.	1.3	49
379	Single-cell genomics unveiled a cryptic cyanobacterial lineage with a worldwide distribution hidden by a dinoflagellate host. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 15973-15978.	3.3	27
380	Impacts of long-term elevated atmospheric CO <sub>2</sub> concentrations on communities of arbuscular mycorrhizal fungi. <i>Molecular Ecology</i> , 2019, 28, 3445-3458.	2.0	20

#	ARTICLE	IF	CITATIONS
381	Identification of two abundant <i>Aerococcus urinae</i> cell wall-anchored proteins. <i>International Journal of Medical Microbiology</i> , 2019, 309, 151325.	1.5	3
382	Draft Genome Sequence of <i>Bacillus coagulans</i> MA-13, a Thermophilic Lactic Acid Producer from Lignocellulose. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	10
383	Temperate Bacteriophages from Chronic <i>Pseudomonas aeruginosa</i> Lung Infections Show Disease-Specific Changes in Host Range and Modulate Antimicrobial Susceptibility. <i>MSystems</i> , 2019, 4, .	1.7	38
384	Metabolic versatility in a modern lineage of cyanobacteria from terrestrial hot springs. <i>Free Radical Biology and Medicine</i> , 2019, 140, 224-232.	1.3	20
385	Kinetic evaluation for rapid degradation of dimethylamine enriched with <i>Agromyces</i> and <i>Ochrobactrum</i> sp.. <i>Journal of Environmental Management</i> , 2019, 245, 322-329.	3.8	8
386	Draft Genome Sequence of <i>Pseudomonas koreensis</i> Strain AB36, Isolated from Gold Mining Soil. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	4
387	Emerging Novel GII.P16 Noroviruses Associated with Multiple Capsid Genotypes. <i>Viruses</i> , 2019, 11, 535.	1.5	53
388	Draft Genome Sequence of a Cold-Adapted <i>Pseudomonas</i> sp. Strain, BGI-2, Isolated from the Ice of Batura Glacier, Pakistan. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	7
389	The Biosynthesis of Rare Homo-Amino Acid Containing Variants of Microcystin by a Benthic Cyanobacterium. <i>Marine Drugs</i> , 2019, 17, 271.	2.2	20
390	Selection of Multidrug-Resistant Bacteria in Medicated Animal Feeds. <i>Frontiers in Microbiology</i> , 2019, 10, 456.	1.5	17
391	Comparison of livestock-associated and community-associated <i>Staphylococcus aureus</i> pathogenicity in a mouse model of skin and soft tissue infection. <i>Scientific Reports</i> , 2019, 9, 6774.	1.6	11
392	Islands of retroelements are major components of <i>Drosophila</i> centromeres. <i>PLoS Biology</i> , 2019, 17, e3000241.	2.6	124
393	Draft Genome Sequence of <i>Enterobacter</i> sp. Strain A8, a Carbazole-Degrading Bacterium. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	1
394	Unprecedented Diversity of Lactococcal Group 936 Bacteriophages Revealed by Amplicon Sequencing of the Portal Protein Gene. <i>Viruses</i> , 2019, 11, 443.	1.5	7
395	Draft Genome Sequences of Sporulation-Impaired <i>Bacillus pumilus</i> Strain NRS576 and Its Native Plasmid p576. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	11
396	ChimeraMiner: An Improved Chimeric Read Detection Pipeline and Its Application in Single Cell Sequencing. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1953.	1.8	13
397	A Forward Chemical Genetic Screen Reveals Gut Microbiota Metabolites That Modulate Host Physiology. <i>Cell</i> , 2019, 177, 1217-1231.e18.	13.5	221
398	Genome analyses of the new model protist <i>Euplotes vannus</i> focusing on genome rearrangement and resistance to environmental stressors. <i>Molecular Ecology Resources</i> , 2019, 19, 1292-1308.	2.2	69

#	ARTICLE	IF	CITATIONS
399	Dicyemida and Orthonectida: Two Stories of Body Plan Simplification. <i>Frontiers in Genetics</i> , 2019, 10, 443.	1.1	37
400	Draft Genome Sequence of Thermophilic Halotolerant <i>Aeribacillus pallidus</i> TD1, Isolated from Tao Dam Hot Spring, Thailand. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	1
401	Genomic epidemiology of erythromycin-resistant <i>Bordetella pertussis</i> in China. <i>Emerging Microbes and Infections</i> , 2019, 8, 461-470.	3.0	46
402	Mitochondrial proline catabolism activates Ras1/cAMP/PKA-induced filamentation in <i>Candida albicans</i> . <i>PLoS Genetics</i> , 2019, 15, e1007976.	1.5	68
403	Draft Genome Sequences of Type Strains of <i>Gordonibacter faecihominis</i> , <i>Paraeggerthella hongkongensis</i> , <i>Parvibacter caecicola</i> , <i>Slackia equolifaciens</i> , <i>Slackia faecicanis</i> , and <i>Slackia isoflavoniconvertens</i> . <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	9
404	Comprehensive Virulence Gene Profiling of Bovine Non- <i>aureus</i> Staphylococci Based on Whole-Genome Sequencing Data. <i>MSystems</i> , 2019, 4, .	1.7	32
405	Interplay among IncA and <i>bla</i> KPC-Carrying Plasmids in <i>Citrobacter freundii</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	1.4	12
406	Draft Genome Sequence of the Putative Marine Pathogen <i>Thalassobius</i> sp. I31.1. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	2
407	Draft Genome Sequence of <i>Bacillus salarius</i> IM0101, Isolated from Hypersaline Soil in Inner Mongolia, China. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	0
408	Draft Genome Sequence of Heavy Metal-Resistant <i>Bacillus cereus</i> NWUAB01. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	4
409	Characterization of the mitochondrial genome of the MAX1 type of cytoplasmic male-sterile sunflower. <i>BMC Plant Biology</i> , 2019, 19, 51.	1.6	18
410	The complete mitochondrial genome of Gunnison's prairie dog subspecies ( <i>Cynomys gunnisoni</i> ) Tj ETQq1 1 0.784314 rgBT /Omer Part B: Resources, 2019, 4, 397-398.	0.2	2
411	Closely related viruses of the marine picoeukaryotic alga <i>Ostreococcus lucimarinus</i> exhibit different ecological strategies. <i>Environmental Microbiology</i> , 2019, 21, 2148-2170.	1.8	15
412	Horizontally-acquired genetic elements in the mitochondrial genome of a centrohelid <i>Marophrys</i> sp. SRT127. <i>Scientific Reports</i> , 2019, 9, 4850.	1.6	16
413	Plasmid-mediated colistin resistance gene <i>mcr-1</i> in <i>Escherichia coli</i> and <i>Klebsiella pneumoniae</i> ; isolated from market retail fruits in Guangzhou, China. <i>Infection and Drug Resistance</i> , 2019, Volume 12, 385-389.	1.1	42
414	Comparative Genomics, Siderophore Production, and Iron Scavenging Potential of Root Zone Soil Bacteria Isolated from Concord™ Grape Vineyards. <i>Microbial Ecology</i> , 2019, 78, 699-713.	1.4	14
415	Molecular evidence for distinct modes of nutrient acquisition between visceral and neurotropic schistosomes of birds. <i>Scientific Reports</i> , 2019, 9, 1347.	1.6	17
416	Archaea, the tree of life, and cellular evolution in eukaryotes. <i>Science China Earth Sciences</i> , 2019, 62, 489-506.	2.3	5



#	ARTICLE	IF	CITATIONS
417	Anabaena/Dolichospermum as the source of lethal microcystin levels responsible for a large cattle toxicosis event. <i>Toxicon</i> , 2019, 1, 100003.	1.2	24
418	Expansion of Vancomycin-Resistant <i>Enterococcus faecium</i> in an Academic Tertiary Hospital in Southwest Germany: a Large-Scale Whole-Genome-Based Outbreak Investigation. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	1.4	37
419	Genomics insights into ecotype formation of ammonia-oxidizing archaea in the deep ocean. <i>Environmental Microbiology</i> , 2019, 21, 716-729.	1.8	39
420	Draft Whole-Genome Sequences of <i>Xylella fastidiosa</i> subsp. <i>fastidiosa</i> Strains TPD3 and TPD4, Isolated from Grapevines in Hou-li, Taiwan. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	6
421	The complete mitochondrial genome of <i>Plautia crossota</i> (Hemiptera: Pentatomidae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2281-2282.	0.2	4
422	System OMICs analysis of <i>Mycobacterium tuberculosis</i> Beijing B0/W148 cluster. <i>Scientific Reports</i> , 2019, 9, 19255.	1.6	7
423	Multiple <i>Klebsiella pneumoniae</i> KPC Clones Contribute to an Extended Hospital Outbreak. <i>Frontiers in Microbiology</i> , 2019, 10, 2767.	1.5	27
424	Comparative Genomics Analysis of Ciliates Provides Insights on the Evolutionary History Within <i>Nassophorea</i> – <i>Synhymenia</i> – <i>Phyllopharyngea</i> Assemblage. <i>Frontiers in Microbiology</i> , 2019, 10, 2819.	1.5	31
425	Draft Genome Sequence of Multidrug-Resistant <i>Vibrio parahaemolyticus</i> Strain PH698, Infecting Penaeid Shrimp in the Philippines. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	3
426	Fourier-Transform Infrared (FTIR) Spectroscopy for Typing of Clinical <i>Enterobacter cloacae</i> Complex Isolates. <i>Frontiers in Microbiology</i> , 2019, 10, 2582.	1.5	51
427	Sequencing of animal viruses: quality data assurance for NGS bioinformatics. <i>Virology Journal</i> , 2019, 16, 140.	1.4	18
428	Genome analysis of <i>Ranavirus frog virus 3</i> isolated from American Bullfrog ( <i>Lithobates catesbeianus</i> ) in South America. <i>Scientific Reports</i> , 2019, 9, 17135.	1.6	11
429	<i>Paenibacillus lutrae</i> sp. nov., A Chitinolytic Species Isolated from A River Otter in Castril Natural Park, Granada, Spain. <i>Microorganisms</i> , 2019, 7, 637.	1.6	2
430	Basal Rot of Narcissus: Understanding Pathogenicity in <i>Fusarium oxysporum</i> f. sp. <i>narcissi</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 2905.	1.5	8
431	<i>Oceanobacillus timonensis</i> sp. nov. and <i>Oceanobacillus senegalensis</i> sp. nov., two new moderately halophilic, Gram-stain positive bacteria isolated from stools sample of healthy young Senegalese. <i>Antonie Van Leeuwenhoek</i> , 2019, 112, 785-796.	0.7	4
432	Identification of <i>bla</i> <sub>VIM-1</sub> Gene in ST307 and ST661 <i>Klebsiella pneumoniae</i> Clones in Italy: Old Acquaintances for New Combinations. <i>Microbial Drug Resistance</i> , 2019, 25, 787-790.	0.9	13
433	Periodic and Spatial Spreading of Alkanes and <i>Alcanivorax</i> Bacteria in Deep Waters of the Mariana Trench. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	17
434	Epidemiology and Whole-Genome Analysis of <i>NDM-1</i> -Producing <i>Klebsiella pneumoniae</i> KP3771 from Tunisia. <i>Microbial Drug Resistance</i> , 2019, 25, 644-651.	0.9	12

#	ARTICLE	IF	CITATIONS
435	Metagenomic engineering of the mammalian gut microbiome in situ. <i>Nature Methods</i> , 2019, 16, 167-170.	9.0	164
436	Bioelectrochemical Nitrogen fixation (e-BNF): Electro-stimulation of enriched biofilm communities drives autotrophic nitrogen and carbon fixation. <i>Bioelectrochemistry</i> , 2019, 125, 105-115.	2.4	28
437	Shaping microbial consortia in coupling glycerol fermentation and carboxylate chain elongation for Co-production of 1,3-propanediol and caproate: Pathways and mechanisms. <i>Water Research</i> , 2019, 148, 281-291.	5.3	30
438	Comparative genomics of the <i>Komagataeibacter</i> strains – Efficient bionanocellulose producers. <i>MicrobiologyOpen</i> , 2019, 8, e00731.	1.2	51
439	Segregational Drift and the Interplay between Plasmid Copy Number and Evolvability. <i>Molecular Biology and Evolution</i> , 2019, 36, 472-486.	3.5	46
440	Fluoroquinolone Prophylaxis Selects for Meropenem-nonsusceptible <i>Pseudomonas aeruginosa</i> in Patients With Hematologic Malignancies and Hematopoietic Cell Transplant Recipients. <i>Clinical Infectious Diseases</i> , 2019, 68, 2045-2052.	2.9	43
441	Genetic and Genome Analyses Reveal Genetically Distinct Populations of the Bee Pathogen <i>Nosema ceranae</i> from Thailand. <i>Microbial Ecology</i> , 2019, 77, 877-889.	1.4	8
442	Characterization and phylogenetic analysis of the complete mitochondrial genome sequence of <i>Rhyticeros undulatus</i> (Bucerotiformes: Bucerotidae). <i>Conservation Genetics Resources</i> , 2019, 11, 27-30.	0.4	0
443	Genomic differences within the phylum Marinimicrobia: From waters to sediments in the Mariana Trench. <i>Marine Genomics</i> , 2020, 50, 100699.	0.4	12
444	<i>In vitro</i> characterization and genetic diversity of <i>Bordetella avium</i> field strains. <i>Avian Pathology</i> , 2020, 49, 36-46.	0.8	2
445	Phylogenetic and structural diversity of aromatically dense pili from environmental metagenomes. <i>Environmental Microbiology Reports</i> , 2020, 12, 49-57.	1.0	22
446	Exploration of the propagation of transpovirons within Mimiviridae reveals a unique example of commensalism in the viral world. <i>ISME Journal</i> , 2020, 14, 727-739.	4.4	22
447	Core genome multi-locus sequence typing as an essential tool in a high-cost livestock-associated methicillin-resistant <i>Staphylococcus aureus</i> CC398 hospital outbreak. <i>Journal of Hospital Infection</i> , 2020, 104, 574-581.	1.4	14
448	Emergence of a Plant Pathogen in Europe Associated with Multiple Intercontinental Introductions. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	57
449	Manganese and cobalt redox cycling in laterites; Biogeochemical and bioprocessing implications. <i>Chemical Geology</i> , 2020, 531, 119330.	1.4	22
450	Defining the eco-enzymological role of the fungal strain <i>Coniochaeta</i> sp. 2T2.1 in a tripartite lignocellulolytic microbial consortium. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	12
451	Comprehensive analysis of the molecular characterization of GM rice G6H1 using a paired-end sequencing approach. <i>Food Chemistry</i> , 2020, 309, 125760.	4.2	10
452	Multispecies Diesel Fuel Biodegradation and Niche Formation Are Ignited by Pioneer Hydrocarbon-Utilizing Proteobacteria in a Soil Bacterial Consortium. <i>Applied and Environmental Microbiology</i> , 2020, 87, .	1.4	20

#	ARTICLE	IF	CITATIONS
453	Differential Gene Expression with an Emphasis on Floral Organ Size Differences in Natural and Synthetic Polyploids of <i>Nicotiana tabacum</i> (Solanaceae). <i>Genes</i> , 2020, 11, 1097.	1.0	15
454	The New <i>Klebsiella pneumoniae</i> ST152 Variants with Hypermucoviscous Phenotype Isolated from Renal Transplant Recipients with Asymptomatic Bacteriuria—Genetic Characteristics by WGS. <i>Genes</i> , 2020, 11, 1189.	1.0	10
455	A Novel RNA Virus, <i>Macrobrachium rosenbergii</i> Golda Virus (MrGV), Linked to Mass Mortalities of the Larval Giant Freshwater Prawn in Bangladesh. <i>Viruses</i> , 2020, 12, 1120.	1.5	11
456	Clinical and Molecular Description of a High-Copy IncQ1 KPC-2 Plasmid Harbored by the International ST15 <i>Klebsiella pneumoniae</i> Clone. <i>MSphere</i> , 2020, 5, .	1.3	19
457	The Complete Chloroplast Genome Sequence of the <i>Speirantha gardenii</i> : Comparative and Adaptive Evolutionary Analysis. <i>Agronomy</i> , 2020, 10, 1405.	1.3	14
458	Borderline resistance to oxacillin in <i>Staphylococcus aureus</i> after treatment with sub-lethal sodium hypochlorite concentrations. <i>Heliyon</i> , 2020, 6, e04070.	1.4	12
459	Metagenomic studies of SAR202 bacteria at the full-ocean depth in the Mariana Trench. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2020, 165, 103396.	0.6	14
460	Genetic Evidence for a Mixed Composition of the Genus <i>Myoxocephalus</i> (Cottoidei: Cottidae) Necessitates Generic Realignment. <i>Genes</i> , 2020, 11, 1071.	1.0	5
461	metaFlye: scalable long-read metagenome assembly using repeat graphs. <i>Nature Methods</i> , 2020, 17, 1103-1110.	9.0	430
462	Targeted Cell Sorting Combined With Single Cell Genomics Captures Low Abundant Microbial Dark Matter With Higher Sensitivity Than Metagenomics. <i>Frontiers in Microbiology</i> , 2020, 11, 1377.	1.5	25
463	Insights into the dynamics between viruses and their hosts in a hot spring microbial mat. <i>ISME Journal</i> , 2020, 14, 2527-2541.	4.4	42
464	Genome-Wide Association Analysis Identifies a Genetic Basis of Infectivity in a Model Bacterial Pathogen. <i>Molecular Biology and Evolution</i> , 2020, 37, 3439-3452.	3.5	20
465	Horizontal Plasmid Transfer among <i>Klebsiella pneumoniae</i> Isolates Is the Key Factor for Dissemination of Extended-Spectrum $\beta$ -Lactamases among Children in Tanzania. <i>MSphere</i> , 2020, 5, .	1.3	9
466	Characterization of the complete chloroplast genome of <i>Apocynum venetum</i> L. (Apocynaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2475-2476.	0.2	1
467	Chemically Defined, High-Density Insect Cell-Based Expression System for Scalable AAV Vector Production. <i>Molecular Therapy - Methods and Clinical Development</i> , 2020, 19, 330-340.	1.8	22
468	Genome Size Versus Genome Assemblies: Are the Genomes Truly Expanded in Polyploid Fungal Symbionts?. <i>Genome Biology and Evolution</i> , 2020, 12, 2384-2390.	1.1	6
469	Whole-genome characterisation of TEM-1 and CMY-2 $\beta$ -lactamase-producing <i>Salmonella</i> Kentucky ST198 in Lebanese broiler chain. <i>Journal of Global Antimicrobial Resistance</i> , 2020, 23, 408-416.	0.9	6
470	Trends in Population Dynamics of <i>Escherichia coli</i> Sequence Type 131, Calgary, Alberta, Canada, 2006–2016. <i>Emerging Infectious Diseases</i> , 2020, 26, 2907-2915.	2.0	26

#	ARTICLE	IF	CITATIONS
471	Evidence of Severe Acute Respiratory Syndrome Coronavirus 2 Reinfection After Recovery from Mild Coronavirus Disease 2019. <i>Clinical Infectious Diseases</i> , 2021, 73, e3002-e3008.	2.9	68
472	Draft Genome Sequence of the Green Microalga <i>Chlorella</i> sp. Strain BAC9706, Isolated from Lake Baikal, Russia. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
473	Distemper, extinction, and vaccination of the Amur tiger. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 31954-31962.	3.3	33
474	Unravelling the importance of the eukaryotic and bacterial communities and their relationship with <i>Legionella</i> spp. ecology in cooling towers: a complex network. <i>Microbiome</i> , 2020, 8, 157.	4.9	19
475	Genetic and Antigenic Evolution of European Swine Influenza A Viruses of HA-1C (Avian-Like) and HA-1B (Human-Like) Lineages in France from 2000 to 2018. <i>Viruses</i> , 2020, 12, 1304.	1.5	7
476	Characteristics of the completed chloroplast genome sequence of <i>Xanthium spinosum</i> : comparative analyses, identification of mutational hotspots and phylogenetic implications. <i>BMC Genomics</i> , 2020, 21, 855.	1.2	23
477	Occurrence of <i>Listeria</i> spp. and <i>Listeria</i> monocytogenes Isolated from PDO Taleggio Production Plants. <i>Foods</i> , 2020, 9, 1636.	1.9	8
478	Genomic analysis of <i>Bacillus cereus</i> NWUAB01 and its heavy metal removal from polluted soil. <i>Scientific Reports</i> , 2020, 10, 19660.	1.6	81
479	Single-Cell Genomic Sequencing of Three Peritrichs (Protista, Ciliophora) Reveals Less Biased Stop Codon Usage and More Prevalent Programmed Ribosomal Frameshifting Than in Other Ciliates. <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	14
480	Genome Sequencing of <i>Escherichia coli</i> and <i>Klebsiella pneumoniae</i> Isolates That Harbor the FOX-5 $\beta$ -Lactamase Gene. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	0
481	Validation of Variant Assembly Using HAPHIPE with Next-Generation Sequence Data from Viruses. <i>Viruses</i> , 2020, 12, 758.	1.5	4
482	Pre-growth conditions and strain diversity affect nisin treatment efficacy against <i>Listeria monocytogenes</i> on cold-smoked salmon. <i>International Journal of Food Microbiology</i> , 2020, 333, 108793.	2.1	9
483	Epigenetic Regulation of <i>Verticillium dahliae</i> Virulence: Does DNA Methylation Level Play A Role?. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5197.	1.8	5
484	Draft Genome Sequence of a <i>Bacteroides fragilis</i> Strain Isolated from Peritoneal Fluid of a Patient from Kazakhstan. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	0
485	Virus and Potential Host Microbes from Viral-Enriched Metagenomic Characterization in the High-Altitude Wetland, Salar de Huasco, Chile. <i>Microorganisms</i> , 2020, 8, 1077.	1.6	14
486	<i>Acinetobacter baumannii</i> NCIMB8209: a Rare Environmental Strain Displaying Extensive Insertion Sequence-Mediated Genome Remodeling Resulting in the Loss of Exposed Cell Structures and Defensive Mechanisms. <i>MSphere</i> , 2020, 5, .	1.3	12
487	Cultivation and Genomics Prove Long-Term Colonization of Donor's Bifidobacteria in Recurrent <i>Clostridioides difficile</i> Patients Treated With Fecal Microbiota Transplantation. <i>Frontiers in Microbiology</i> , 2020, 11, 1663.	1.5	7
488	Identification of Antimicrobial Resistance-Associated Genes through Whole Genome Sequencing of <i>Mycoplasma bovis</i> Isolates with Different Antimicrobial Resistances. <i>Pathogens</i> , 2020, 9, 588.	1.2	8

#	ARTICLE	IF	CITATIONS
489	Acquisition and Adaptation of Ultra-small Parasitic Reduced Genome Bacteria to Mammalian Hosts. <i>Cell Reports</i> , 2020, 32, 107939.	2.9	152
490	Detection and Characterization of Diphtheria Toxin Gene-Bearing <i>Corynebacterium</i> Species through a New Real-Time PCR Assay. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	1.8	18
491	Genomic and transcriptomic evidence for descent from Plasmodium and loss of blood schizogony in Hepatocystis parasites from naturally infected red colobus monkeys. <i>PLoS Pathogens</i> , 2020, 16, e1008717.	2.1	18
492	Highly Reduced Genomes of Protist Endosymbionts Show Evolutionary Convergence. <i>Current Biology</i> , 2020, 30, 925-933.e3.	1.8	41
493	Formation of new PHE plasmids in pseudomonads in a phenol-polluted environment. <i>Plasmid</i> , 2020, 110, 102504.	0.4	4
494	Using full chloroplast genomes of "red"™ and "yellow"™ <i>Bixa orellana</i> (achiote) for kmer based identification and phylogenetic inference. <i>BMC Genomics</i> , 2020, 21, 544.	1.2	3
495	<i>Sphingomonas hominis</i> sp. nov., isolated from hair of a 21-year-old girl. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1523-1530.	0.7	27
496	Draft Genome Sequences of 171 <i>Listeria monocytogenes</i> Isolates from Food-Related Listeriosis Outbreaks in California from 2007 to 2017. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	0
497	New Insights Into DAEC and EAEC Pathogenesis and Phylogeny. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 572951.	1.8	11
498	Complete Mitochondrial Genomes Reveal Population-Level Patterns in the Widespread Red Alga <i>Gelidiella fanii</i> (Gelidiales, Rhodophyta). <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	8
499	Breast-milk derived potential probiotics as strategy for the management of childhood obesity. <i>Food Research International</i> , 2020, 137, 109673.	2.9	13
500	Assessing the Genomic Variability of <i>Gardnerella vaginalis</i> through Comparative Genomic Analyses: Evolutionary and Ecological Implications. <i>Applied and Environmental Microbiology</i> , 2020, 87, .	1.4	8
501	An enhanced target-enrichment bait set for <i>Hexacorallia</i> provides phylogenomic resolution of the staghorn corals (Acroporidae) and close relatives. <i>Molecular Phylogenetics and Evolution</i> , 2020, 153, 106944.	1.2	59
502	Distinct Polysaccharide Utilization Determines Interspecies Competition between Intestinal <i>Prevotella</i> spp.. <i>Cell Host and Microbe</i> , 2020, 28, 838-852.e6.	5.1	86
503	Whole-Genome Sequencing of Bacterial Isolates That Degrade the Cyanobacterial Toxin Microcystin-LR. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	4
504	Mucoidy, a general mechanism for maintaining lytic phage in populations of bacteria. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	21
505	Aerobic microbial communities in the sediments of a marine oxygen minimum zone. <i>FEMS Microbiology Letters</i> , 2020, 367, .	0.7	16
506	Metabolic diversification of anaerobic methanotrophic archaea in a deep-sea cold seep. <i>Marine Life Science and Technology</i> , 2020, 2, 431-441.	1.8	17

#	ARTICLE	IF	CITATIONS
507	Recombination at the emergence of the pathogenic rabbit haemorrhagic disease virus Lagovirus europaeus/GI.2. Scientific Reports, 2020, 10, 14502.	1.6	36
508	First Report of Pathogenic Bacterium Kalamiaella piersonii Isolated from Urine of a Kidney Stone Patient: Draft Genome and Evidence for Role in Struvite Crystallization. Pathogens, 2020, 9, 711.	1.2	18
509	Genome Sequencing of a Camelpox Vaccine Reveals Close Similarity to Modified Vaccinia virus Ankara (MVA). Viruses, 2020, 12, 786.	1.5	3
510	Microbial single-cell omics: the crux of the matter. Applied Microbiology and Biotechnology, 2020, 104, 8209-8220.	1.7	38
511	Gut microorganisms act together to exacerbate inflammation in spinal cords. Nature, 2020, 585, 102-106.	13.7	153
512	Bifidobacterium adolescentis as a key member of the human gut microbiota in the production of GABA. Scientific Reports, 2020, 10, 14112.	1.6	140
513	Ancestral Absence of Electron Transport Chains in Patescibacteria and DPANN. Frontiers in Microbiology, 2020, 11, 1848.	1.5	62
514	Examination of 189 <i>Campylobacter</i> Species Isolates from the Global Enteric Multicenter Study. Microbiology Resource Announcements, 2020, 9, .	0.3	0
515	Antibiotic Resistance Characteristics of Pseudomonas aeruginosa Isolated from Keratitis in Australia and India. Antibiotics, 2020, 9, 600.	1.5	26
516	Differences in the Endophytic Microbiome of Olive Cultivars Infected by Xylella fastidiosa across Seasons. Pathogens, 2020, 9, 723.	1.2	39
517	First Draft Genome Sequence of Thermophilic Laceyella tengchongensis BKK01, Isolated from Municipal Solid Waste in Thailand. Microbiology Resource Announcements, 2020, 9, .	0.3	0
518	Draft Genome Sequence of Aeromonas sobria Strain CHT-30, Isolated from a Diseased Rainbow Trout (Oncorhynchus mykiss) in Peru. Microbiology Resource Announcements, 2020, 9, .	0.3	0
519	Covariation patterns of phytoplankton and bacterioplankton in hypertrophic shallow lakes. FEMS Microbiology Ecology, 2020, 96, .	1.3	5
520	Spacer acquisition by Type III CRISPR-Cas system during bacteriophage infection of Thermus thermophilus. Nucleic Acids Research, 2020, 48, 9787-9803.	6.5	24
521	Mutation of hilD in a Salmonella Derby lineage linked to swine adaptation and reduced risk to human health. Scientific Reports, 2020, 10, 21539.	1.6	7
522	Distribution of Important Probiotic Genes and Identification of the Biogenic Amines Produced by Lactobacillus acidophilus PNW3. Foods, 2020, 9, 1840.	1.9	5
523	Draft Genome Sequences of Five Diverse Klebsiella Species Isolates from Intensive Care Unit Patients. Microbiology Resource Announcements, 2020, 9, .	0.3	0
524	X-ray inactivation of RNA viruses without loss of biological characteristics. Scientific Reports, 2020, 10, 21431.	1.6	8

#	ARTICLE	IF	CITATIONS
525	Virulence role of the outer membrane protein CarO in carbapenem-resistant <i>Acinetobacter baumannii</i> . <i>Virulence</i> , 2020, 11, 1727-1737.	1.8	16
526	Diverse Horizontally-Acquired Gene Clusters Confer Sucrose Utilization to Different Lineages of the Marine Pathogen <i>Photobacterium damsela</i> subsp. <i>damsela</i> . <i>Genes</i> , 2020, 11, 1244.	1.0	4
527	Draft Genome Sequences of 11 Bacterial Strains Isolated from Commercial Corn-Based Poultry Feed. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	3
528	Genome Sequence of a <i>Weissella confusa</i> Strain Isolated from the First Reported Case of Neonatal Sepsis in an Equid. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	2
529	Next-Generation Sequencing and MALDI Mass Spectrometry in the Study of Multiresistant Processed Meat Vancomycin-Resistant Enterococci (VRE). <i>Biology</i> , 2020, 9, 89.	1.3	13
530	Draft Genome Sequences of 10 Bacterial Strains Isolated from Root Nodules of <i>Alnus</i> Trees in New Hampshire. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	4
531	Within-patient plasmid dynamics in <i>Klebsiella pneumoniae</i> during an outbreak of a carbapenemase-producing <i>Klebsiella pneumoniae</i> . <i>PLoS ONE</i> , 2020, 15, e0233313.	1.1	13
532	Fetal inheritance of chromosomally integrated human herpesvirus 6 predisposes the mother to pre-eclampsia. <i>Nature Microbiology</i> , 2020, 5, 901-908.	5.9	29
533	Metagenome-assembled genomes reveal unique metabolic adaptations of a basal marine Thaumarchaeota lineage. <i>ISME Journal</i> , 2020, 14, 2105-2115.	4.4	54
534	Emerging Threat of Antimicrobial Resistance in $\hat{H}^2$ -Hemolytic Streptococci. <i>Frontiers in Microbiology</i> , 2020, 11, 797.	1.5	15
535	Population Genomic Analysis Reveals a Highly Conserved Mitochondrial Genome in <i>Fusarium asiaticum</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 839.	1.5	14
536	Draft Genome Sequences of 13 Isolates of <i>Adlercreutzia equolifaciens</i> , <i>Eggerthella lenta</i> , and <i>Gordonibacter urolithinifaciens</i> , Isolated from Human Fecal Samples in Karlsruhe, Germany. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	6
537	Whole-Genome Sequences of an Abortive <i>Bacillus safensis</i> Strain Isolated from a Mare's Uterus. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
538	Detection of Astrovirus in a Cow with Neurological Signs by Nanopore Technology, Italy. <i>Viruses</i> , 2020, 12, 530.	1.5	7
539	First detection of autochthonous extensively drug-resistant NDM-1 <i>Pseudomonas aeruginosa</i> ST235 from a patient with bloodstream infection in Italy, October 2019. <i>Antimicrobial Resistance and Infection Control</i> , 2020, 9, 73.	1.5	7
540	The complete chloroplast genome sequence of <i>Bupleurum scorzonerifolium</i> Willd. (Apiaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1998-1999.	0.2	2
541	A Novel Microbialite-Associated Phototrophic Chloroflexi Lineage Exhibiting a Quasi-Clonal Pattern along Depth. <i>Genome Biology and Evolution</i> , 2020, 12, 1207-1216.	1.1	11
542	Importance of <i>Defluviitalea ramosedens</i> for Hydrolytic Biomass Degradation in Co-Culture with <i>Hungateiclostridium thermocellum</i> . <i>Microorganisms</i> , 2020, 8, 915.	1.6	13

#	ARTICLE	IF	CITATIONS
543	A new metagenome binning method based on gene uniqueness. <i>Genes and Genomics</i> , 2020, 42, 883-892.	0.5	0
544	Using SPAdes De Novo Assembler. <i>Current Protocols in Bioinformatics</i> , 2020, 70, e102.	25.8	1,113
545	Prevalence and molecular epidemiology of mcr-1-positive <i>Klebsiella pneumoniae</i> in healthy adults from China. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 2485-2494.	1.3	17
546	Origin and evolution of dengue virus type 2 causing outbreaks in Kenya: Evidence of circulation of two cosmopolitan genotype lineages. <i>Virus Evolution</i> , 2020, 6, veaa026.	2.2	9
547	Mitochondrial Genomes of <i>Hemiarma marina</i> and <i>Leucocryptos marina</i> Revised the Evolution of Cytochrome c Maturation in Cryptista. <i>Frontiers in Ecology and Evolution</i> , 2020, 8, .	1.1	9
548	Genotyping of Salmon Gill Poxvirus Reveals One Main Predominant Lineage in Europe, Featuring Fjord- and Fish Farm-Specific Sub-Lineages. <i>Frontiers in Microbiology</i> , 2020, 11, 1071.	1.5	8
549	Identification of Persistent Sulfidogenic Bacteria in Shale Gas Produced Waters. <i>Frontiers in Microbiology</i> , 2020, 11, 286.	1.5	15
550	Comparative Genome Analysis of the Lignocellulose Degrading Bacteria <i>Citrobacter freundii</i> so4 and <i>Sphingobacterium multivorum</i> w15. <i>Frontiers in Microbiology</i> , 2020, 11, 248.	1.5	10
551	Draft Genome Sequences of 12 <i>Lactobacillus reuteri</i> Strains of Rodent Origin. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	2
552	Genomic Stability of Composite SCCmec ACME and COMER-Like Genetic Elements in <i>Staphylococcus epidermidis</i> Correlates With Rate of Excision. <i>Frontiers in Microbiology</i> , 2020, 11, 166.	1.5	12
553	<i>Streptococcus pneumoniae</i> Nasopharyngeal Carriage among PCV-10-Vaccinated HIV-1-Infected Children with Maintained Serological Memory in Ethiopia. <i>Pathogens</i> , 2020, 9, 159.	1.2	1
554	Comparative Genomics and Antimicrobial Resistance Profiling of <i>Elizabethkingia</i> Isolates Reveal Nosocomial Transmission and <i>In Vitro</i> Susceptibility to Fluoroquinolones, Tetracyclines, and Trimethoprim-Sulfamethoxazole. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	1.8	27
555	Secondary Metabolism in the Gill Microbiota of Shipworms (Teredinidae) as Revealed by Comparison of Metagenomes and Nearly Complete Symbiont Genomes. <i>MSystems</i> , 2020, 5, .	1.7	15
556	Draft Genome Sequence of <i>Flavobacterium</i> sp. Strain SLB02, Isolated from the Diseased Sponge <i>Lubomirskia baicalensis</i> . <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	5
557	Genomic Analysis of Bovine <i>Staphylococcus aureus</i> Isolates from Milk To Elucidate Diversity and Determine the Distributions of Antimicrobial and Virulence Genes and Their Association with Mastitis. <i>MSystems</i> , 2020, 5, .	1.7	35
558	Genomic Analysis of <i>Staphylococcus aureus</i> Strains Originating from Hungarian Rabbit Farms Reinforce the Clonal Origin of Various Virulence Types. <i>Animals</i> , 2020, 10, 1128.	1.0	4
559	<i>Methanohalophilus profundus</i> sp. nov., a methylotrophic halophilic piezophilic methanogen isolated from a deep hypersaline anoxic basin. <i>Systematic and Applied Microbiology</i> , 2020, 43, 126107.	1.2	10
560	Characterization of <i>Staphylococcus intermedius</i> Group Isolates Associated with Animals from Antarctica and Emended Description of <i>Staphylococcus delphini</i> . <i>Microorganisms</i> , 2020, 8, 204.	1.6	19



#	ARTICLE	IF	CITATIONS
561	Epidemiology of colistin-resistant, carbapenemase-producing Enterobacteriaceae and Acinetobacter baumannii in Croatia. <i>Infection, Genetics and Evolution</i> , 2020, 81, 104263.	1.0	34
562	Metabolic Changes of Mycobacterium tuberculosis during the Anti-Tuberculosis Therapy. <i>Pathogens</i> , 2020, 9, 131.	1.2	11
563	Genome sequence of an aichivirus detected in a common pipistrelle bat ( <i>Pipistrellus pipistrellus</i> ). <i>Archives of Virology</i> , 2020, 165, 1019-1022.	0.9	5
564	Paralogization and New Protein Architectures in Planctomycetes Bacteria with Complex Cell Structures. <i>Molecular Biology and Evolution</i> , 2020, 37, 1020-1040.	3.5	6
565	Complete Coding Sequence of a Lumpy Skin Disease Virus Strain Isolated during the 2016 Outbreak in Kazakhstan. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	10
566	Acquisition, transmission and strain diversity of human gut-colonizing crAss-like phages. <i>Nature Communications</i> , 2020, 11, 280.	5.8	55
567	Mineralization and nitrification: Archaea dominate ammonia-oxidising communities in grassland soils. <i>Soil Biology and Biochemistry</i> , 2020, 143, 107725.	4.2	44
568	Metagenomics methods for the study of plant-associated microbial communities: A review. <i>Journal of Microbiological Methods</i> , 2020, 170, 105860.	0.7	91
569	A multicentre outbreak of ST45 MRSA containing deletions in the spa gene in New South Wales, Australia. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 1112-1116.	1.3	10
570	Coral microbiome composition along the northern Red Sea suggests high plasticity of bacterial and specificity of endosymbiotic dinoflagellate communities. <i>Microbiome</i> , 2020, 8, 8.	4.9	75
571	Genomic Insights Into the Mycobacterium kansasii Complex: An Update. <i>Frontiers in Microbiology</i> , 2019, 10, 2918.	1.5	29
572	Detecting Introgression Between Members of the Fusarium fujikuroi and F. oxysporum Species Complexes by Comparative Mitogenomics. <i>Frontiers in Microbiology</i> , 2020, 11, 1092.	1.5	9
573	Complete Genome Sequence of <i>Candidatus</i> Syntrophocurvum alkaliphilum Strain B(2M), Obtained from the Metagenome of a Salt-Tolerant Alkaliphilic Anaerobic Syntrophic Butyrate-Degrading Consortium. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
574	Parallel Evolution in the Integration of a Co-obligate Aphid Symbiosis. <i>Current Biology</i> , 2020, 30, 1949-1957.e6.	1.8	54
575	Genomic characteristics of clinically important ST11 <i>Klebsiella pneumoniae</i> strains worldwide. <i>Journal of Global Antimicrobial Resistance</i> , 2020, 22, 519-526.	0.9	36
576	Microbiome structure and function in rhizosphere of Jerusalem artichoke grown in saline land. <i>Science of the Total Environment</i> , 2020, 724, 138259.	3.9	44
577	Development of a workflow for identification of nuclear genotyping markers for <i>Cyclospora cayatanensis</i> . <i>Parasite</i> , 2020, 27, 24.	0.8	13
578	Draft Genome Sequence of <i>Yersinia ruckeri</i> Strain FMV-22, Isolated from Diseased Rainbow Trout ( <i>Oncorhynchus mykiss</i> ) in Peru. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	0

#	ARTICLE	IF	CITATIONS
579	Early OXA-48-Producing <i>Enterobacterales</i> Isolates Recovered in a Spanish Hospital Reveal a Complex Introduction Dominated by Sequence Type 11 (ST11) and ST405 <i>Klebsiella pneumoniae</i> Clones. <i>MSphere</i> , 2020, 5, .	1.3	15
580	A Novel "Microbial Bait" Technique for Capturing Fe(III)-Reducing Bacteria. <i>Frontiers in Microbiology</i> , 2020, 11, 330.	1.5	4
581	CRISPR/Cas9-mediated targeted mutagenesis of TAS4 and MYBA7 loci in grapevine rootstock 101-14. <i>Transgenic Research</i> , 2020, 29, 355-367.	1.3	38
582	Draft Genome Sequences of Two Boron-Tolerant, Arsenic-Resistant, Gram-Positive Bacterial Strains, <i>Lysinibacillus</i> sp. OL1 and <i>Enterococcus</i> sp. OL5, Isolated from Boron-Fortified Cauliflower-Growing Field Soils of Northern West Bengal, India. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	9
583	" <i>Candidatus</i> <i>Ethanoperedens</i> , a Thermophilic Genus of <i>Archaea</i> Mediating the Anaerobic Oxidation of Ethane. <i>MBio</i> , 2020, 11, .	1.8	66
584	Draft Genome Sequence of an Extensively Drug-Resistant <i>Mycobacterium tuberculosis</i> Clinical Isolate, 3485_MTB, from Nur-Sultan, Kazakhstan. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	3
585	Natural Transmission of <i>Helicobacter saguini</i> Causes Multigenerational Inflammatory Bowel Disease in C57/129 IL-10 <sup>−/−</sup> Mice. <i>MSphere</i> , 2020, 5, .	1.3	3
586	Underpinning unique genes in <i>Ca. Brocadia</i> sp. and its interspecies association potentials in a partial nitrification/anammox system with low-strength wastewater. <i>Chemical Engineering Journal</i> , 2021, 405, 125904.	6.6	13
587	Epidemiology of Respiratory Syncytial Virus Across Five Influenza Seasons Among Adults and Children One Year of Age and Older—Washington State, 2011/2012–2015/2016. <i>Journal of Infectious Diseases</i> , 2021, 223, 147-156.	1.9	10
588	Surveillance of antimicrobial resistance in <i>Escherichia coli</i> and enterococci from food products at retail in Beijing, China. <i>Food Control</i> , 2021, 119, 107483.	2.8	9
589	Evaluation of a real-time PCR assay for the differentiation of <i>Bacillus cereus</i> group species. <i>Food Control</i> , 2021, 120, 107530.	2.8	3
590	Identification of ancient viruses from metagenomic data of the Jomon people. <i>Journal of Human Genetics</i> , 2021, 66, 287-296.	1.1	5
591	Relationships between nitrogen cycling microbial community abundance and composition reveal the indirect effect of soil pH on oak decline. <i>ISME Journal</i> , 2021, 15, 623-635.	4.4	63
592	Whole-genome sequence analysis of <i>Salmonella</i> <i>Infantis</i> isolated from raw chicken meat samples and insights into pESI-like megaplasmid. <i>International Journal of Food Microbiology</i> , 2021, 337, 108956.	2.1	24
593	Phylogenetic and Biogeographic Patterns of <i>Vibrio parahaemolyticus</i> Strains from North America Inferred from Whole-Genome Sequence Data. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	6
594	Assessing the Genetic Diversity of Austrian <i>Corynebacterium diphtheriae</i> Clinical Isolates, 2011 to 2019. <i>Journal of Clinical Microbiology</i> , 2021, 59, .	1.8	9
595	Mini-metagenome analysis of psychrophilic electroactive biofilms based on single cell sorting. <i>Science of the Total Environment</i> , 2021, 762, 144328.	3.9	9
596	Oxazolidinone Resistance Mediated by <i>optrA</i> in Clinical <i>Enterococcus faecalis</i> Isolates in Upper Austria: First Report and Characterization by Whole Genome Sequencing. <i>Microbial Drug Resistance</i> , 2021, 27, 685-690.	0.9	6

#	ARTICLE	IF	CITATIONS
597	Evolutionary History of Endogenous Human Herpesvirus 6 Reflects Human Migration out of Africa. <i>Molecular Biology and Evolution</i> , 2021, 38, 96-107.	3.5	31
598	Analysis of Genome Sequences of Coagulase-Negative Staphylococci Isolates from South Africa and Nigeria Highlighted Environmentally Driven Heterogeneity. <i>Journal of Genomics</i> , 2021, 9, 26-37.	0.6	0
599	Library Preparation Based on Transposase Assisted RNA/DNA Hybrid Co-Tagmentation for Next-Generation Sequencing of Human Noroviruses. <i>Viruses</i> , 2021, 13, 65.	1.5	3
601	Description of <i>Salinimonas profundus</i> sp. nov., a deep-sea bacterium harboring a transposon Tn6333. <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 69-81.	0.7	10
602	Whole Genome Sequencing of Sunflower Root-Associated <i>Bacillus cereus</i> . <i>Evolutionary Bioinformatics</i> , 2021, 17, 117693432110389.	0.6	11
603	Genome-wide comparison of four MRSA clinical isolates from Germany and Hungary. <i>PeerJ</i> , 2021, 9, e10185.	0.9	6
605	Comparative genomics of ESBL-producing <i>Escherichia coli</i> (ESBL-Ec) reveals a similar distribution of the 10 most prevalent ESBL-Ec clones and ESBL genes among human community faecal and extra-intestinal infection isolates in the Netherlands (2014–17). <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 901-908.	1.3	17
607	Draft Genome Sequences of 19 Clinical Isolates of <i>Candida auris</i> from Hong Kong. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	11
608	Rescue of Senecavirus A to uncover mutation profiles of its progenies during 80 serial passages in vitro. <i>Veterinary Microbiology</i> , 2021, 253, 108969.	0.8	22
609	Harnessing the Genetic Diversity and Metabolic Potential of Extremophilic Microorganisms through the Integration of Metagenomics and Single-Cell Genomics. , 0, , .		0
610	An Expanded Gene Catalog of Mouse Gut Metagenomes. <i>MSphere</i> , 2021, 6, .	1.3	13
611	Antimicrobial resistance and interspecies gene transfer in <i>Campylobacter coli</i> and <i>Campylobacter jejuni</i> isolated from food animals, poultry processing, and retail meat in North Carolina, 2018–2019. <i>PLoS ONE</i> , 2021, 16, e0246571.	1.1	34
612	Emerimicins X, 15-Residue Peptaibols Discovered from an <i>Acremonium</i> sp. through Integrated Genomic and Chemical Approaches. <i>Journal of Natural Products</i> , 2021, 84, 1113-1126.	1.5	9
613	Tracking the Origin of Austrian Human Brucellosis Cases Using Whole Genome Sequencing. <i>Frontiers in Medicine</i> , 2021, 8, 635547.	1.2	14
614	<i>Pseudomonas paracarnis</i> sp. nov., isolated from refrigerated beef. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	8
615	Genomic Characterization of Two Shiga Toxin-Producing Bacteriophages Induced From Environmental Shiga Toxin-Producing <i>Escherichia coli</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 587696.	1.5	3
616	Triclosan Tolerance Is Driven by a Conserved Mechanism in Diverse <i>Pseudomonas</i> Species. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	8
619	The complete plastomes of two flowering epiparasites ( <i>Phacellaria glomerata</i> and <i>P. compressa</i> ): Gene content, organization, and plastome degradation. <i>Genomics</i> , 2021, 113, 447-455.	1.3	5

#	ARTICLE	IF	CITATIONS
620	Full pathogen characterisation: species identification including the detection of virulence factors and antibiotic resistance genes via multiplex DNA-assays. <i>Scientific Reports</i> , 2021, 11, 6001.	1.6	8
621	Comparative Genomics Reveals Prophylactic and Catabolic Capabilities of <i>Actinobacteria</i> within the Fungus-Farming Termite Symbiosis. <i>MSphere</i> , 2021, 6, .	1.3	17
622	A large food-borne outbreak of campylobacteriosis in kindergartens and primary schools in Pescara, Italy, May–June 2018. <i>Journal of Medical Microbiology</i> , 2021, 70, .	0.7	7
623	The complete mitochondrial genome of white-tailed mole ( <i>Parascaptor leucura</i> ). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1112-1113.	0.2	2
624	Isolation and Characterization of a Novel Jumbo Phage from Leaf Litter Compost and Its Suppressive Effect on Rice Seedling Rot Diseases. <i>Viruses</i> , 2021, 13, 591.	1.5	6
625	Draft Genomic Analysis of <i>Pseudomonas</i> sp. Strain OA3, a Potential Plant Growth-Promoting Rhizospheric Bacterium. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	0
626	Multidrug Resistance Dissemination in <i>Escherichia coli</i> Isolated from Wild Animals: Bacterial Clones and Plasmid Complicity. <i>Microbiology Research</i> , 2021, 12, 123-137.	0.8	4
628	The complete mitochondrial genome of long-tailed red-toothed shrew ( <i>Episoriculus leucops</i> ) and implication of phylogenetic status. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1308-1309.	0.2	0
630	<i>Altererythrobacter flava</i> sp. nov., a new member of the family Erythrobacteraceae, isolated from a surface seawater sample. <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 497-506.	0.7	2
631	Decoding the interspecies interaction in anammox process with inorganic feeding through metagenomic and metatranscriptomic analysis. <i>Journal of Cleaner Production</i> , 2021, 288, 125691.	4.6	33
632	Vertical and horizontal dissemination of an IncC plasmid harbouring rmtB 16S rRNA methylase gene, conferring resistance to plazomicin, among invasive ST258 and ST16 KPC-producing <i>Klebsiella pneumoniae</i> . <i>Journal of Global Antimicrobial Resistance</i> , 2021, 24, 183-189.	0.9	14
633	Metagenomic Data Assembly – The Way of Decoding Unknown Microorganisms. <i>Frontiers in Microbiology</i> , 2021, 12, 613791.	1.5	67
634	Evidence of gene nucleotide composition favoring replication and growth in a fastidious plant pathogen. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	5
635	Nutrient-driven genome evolution revealed by comparative genomics of chryomonad flagellates. <i>Communications Biology</i> , 2021, 4, 328.	2.0	7
636	Amoxicillin-Clavulanic Acid Resistance in the Genus <i>Bifidobacterium</i> . <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	16
637	Allopatric Plant Pathogen Population Divergence following Disease Emergence. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	14
638	Comparative Genome Analyses of <i>Lactobacillus crispatus</i> Isolates from Different Ecological Niches Reveal an Adaptation of This Species to the Human Vaginal Environment. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	8
639	Antimicrobial Resistance Genes in Bacteria Isolated From Japanese Honey, and Their Potential for Conferring Macrolide and Lincosamide Resistance in the American Foulbrood Pathogen <i>Paenibacillus larvae</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 667096.	1.5	15

#	ARTICLE	IF	CITATIONS
640	Data on the polymorphic sites in the chloroplast genomes of seven perennial <i>Helianthus</i> species. Data in Brief, 2021, 35, 106904.	0.5	0
641	Complete Genome Sequence of <i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> Strain 42-13-1, Isolated in Japan. Microbiology Resource Announcements, 2021, 10, .	0.3	1
642	Detection and genome characterization of bovine kobuvirus (BKV) in faecal samples from diarrhoeic calves in Quebec, Canada. Transboundary and Emerging Diseases, 2022, 69, 1649-1655.	1.3	4
643	<i>Actirhodobacter atriluteus</i> gen. nov., sp. nov., isolated from the surface water of the Yellow Sea. Antonie Van Leeuwenhoek, 2021, 114, 1059-1068.	0.7	16
644	Identification of a Novel Papillomavirus Type (MfoiPV1) Associated with Acrochordon in a Stone Marten ( <i>Martes foina</i> ). Pathogens, 2021, 10, 539.	1.2	1
645	A Primer on the Analysis of High-Throughput Sequencing Data for Detection of Plant Viruses. Microorganisms, 2021, 9, 841.	1.6	36
646	Molecular Detection and Characterization of Porcine Epidemic Diarrhea Virus and Porcine Aichivirus C Coinfection in MÃ©xico. Viruses, 2021, 13, 738.	1.5	13
647	Rationally designed bacterial consortia to treat chronic immune-mediated colitis and restore intestinal homeostasis. Nature Communications, 2021, 12, 3105.	5.8	82
648	Genome Sequence of <i>Streptomyces cavourensis</i> BUU135, Isolated from Soil from a Tropical Fruit Farm in Thailand. Microbiology Resource Announcements, 2021, 10, .	0.3	0
649	Ceftazidime-Avibactam Resistance in <i>Klebsiella pneumoniae</i> Sequence Type 11 Due to a Mutation in Plasmid-Borne <i>bla</i> pc-2 to <i>bla</i> pc-33, in Henan, China. Infection and Drug Resistance, 2021, Volume 14, 1725-1731.	1.1	10
650	Anchored Phylogenomics, Evolution and Systematics of Elateridae: Are All Bioluminescent Elateroidea Derived Click Beetles?. Biology, 2021, 10, 451.	1.3	39
652	An Integrative Bioinformatic Analysis for Keratinase Detection in Marine-Derived <i>Streptomyces</i> . Marine Drugs, 2021, 19, 286.	2.2	2
653	Stability of the human gut virome and effect of gluten-free diet. Cell Reports, 2021, 35, 109132.	2.9	34
654	Target sequence capture in orchids: Developing a kit to sequence hundreds of singleâ€œcopy loci. Applications in Plant Sciences, 2021, 9, e11416.	0.8	21
657	Appearances are deceptive: Three RNA viruses co-infected with the nucleopolyhedrovirus in host <i>Lymantria dispar</i> . Virus Research, 2021, 297, 198371.	1.1	4
658	Isoprene-Degrading Bacteria from Soils Associated with Tropical Economic Crops and Framework Forest Trees. Microorganisms, 2021, 9, 1024.	1.6	2
659	Viruses infecting a warm water picoeukaryote shed light on spatial co-occurrence dynamics of marine viruses and their hosts. ISME Journal, 2021, 15, 3129-3147.	4.4	10
660	Printing Microbial Dark Matter: Using Single Cell Dispensing and Genomics to Investigate the Patescibacteria/Candidate Phyla Radiation. Frontiers in Microbiology, 2021, 12, 635506.	1.5	14

#	ARTICLE	IF	CITATIONS
661	<i>Pseudomonas paraversuta</i> sp. nov. isolated from refrigerated dry-aged beef. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	7
662	Implementing metatranscriptomics to unveil the mechanism of bioaugmentation adopted in a continuous anaerobic process treating cow manure. <i>Bioresource Technology</i> , 2021, 330, 124962.	4.8	21
663	Genomic Analysis of <i>Pasteurella atlantica</i> Provides Insight on Its Virulence Factors and Phylogeny and Highlights the Potential of Reverse Vaccinology in Aquaculture. <i>Microorganisms</i> , 2021, 9, 1215.	1.6	4
664	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
666	The First Data on the Complete Genome of a Tetrodotoxin-Producing Bacterium. <i>Toxins</i> , 2021, 13, 410.	1.5	1
667	Genomic assessment of <i>Stenotrophomonas indicatrix</i> for improved sunflower plant. <i>Current Genetics</i> , 2021, 67, 891-907.	0.8	11
668	Whole-Genome Sequencing Investigation of a Large Nosocomial Outbreak Caused by ST131 H30Rx KPC-Producing <i>Escherichia coli</i> in Italy. <i>Antibiotics</i> , 2021, 10, 718.	1.5	7
669	Subtypes, resistance and virulence platforms in extended-drug resistant <i>Acinetobacter baumannii</i> Romanian isolates. <i>Scientific Reports</i> , 2021, 11, 13288.	1.6	16
670	Three transmission events of <i>Vibrio cholerae</i> O1 into Lusaka, Zambia. <i>BMC Infectious Diseases</i> , 2021, 21, 570.	1.3	5
671	Antimicrobial resistant bacteria recovered from retail ground meat products in the US include a <i>Raoultella ornithinolytica</i> co-harboring blaKPC-2 and blaNDM-5. <i>Scientific Reports</i> , 2021, 11, 14041.	1.6	10
672	The complete mitochondrial genome of the photosymbiotic sea slug <i>Berghia stephanieae</i> (ValdÃ©s, 2005) (Gastropoda, Nudibranchia). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2281-2284.	0.2	4
673	Draft Genome Sequences of Nitrogen-Fixing Bradyrhizobia Isolated from Root Nodules of Peanut, <i>Arachis hypogaea</i> , Cultivated in Southern Tunisia. <i>Microbiology Resource Announcements</i> , 2021, 10, e0043421.	0.3	1
674	Successful Dissemination of Plasmid-Mediated Extended-Spectrum $\beta$ -Lactamases in Enterobacterales over Humans to Wild Fauna. <i>Microorganisms</i> , 2021, 9, 1471.	1.6	2
675	Population-based surveillance of <i>Enterobacter cloacae</i> complex causing blood stream infections in a centralized Canadian region. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2022, 41, 119-125.	1.3	8
677	Novel hyperthermophilic crenarchaeon <i>Infirmifilum lucidum</i> gen. nov. sp. nov., reclassification of <i>Thermofilum uzonense</i> as <i>Infirmifilum uzonense</i> comb. nov. and assignment of the family Thermofilaceae to the order Thermofilales ord. nov.. <i>Systematic and Applied Microbiology</i> , 2021, 44, 126230.	1.2	15
678	Draft Genome Sequencing of <i>Stenotrophomonas indicatrix</i> BOVIS40 and <i>Stenotrophomonas maltophilia</i> JVB5, Two Strains with Identifiable Genes Involved in Plant Growth Promotion. <i>Microbiology Resource Announcements</i> , 2021, 10, e0048221.	0.3	3
679	Deep-Sea Carbonates Are a Reservoir of Fossil Microbes Previously Inhabiting Cold Seeps. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	1
680	Mating-Type Locus Organization and Mating-Type Chromosome Differentiation in the Bipolar Edible Button Mushroom <i>Agaricus bisporus</i> . <i>Genes</i> , 2021, 12, 1079.	1.0	17

#	ARTICLE	IF	CITATIONS
681	Comprehending Cornales: phylogenetic reconstruction of the order using the Angiosperms353 probe set. <i>American Journal of Botany</i> , 2021, 108, 1112-1121.	0.8	23
682	Both Conifer II and Gnetales are characterized by a high frequency of ancient mitochondrial gene transfer to the nuclear genome. <i>BMC Biology</i> , 2021, 19, 146.	1.7	18
683	Linking plasmid-based beta-lactamases to their bacterial hosts using single-cell fusion PCR. <i>ELife</i> , 2021, 10, .	2.8	18
684	Complete Genome Sequences of Eight <i>Streptococcus equi</i> subsp. <i>zooepidemicus</i> Strains Isolated from Mares in Estrus with Endometritis. <i>Microbiology Resource Announcements</i> , 2021, 10, e0132120.	0.3	0
685	An <i>Agrobacterium</i> -mediated stable transformation technique for the hornwort model <i>Anthoceros agrestis</i> . <i>New Phytologist</i> , 2021, 232, 1488-1505.	3.5	18
686	A new family of globally distributed lytic roseophages with unusual deoxythymidine to deoxyuridine substitution. <i>Current Biology</i> , 2021, 31, 3199-3206.e4.	1.8	13
687	Diverse methanogens, bacteria and tannase genes in the feces of the endangered volcano rabbit ( <i>Romerolagus diazi</i> ). <i>PeerJ</i> , 2021, 9, e11942.	0.9	6
688	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
689	Adaptive laboratory evolution of microbial co-cultures for improved metabolite secretion. <i>Molecular Systems Biology</i> , 2021, 17, e10189.	3.2	21
690	The Insights into Mitochondrial Genomes of Sunflowers. <i>Plants</i> , 2021, 10, 1774.	1.6	7
691	coronaSPAdes: from biosynthetic gene clusters to RNA viral assemblies. <i>Bioinformatics</i> , 2021, 38, 1-8.	1.8	30
692	Genomic Analysis of Endophytic <i>Bacillus cereus</i> T4S and Its Plant Growth-Promoting Traits. <i>Plants</i> , 2021, 10, 1776.	1.6	30
693	Rapid Shifts in Mitochondrial tRNA Import in a Plant Lineage with Extensive Mitochondrial tRNA Gene Loss. <i>Molecular Biology and Evolution</i> , 2021, 38, 5735-5751.	3.5	13
694	Sea-Ice Bacteria <i>Halomonas</i> sp. Strain 363 and <i>Paracoccus</i> sp. Strain 392 Produce Multiple Types of Poly-3-Hydroxyalkanoic Acid (PHA) Storage Polymers at Low Temperature. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0092921.	1.4	9
695	Characterization of plant-growth-promoting rhizobacterial isolates associated with food plants in South Africa. <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 1683-1708.	0.7	8
696	Genome Sequence of Lymphocystis Disease Virus 2 LCDV-JP_Oita_2018, Isolated from a Diseased Japanese Flounder ( <i>Paralichthys olivaceus</i> ) in Japan. <i>Microbiology Resource Announcements</i> , 2021, 10, e0054721.	0.3	5
697	Environmental Surveillance and Characterization of Antibiotic Resistant <i>Staphylococcus aureus</i> at Coastal Beaches and Rivers on the Island of Hawaii. <i>Antibiotics</i> , 2021, 10, 980.	1.5	9
698	Whole-genome sequencing reveals forgotten lineages and recurrent hybridizations within the kelp genus <i>Alaria</i> (Phaeophyceae). <i>Journal of Phycology</i> , 2021, 57, 1721-1738.	1.0	10

#	ARTICLE	IF	CITATIONS
699	Metagenome Assembly and Metagenome-Assembled Genome of <i>Candidatus</i> Aramenus sulfurataquae from Thermal Sediments from the Los Azufres Volcanic Complex. Microbiology Resource Announcements, 2021, 10, e0037921.	0.3	3
700	Intracellular DNA transfer events restricted to the genus <i>Convallaria</i> within the Asparagaceae family: Possible mechanisms and potential as genetic markers for biographical studies. Genomics, 2021, 113, 2906-2918.	1.3	8
701	A complete mitochondrial genome for fragrant Chinese rosewood ( <i>Dalbergia odorifera</i> , Fabaceae) with comparative analyses of genome structure and intergenomic sequence transfers. BMC Genomics, 2021, 22, 672.	1.2	25
702	Imported human norovirus in travelers, Shanghai port, China 2018: An epidemiological and whole genome sequencing study. Travel Medicine and Infectious Disease, 2021, 43, 102140.	1.5	5
703	Whole genome sequences reveal the <i>Xanthomonas perforans</i> population is shaped by the tomato production system. ISME Journal, 2022, 16, 591-601.	4.4	6
704	Whole Genome Sequencing Based Taxonomic Classification, and Comparative Genomic Analysis of Potentially Human Pathogenic <i>Enterobacter</i> spp. Isolated from Chlorinated Wastewater in the North West Province, South Africa. Microorganisms, 2021, 9, 1928.	1.6	3
705	Draft Genome Sequences of Four Novel Strains of Microbes Isolated from <i>Lepidocephalichthys guntea</i> . Microbiology Resource Announcements, 2021, 10, e0062121.	0.3	0
706	In vivo Selection of Imipenem Resistance Among Ceftazidime-Avibactam-Resistant, Imipenem-Susceptible <i>Klebsiella pneumoniae</i> Isolate With KPC-33 Carbapenemase. Frontiers in Microbiology, 2021, 12, 727946.	1.5	6
707	Isolation, characterization, and genome assembly of <i>Barnettozyma botsteinii</i> sp. nov. and novel strains of <i>Kurtzmaniella quercitrusa</i> isolated from the intestinal tract of the termite <i>Macrotermes bellicosus</i> . G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	7
708	Sedimentation rate and organic matter dynamics shape microbiomes across a continental margin. Biogeosciences, 2021, 18, 5203-5222.	1.3	8
709	Rescuing eGFP-Tagged Canine Distemper Virus for 40 Serial Passages Separately in Ribavirin- and Non-Treated Cells: Comparative Analysis of Viral Mutation Profiles. Frontiers in Cellular and Infection Microbiology, 2021, 11, 746926.	1.8	4
710	Genome Mining of Three Plant Growth-Promoting <i>Bacillus</i> Species from Maize Rhizosphere. Applied Biochemistry and Biotechnology, 2021, 193, 3949-3969.	1.4	22
711	Whole-Genome Sequence and Comparative Analysis of Human Papillomavirus Type 18 Isolated from a Nasopharyngeal Carcinoma from South Africa. Microbiology Resource Announcements, 2021, 10, e0063021.	0.3	0
712	Biogeography, reproductive biology and phylogenetic divergence within the Fungiidae (mushroom) <i>Tj ETQq1 1 0.784314 rgBJ /Overl</i>	1.2	7
713	Metathramycin, a new bioactive aureolic acid discovered by heterologous expression of a metagenome derived biosynthetic pathway. RSC Chemical Biology, 2021, 2, 556-567.	2.0	11
714	Genomic Drivers of Multidrug-Resistant <i>Shigella</i> Affecting Vulnerable Patient Populations in the United States and Abroad. MBio, 2021, 12, .	1.8	19
715	Popping Superbubbles and Discovering Clumps: Recent Developments in Biological Sequence Analysis. Lecture Notes in Computer Science, 2016, , 3-14.	1.0	6
716	The characteristics and genome analysis of vB_ApiP_XC38, a novel phage infecting <i>Acinetobacter pittii</i> . Virus Genes, 2020, 56, 498-507.	0.7	7



#	ARTICLE	IF	CITATIONS
717	<i>Aliarcobacter vitoriensis</i> sp. nov., isolated from carrot and urban wastewater. <i>Systematic and Applied Microbiology</i> , 2020, 43, 126091.	1.2	17
718	<i>Legionella saudiensis</i> sp. nov., isolated from a sewage water sample. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 4367-4371.	0.8	12
719	<i>Arcobacter canalis</i> sp. nov., isolated from a water canal contaminated with urban sewage. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 1258-1264.	0.8	37
720	<i>Arcobacter haliotis</i> Tanaka et al. 2017 is a later heterotypic synonym of <i>Arcobacter lekithochrous</i> DiÃ©guez et al. 2017. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 2851-2854.	0.8	10
721	<i>Frankia canadensis</i> sp. nov., isolated from root nodules of <i>Alnus incana</i> subspecies <i>rugosa</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 3001-3011.	0.8	33
722	<i>Arcobacter lacus</i> sp. nov. and <i>Arcobacter caeni</i> sp. nov., two novel species isolated from reclaimed water. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 3326-3331.	0.8	18
723	<i>Apibacter muscae</i> sp. nov., a novel bacterial species isolated from house flies. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 3586-3592.	0.8	7
724	<i>Pseudomonas bubulae</i> sp. nov., isolated from beef. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 292-301.	0.8	9
725	<i>Borrelia maritima</i> sp. nov., a novel species of the <i>Borrelia burgdorferi</i> sensu lato complex, occupying a basal position to North American species. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 849-856.	0.8	27
726	<i>Pseudomonas carnis</i> sp. nov., isolated from meat. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 1528-1540.	0.8	19
727	Description of <i>Citrobacter cronae</i> sp. nov., isolated from human rectal swabs and stool samples. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 2998-3003.	0.8	18
728	Molecular epidemiological study on Infectious Pancreatic Necrosis Virus isolates from aquafarms in Scotland over three decades. <i>Journal of General Virology</i> , 2018, 99, 1567-1581.	1.3	18
729	Rapid detection of extra-intestinal pathogenic <i>Escherichia coli</i> multi-locus sequence type 127 using a specific PCR assay. <i>Journal of Medical Microbiology</i> , 2019, 68, 188-196.	0.7	6
730	Urinary microbiota â€“ a potential biomarker and therapeutic target for bladder cancer. <i>Journal of Medical Microbiology</i> , 2019, 68, 1471-1478.	0.7	59
731	In vivo acquisition and risk of inter-species spread of bla KPC-3-plasmid from <i>Klebsiella pneumoniae</i> to <i>Serratia marcescens</i> in the lower respiratory tract. <i>Journal of Medical Microbiology</i> , 2020, 69, 82-86.	0.7	5
732	The comparative genomics of <i>Bifidobacterium callitrichos</i> reflects dietary carbohydrate utilization within the common marmoset gut. <i>Microbial Genomics</i> , 2018, 4, .	1.0	16
733	Comparison of core-genome MLST, coreSNP and PFGE methods for <i>Klebsiella pneumoniae</i> cluster analysis. <i>Microbial Genomics</i> , 2020, 6, .	1.0	34
734	Molecular epidemiology of <i>Salmonella Infantis</i> in Europe: insights into the success of the bacterial host and its parasitic pESI-like megaplasmid. <i>Microbial Genomics</i> , 2020, 6, .	1.0	68

#	ARTICLE	IF	CITATIONS
735	Diminutive, degraded but dissimilar: Wolbachia genomes from filarial nematodes do not conform to a single paradigm. <i>Microbial Genomics</i> , 2020, 6, .	1.0	24
750	Rapid Identification of Different <i>Escherichia coli</i> Sequence Type 131 Clades. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	94
751	Primer Design for an Accurate View of Picocyanobacterial Community Structure by Using High-Throughput Sequencing. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	9
752	Plasmid Dynamics in KPC-Positive <i>Klebsiella pneumoniae</i> during Long-Term Patient Colonization. <i>MBio</i> , 2016, 7, .	1.8	126
753	Whole-Genome Sequences of Seven <i>Listeria monocytogenes</i> Strains from Different Stages of a Poultry Meat Production Chain. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	3
754	<i>Salmonella enterica</i> subsp. <i>arizonae</i> Isolated from a Canine Clinical Case of Prostatitis. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	2
755	Draft Genome Sequence of <i>Bacillus velezensis</i> Strain ZeaDK315Endo16. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	2
756	Draft Genome Sequence of <i>Massilia</i> sp. Strain ONC3, a Novel Bacterial Species of the <i>Oxalobacteraceae</i> Family Isolated from Garden Soil. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	9
757	MiSeq Sequencing of <i>Salmonella enterica</i> subsp. <i>houtenae</i> Isolates from a Dog Treated for Hind-Limb Paresis. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	3
758	Draft Genome Sequences of 10 Bacterial Strains Isolated from an Abandoned Coal Mine in Southeast Kansas. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	3
759	Draft Genome Sequence of <i>Vibrio parahaemolyticus</i> Strain PH1339, Which Causes Acute Hepatopancreatic Necrosis Disease in Shrimp in the Philippines. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	4
760	Draft Genome Sequence of <i>Janthinobacterium</i> sp. Strain SLB01, Isolated from the Diseased Sponge <i>Lubomirskia baicalensis</i> . <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	5
761	Complete Genome Sequence of a Hyperthermophilic Archaeon, <i>Thermosphaera</i> sp. Strain 3507, Isolated from a Chilean Hot Spring. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	2
762	Draft Genome Sequences of Type Strains of <i>Adlercreutzia muris</i> and <i>Ellagibacter urolithinifaciens</i> , Belonging to the Family <i>Eggerthellaceae</i> . <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	5
763	Evolution of Ciprofloxacin Resistance-Encoding Genetic Elements in <i>Salmonella</i> . <i>MSystems</i> , 2020, 5, .	1.7	11
764	Impacts of local population history and ecology on the evolution of a globally dispersed pathogen. <i>BMC Genomics</i> , 2020, 21, 369.	1.2	19
765	Typing and classification of non-tuberculous mycobacteria isolates. <i>F1000Research</i> , 0, 9, 249.	0.8	1
766	Complete assembly of a dengue virus type 3 genome from a recent genotype III clade by metagenomic sequencing of serum. <i>Wellcome Open Research</i> , 2018, 3, 44.	0.9	4

#	ARTICLE	IF	CITATIONS
767	Complete assembly of a dengue virus type 3 genome from a recent genotype III clade by metagenomic sequencing of serum. Wellcome Open Research, 2018, 3, 44.	0.9	6
768	Comparative Transcriptomic Exploration Reveals Unique Molecular Adaptations of Neuropathogenic <i>Trichobilharzia</i> to Invade and Parasitize Its Avian Definitive Host. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004406.	1.3	25
769	MLST and Whole-Genome-Based Population Analysis of <i>Cryptococcus gattii</i> VGIII Links Clinical, Veterinary and Environmental Strains, and Reveals Divergent Serotype Specific Sub-populations and Distant Ancestors. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004861.	1.3	49
770	Capture-based enrichment of <i>Theileria parva</i> DNA enables full genome assembly of first buffalo-derived strain and reveals exceptional intra-specific genetic diversity. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008781.	1.3	6
771	A Method Enabling High-Throughput Sequencing of Human Cytomegalovirus Complete Genomes from Clinical Isolates. <i>PLoS ONE</i> , 2014, 9, e95501.	1.1	23
772	Monodisperse Picoliter Droplets for Low-Bias and Contamination-Free Reactions in Single-Cell Whole Genome Amplification. <i>PLoS ONE</i> , 2015, 10, e0138733.	1.1	55
773	Genomic surveillance detects <i>Salmonella enterica</i> serovar Paratyphi A harbouring blaCTX-M-15 from a traveller returning from Bangladesh. <i>PLoS ONE</i> , 2020, 15, e0228250.	1.1	15
774	Emergence of a novel chikungunya virus strain bearing the E1:V80A substitution, out of the Mombasa, Kenya 2017-2018 outbreak. <i>PLoS ONE</i> , 2020, 15, e0241754.	1.1	10
775	Molecular-Genetic Characteristics of <i>Yersinia pestis</i> Strains Isolated in the Mongolian Territory of Transboundary Sailyugem Natural Plague Focus. <i>Problemy Osobo Opasnykh Infektsii</i> , 2019, , 34-42.	0.2	6
776	Genome Sequence of a Highly Virulent pvl-positive Vancomycin intermediate-resistant <i>Staphylococcus aureus</i> Sequence Type 30. <i>Current Genomics</i> , 2020, 21, 128-137.	0.7	2
777	Listeriosis outbreak likely due to contaminated liver pâté consumed in a tavern, Austria, December 2018. <i>Eurosurveillance</i> , 2019, 24, .	3.9	19
778	Serendipitous Discovery of a Novel Murine Astrovirus Contaminating a Murine Helper T-cell Line and Incapable of Infecting Highly Immunodeficient Mice. <i>Comparative Medicine</i> , 2020, 70, 359-369.	0.4	5
779	Snails as Taxis for a Large Yeast Biodiversity. <i>Fermentation</i> , 2020, 6, 90.	1.4	9
780	Osmotic Adaptation and Compatible Solute Biosynthesis of Phototrophic Bacteria as Revealed from Genome Analyses. <i>Microorganisms</i> , 2021, 9, 46.	1.6	37
781	Cryptic roles of tetrathionate in the sulfur cycle of marine sediments: microbial drivers and indicators. <i>Biogeosciences</i> , 2020, 17, 4611-4631.	1.3	15
782	Recurrent loss of CenH3 is associated with independent transitions to holocentricity in insects. <i>ELife</i> , 2014, 3, .	2.8	174
783	Long-term balancing selection drives evolution of immunity genes in <i>Capsella</i> . <i>ELife</i> , 2019, 8, .	2.8	69
784	A unicellular relative of animals generates a layer of polarized cells by actomyosin-dependent cellularization. <i>ELife</i> , 2019, 8, .	2.8	41

#	ARTICLE	IF	CITATIONS
785	Evolutionary origins of the emergent ST796 clone of vancomycin resistant <i>Enterococcus faecium</i> . PeerJ, 2017, 5, e2916.	0.9	46
786	Mitochondrial genomes organization in alloplasmic lines of sunflower ( <i>Helianthus annuus</i> L.) with various types of cytoplasmic male sterility. PeerJ, 2018, 6, e5266.	0.9	13
787	A comparative analysis of the complete chloroplast genome sequences of four peanut botanical varieties. PeerJ, 2018, 6, e5349.	0.9	28
788	First steps towards mitochondrial pan-genomics: detailed analysis of <i>Fusarium graminearum</i> mitogenomes. PeerJ, 2018, 6, e5963.	0.9	37
789	Optimizing <i>de novo</i> genome assembly from PCR-amplified metagenomes. PeerJ, 2019, 7, e6902.	0.9	28
790	A survey of the sperm whale ( <i>Physeter catodon</i> ) commensal microbiome. PeerJ, 2019, 7, e7257.	0.9	15
791	Chlamydia pecorum Ovine Abortion: Associations between Maternal Infection and Perinatal Mortality. Pathogens, 2021, 10, 1367.	1.2	4
792	Acinetobacter geminorum sp. nov., isolated from human throat swabs. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	10
793	In vitro and in vivo activity of new strains of Bacillus subtilis against ESBL-producing Escherichia coli: an experimental study. Journal of Applied Microbiology, 2022, 132, 2270-2279.	1.4	4
794	Comparative mitogenomics of Drosophilidae and the evolution of the Zygothrica genus group (Diptera, Drosophilidae). Genetica, 2021, 149, 267-281.	0.5	5
795	A phylogenomic perspective on the evolutionary history of the stonefly genus Suwallia (Plecoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 Evolution, 2022, 166, 107320.	1.2	3
796	Microbial ecology of sulfur cycling near the sulfate-methane transition of deep-sea cold seep sediments. Environmental Microbiology, 2021, 23, 6844-6858.	1.8	31
797	Ubericin K, a New Pore-Forming Bacteriocin Targeting mannose-PTS. Microbiology Spectrum, 2021, 9, e0029921.	1.2	11
799	Encephalitis and Death in Wild Mammals at a Rehabilitation Center after Infection with Highly Pathogenic Avian Influenza A(H5N8) Virus, United Kingdom. Emerging Infectious Diseases, 2021, 27, 2856-2863.	2.0	53
800	Pneumococcal pneumonia among shipyard workers: Inside the features of disease onset. Travel Medicine and Infectious Disease, 2021, 44, 102183.	1.5	1
801	Structural Variation Detection with Read Pair Information: An Improved Null-Hypothesis Reduces Bias. Lecture Notes in Computer Science, 2016, , 176-188.	1.0	0
812	Paeniglutamibacter terrestris sp. nov., isolated from phenanthrene-degrading consortium enriched from Antarctic soil. International Journal of Systematic and Evolutionary Microbiology, 2019, 71, .	0.8	8
815	Draft Genome Sequence of Multidrug-Resistant Proteus mirabilis CKTH01, Isolated from Raw Chicken Meat. Microbiology Resource Announcements, 2019, 8, .	0.3	0

#	ARTICLE	IF	CITATIONS
816	Examination of 388 <i>Staphylococcus aureus</i> Isolates from Intensive Care Unit Patients. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	3
817	Draft Genome Sequence of <i>Haloferax volcanii</i> SS0101, Isolated from Salt Farms in Samut Sakhon, Thailand. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	0
819	Draft Genome Sequences of <i>Mycobacterium tuberculosis</i> Clinical Isolates from the Ural Region of Russia That Carry the <i>pks15/1</i> Gene. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	1
820	<i>Psychrobacillus vulpis</i> sp. nov., a new species isolated from faeces of a red fox in Spain. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 882-888.	0.8	10
822	Molecular typing, and integron and associated gene cassette analyses in <i>Acinetobacter baumannii</i> strains isolated from clinical samples. <i>Experimental and Therapeutic Medicine</i> , 2020, 20, 1943-1952.	0.8	3
823	Draft Genome Sequence of <i>Erysipelothrix rhusiopathiae</i> , Isolated from a Canine Case of Diskospondylitis. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	0
824	Examination of <i>Staphylococcus aureus</i> Isolates from the Gloves and Gowns of Intensive Care Unit Health Care Workers. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
825	Genome Sequence of a <i>Blattabacterium</i> Strain Isolated from the Viviparous Cockroach, <i>Diploptera punctata</i> . <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	2
826	Draft Genome Sequence of <i>Brucella ceti</i> Isolated in the Western Pacific Ocean. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	2
827	<i>Mycobacterium intracellulare</i> subsp. <i>chimaera</i> from Cardio Surgery Heating-Cooling Units and from Clinical Samples in Israel Are Genetically Unrelated. <i>Pathogens</i> , 2021, 10, 1392.	1.2	3
828	Complete genome reveals genetic repertoire and potential metabolic strategies involved in lignin degradation by environmental ligninolytic <i>Klebsiella variicola</i> P1CD1. <i>PLoS ONE</i> , 2020, 15, e0243739.	1.1	19
829	Genome Sequence of <i>Vibrio nigripulchritudo</i> Strain TUMSAT-TG-2018, Isolated from Diseased Pacific White Shrimp, <i>Litopenaeus vannamei</i> . <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	0
830	Draft Genome Sequence of <i>Lactobacillus rhamnosus</i> NCB 441, Isolated from Egyptian White Domiati Cheese. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	0
831	Disseminated <i>Mycobacterium marinum</i> in Human Immunodeficiency Virus Unmasked by Immune Reconstitution Inflammatory Syndrome. <i>Journal of Infectious Diseases</i> , 2021, 224, 453-457.	1.9	3
833	Draft Genome Sequence of the Symbiotic <i>Frankia</i> sp. strain B2 isolated from root nodules of <i>Casuarina cunninghamiana</i> found in Algeria. <i>Journal of Genomics</i> , 2020, 8, 11-15.	0.6	3
834	Genomic analysis of Latin American-Mediterranean family of <i>Mycobacterium tuberculosis</i> clinical strains from Kazakhstan. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2020, 115, e200215.	0.8	5
839	Typing and classification of non-tuberculous mycobacteria isolates. <i>F1000Research</i> , 0, 9, 249.	0.8	1
840	Antimicrobial Activity of Aztreonam in Combination with Old and New $\beta$ -Lactamase Inhibitors against MBL and ESBL Co-Producing Gram-Negative Clinical Isolates: Possible Options for the Treatment of Complicated Infections. <i>Antibiotics</i> , 2021, 10, 1341.	1.5	13

#	ARTICLE	IF	CITATIONS
841	Detection of extended-spectrum beta-lactamase (ESBL) genes and plasmid replicons in Enterobacteriaceae using PlasmidSPAdes assembly of short-read sequence data. <i>Microbial Genomics</i> , 2020, 6, .	1.0	3
842	<i>Methanobolus halotolerans</i> sp. nov., isolated from the saline Lake Tus in Siberia. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 5586-5593.	0.8	9
844	DATMA: Distributed AuTomatic Metagenomic Assembly and annotation framework. <i>PeerJ</i> , 2020, 8, e9762.	0.9	2
845	Regional outbreak of methicillin-resistant <i>Staphylococcus aureus</i> ST2725-t1784 in rural Japan. <i>Infection Control and Hospital Epidemiology</i> , 2021, 42, 1294-1296.	1.0	1
846	Draft Genome Sequence of <i>Pseudomonas aeruginosa</i> Strain PA14-UM. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	0
847	Draft Genome Sequence of <i>Escherichia coli</i> Strain UMD142. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	0
848	Draft Genome Sequence of <i>Scheffersomyces spartinae</i> ARV011, a Marine Yeast Isolate. <i>Microbiology Resource Announcements</i> , 2021, 10, e0065221.	0.3	1
849	Genomic features of <i>Mycobacterium avium</i> subsp. <i>hominissuis</i> isolated from pigs in Japan. <i>GigaByte</i> , 0, 2021, 1-12.	0.0	3
850	New data on the fine structure of <i>Deuteramoeba mycophaga</i> CCAP 1586/1 (Amoebozoa, Tubulinea). <i>European Journal of Protistology</i> , 2021, 82, 125853.	0.5	0
851	Whole genome sequencing and characteristics of <i>Escherichia coli</i> with co-existence of ESBL and <i>mcr</i> genes from pigs. <i>PLoS ONE</i> , 2021, 16, e0260011.	1.1	8
852	Preparation of Soil Metagenome Libraries and Screening for Gene-Specific Amplicons. <i>Methods in Molecular Biology</i> , 2022, 2397, 3-17.	0.4	4
854	Remarkably coherent population structure for a dominant Antarctic <i>Chlorobium</i> species. <i>Microbiome</i> , 2021, 9, 231.	4.9	5
855	<i>Prauserella cavernicola</i> sp. nov., isolated from cave rock. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	4
856	Survival Comes at a Cost: A Coevolution of Phage and Its Host Leads to Phage Resistance and Antibiotic Sensitivity of <i>Pseudomonas aeruginosa</i> Multidrug Resistant Strains. <i>Frontiers in Microbiology</i> , 2021, 12, 783722.	1.5	12
857	Isolation, Whole-Genome Sequencing, and Annotation of Three Unclassified Antibiotic-Producing Bacteria, <i>Enterobacter</i> sp. Strain RIT 637, <i>Pseudomonas</i> sp. Strain RIT 778, and <i>Deinococcus</i> sp. Strain RIT 780. <i>Microbiology Resource Announcements</i> , 2021, 10, e0086321.	0.3	1
858	Discovery of an Antarctic Ascidian-Associated Uncultivated <i>Verrucomicrobia</i> with Antimelanoma Palmerolide Biosynthetic Potential. <i>MSphere</i> , 2021, 6, e0075921.	1.3	7
859	Comparative genomic and transmission analysis of <i>Clostridioides difficile</i> between environmental, animal, and clinical sources in China. <i>Emerging Microbes and Infections</i> , 2021, 10, 2244-2255.	3.0	9
860	Clonal Dissemination of Clinical Carbapenem-Resistant <i>Klebsiella pneumoniae</i> Isolates Carrying <i>fosA3</i> and <i>blaKPC-2</i> Coharboring Plasmids in Shandong, China. <i>Frontiers in Microbiology</i> , 2021, 12, 771170.	1.5	5

#	ARTICLE	IF	CITATIONS
861	Genome Analysis of the <i>Janthinobacterium</i> sp. Strain SLB01 from the Diseased Sponge of the <i>Lubomirskia baicalensis</i> . <i>Current Issues in Molecular Biology</i> , 2021, 43, 2220-2237.	1.0	3
862	Clinical and Microbiological Characteristics of <i>Mycobacterium kansasii</i> Pulmonary Infections in China. <i>Microbiology Spectrum</i> , 2022, 10, e0147521.	1.2	6
863	Isolation and characterization of a novel Lambda-like phage infecting the bloom-forming cyanobacteria <i>Cylindrospermopsis raciborskii</i> . <i>Environmental Microbiology</i> , 2022, 24, 2435-2448.	1.8	6
864	Enrichment of gut microbiome strains for cultivation-free genome sequencing using droplet microfluidics. <i>Cell Reports Methods</i> , 2022, 2, 100137.	1.4	14
865	<i>Apophysomyces Variabilis</i> Infection in Transplant Recipients due to Unrecognized Infection in an Intravenous Drug-Using Donor. <i>Transplantation</i> , 2022, 106, e169-e171.	0.5	4
866	<i>Erythrobacter rubeus</i> sp. nov., a carotenoid-producing alphaproteobacterium isolated from coastal seawater. <i>Archives of Microbiology</i> , 2022, 204, 125.	1.0	9
867	Roseobacter group probiotics exhibit differential killing of fish pathogenic <i>Tenacibaculum</i> species. <i>Applied and Environmental Microbiology</i> , 2022, , aem0241821.	1.4	11
868	Whole-Genome Sequence of <i>Paenibacillus polymyxa</i> Strain SRT9.1, a Promising Plant Growth-Promoting Bacterium. <i>Microbiology Resource Announcements</i> , 2022, 11, e0109721.	0.3	2
869	Draft Genome Sequences of Six <i>Yersinia kristensenii</i> Strains. <i>Microbiology Resource Announcements</i> , 2022, 11, e0106321.	0.3	0
870	<i>Latilactobacillus fragifolii</i> sp. nov., isolated from leaves of a strawberry plant ( <i>Fragaria x ananassa</i> ). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	7
871	Proteomic Signatures of Antimicrobial Resistance in <i>Yersinia pestis</i> and <i>Francisella tularensis</i> . <i>Frontiers in Medicine</i> , 2022, 9, 821071.	1.2	3
872	<i>Spongibacter pelagi</i> sp. nov., a marine gammaproteobacterium isolated from coastal seawater. <i>Antonie Van Leeuwenhoek</i> , 2022, 115, 487.	0.7	6
873	Exploration of the molecular mechanisms underlying the antibiotic resistance of <i>Helicobacter pylori</i> : A whole-genome sequencing-based study in Southern China. <i>Helicobacter</i> , 2022, 27, e12879.	1.6	7
874	Draft Genome Sequence of <i>Microbacterium</i> sp. Strain KKR3/1, an Antimicrobial-Substance-Producing Strain Isolated from Banana Shrimp ( <i>Atyopsis moluccensis</i> ). <i>Microbiology Resource Announcements</i> , 2022, , e0124221.	0.3	0
875	Bacterial Antagonistic Species of the Pathogenic Genus <i>Legionella</i> Isolated from Cooling Tower. <i>Microorganisms</i> , 2022, 10, 392.	1.6	2
876	Draft Genome Sequence of Sweet Pepper Fruit Epiphyte-Associated <i>Bacillus cereus</i> HRT7.7. <i>Microbiology Resource Announcements</i> , 2022, 11, e0112521.	0.3	0
877	Side-by-Side Comparison of Post-Entry Quarantine and High Throughput Sequencing Methods for Virus and Viroid Diagnosis. <i>Biology</i> , 2022, 11, 263.	1.3	12
878	<i>Desulfovulcanus ferrireducens</i> gen. nov., sp. nov., a thermophilic autotrophic iron and sulfate-reducing bacterium from subseafloor basalt that grows on akaganite and lepidocrocite minerals. <i>Extremophiles</i> , 2022, 26, 13.	0.9	2

#	ARTICLE	IF	CITATIONS
879	Whole-Genome Sequence of the <i>Wolbachia</i> Strain <i>w</i> Tcon, an Endosymbiont of the Confused Flour Beetle, <i>Tribolium confusum</i> . <i>Microbiology Resource Announcements</i> , 2022, 11, e0114421.	0.3	0
880	Draft Genome Sequences from Two Gram-Negative Bacteria, <i>Serratia</i> sp. Strain EWG9 and <i>Leclercia</i> sp. Strain EMC7, Isolated from the Earthworm <i>Eisenia fetida</i> . <i>Microbiology Resource Announcements</i> , 2022, 11, e0093921.	0.3	0
881	Secreted Autotransporter Toxin (Sat) Mediates Innate Immune System Evasion. <i>Frontiers in Immunology</i> , 2022, 13, 844878.	2.2	10
882	Antimicrobial Susceptibility, Virulence, and Genomic Features of a Hypervirulent Serotype K2, ST65 <i>Klebsiella pneumoniae</i> Causing Meningitis in Italy. <i>Antibiotics</i> , 2022, 11, 261.	1.5	8
883	Draft Genome Sequence of <i>Lactococcus lactis</i> Subsp. <i>cremoris</i> WA2-67: A Promising Nisin-Producing Probiotic Strain Isolated from the Rearing Environment of a Spanish Rainbow Trout ( <i>Oncorhynchus mykiss</i> ). <i>Microbiology Resource Announcements</i> , 2022, 11, e0114421.	0.3	0
884	Disentangle genus microdiversity within a complex microbial community by using a multi-omic distance long-read binning method: example of <i>Candidatus</i> <i>Accumulibacter</i> . <i>Environmental Microbiology</i> , 2022, 24, 2136-2156.	1.8	4
885	Down-regulation of the bacterial protein biosynthesis machinery in response to weeks, years, and decades of soil warming. <i>Science Advances</i> , 2022, 8, eabm3230.	4.7	18
886	Whole-Genome Analysis of <i>Escherichia</i> Phage $\nu$ B_EcoM-S1P5QW, Isolated from Manures Collected from Cattle Farms in Maine. <i>Microbiology Resource Announcements</i> , 2022, 11, e0004122.	0.3	1
887	Comparative Genome Analysis of the Photosynthetic Betaproteobacteria of the Genus <i>Rhodocyclus</i> : Heterogeneity within Strains Assigned to <i>Rhodocyclus tenuis</i> and Description of <i>Rhodocyclus gracilis</i> sp. nov. as a New Species. <i>Microorganisms</i> , 2022, 10, 649.	1.6	11
888	Genomics of human and chicken <i>Salmonella</i> isolates in Senegal: Broilers as a source of antimicrobial resistance and potentially invasive nontyphoidal salmonellosis infections. <i>PLoS ONE</i> , 2022, 17, e0266025.	1.1	7
889	Genome Sequencing of <i>Pseudomonas aeruginosa</i> strain M2 illuminates traits of an opportunistic pathogen of burn wounds. <i>G3: Genes, Genomes, Genetics</i> , 2022, , .	0.8	4
890	VPipe: an Automated Bioinformatics Platform for Assembly and Management of Viral Next-Generation Sequencing Data. <i>Microbiology Spectrum</i> , 2022, 10, e0256421.	1.2	8
891	Quantifying and Cataloguing Unknown Sequences within Human Microbiomes. <i>MSystems</i> , 2022, 7, e0146821.	1.7	2
892	Determination of Antiviral Mechanism of Centenarian Gut-Derived <i>Limosilactobacillus fermentum</i> Against Norovirus. <i>Frontiers in Nutrition</i> , 2022, 9, 812623.	1.6	4
893	Draft Genome Sequence Resource of <i>Fragaria</i> $\times$ <i>Ananassa</i> ™ Phylloidy Phytoplasma Strain StrPh-CL from Chilean Strawberry. <i>Plant Disease</i> , 2022, 106, 1031-1034.	0.7	1
895	The pathogens of secondary infection in septic patients share a similar genotype to those that predominate in the gut. <i>Critical Care</i> , 2022, 26, 68.	2.5	12
896	Draft Genome Sequences of 6 Actinobacterial Strains Isolated from Rock Surfaces Obtained from Indian Stone Ruins in Tamil Nadu, India, and Rocks from New England, United States. <i>Microbiology Resource Announcements</i> , 2022, 11, e0002422.	0.3	2
897	Evidence of Genomic Diversification in a Natural Symbiotic Population Within Its Host. <i>Frontiers in Microbiology</i> , 2022, 13, 854355.	1.5	3



#	ARTICLE	IF	CITATIONS
898	Phage anti-CBASS and anti-Pycsar nucleases subvert bacterial immunity. <i>Nature</i> , 2022, 605, 522-526.	13.7	70
899	Surveillance of <i>Enterobacter cloacae</i> complex colonization and comparative analysis of different typing methods on a neonatal intensive care unit in Germany. <i>Antimicrobial Resistance and Infection Control</i> , 2022, 11, 54.	1.5	8
901	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
902	Patterns of Diversity of <i>Fusarium</i> Fungi Contaminating Soybean Grains. <i>Toxins</i> , 2021, 13, 884.	1.5	5
903	The genetic basis of phage susceptibility, cross-resistance and host-range in <i>Salmonella</i> . <i>Microbiology (United Kingdom)</i> , 2021, 167, .	0.7	20
904	Genetic differentiation of <i>Xylella fastidiosa</i> following the introduction into Taiwan. <i>Microbial Genomics</i> , 2021, 7, .	1.0	2
905	Evidence for the agricultural origin of resistance to multiple antimicrobials in <i>Aspergillus fumigatus</i> , a fungal pathogen of humans. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	24
906	Draft Genome Sequence of <i>Weissella cibaria</i> P71, a Promising Aquaculture Probiotic Strain Isolated from Common Octopus ( <i>Octopus vulgaris</i> ). <i>Microbiology Resource Announcements</i> , 2021, 10, e0079221.	0.3	1
907	Highly Stretchable Bacterial Cellulose Produced by <i>Komagataeibacter hansenii</i> SI1. <i>Polymers</i> , 2021, 13, 4455.	2.0	12
908	<i>Desulfovibrio desulfuricans</i> AY5 Isolated from a Patient with Autism Spectrum Disorder Binds Iron in Low-Soluble Greigite and Pyrite. <i>Microorganisms</i> , 2021, 9, 2558.	1.6	6
909	Reverting the mode of action of the mitochondrial FOF1-ATPase by <i>Legionella pneumophila</i> preserves its replication niche. <i>ELife</i> , 2021, 10, .	2.8	8
912	Updating the Phylodynamics of Yellow Fever Virus 2016–2019 Brazilian Outbreak With New 2018 and 2019 São Paulo Genomes. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	2
913	Comparative Analyses of 35 Complete Chloroplast Genomes from the Genus <i>Dalbergia</i> (Fabaceae) and the Identification of DNA Barcodes for Tracking Illegal Logging and Counterfeit Rosewood. <i>Forests</i> , 2022, 13, 626.	0.9	14
914	A Yersiniabactin-producing <i>Klebsiella aerogenes</i> Strain Causing an Outbreak in an Austrian Neonatal Intensive Care Unit. <i>Pediatric Infectious Disease Journal</i> , 2022, 41, 593-599.	1.1	3
915	Draft Genomes of Six Philippine <i>Erwinia mallotivora</i> Isolates: Comparative Genomics and Genome-Wide Analysis of Candidate Secreted Proteins. <i>Current Microbiology</i> , 2022, 79, 164.	1.0	1
916	Variations in the Adaptive Response of <i>Burkholderia pseudomallei</i> to Cold Stress. <i>Problemy Osobo Opasnykh Infektsii</i> , 2022, , 106-112.	0.2	0
917	Genomic analysis of CTX-M-115 and OXA-23/-72 co-producing <i>Acinetobacter baumannii</i> , and their potential to spread resistance genes by natural transformation. <i>Journal of Antimicrobial Chemotherapy</i> , 2022, 77, 1542-1552.	1.3	4
918	Large-Scale Genomic Epidemiology of <i>Klebsiella pneumoniae</i> Identified Clone Divergence with Hypervirulent Plus Antimicrobial-Resistant Characteristics Causing Within-Ward Strain Transmissions. <i>Microbiology Spectrum</i> , 2022, 10, e0269821.	1.2	7

#	ARTICLE	IF	CITATIONS
919	Fecal Shedding of Multidrug Resistant <i>Escherichia coli</i> Isolates in Dogs Fed with Raw Meat-Based Diets in Brazil. <i>Antibiotics</i> , 2022, 11, 534.	1.5	6
921	Effect of endophytic bacterium, <i>Stenotrophomonas maltophilia</i> JVB5 on sunflowers. <i>Plant Protection Science</i> , 2022, 58, 185-198.	0.7	11
1012	<i>Spongibacter thalassae</i> sp. nov., a marine gammaproteobacterium isolated from seawater. <i>Archives of Microbiology</i> , 2022, 204, 273.	1.0	5
1013	Genome sequences of <i>Rhizopogon roseolus</i> , <i>Mariannaea elegans</i> , <i>Myrothecium verrucaria</i> and <i>Sphaerostilbella broomeana</i> and the identification of biosynthetic gene clusters for fungal peptide natural products. <i>G3: Genes, Genomes, Genetics</i> , 2022, , .	0.8	0
1014	Genomic Epidemiology of Global Carbapenemase-Producing <i>Escherichia coli</i> , 2015–2017. <i>Emerging Infectious Diseases</i> , 2022, 28, .	2.0	39
1015	Exploration of the Molecular Mechanisms Underlying the Anti-Photoaging Effect of <i>Limosilactobacillus fermentum</i> XJC60. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 838060.	1.8	9
1016	Whole genome sequencing and phylogenomic analyses of a novel glufosinate-tolerant <i>Pseudomonas</i> species. <i>3 Biotech</i> , 2022, 12, 123.	1.1	3
1017	Antimicrobial Susceptibility of <i>Enterococcus</i> Isolates from Cattle and Pigs in Portugal: Linezolid Resistance Genes <i>optrA</i> and <i>poxTA</i> . <i>Antibiotics</i> , 2022, 11, 615.	1.5	7
1018	Integration of Maps Enables a Cytogenomics Analysis of the Complete Karyotype in <i>Solea senegalensis</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 5353.	1.8	4
1019	Draft Genome Sequences for Three <i>Ophiostoma</i> Species Acquired during Revisions of Australian Plant Pathogen Reference Collections. <i>Microbiology Resource Announcements</i> , 2022, 11, e0017522.	0.3	2
1020	Meta-Omics reveal the metabolic acclimation of freshwater anammox bacteria for saline wastewater treatment. <i>Journal of Cleaner Production</i> , 2022, 362, 132184.	4.6	5
1021	Two Novel Iflaviruses Discovered in Bat Samples in Washington State. <i>Viruses</i> , 2022, 14, 994.	1.5	3
1022	Single-cell metagenomics and metagenomics approaches reveal extracellular electron transfer of psychrophilic electroactive biofilms. <i>Science of the Total Environment</i> , 2022, 836, 155606.	3.9	4
1023	Diversity and Long-Term Dynamics of Human Blood Anelloviruses. <i>Journal of Virology</i> , 2022, 96, e0010922.	1.5	18
1024	Potential Use of Microbial Community Genomes in Various Dimensions of Agriculture Productivity and Its Management: A Review. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	12
1025	Characterization of Immunological Responses to <i>Borrelia</i> Immunogenic Protein A (BipA), a Species-Specific Antigen for North American Tick-Borne Relapsing Fever. <i>Microbiology Spectrum</i> , 2022, 10, e0172221.	1.2	6
1027	<i>Paraburkholderia bengalensis</i> sp. nov. isolated from roots of <i>Oryza sativa</i> , IR64. <i>Archives of Microbiology</i> , 2022, 204, .	1.0	1
1028	<i>Pseudophaeobacter flagellatus</i> sp. nov., isolated from coastal water. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	6

#	ARTICLE	IF	CITATIONS
1029	The characterization of <i>Moraxella catarrhalis</i> carried in the general population. <i>Microbial Genomics</i> , 2022, 8, .	1.0	5
1030	Metagenomics Reveals Dominant Unusual Sulfur Oxidizers Inhabiting Active Hydrothermal Chimneys From the Southwest Indian Ridge. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	4
1032	Denitrification in foraminifera has an ancient origin and is complemented by associated bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	9
1033	Complete Genome Analysis of <i>Rhodococcus opacus</i> S8 Capable of Degrading Alkanes and Producing Biosurfactant Reveals Its Genetic Adaptation for Crude Oil Decomposition. <i>Microorganisms</i> , 2022, 10, 1172.	1.6	4
1034	Rifampicin Resistance Associated with <i>rpoB</i> Mutations in <i>Neisseria gonorrhoeae</i> Clinical Strains Isolated in Austria, 2016 to 2020. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	3
1035	The influence of bioclimate on soil microbial communities of cork oak. <i>BMC Microbiology</i> , 2022, 22, .	1.3	10
1036	<i>Sphingopyxis jiangsuensis</i> sp. nov. Isolated From the Surface Water of the Yellow Sea. <i>Current Microbiology</i> , 2022, 79, .	1.0	2
1037	Genomic Analysis Reveals That Isolation Temperature on Selective Media Introduces Genetic Variation in <i>Campylobacter jejuni</i> from Bovine Feces. <i>Pathogens</i> , 2022, 11, 678.	1.2	1
1038	<i>Peribacillus castrilensis</i> sp. nov.: A Plant-Growth-Promoting and Biocontrol Species Isolated From a River Otter in Castril, Granada, Southern Spain. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	7
1039	<i>Xylella fastidiosa</i> Outbreak in Israel: Population Genetics, Host Range, and Temporal and Spatial Distribution Analysis. <i>Phytopathology</i> , 2022, 112, 2296-2309.	1.1	6
1040	Anthroponotic-Based Transfer of <i>Staphylococcus</i> to Dog: A Case Study. <i>Pathogens</i> , 2022, 11, 802.	1.2	3
1041	Whole-genome single nucleotide polymorphism analysis for typing the pandemic pathogen <i>Fusarium graminearum</i> sensu stricto. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
1042	Two Newly Isolated Enterobacter-Specific Bacteriophages: Biological Properties and Stability Studies. <i>Viruses</i> , 2022, 14, 1518.	1.5	8
1043	Forecasting <i>Staphylococcus aureus</i> Infections Using Genome-Wide Association Studies, Machine Learning, and Transcriptomic Approaches. <i>MSystems</i> , 2022, 7, .	1.7	3
1044	Evaluation of an Antibiotic Susceptibility Testing Method on Enterobacterales-Positive Blood Cultures in Less Than 8 h Using the Rapid Mueller-Hinton Diffusion Method in Conjunction with the SIRscan 2000 Automatic Reading Device. <i>Microorganisms</i> , 2022, 10, 1377.	1.6	0
1045	Morphological and Genetic Characterization of <i>Eggerthella lenta</i> Bacteriophage PMBT5. <i>Viruses</i> , 2022, 14, 1598.	1.5	2
1046	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
1047	Genomics of <i>Staphylococcus aureus</i> Strains Isolated from Infectious and Non-Infectious Ocular Conditions. <i>Antibiotics</i> , 2022, 11, 1011.	1.5	5

#	ARTICLE	IF	CITATIONS
1049	Molecular characterization of extended spectrum cephalosporin resistant <i>Escherichia coli</i> isolated from livestock and in-contact humans in Southeast Nigeria. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
1050	<i>Hyphomonas sediminis</i> sp. nov., isolated from marine sediment. <i>Antonie Van Leeuwenhoek</i> , 2022, 115, 1177-1185.	0.7	1
1051	Freshwater macrophytes harbor viruses representing all five major phyla of the RNA viral kingdom <i>Orthornavirae</i>. <i>PeerJ</i> , 0, 10, e13875.	0.9	6
1052	Thecochaos is not a myth: study of the genus <i>Thecochaos</i> (Amoebozoa, Discosea) â€“ a rediscovered group of lobose amoeba, with short SSU gene. <i>Organisms Diversity and Evolution</i> , 2023, 23, 7-24.	0.7	2
1053	Geographic isolation drives speciation in Nearctic aphids. <i>Communications Biology</i> , 2022, 5, .	2.0	2
1054	Why are there so many species of mining bees (Hymenoptera, Andrenidae)? The possible roles of phenology and <i>Wolbachia</i> incompatibility in maintaining species boundaries in the <i>Andrena proxima</i> complex. <i>Systematic Entomology</i> , 2023, 48, 127-141.	1.7	7
1055	Microbiological and Molecular Features Associated with Persistent and Relapsing <i>Staphylococcus aureus</i> Prosthetic Joint Infection. <i>Antibiotics</i> , 2022, 11, 1119.	1.5	5
1056	<i>Siccirubricoccus soli</i> sp. nov., a novel bacterial species isolated from Jiaozhi Mountain soil. <i>Antonie Van Leeuwenhoek</i> , 0, , .	0.7	0
1058	Characterization of <i>Marinilongibacter aquaticus</i> gen. nov., sp. nov., a unique marine bacterium harboring four CRISPR-Cas systems in the phylum Bacteroidota. <i>Journal of Microbiology</i> , 2022, 60, 905-915.	1.3	4
1059	Genetic characterization of hypervirulent <i>Klebsiella pneumoniae</i> responsible for acute death in captive marmosets. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	0
1061	<i>Aestuariicella albida</i> sp. nov., isolated from surface water of the Yellow Sea, and proposal of the genus <i>Aestuariicella</i> as a member of the family Cellvibrionaceae. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	3
1062	The effect of sequencing and assembly on the inference of horizontal gene transfer on chromosomal and plasmid phylogenies. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2022, 377, .	1.8	3
1063	<i>Listeria monocytogenes</i> post-outbreak management - When could a food production be considered under control again?. <i>International Journal of Food Microbiology</i> , 2022, 379, 109844.	2.1	6
1064	Draft Genomes Sequences of 11 <i>Geodermatophilaceae</i> Strains Isolated from Building Stones from New England and Indian Stone Ruins found at historic sites in Tamil Nadu, India. <i>Journal of Genomics</i> , 2022, 10, 69-77.	0.6	1
1065	Functional characterization of prokaryotic dark matter: the road so far and what lies ahead. <i>Current Research in Microbial Sciences</i> , 2022, 3, 100159.	1.4	2
1066	Molecular epidemiology and antibiotic resistance profiles of invasive <i>Haemophilus influenzae</i> from Norway 2017â€“2021. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	9
1067	Genomic profile of eGFP-expressing canine distemper virus that undergoes serial plaque-to-plaque transfers. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	0
1068	Isolation of <i>Pseudomonas aromaticivorans</i> sp. nov from a hydrocarbon-contaminated groundwater capable of degrading benzene-, toluene-, m- and p-xylene under microaerobic conditions. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	7

#	ARTICLE	IF	CITATIONS
1069	Effect of the vaccination against Shiga toxin 2e in a farm with history of oedema disease, caused by atypical <i>Escherichia coli</i> producing Shiga toxin (STEC). <i>Veterinari Medicina</i> , 2022, 67, 510-518.	0.2	1
1070	Nitrogen and phosphorus significantly alter growth, nitrogen fixation, anatoxin-a content, and the transcriptome of the bloom-forming cyanobacterium, <i>Dolichospermum</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5
1071	Geochemistry and microbiology of tropical serpentine soils in the Santa Elena Ophiolite, a landscape-biogeographical approach. <i>Geochemical Transactions</i> , 2022, 23, .	1.8	0
1072	Acquisition of genomic elements were pivotal for the success of <i>Escherichia coli</i> ST410. <i>Journal of Antimicrobial Chemotherapy</i> , 2022, 77, 3399-3407.	1.3	8
1073	Genetic and drug susceptibility profiles of mcr-1-bearing foodborne <i>Salmonella</i> strains collected in Shenzhen, China during the period 2014–2017. <i>Microbiological Research</i> , 2022, 265, 127211.	2.5	6
1074	Draft Genome Sequences of Four Strains of Plant Growth-Promoting Bacteria Associated with Maize Rhizosphere. <i>Microbiology Resource Announcements</i> , 0, , .	0.3	0
1075	Metabolic Characteristics of Porcine LA-MRSA CC398 and CC9 Isolates from Germany and China via Biolog Phenotype MicroArray™. <i>Microorganisms</i> , 2022, 10, 2116.	1.6	4
1076	Evolution of the Piau–Laterite, Brazil: Mineralogical, Geochemical and Geomicrobiological Mechanisms for Cobalt and Nickel Enrichment. <i>Minerals (Basel, Switzerland)</i> , 2022, 12, 1298.	0.8	3
1077	Genomic insights into the physiology of <i>Quinella</i> , an iconic uncultured rumen bacterium. <i>Nature Communications</i> , 2022, 13, .	5.8	10
1078	First Finding of a Methicillin-Resistant <i>Staphylococcus aureus</i> (MRSA) t304/ST6 from Bovine Clinical Mastitis. <i>Antibiotics</i> , 2022, 11, 1393.	1.5	3
1079	Draft Genome Sequences of the <i>Vibrio parahaemolyticus</i> Strains VHT1 and VHT2, Pasteurization-Resistant Isolates from Environmental Seafood. <i>Microbiology Resource Announcements</i> , 2022, 11, .	0.3	2
1080	Draft Genome Sequence of a Multidrug-Resistant Strain of <i>Salmonella enterica</i> Serovar Typhimurium Isolated from a Pine Siskin ( <i>Spinus pinus</i> ). <i>Microbiology Resource Announcements</i> , 0, , .	0.3	0
1081	Comparative analysis of <i>Vibrio cholerae</i> isolates from Ghana reveals variations in genome architecture and adaptation of outbreak and environmental strains. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
1082	Activities of Manogepix and Comparators against 1,435 Recent Fungal Isolates Collected during an International Surveillance Program (2020). <i>Antimicrobial Agents and Chemotherapy</i> , 2022, 66, .	1.4	7
1083	Commensal microbiota from patients with inflammatory bowel disease produce genotoxic metabolites. <i>Science</i> , 2022, 378, .	6.0	74
1084	Draft Genome Sequence of <i>Enterobacter mori</i> AYS9, a Potential Plant Growth-Promoting Rhizobacterium. <i>Microbiology Resource Announcements</i> , 0, , .	0.3	0
1085	Draft Genome Sequences for Bacteria Associated with Root Nodules of <i>Alnus incana</i> in New England. <i>Microbiology Resource Announcements</i> , 2022, 11, .	0.3	2
1086	Draft Genome Sequence of a Ketoprofen Degradar, <i>Rhodococcus erythropolis</i> IEGM 746. <i>Microbiology Resource Announcements</i> , 0, , .	0.3	0

#	ARTICLE	IF	CITATIONS
1087	Draft Genome Sequence of <i>Aeromonas caviae</i> Strain A1-2, a Potential Plant Growth-Promoting Rhizospheric Bacterium. <i>Microbiology Resource Announcements</i> , 0, , .	0.3	0
1088	Control of Human Anelloviruses by Cytosine to Uracil Genome Editing. <i>MSphere</i> , 2022, 7, .	1.3	5
1089	<i>Glycomyces amatae</i> sp. nov., isolated from a yellow-ringed grass moth ( <i>Amata sperbius</i> ). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	0
1090	Characterization of the complete chloroplast genome sequence of <i>Stipa bungeana</i> (Poaceae), an important forage grass in the temperate steppe of Northern China. <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1948-1951.	0.2	0
1091	The Relationship between Ciprofloxacin Resistance and Genotypic Changes in <i>S. aureus</i> Ocular Isolates. <i>Pathogens</i> , 2022, 11, 1354.	1.2	4
1092	Isolation, characterization and complete genome sequencing of a <i>Streptococcus dysgalactiae</i> associated with cultured channel catfish mortalities in China. <i>Aquaculture Reports</i> , 2022, 27, 101408.	0.7	0
1093	Rose Virome Analysis and Identification of a Novel Iarvirus in Taiwan. <i>Viruses</i> , 2022, 14, 2537.	1.5	1
1094	High diversity of clinical <i>Mycobacterium intracellulare</i> in China revealed by whole genome sequencing. <i>Frontiers in Public Health</i> , 0, 10, .	1.3	1
1095	C-N-S synergy in a pilot-scale mainstream anammox fluidized-bed membrane bioreactor for treating chemically enhanced primary treatment saline sewage. <i>Water Research</i> , 2023, 229, 119475.	5.3	15
1096	Genomic signatures of recent convergent transitions to social life in spiders. <i>Nature Communications</i> , 2022, 13, .	5.8	7
1097	Ultrastructure of <i>Diophrys appendiculata</i> and new systematic consideration of the euplotid family Uronychiidae (Protista, Ciliophora). <i>Marine Life Science and Technology</i> , 2022, 4, 551-568.	1.8	7
1098	Lack of host phylogenetic structure in the gut bacterial communities of New Zealand cicadas and their interspecific hybrids. <i>Scientific Reports</i> , 2022, 12, .	1.6	4
1100	Genomic Insights into Two Endophytic Strains: <i>Stenotrophomonas geniculata</i> NWUBe21 and <i>Pseudomonas carnis</i> NWUBe30 from Cowpea with Plant Growth-Stimulating Attributes. <i>Applied Sciences (Switzerland)</i> , 2022, 12, 12953.	1.3	3
1101	Decoupling of respiration rates and abundance in marine prokaryoplankton. <i>Nature</i> , 2022, 612, 764-770.	13.7	19
1102	<i>Paeniglutamibacter quisquiliarum</i> sp. nov., isolated from midden soil waste. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	0
1103	Horizontal Transfer of Bacteriocin Biosynthesis Genes Requires Metabolic Adaptation To Improve Compound Production and Cellular Fitness. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	4
1104	Extensive reorganization of the chloroplast genome of <i>Corydalis platycarpa</i> : A comparative analysis of their organization and evolution with other <i>Corydalis</i> plastomes. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	5
1105	Whole genome sequencing data of <i>Chromobacterium amazonense</i> BASUSDA_45 isolated from soil in Bangladesh capable of degrading pesticide. <i>Data in Brief</i> , 2022, , 108853.	0.5	0

#	ARTICLE	IF	CITATIONS
1106	Prevalence and whole genome phylogenetic analysis reveal genetic relatedness between antibiotic resistance <i>Salmonella</i> in hatchlings and older chickens from farms in Nigeria. <i>Poultry Science</i> , 2023, 102, 102427.	1.5	2
1107	<i>Janthinobacterium</i> sp. Strain SLB01 as Pathogenic Bacteria for Sponge <i>Lubomirskia baikalensis</i> . <i>Pathogens</i> , 2023, 12, 8.	1.2	1
1108	Transmission of <i>Escherichia coli</i> Causing Pyometra between Two Female Dogs. <i>Microorganisms</i> , 2022, 10, 2465.	1.6	3
1109	Whole genome sequence characterization of <i>Aspergillus terreus</i> ATCC 20541 and genome comparison of the fungi <i>A. terreus</i> . <i>Scientific Reports</i> , 2023, 13, .	1.6	5
1110	Draft Genome Sequence of <i>Lactiplantibacillus plantarum</i> Strain ISO1, a Potential Probiotic Bacterium Isolated from the Milk of South African Saanen Goats. <i>Microbiology Resource Announcements</i> , 0, , .	0.3	0
1111	Description of <i>Nocardioides jiangsuensis</i> sp. nov., and Proposal for Reclassification of the Genus <i>Marmoricola</i> as <i>Nocardioides</i> . <i>Current Microbiology</i> , 2023, 80, .	1.0	3
1112	<i>De novo</i> Genome Assessment of <i>Serratia marcescens</i> SGT5.3, a Potential Plant Growth-Promoting Bacterium Isolated from the Surface of <i>Capsicum annuum</i> Fruit. <i>Microbiology Resource Announcements</i> , 0, , .	0.3	0
1113	Identification of Novel Mobile Genetic Elements Associated With Resistance to Macrolide and Lincosamide in <i>Streptococcus Dysgalactiae</i> Subsp. <i>Equisimilis</i> . <i>Open Microbiology Journal</i> , 2023, 17, .	0.2	0
1114	The complete chloroplast genome sequence of <i>Astragalus melilotoides</i> (Fabaceae), a leguminous forage in Northern China. <i>Mitochondrial DNA Part B: Resources</i> , 2023, 8, 141-144.	0.2	0
1115	The compact Cas12 (Cas12l) "bracelet"™ provides a unique structural platform for DNA manipulation. <i>Cell Research</i> , 2023, 33, 229-244.	5.7	15
1116	Cytotoxicity and Antimicrobial Resistance of <i>Salmonella enterica</i> Subspecies Isolated from Raised Reptiles in Beijing, China. <i>Animals</i> , 2023, 13, 315.	1.0	3
1117	Biological Properties of 12 Newly Isolated <i>Acinetobacter baumannii</i> -Specific Bacteriophages. <i>Viruses</i> , 2023, 15, 231.	1.5	9
1118	Effect of a karst system (France) on extended spectrum beta-lactamase (ESBL)-producing <i>Escherichia coli</i> . <i>Water Research</i> , 2023, 230, 119582.	5.3	3
1119	Draft Genome Sequence of <i>Vibrio parahaemolyticus</i> PSU5579, Isolated during an Outbreak of Acute Hepatopancreatic Necrosis Disease in Thailand. <i>Microbiology Resource Announcements</i> , 2023, 12, .	0.3	2
1120	Strain-specific alterations in gut microbiome and host immune responses elicited by tolerogenic <i>Bifidobacterium pseudolongum</i> . <i>Scientific Reports</i> , 2023, 13, .	1.6	8
1121	Draft Genome Sequence of <i>Listeria monocytogenes</i> Clonal Complex 1 Strain SNU3 from South Korea. <i>Microbiology Resource Announcements</i> , 2023, 12, .	0.3	1
1122	Genome Assembly of a Putative Plant Growth-Stimulating Bacterial Sweet Pepper Fruit Isolate, <i>Enterobacter hormaechei</i> SRU4.4. <i>Microbiology Resource Announcements</i> , 0, , .	0.3	0
1123	Molecular characterization of eliminated chromosomes in Hessian fly ( <i>Mayetiola destructor</i> (Say)). <i>Chromosome Research</i> , 2023, 31, .	1.0	0

#	ARTICLE	IF	CITATIONS
1124	Retrospective Study of the Epidemiology of Clostridioides difficile Infection in the Neurosurgery Department of a Tertiary Hospital in China. Infection and Drug Resistance, 0, Volume 16, 545-554.	1.1	1
1126	Despite Shared Geography, Campylobacter Isolated from Surface Water Are Genetically Distinct from Campylobacter Isolated from Chickens. Microbiology Spectrum, 2023, 11, .	1.2	1
1127	Sequencing the genomes of LPP-1, the first isolated cyanophage, and its relative LPP-2 reveal different integration mechanisms in closely related phages. Harmful Algae, 2023, 124, 102409.	2.2	2
1128	Genomic and metabolic properties of Staphylococcus gallinarum FCW1 MCC4687 isolated from naturally fermented coconut water towards GRAS assessment. Gene, 2023, 867, 147356.	1.0	1
1129	Study on characteristic and mechanism involved in the formation of N-nitrosodimethylamine precursors during microbial metabolism of amino acids. Science of the Total Environment, 2023, 874, 162469.	3.9	2
1131	Fourier transform infrared spectroscopy; can it be used as a rapid typing method of Neisseria gonorrhoeae?. Journal of Microbiological Methods, 2023, 205, 106675.	0.7	1
1132	Contrasting Genetic Diversity of <i>Listeria</i> Pathogenicity Islands 3 and 4 Harbored by Nonpathogenic <i>Listeria</i> spp.. Applied and Environmental Microbiology, 2023, 89, .	1.4	4
1133	Genomics discovery of giant fungal viruses from subsurface oceanic crustal fluids. ISME Communications, 2023, 3, .	1.7	6
1136	Amazonian birds in more dynamic habitats have less population genetic structure and higher gene flow. Molecular Ecology, 2023, 32, 2186-2205.	2.0	8
1137	A novel binary pesticidal protein from Chryseobacterium arthrosphaerae controls western corn rootworm by a different mode of action to existing commercial pesticidal proteins. PLoS ONE, 2023, 18, e0267220.	1.1	2
1138	Resistance to the Bacteriocin Lcn972 Deciphered by Genome Sequencing. Microorganisms, 2023, 11, 501.	1.6	2
1139	Draft Genome Sequences of Three <i>Listeria monocytogenes</i> Strains Isolated from Chicken Carcasses in South Korea. Microbiology Resource Announcements, 2023, 12, .	0.3	0
1140	Chimera: The spoiler in multiple displacement amplification. Computational and Structural Biotechnology Journal, 2023, 21, 1688-1696.	1.9	3
1141	Survey of mosquito species and mosquito-borne viruses in residential areas along the Sino-Vietnam border in Yunnan Province in China. Frontiers in Microbiology, 0, 14, .	1.5	1
1142	Comprehensive phylogenomic analyses reveal that order Armophorida is most closely related to class Armophorea (Protista, Ciliophora). Molecular Phylogenetics and Evolution, 2023, 182, 107737.	1.2	5
1143	Draft Genome Sequences of Three <i>Candidatus</i> Symbiopectobacterium Isolates Collected from Potato Tubers Grown in New Zealand. Microbiology Resource Announcements, 2023, 12, .	0.3	1
1144	Chromosomal Position of Ribosomal Protein Genes Affects Long-Term Evolution of <i>Vibrio cholerae</i> . MBio, 2023, 14, .	1.8	2
1145	Genomic Comparisons Reveal Selection Pressure and Functional Variation Between Nutritional Endosymbionts of Cave-Adapted and Epigeal Hawaiian Planthoppers. Genome Biology and Evolution, 2023, 15, .	1.1	5



#	ARTICLE	IF	CITATIONS
1146	Conservation of Genomic Information in Multiple Displacement Amplified Low-Quantity Metagenomic Material from Marine Invertebrates. <i>Marine Drugs</i> , 2023, 21, 165.	2.2	0
1147	Phylogeny of the flea beetles (Galerucinae: Alticini) and the position of <i>Aulacothorax</i> elucidated through anchored phylogenomics (Coleoptera: Chrysomelidae: Alticini). <i>Systematic Entomology</i> , 2023, 48, 361-386.	1.7	5
1148	Near-Complete Genome Sequence of L�tschberg Virus ( <i>Mononegavirales</i> : <i>Filoviridae</i> ) Identified in European Perch ( <i>Perca fluviatilis</i> Linnaeus, 1758). <i>Microbiology Resource Announcements</i> , 2023, 12, .	0.3	0
1149	Risk Factors, Genetic Diversity, and Antimicrobial Resistance of <i>Staphylococcus</i> spp. Isolates in Dogs Admitted to an Intensive Care Unit of a Veterinary Hospital. <i>Antibiotics</i> , 2023, 12, 621.	1.5	1
1150	Description of <i>Limnobaculum eriocheiris</i> sp. nov., an intestinal bacterium of <i>Eriocheir sinensis</i> , and reclassification of the genera <i>Jinshanibacter</i> and <i>Insectihabitans</i> as <i>Limnobaculum</i> . <i>Antonie Van Leeuwenhoek</i> , 2023, 116, 487-497.	0.7	2
1151	A Potential Draft Sequence Analysis of <i>Enterobacter asburiae</i> Strain B6_18 of an Endophytic Bacterium. <i>Microbiology Resource Announcements</i> , 0, , .	0.3	0
1152	High incidence of carbapenemase-producing <i>Pseudomonas aeruginosa</i> clinical isolates from Lagos, Nigeria. <i>JAC-Antimicrobial Resistance</i> , 2023, 5, .	0.9	3
1153	Staphylococcal diversity in atopic dermatitis from an individual to a global scale. <i>Cell Host and Microbe</i> , 2023, 31, 578-592.e6.	5.1	9
1154	Design and validation of <i>Dolosigranulum pigrum</i> specific PCR primers using the bacterial core genome. <i>Scientific Reports</i> , 2023, 13, .	1.6	0
1155	Draft Genome Sequence and Annotation of the Halotolerant Carotenoid-Producing Strain <i>Paracoccus bogoriensis</i> BOG6 <sup>T</sup> . <i>Microbiology Resource Announcements</i> , 0, , .	0.3	0
1157	Human Milk Microbiota Profile Affected by Prematurity in Argentinian Lactating Women. <i>Microorganisms</i> , 2023, 11, 1090.	1.6	0
1172	DNA-Sequenzmontage und Genannotation. , 2023, , 11-28.		0