

Canu: scalable and accurate long-read assembly via adaptive repeat separation

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Citation Report

#	ARTICLE	IF	CITATIONS
6	<i>In Silico</i> Whole Genome Sequencer and Analyzer (iWGS): a Computational Pipeline to Guide the Design and Analysis of <i>de novo</i> Genome Sequencing Studies. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 3655-3662.	0.8	39
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9	Fast and accurate de novo genome assembly from long uncorrected reads. <i>Genome Research</i> , 2017, 27, 737-746.	2.4	2,071
10	HySA: a Hybrid Structural variant Assembly approach using next-generation and single-molecule sequencing technologies. <i>Genome Research</i> , 2017, 27, 793-800.	2.4	32
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13	Whole genome sequencing and analysis of <i>Campylobacter coli</i> YH502 from retail chicken reveals a plasmid-borne type VI secretion system. <i>Genomics Data</i> , 2017, 11, 128-131.	1.3	20
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15	Structure and Origin of the <i>White Cap</i> Locus and Its Role in Evolution of Grain Color in Maize. <i>Genetics</i> , 2017, 206, 135-150.	1.2	36
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17	Complete Genome Sequence of <i>Paenibacillus polymyxa</i> YC0573, a Plant Growth-Promoting Rhizobacterium with Antimicrobial Activity. <i>Genome Announcements</i> , 2017, 5, .	0.8	16
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19	Resolving Multicopy Duplications de novo Using Polyploid Phasing. <i>Lecture Notes in Computer Science</i> , 2017, 10229, 117-133.	1.0	22
20	Complete Genome Sequence of the Disinfectant Susceptibility Testing Reference Strain <i>Staphylococcus aureus</i> subsp. <i>aureus</i> ATCC 6538. <i>Genome Announcements</i> , 2017, 5, .	0.8	18
21	New advances in sequence assembly. <i>Genome Research</i> , 2017, 27, xi-xiii.	2.4	63
22	Nanopore sequencing data analysis: state of the art, applications and challenges. <i>Briefings in Bioinformatics</i> , 2018, 19, 1256-1272.	3.2	91
23	De novo yeast genome assemblies from MinION, PacBio and MiSeq platforms. <i>Scientific Reports</i> , 2017, 7, 3935.	1.6	146

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24	<i>GfaPy</i> : a flexible and extensible software library for handling sequence graphs in Python. <i>Bioinformatics</i> , 2017, 33, 3094-3095.	1.8	6
25	Complete Genome Sequence of the Autotrophic Acetogen <i>Clostridium formicaceticum</i> DSM 92^T Using Nanopore and Illumina Sequencing Data. <i>Genome Announcements</i> , 2017, 5, .	0.8	12
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27	Single-molecule sequencing resolves the detailed structure of complex satellite DNA loci in <i>Drosophila melanogaster</i> . <i>Genome Research</i> , 2017, 27, 709-721.	2.4	88
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29	Complete genome sequence of <i>Acidihalobacter prosperus</i> strain F5, an extremely acidophilic, iron- and sulfur-oxidizing halophile with potential industrial applicability in saline water bioleaching of chalcopyrite. <i>Journal of Biotechnology</i> , 2017, 262, 56-59.	1.9	17
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40	Nanopore sequencing enables near-complete de novo assembly of <i>Saccharomyces cerevisiae</i> reference strain CEN.PK113-7D. <i>FEMS Yeast Research</i> , 2017, 17, .	1.1	84
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49	Efficient data structures for mobile de novo genome assembly by third-generation sequencing. <i>Procedia Computer Science</i> , 2017, 110, 440-447.	1.2	5
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51	Genome Sequence of <i>Zymomonas mobilis</i> subsp. <i>mobilis</i> NRRL B-1960. <i>Genome Announcements</i> , 2017, 5, .	0.8	10
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79	Describing Genomic and Epigenomic Traits Underpinning Emerging Fungal Pathogens. <i>Advances in Genetics</i> , 2017, 100, 73-140.	0.8	17
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83	The long reads ahead: de novo genome assembly using the MinION. <i>F1000Research</i> , 2017, 6, 1083.	0.8	54
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96	High-Quality Complete Genome Sequences of Three Bovine Shiga Toxin-Producing <i>Escherichia coli</i> O177:H- (<i>fl</i> C H25) Isolates Harboring Virulent <i>stx</i> 2 and Multiple Plasmids. <i>Genome Announcements</i> , 2018, 6, .	0.8	3
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110	Complete mitochondrial genome of the green-lipped mussel, <i>Perna canaliculus</i> (Mollusca: Mytiloidea), from long nanopore sequencing reads. <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 175-176.	0.2	12
111	Real-time DNA barcoding in a rainforest using nanopore sequencing: opportunities for rapid biodiversity assessments and local capacity building. <i>GigaScience</i> , 2018, 7, .	3.3	176
112	DeepSimulator: a deep simulator for Nanopore sequencing. <i>Bioinformatics</i> , 2018, 34, 2899-2908.	1.8	65
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133	High-quality assembly of <i>Dermatophagoides pteronyssinus</i> genome and transcriptome reveals a wide range of novel allergens. <i>Journal of Allergy and Clinical Immunology</i> , 2018, 141, 2268-2271.e8.	1.5	34
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141	The global distribution and spread of the mobilized colistin resistance gene <i>mcr-1</i> . <i>Nature Communications</i> , 2018, 9, 1179.	5.8	464
142	Genome Sequence of the Amphotericin B-Resistant <i>Candida duobushaemulonii</i> Strain B09383. <i>Genome Announcements</i> , 2018, 6, .	0.8	9
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144	Complete and assembled genome sequence of an NDM-9- and CTX-M-15-producing <i>Klebsiella pneumoniae</i> ST147 wastewater isolate from Switzerland. <i>Journal of Global Antimicrobial Resistance</i> , 2018, 13, 53-54.	0.9	16
145	Finished Genome Sequence of a Polyurethane-Degrading <i>Pseudomonas</i> Isolate. <i>Genome Announcements</i> , 2018, 6, .	0.8	1
146	Tracing Genomic Divergence of <i>Vibrio</i> Bacteria in the <i>Harveyi</i> Clade. <i>Journal of Bacteriology</i> , 2018, 200, .	1.0	8
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1013	Whole-Genome Sequencing and Bioinformatics Analysis of <i>Apiotrichum mycotoxinivorans</i> : Predicting Putative Zearalenone-Degradation Enzymes. <i>Frontiers in Microbiology</i> , 2020, 11, 1866.	1.5	15
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1031	Genome assembly and annotation of <i>Meloidogyne enterolobii</i> , an emerging parthenogenetic root-knot nematode. <i>Scientific Data</i> , 2020, 7, 324.	2.4	33
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1082	Generation of a chromosome-scale genome assembly of the insect-repellent terpenoid-producing <i>Lamiaceae</i> species, <i>Callicarpa americana</i> . <i>GigaScience</i> , 2020, 9, .	3.3	21
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1089	Genome sequencing and population genomics modeling provide insights into the local adaptation of weeping forsythia. Horticulture Research, 2020, 7, 130.	2.9	33
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1095	Whole-Genome Sequencing of <i>Sphingobium</i> sp. Strain RSMS, a Highly Efficient Tributyl Phosphate-Degrading Bacterium. Microbiology Resource Announcements, 2020, 9, .	0.3	4
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1103	Targeted Disruption of Scytalone Dehydratase Gene Using <i>Agrobacterium tumefaciens</i> -Mediated Transformation Leads to Altered Melanin Production in <i>Ascochyta lentis</i> . Journal of Fungi (Basel,) Tj ETQq1 1 0.784314 rgBT /Overlock 1	1.4	1
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1107	Characterization of an IncR Plasmid with Two Copies of ISCR-Linked <i>qnrB6</i> from ST968 <i>Klebsiella pneumoniae</i> . <i>International Journal of Genomics</i> , 2020, 2020, 1-8.	0.8	4
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1110	Benchmarking Long-Read Assemblers for Genomic Analyses of Bacterial Pathogens Using Oxford Nanopore Sequencing. <i>International Journal of Molecular Sciences</i> , 2020, 21, 9161.	1.8	26
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1119	Identification and Isolation of Two Different Subpopulations Within African Swine Fever Virus Arm/07 Stock. <i>Vaccines</i> , 2020, 8, 625.	2.1	16
1120	A survey on deep learning in DNA/RNA motif mining. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	59
1121	Genome Sequences of Four <i>Shigella boydii</i> Strains Representative of the Major <i>S. boydii</i> Clades. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
1122	The Collection of Zoosporic Eufungi at the University of Michigan (CZEUM): introducing a new repository of barcoded Chytridiomycota and Blastocladiomycota cultures. <i>IMA Fungus</i> , 2020, 11, 20.	1.7	22
1123	The genetic adaptations of fall armyworm <i>Spodoptera frugiperda</i> facilitated its rapid global dispersal and invasion. <i>Molecular Ecology Resources</i> , 2020, 20, 1050-1068.	2.2	88

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1124	Complete Genome Sequence of <i>Mycoplasma bovis</i> Strain XBY01, Isolated from Henan Province, China. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	0
1125	Complete Genome Sequence of <i>Bacillus</i> sp. Strain KH172YL63, Isolated from Deep-Sea Sediment. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
1126	Complete Genome Sequence of <i>Lactococcus lactis</i> subsp. <i>lactis</i> bv. <i>diacetylactis</i> SD96. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	5
1127	Complete Genome Sequence of the Deep-Sea Bacterium <i>Moritella marina</i> MP-1 (ATCC 15381). <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
1128	Genome Sequences of Both Organelles of the Grapevine Rootstock Cultivar 'Bârner'™. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	3
1129	A long road/read to rapid high-resolution HLA typing: The nanopore perspective. <i>Human Immunology</i> , 2021, 82, 488-495.	1.2	25
1130	Complete Genome Sequence of the Cryptophycin-Producing Cyanobacterium <i>Nostoc</i> sp. Strain ATCC 53789. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	6
1131	Nanopore sequencing and the Shasta toolkit enable efficient de novo assembly of eleven human genomes. <i>Nature Biotechnology</i> , 2020, 38, 1044-1053.	9.4	344
1132	Genomic Variability of <i>Phytophthora palmivora</i> Isolates from Different Oil Palm Cultivation Regions in Colombia. <i>Phytopathology</i> , 2020, 110, 1553-1564.	1.1	4
1133	Genome Sequence Resources of <i>Colletotrichum truncatum</i> , <i>C. plurivorum</i> , <i>C. musicola</i> , and <i>C. sojiae</i> : Four Species Pathogenic to Soybean (<i>Glycine max</i>). <i>Phytopathology</i> , 2020, 110, 1497-1499.	1.1	12
1134	Closed Genome Sequences of 28 Foodborne Pathogens from the CFSAN Verification Set, Determined by a Combination of Long and Short Reads. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	3
1135	Complete Genome Sequence of <i>Mycoplasma feriruminatoris</i> Strain IVB14/OD_0535, Isolated from an Alpine Ibex in a Swiss Zoo. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	2
1136	Complete Genome Sequence of <i>Leptospira interrogans</i> Strains FMAS_KW1, FMAS_KW2 and FMAS_AW1 Isolated from Leptospirosis Patients from Karawanalla and Awissawella, Sri Lanka. <i>Journal of Genomics</i> , 2020, 8, 49-52.	0.6	9
1137	Complete Genomic Data of <i>Burkholderia glumae</i> Strain GX Associated with Bacterial Panicle Blight of Rice in China. <i>Plant Disease</i> , 2020, 104, 1578-1580.	0.7	2
1138	Complete Genome Sequence of Lignin-Degrading <i>Streptomyces</i> sp. Strain S6, Isolated from an Oil Palm Plantation in Malaysia. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
1139	A high-quality reference genome of wild <i>Cannabis sativa</i> . <i>Horticulture Research</i> , 2020, 7, 73.	2.9	73
1140	Genomes of the Venus Flytrap and Close Relatives Unveil the Roots of Plant Carnivory. <i>Current Biology</i> , 2020, 30, 2312-2320.e5.	1.8	60
1141	Complete Genome Sequence of the Plant Growth-Promoting Bacterium <i>Pantoea agglomerans</i> Strain UAEU18, Isolated from Date Palm Rhizosphere Soil in the United Arab Emirates. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	6

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1143	Rapid, highly accurate and cost-effective open-source simultaneous complete <i>HLA</i> typing and phasing of class I and <i>HLA-B</i> alleles using nanopore sequencing. <i>Hla</i> , 2020, 96, 163-178.	0.4	20
1144	Allele-aware chromosome-level genome assembly and efficient transgene-free genome editing for the autotetraploid cultivated alfalfa. <i>Nature Communications</i> , 2020, 11, 2494.	5.8	224
1145	Improved Genome Assembly and Annotation of the Soybean Aphid (<i>Aphis glycines</i> Matsumura). <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 899-906.	0.8	22
1146	A Highly Contiguous Genome for the Golden-Fronted Woodpecker (<i>Melanerpes aurifrons</i>) via Hybrid Oxford Nanopore and Short Read Assembly. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1829-1836.	0.8	9
1147	Plasmid-Encoded <i>bla</i> _{NDM-5} Gene That Confers High-Level Carbapenem Resistance in <i>Salmonella</i> Typhimurium of Pork Origin. <i>Infection and Drug Resistance</i> , 2020, Volume 13, 1485-1490.	1.1	15
1148	Molecular Typing, Characterization of Antimicrobial Resistance, Virulence Profiling and Analysis of Whole-Genome Sequence of Clinical <i>Klebsiella pneumoniae</i> Isolates. <i>Antibiotics</i> , 2020, 9, 261.	1.5	29
1149	Assessing Population Diversity of <i>Brettanomyces</i> Yeast Species and Identification of Strains for Brewing Applications. <i>Frontiers in Microbiology</i> , 2020, 11, 637.	1.5	21
1150	Ancestral niche separation and evolutionary rate differentiation between sister marine flavobacteria lineages. <i>Environmental Microbiology</i> , 2020, 22, 3234-3247.	1.8	8
1151	Effect of sequence depth and length in long-read assembly of the maize inbred NC358. <i>Nature Communications</i> , 2020, 11, 2288.	5.8	39
1152	A de novo chromosome-level genome assembly of <i>Coregonus</i> sp. <i>Balchen</i> : One representative of the Swiss Alpine whitefish radiation. <i>Molecular Ecology Resources</i> , 2020, 20, 1093-1109.	2.2	29
1153	De novo Assembly and Genome-Wide SNP Discovery in Rohu Carp, <i>Labeo rohita</i> . <i>Frontiers in Genetics</i> , 2020, 11, 386.	1.1	17
1154	A High-Quality Genome Sequence of Model Legume <i>Lotus japonicus</i> (MG-20) Provides Insights into the Evolution of Root Nodule Symbiosis. <i>Genes</i> , 2020, 11, 483.	1.0	31
1155	Profiling of Human Gut Virome with Oxford Nanopore Technology. <i>Medicine in Microecology</i> , 2020, 4, 100012.	0.7	16
1156	The origin and diversification of a novel protein family in venomous snakes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 10911-10920.	3.3	62
1157	Chromosome-level genome assembly of the greenfin horse-faced filefish (<i>Thamnaconus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Ecology Resources, 2020, 20, 1069-1079.	2.2	27
1158	Functional insights from the GC-poor genomes of two aphid parasitoids, <i>Aphidius ervi</i> and <i>Lysiphlebus fabarum</i> . <i>BMC Genomics</i> , 2020, 21, 376.	1.2	19
1159	Genetic Underpinnings of Host Manipulation by <i>Ophiocordyceps</i> as Revealed by Comparative Transcriptomics. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2275-2296.	0.8	33

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1161	The third generation sequencing: the advanced approach to genetic diseases. <i>Translational Pediatrics</i> , 2020, 9, 163-173.	0.5	77
1162	Hydrogen and Carbon Monoxide-Utilizing <i>Kyrpidia spormannii</i> Species From Pantelleria Island, Italy. <i>Frontiers in Microbiology</i> , 2020, 11, 951.	1.5	18
1163	Recent advances and future perspectives in vector-omics. <i>Current Opinion in Insect Science</i> , 2020, 40, 94-103.	2.2	6
1164	Natural hybridization reveals incompatible alleles that cause melanoma in swordtail fish. <i>Science</i> , 2020, 368, 731-736.	6.0	86
1165	Complete Genome Sequences of the Human Pathogen <i>Paenibacillus thiaminolyticus</i> Mbale and Type Strain <i>P. thiaminolyticus</i> NRRL B-4156. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	10
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1167	Identification and characterization of a novel extracellular polyhydroxyalkanoate depolymerase in the complete genome sequence of <i>Undibacterium</i> sp. KW1 and YM2 strains. <i>PLoS ONE</i> , 2020, 15, e0232698.	1.1	9
1168	Complete Genome Sequence of <i>Acinetobacter baumannii</i> ATCC 19606 ^T , a Model Strain of Pathogenic Bacteria Causing Nosocomial Infection. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	8
1169	Whole Genome Sequencing and Comparative Genomic Analyses of <i>Lysinibacillus pakistanensis</i> LZH-9, a Halotolerant Strain with Excellent COD Removal Capability. <i>Microorganisms</i> , 2020, 8, 716.	1.6	3
1170	Mitochondrial Genome of <i>Fagopyrum esculentum</i> and the Genetic Diversity of Extranuclear Genomes in Buckwheat. <i>Plants</i> , 2020, 9, 618.	1.6	16
1171	Chromosome-Level Reference Genome and Population Genomic Analysis Provide Insights into the Evolution and Improvement of Domesticated Mulberry (<i>Morus alba</i>). <i>Molecular Plant</i> , 2020, 13, 1001-1012.	3.9	59
1172	Whole genome sequencing and antibiotic diffusion assays, provide new insight on drug resistance in the genus <i>Pedobacter</i> . <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	5
1173	Complete Genome Sequences of Six <i>Lactobacillus iners</i> Strains Isolated from the Human Vagina. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	8
1174	Genome and single-cell RNA-sequencing of the earthworm <i>Eisenia andrei</i> identifies cellular mechanisms underlying regeneration. <i>Nature Communications</i> , 2020, 11, 2656.	5.8	43
1175	HiC-Hiker: a probabilistic model to determine contig orientation in chromosome-length scaffolds with Hi-C. <i>Bioinformatics</i> , 2020, 36, 3966-3974.	1.8	11
1176	CSA: A high-throughput chromosome-scale assembly pipeline for vertebrate genomes. <i>GigaScience</i> , 2020, 9, .	3.3	4
1177	Chromosome-Level Genome Reveals the Origin of Neo-Y Chromosome in the Male Barred Knifejaw <i>Oplegnathus fasciatus</i> . <i>IScience</i> , 2020, 23, 101039.	1.9	14

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1179	Draft Genome Assembly of <i>Floccularia luteovirens</i> , an Edible and Symbiotic Mushroom on Qinghai-Tibet Plateau. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1167-1173.	0.8	5
1180	Mitochondrial genome sequencing and phylogenetic analysis of <i>Cynodon dactylon</i> — <i>Cynodon transvaalensis</i> . <i>Turkish Journal of Botany</i> , 2020, 44, 14-24.	0.5	0
1181	Whole-genome sequence of <i>Phellinus gilvus</i> (mulberry Sanghuang) reveals its unique medicinal values. <i>Journal of Advanced Research</i> , 2020, 24, 325-335.	4.4	24
1182	Oxford Nanopore sequencing: new opportunities for plant genomics?. <i>Journal of Experimental Botany</i> , 2020, 71, 5313-5322.	2.4	46
1183	Genome Sequence of <i>Phoma sorghina</i> var. <i>saccharum</i> That Causes Sugarcane Twisted Leaf Disease in China. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 1092-1094.	1.4	1
1184	Nanopore sequencing reveals genomic map of CTX-M-type extended-spectrum β -lactamases carried by <i>Escherichia coli</i> strains isolated from blue mussels (<i>Mytilus edulis</i>) in Norway. <i>BMC Microbiology</i> , 2020, 20, 134.	1.3	13
1185	The <i>Gossypium longicalyx</i> Genome as a Resource for Cotton Breeding and Evolution. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1457-1467.	0.8	32
1186	Determining the Genetic Characteristics of Resistance and Virulence of the α -Epidermidis Cluster Group Through Pan-Genome Analysis. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 274.	1.8	16
1187	Bacterial symbionts support larval sap feeding and adult folivory in (semi-)aquatic reed beetles. <i>Nature Communications</i> , 2020, 11, 2964.	5.8	42
1188	Comparative Evaluation of Genome Assemblers from Long-Read Sequencing for Plants and Crops. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 7670-7677.	2.4	18
1189	Trans-NanoSim characterizes and simulates nanopore RNA-sequencing data. <i>GigaScience</i> , 2020, 9, .	3.3	20
1190	Dual-Seq reveals genome and transcriptome of <i>Caedibacter taeniospiralis</i> , obligate endosymbiont of <i>Paramecium</i> . <i>Scientific Reports</i> , 2020, 10, 9727.	1.6	8
1191	Prevalence of Aminoglycoside Resistance Genes and Molecular Characterization of a Novel Gene, <i>aac(3)-Ilg</i> , among Clinical Isolates of the <i>Enterobacter cloacae</i> Complex from a Chinese Teaching Hospital. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	1.4	9
1192	Complete Genome Sequence of <i>Halomonas hydrothermalis</i> Strain Slthf2, a Halophilic Bacterium Isolated from a Deep-Sea Hydrothermal-Vent Environment. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
1193	The Genome Sequence of Five Highly Pathogenic Isolates of <i>Fusarium oxysporum</i> f. sp. lini. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 1112-1115.	1.4	14
1194	Two Synthetic 18-Way Outcrossed Populations of Diploid Budding Yeast with Utility for Complex Trait Dissection. <i>Genetics</i> , 2020, 215, 323-342.	1.2	17
1195	Mobile Genetic Elements Harboring Antibiotic Resistance Determinants in <i>Acinetobacter baumannii</i> Isolates From Bolivia. <i>Frontiers in Microbiology</i> , 2020, 11, 919.	1.5	26

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1197	Complete, high-quality genomes from long-read metagenomic sequencing of two wolf lichen thalli reveals enigmatic genome architecture. <i>Genomics</i> , 2020, 112, 3150-3156.	1.3	16
1198	Long-read human genome sequencing and its applications. <i>Nature Reviews Genetics</i> , 2020, 21, 597-614.	7.7	542
1199	Nanopore sequencing from extraction-free direct PCR of dried serum spots for portable hepatitis B virus drug-resistance typing. <i>Journal of Clinical Virology</i> , 2020, 129, 104483.	1.6	9
1200	Complete Genome Sequences of 16 <i>Mycoplasma bovis</i> Isolates from Canadian Bison and Cattle. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	3
1201	Complete Genome Sequence of the Lignocellulose-Degrading Actinomycete <i>Streptomyces albus</i> CAS922. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	3
1202	Lineage dynamics of the endosymbiotic cell type in the soft coral <i>Xenia</i> . <i>Nature</i> , 2020, 582, 534-538.	13.7	71
1203	A neurotransmitter produced by gut bacteria modulates host sensory behaviour. <i>Nature</i> , 2020, 583, 415-420.	13.7	155
1204	Pan-Genome of Wild and Cultivated Soybeans. <i>Cell</i> , 2020, 182, 162-176.e13.	13.5	508
1205	Taro Genome Assembly and Linkage Map Reveal QTLs for Resistance to Taro Leaf Blight. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2763-2775.	0.8	15
1206	Major Impacts of Widespread Structural Variation on Gene Expression and Crop Improvement in Tomato. <i>Cell</i> , 2020, 182, 145-161.e23.	13.5	464
1207	Co-existence of <i>mphA</i> , <i>oqxAB</i> and <i>blaCTX-M-65</i> on the <i>IncHI2</i> Plasmid in highly drug-resistant <i>Salmonella enterica</i> serovar Indiana ST17 isolated from retail foods and humans in China. <i>Food Control</i> , 2020, 118, 107269.	2.8	14
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1209	Tandem gene duplications drive divergent evolution of caffeine and crocin biosynthetic pathways in plants. <i>BMC Biology</i> , 2020, 18, 63.	1.7	94
1210	Cartography of opportunistic pathogens and antibiotic resistance genes in a tertiary hospital environment. <i>Nature Medicine</i> , 2020, 26, 941-951.	15.2	130
1211	Chromosome Level Genome Assembly of <i>Andrographis paniculata</i> . <i>Frontiers in Genetics</i> , 2020, 11, 701.	1.1	14
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1213	Tracing Back the Evolutionary Route of Enteroinvasive <i>Escherichia coli</i> (EIEC) and <i>Shigella</i> Through the Example of the Highly Pathogenic O96:H19 EIEC Clone. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 260.	1.8	7

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1215	Whole Genome Sequencing of Hepatitis A Virus Using a PCR-Free Single-Molecule Nanopore Sequencing Approach. <i>Frontiers in Microbiology</i> , 2020, 11, 874.	1.5	14
1216	Phytopathogenic <i>Rhodococcus</i> Have Diverse Plasmids With Few Conserved Virulence Functions. <i>Frontiers in Microbiology</i> , 2020, 11, 1022.	1.5	18
1217	Complete Genome of <i>Lactobacillus iners</i> KY Using Flongle Provides Insight Into the Genetic Background of Optimal Adaption to Vaginal Ecoiniche. <i>Frontiers in Microbiology</i> , 2020, 11, 1048.	1.5	16
1218	A Chromosome-Scale Assembly of the Garden Orach (<i>Atriplex hortensis</i> L.) Genome Using Oxford Nanopore Sequencing. <i>Frontiers in Plant Science</i> , 2020, 11, 624.	1.7	11
1219	Genome Sequences of Chikungunya Virus Isolates from Bolivia. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	0
1220	Ultraplexing: increasing the efficiency of long-read sequencing for hybrid assembly with k-mer-based multiplexing. <i>Genome Biology</i> , 2020, 21, 68.	3.8	6
1221	Whole Genome Sequence of <i>Xylella fastidiosa</i> ATCC 35879T and Detection of Genome Rearrangements Within Subsp. <i>fastidiosa</i> . <i>Current Microbiology</i> , 2020, 77, 1858-1863.	1.0	4
1222	Apollo: a sequencing-technology-independent, scalable and accurate assembly polishing algorithm. <i>Bioinformatics</i> , 2020, 36, 3669-3679.	1.8	26
1223	The honeysuckle genome provides insight into the molecular mechanism of carotenoid metabolism underlying dynamic flower coloration. <i>New Phytologist</i> , 2020, 227, 930-943.	3.5	68
1224	Genome of the webworm <i>Hyphantria cunea</i> unveils genetic adaptations supporting its rapid invasion and spread. <i>BMC Genomics</i> , 2020, 21, 242.	1.2	12
1225	High Contiguity de novo Genome Sequence Assembly of Trifoliolate Yam (<i>Dioscorea dumetorum</i>) Using Long Read Sequencing. <i>Genes</i> , 2020, 11, 274.	1.0	54
1226	Closing <i>Clostridium botulinum</i> Group I Genomes Using a Combination of Short- and Long-Reads. <i>Frontiers in Microbiology</i> , 2020, 11, 239.	1.5	10
1227	Combining short and long read sequencing to characterize antimicrobial resistance genes on plasmids applied to an unauthorized genetically modified <i>Bacillus</i> . <i>Scientific Reports</i> , 2020, 10, 4310.	1.6	57
1228	Highly Contiguous Genome Resource of <i>Colletotrichum fructicola</i> Generated Using Long-Read Sequencing. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 790-793.	1.4	12
1229	The genome evolution and domestication of tropical fruit mango. <i>Genome Biology</i> , 2020, 21, 60.	3.8	104
1230	Chromosome-level genome assembly and annotation of the loquat (<i>Eriobotrya japonica</i>) genome. <i>GigaScience</i> , 2020, 9, .	3.3	43
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1233	Assembly and analysis of the whole genome of <i>Arthroderma uncinatum</i> strain T10, compared with <i>Microsporium canis</i> and <i>Trichophyton rubrum</i> . <i>Mycoses</i> , 2020, 63, 683-693.	1.8	6
1234	Comparison of third-generation sequencing approaches to identify viral pathogens under public health emergency conditions. <i>Virus Genes</i> , 2020, 56, 288-297.	0.7	17
1235	Centromere scission drives chromosome shuffling and reproductive isolation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 7917-7928.	3.3	47
1236	Phylogenetic relationship between Australian <i>Fusarium oxysporum</i> isolates and resolving the species complex using the multispecies coalescent model. <i>BMC Genomics</i> , 2020, 21, 248.	1.2	25
1237	A <i>Staphylococcus</i> pro-apoptotic peptide induces acute exacerbation of pulmonary fibrosis. <i>Nature Communications</i> , 2020, 11, 1539.	5.8	43
1238	Can we use it? On the utility of de novo and reference-based assembly of Nanopore data for plant plastome sequencing. <i>PLoS ONE</i> , 2020, 15, e0226234.	1.1	33
1239	Draft Genome Resource for the Ex-types of <i>Phytophthora ramorum</i> , <i>P. kernoviae</i> , and <i>P. melonis</i> , Species of Regulatory Concern, Using Ultra-Long Read MinION Nanopore Sequencing. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 794-797.	1.4	8
1240	Genome sequence of the fungus <i>Pycnoporus sanguineus</i> , which produces cinnabarinic acid and pH- and thermo- stable laccases. <i>Gene</i> , 2020, 742, 144586.	1.0	8
1241	Chromosome-level genome assembly of the greenhouse whitefly (<i>Trialeurodes vaporariorum</i>) Tj ETQq1 1 0,784314 rgBT /Over 2.2 21	2.2	21
1242	The chromosome-scale assembly of the willow genome provides insight into Salicaceae genome evolution. <i>Horticulture Research</i> , 2020, 7, 45.	2.9	35
1243	An improved de novo genome assembly of the common marmoset genome yields improved contiguity and increased mapping rates of sequence data. <i>BMC Genomics</i> , 2020, 21, 243.	1.2	9
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1247	New genome assemblies reveal patterns of domestication and adaptation across <i>Brettanomyces</i> (<i>Dekkera</i>) species. <i>BMC Genomics</i> , 2020, 21, 194.	1.2	21
1248	Benchmarking hybrid assemblies of <i>Giardia</i> and prediction of widespread intra-isolate structural variation. <i>Parasites and Vectors</i> , 2020, 13, 108.	1.0	8
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1285	A chromosome-scale reference genome for <i>Giardia intestinalis</i> WB. <i>Scientific Data</i> , 2020, 7, 38.	2.4	69
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1319	Genomic Acquisitions in Emerging Populations of <i>Xanthomonas vasicola</i> pv. <i>vasculorum</i> Infecting Corn in the United States and Argentina. <i>Phytopathology</i> , 2020, 110, 1161-1173.	1.1	16
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1361	Draft Genome Sequences of Two <i>Vibrio fortis</i> Strains Isolated from Coral (<i>Fungia</i> sp.) from the Andaman Sea. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	2
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1363	Genome Sequence of <i>Escherichia coli</i> K1683, Isolated from a Urosepsis Patient. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	0
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1365	Complete Genome Sequences for Two <i>Talaromyces marneffeii</i> Clinical Isolates from Northern and Southern Vietnam. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	7
1366	Draft Genome Sequence of <i>Idiomarina</i> sp. Strain W-5T, Isolated from the Andaman Sea. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	0
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1379	Comparative genomics analysis of <i>Acinetobacter haemolyticus</i> isolates from sputum samples of respiratory patients. <i>Genomics</i> , 2020, 112, 2784-2793.	1.3	11
1380	Complete Genome Sequence of <i>Bordetella bronchiseptica</i> Strain KM22. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	4
1381	Genome Sequences of <i>Brevundimonas naejangsanensis</i> Strain FS1091 and <i>Bacillus amyloliquefaciens</i> Strain FS1092, Isolated from a Fresh-Cut-Produce-Processing Plant. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
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1387	Genome elimination mediated by gene expression from a selfish chromosome. <i>Science Advances</i> , 2020, 6, eaaz9808.	4.7	48
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1390	Complete Genome Sequence of <i>Mycobacterium xenopi</i> JCM15661 T, Obtained Using Nanopore and Illumina Sequencing Technologies. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	2
1391	Complete Genome Sequence of <i>Pseudomonas putida</i> Strain TS312, Harboring an HdtS-Type <i>N</i> -Acyl-Homoserine Lactone Synthase, Isolated from a Paper Mill. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	3
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1393	Rapid mitochondrial genome sequencing based on Oxford Nanopore Sequencing and a proxy for vertebrate species identification. <i>Ecology and Evolution</i> , 2020, 10, 3544-3560.	0.8	20
1394	Research in Computational Molecular Biology. <i>Lecture Notes in Computer Science</i> , 2020, , .	1.0	0
1395	Whole genome sequence analysis of the mosquitocidal <i>Bacillus thuringiensis</i> LLP29. <i>Archives of Microbiology</i> , 2020, 202, 1693-1700.	1.0	5

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1398	A platinum standard pan-genome resource that represents the population structure of Asian rice. <i>Scientific Data</i> , 2020, 7, 113.	2.4	86
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1406	De novo assembly of the olive fruit fly (<i>Bactrocera oleae</i>) genome with linked-reads and long-read technologies minimizes gaps and provides exceptional Y chromosome assembly. <i>BMC Genomics</i> , 2020, 21, 259.	1.2	21
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1408	Complete genome sequence and annotation of the laboratory reference strain <i>Shigella flexneri</i> serotype 5a M90T and genome-wide transcriptional start site determination. <i>BMC Genomics</i> , 2020, 21, 285.	1.2	7
1409	MetaEuk" sensitive, high-throughput gene discovery, and annotation for large-scale eukaryotic metagenomics. <i>Microbiome</i> , 2020, 8, 48.	4.9	119
1410	Adaptation to Industrial Stressors Through Genomic and Transcriptional Plasticity in a Bioethanol Producing Fission Yeast Isolate. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1375-1391.	0.8	1
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1412	Real-time, MinION-based, amplicon sequencing for lineage typing of infectious bronchitis virus from upper respiratory samples. <i>Journal of Veterinary Diagnostic Investigation</i> , 2021, 33, 179-190.	0.5	7
1413	Next Generation Sequencing Methods: Pushing the Boundaries. , 2021, , 19-46.		0

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1415	High quality genome sequences of thirteen Hypoxylaceae (Ascomycota) strengthen the phylogenetic family backbone and enable the discovery of new taxa. <i>Fungal Diversity</i> , 2021, 106, 7-28.	4.7	65
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1418	Bacterial-fungal interactions revealed by genome-wide analysis of bacterial mutant fitness. <i>Nature Microbiology</i> , 2021, 6, 87-102.	5.9	49
1419	Genomic Analysis Revealed a Convergent Evolution of LINE-1 in Coat Color: A Case Study in Water Buffaloes (<i>Bubalus bubalis</i>). <i>Molecular Biology and Evolution</i> , 2021, 38, 1122-1136.	3.5	32
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1422	Chromosomal genomes of three rice planthoppers provide new insights into sex chromosome evolution. <i>Molecular Ecology Resources</i> , 2021, 21, 226-237.	2.2	44
1423	De novo assemblies of <i>Luffa acutangula</i> and <i>Luffa cylindrica</i> genomes reveal an expansion associated with substantial accumulation of transposable elements. <i>Molecular Ecology Resources</i> , 2021, 21, 212-225.	2.2	23
1424	Genome Resource for <i>Pseudomonas</i> sp. Strain L22-9: A Potential Novel Species with Antifungal Activity. <i>Phytopathology</i> , 2021, 111, 425-428.	1.1	5
1425	A chromosome-level genome assembly of the wild rice <i>Oryza rufipogon</i> facilitates tracing the origins of Asian cultivated rice. <i>Science China Life Sciences</i> , 2021, 64, 282-293.	2.3	24
1426	Complete Genome Resource of <i>Serratia plymuthica</i> C-1 that Causes Root Rot Disease in Korean Ginseng. <i>Plant Disease</i> , 2021, 105, 202-204.	0.7	0
1427	Assessing the utility of long-read nanopore sequencing for rapid and efficient characterization of mobile element insertions. <i>Laboratory Investigation</i> , 2021, 101, 442-449.	1.7	9
1428	A General Model to Explain Repeated Turnovers of Sex Determination in the Salicaceae. <i>Molecular Biology and Evolution</i> , 2021, 38, 968-980.	3.5	53
1429	Finding long tandem repeats in long noisy reads. <i>Bioinformatics</i> , 2021, 37, 612-621.	1.8	4
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1434	Giant African snail genomes provide insights into molluscan whole-genome duplication and aquatic-terrestrial transition. <i>Molecular Ecology Resources</i> , 2021, 21, 478-494.	2.2	33
1435	A chromosome-scale assembly of allotetraploid <i>Brassica juncea</i> (AABB) elucidates comparative architecture of the A and B genomes. <i>Plant Biotechnology Journal</i> , 2021, 19, 602-614.	4.1	62
1436	Complete genome sequence and comparative genome analysis of <i>Alcanivorax</i> sp. IO_7, a marine alkane-degrading bacterium isolated from hydrothermally-influenced deep seawater of southwest Indian ridge. <i>Genomics</i> , 2021, 113, 884-891.	1.3	14
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1438	A <i>Pseudomonas</i> sp. strain uniquely degrades PAHs and heterocyclic derivatives via lateral dioxygenation pathways. <i>Journal of Hazardous Materials</i> , 2021, 403, 123956.	6.5	51
1439	Genome Resource for Peanut Web Blotch Causal Agent <i>Peyronellaea arachidicola</i> Strain YY187. <i>Plant Disease</i> , 2021, 105, 1177-1178.	0.7	10
1440	Antagonistic action of <i>Streptomyces pratensis</i> S10 on <i>Fusarium graminearum</i> and its complete genome sequence. <i>Environmental Microbiology</i> , 2021, 23, 1925-1940.	1.8	18
1441	A high-quality <i>Brassica napus</i> genome reveals expansion of transposable elements, subgenome evolution and disease resistance. <i>Plant Biotechnology Journal</i> , 2021, 19, 615-630.	4.1	56
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1445	Chromosome-level de novo assembly of <i>Coprinopsis cinerea</i> A43mut B43mut pab1-1 #326 and genetic variant identification of mutants using Nanopore MinION sequencing. <i>Fungal Genetics and Biology</i> , 2021, 146, 103485.	0.9	7
1446	Improved high-molecular-weight DNA extraction, nanopore sequencing and metagenomic assembly from the human gut microbiome. <i>Nature Protocols</i> , 2021, 16, 458-471.	5.5	65
1447	Carbapenemase-producing Enterobacterales causing secondary infections during the COVID-19 crisis at a New York City hospital. <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 380-384.	1.3	58
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1451	Enrichment and physiological characterization of a novel comammox <i>Nitrospira</i> indicates ammonium inhibition of complete nitrification. <i>ISME Journal</i> , 2021, 15, 1010-1024.	4.4	117
1452	Genomic characterization of an extensively drug-resistant chicken-borne <i>Salmonella</i> Indiana isolate carrying an IncHI2-IncHI2A plasmid. <i>Food Control</i> , 2021, 125, 107761.	2.8	9
1453	<i>Pseudonocardia cytotoxica</i> sp. nov., a novel actinomycete isolated from an Arctic fjord with potential to produce cytotoxic compound. <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 23-35.	0.7	9
1454	Comparative genomics reveals the <i>in planta</i> secreted <i>Verticillium dahliae</i> Av2 effector protein recognized in tomato plants that carry the <i>V2</i> resistance locus. <i>Environmental Microbiology</i> , 2021, 23, 1941-1958.	1.8	32
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1461	The novel macrolide resistance genes <i>mef</i> (F) and <i>msr</i> (G) are located on a plasmid in <i>Macroccoccus canis</i> and a transposon in <i>Macroccoccus caseolyticus</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 48-54.	1.3	5
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1463	Chromosome-level genome of the peach fruit moth <i>Carposina sasakii</i> (Lepidoptera: Carposinidae) provides a resource for evolutionary studies on moths. <i>Molecular Ecology Resources</i> , 2021, 21, 834-848.	2.2	25
1464	The large plasmidome of <i>Lactococcus lactis</i> subsp. <i>lactis</i> bv. <i>diacetylactis</i> S50 confers its biotechnological properties. <i>International Journal of Food Microbiology</i> , 2021, 337, 108935.	2.1	12
1465	gcType: a high-quality type strain genome database for microbial phylogenetic and functional research. <i>Nucleic Acids Research</i> , 2021, 49, D694-D705.	6.5	53
1467	Genome Resources of Four Distinct Pathogenic Races Within <i>Fusarium oxysporum</i> f. sp. <i>vasinfectum</i> that Cause Vascular Wilt Disease of Cotton. <i>Phytopathology</i> , 2021, 111, 593-596.	1.1	7
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1470	Chromosome-level de novo genome assembly of <i>Sarcophaga peregrina</i> provides insights into the evolutionary adaptation of flesh flies. <i>Molecular Ecology Resources</i> , 2021, 21, 251-262.	2.2	16
1471	Distribution of β -Lactamase Genes and Genetic Context of blaKPC-2 in Clinical Carbapenemase-Producing <i>Klebsiella pneumoniae</i> Isolates. <i>Infection and Drug Resistance</i> , 2021, Volume 14, 237-247.	1.1	11
1472	Compacting a synthetic yeast chromosome arm. <i>Genome Biology</i> , 2021, 22, 5.	3.8	28
1473	The complete chloroplast genome of <i>Adenophora triphylla</i> (Asterales: Campanulaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 82-83.	0.2	0
1474	Whole-genome sequencing reveals sex determination and liver high-fat storage mechanisms of yellowstripe goby (<i>Mugilogobius chulae</i>). <i>Communications Biology</i> , 2021, 4, 15.	2.0	11
1477	Sat-BSA: an NGS-based method using local <i>de novo</i> assembly of long reads for rapid identification of genomic structural variations associated with agronomic traits. <i>Breeding Science</i> , 2021, 71, 299-312.	0.9	6
1478	Genome Assembly and Analyses of the Macrofungus <i>Macrocybe gigantea</i> . <i>BioMed Research International</i> , 2021, 2021, 1-14.	0.9	4
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1480	Identifying a melanogenesis-related candidate gene by a high-quality genome assembly and population diversity analysis in <i>Hypsizygus marmoreus</i> . <i>Journal of Genetics and Genomics</i> , 2021, 48, 75-87.	1.7	14
1481	Error correction enables use of Oxford Nanopore technology for reference-free transcriptome analysis. <i>Nature Communications</i> , 2021, 12, 2.	5.8	94
1482	Methods for Proteogenomics Data Analysis, Challenges, and Scalability Bottlenecks: A Survey. <i>IEEE Access</i> , 2021, 9, 5497-5516.	2.6	14
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1484	The assembled and annotated genome of the pigeon louse <i>Columbicola columbae</i> , a model ectoparasite. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	18
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1487	Application of long-read sequencing to the detection of structural variants in human cancer genomes. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 4207-4216.	1.9	25
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1490	Comprehensive Genomic Investigation of Coevolution of <i>mcr</i> genes in <i>Escherichia coli</i> Strains via Nanopore Sequencing. <i>Global Challenges</i> , 2021, 5, 2000014.	1.8	19
1491	A strategy for complete telomere-to-telomere assembly of ciliate macronuclear genome using ultra-high coverage Nanopore data. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 1928-1932.	1.9	10
1492	Comparative multi-omics analyses reveal differential expression of key genes relevant for parasitism between non-encapsulated and encapsulated <i>Trichinella</i> . <i>Communications Biology</i> , 2021, 4, 134.	2.0	4
1493	Whole Genome Sequencing and Root Colonization Studies Reveal Novel Insights in the Biocontrol Potential and Growth Promotion by <i>Bacillus subtilis</i> MBI 600 on Cucumber. <i>Frontiers in Microbiology</i> , 2020, 11, 600393.	1.5	41
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1498	Long read sequencing of <i>Toona sinensis</i> (A. Juss) Roem: A chromosome-level reference genome for the family Meliaceae. <i>Molecular Ecology Resources</i> , 2021, 21, 1243-1255.	2.2	20
1499	Draft Genome Resource of <i>Fusarium oxysporum</i> f. sp. <i>capsici</i> , the Infectious Agent of Pepper <i>Fusarium</i> Wilt. <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 715-717.	1.4	7
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1502	Comparative Virulence and Genomic Analysis of <i>Streptococcus suis</i> Isolates. <i>Frontiers in Microbiology</i> , 2020, 11, 620843.	1.5	11
1503	Efficient assembly of nanopore reads via highly accurate and intact error correction. <i>Nature Communications</i> , 2021, 12, 60.	5.8	166
1505	A type VII secretion system of <i>Streptococcus gallolyticus</i> subsp. <i>gallolyticus</i> contributes to gut colonization and the development of colon tumors. <i>PLoS Pathogens</i> , 2021, 17, e1009182.	2.1	41
1506	Complete Genome Sequence of <i>Aeromonas salmonicida</i> subsp. <i>masoucida</i> Strain BR19001YR, Isolated from Diseased Korean Rockfish (<i>Sebastes schlegelii</i>). <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	4
1507	Complete Genome Sequence of <i>Paludibaculum fermentans</i> P105 ^T , a Facultatively Anaerobic Acidobacterium Capable of Dissimilatory Fe(III) Reduction. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	2
1508	Bioinformatics Approaches for Fungal Biotechnology. , 2021, , 536-554.		0

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1510	BlockPolish: accurate polishing of long-read assembly via block divide-and-conquer. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	2
1511	Combined genomic, transcriptomic, and metabolomic analyses provide insights into chayote (<i>Sechium</i>) Tj ETQq0 0,0 rgBT /Overlock 10	2.9	39
1512	A Multi-Omics Characterization of the Natural Product Potential of Tropical Filamentous Marine Cyanobacteria. <i>Marine Drugs</i> , 2021, 19, 20.	2.2	19
1513	Dissemination mechanisms of NDM genes in hospitalized patients. <i>JAC-Antimicrobial Resistance</i> , 2021, 3, dlab032.	0.9	6
1514	<i>Bodo saltans</i> (Kinetoplastida) is dependent on a novel <i>Paracaedibacter</i> -like endosymbiont that possesses multiple putative toxin-antitoxin systems. <i>ISME Journal</i> , 2021, 15, 1680-1694.	4.4	11
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1516	Bioinformatics resources for SARS-CoV-2 discovery and surveillance. <i>Briefings in Bioinformatics</i> , 2021, 22, 631-641.	3.2	38
1517	Complete Genome Sequence of <i>Alistipes indistinctus</i> Strain 2BBH45, Isolated from the Feces of a Healthy Japanese Male. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	1
1518	Draft Genome Sequences of 284 <i>Xanthomonas citri</i> pv. <i>citri</i> Strains Causing Asiatic Citrus Canker. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	6
1519	Whole-Genome Shotgun Sequence of <i>Bacillus mycoides</i> Strain U53, a Psychrotolerant Bacterium Isolated from the Sakhalin Region in Russia. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	1
1520	<i>S. pseudintermedius</i> and <i>S. aureus</i> lineages with transmission ability circulate as causative agents of infections in pets for years. <i>BMC Veterinary Research</i> , 2021, 17, 42.	0.7	31
1521	The complete mitochondrial genome of Eaton's skate, <i>Bathyraja eatonii</i> (Rajiformes,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 2	0.2	1
1522	Genome sequence of the coffee root-knot nematode <i>Meloidogyne exigua</i> . <i>Journal of Nematology</i> , 2021, 53, 1-6.	0.4	3
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1524	Genome structure variation analyses of peach reveal population dynamics and a 1.67% Mb causal inversion for fruit shape. <i>Genome Biology</i> , 2021, 22, 13.	3.8	50
1525	Genome Sequencing of Fiber Flax Cultivar Atlant Using Oxford Nanopore and Illumina Platforms. <i>Frontiers in Genetics</i> , 2020, 11, 590282.	1.1	28
1526	Complete Genome Sequencing and Comparative Genomic Analysis of <i>Streptococcus thermophilus</i> CKDB027, a Promising Probiotic Bacterial Strain. <i>Food Supplements and Biomaterials for Health</i> , 2021, 1, .	0.3	2

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1527	Scalable long read self-correction and assembly polishing with multiple sequence alignment. <i>Scientific Reports</i> , 2021, 11, 761.	1.6	27
1528	Nitrogen-fixing Ability and Nitrogen Fixation-related Genes of Thermophilic Fermentative Bacteria in the Genus <i>Caldicellulosiruptor</i> . <i>Microbes and Environments</i> , 2021, 36, n/a.	0.7	15
1529	Four Reference Quality Genome Assemblies of <i>Pyrenophora teres</i> f. <i>maculata</i> : A Resource for Studying the Barley Spot Form Net Blotch Interaction. <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 135-139.	1.4	8
1530	NexGen Sequencing Data: Bioinformatic Tools for Visualization and Analysis. , 2021, , 47-90.		0
1532	Identification and Characterization of Mycobacterial Species Using Whole-Genome Sequences. <i>Methods in Molecular Biology</i> , 2021, 2314, 399-457.	0.4	0
1533	Effective Identification of Bacterial Genomes From Short and Long Read Sequencing Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 2806-2816.	1.9	1
1534	Phytoplankton consortia as a blueprint for mutually beneficial eukaryote-bacteria ecosystems based on the biocoenosis of <i>Botryococcus</i> consortia. <i>Scientific Reports</i> , 2021, 11, 1726.	1.6	12
1536	The draft genome sequence of the grove snail <i>Cepaea nemoralis</i> . <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	15
1537	Plastid Genomes of the Early Vascular Plant Genus <i>Selaginella</i> Have Unusual Direct Repeat Structures and Drastically Reduced Gene Numbers. <i>International Journal of Molecular Sciences</i> , 2021, 22, 641.	1.8	10
1538	Chromosome-level genomes of seeded and seedless date plum based on third-generation DNA sequencing and Hi-C analysis. <i>Forestry Research</i> , 2021, 1, 0-0.	0.5	2
1539	White pupae phenotype of tephritids is caused by parallel mutations of a MFS transporter. <i>Nature Communications</i> , 2021, 12, 491.	5.8	25
1540	A biological and genomic comparison of a drug-resistant and a drug-susceptible strain of <i>Candida auris</i> isolated from Beijing, China. <i>Virulence</i> , 2021, 12, 1388-1399.	1.8	11
1541	Chromosome-level genome assembly of the Chinese longsnout catfish <i>Leiocassis longirostris</i> . <i>Zoological Research</i> , 2021, 42, 417-422.	0.9	14
1543	Chromosome-level genome assembly of <i>Ophiorrhiza pumila</i> reveals the evolution of camptothecin biosynthesis. <i>Nature Communications</i> , 2021, 12, 405.	5.8	77
1544	Complete Genome Sequence of <i>Halomonas</i> sp. Strain SH5A2, a Dye-Degrading Halotolerant Bacterium Isolated from the Salinas and Aguada Blanca National Reserve in Peru. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	1
1545	Selfing is the safest sex for <i>Caenorhabditis tropicalis</i> . <i>ELife</i> , 2021, 10, .	2.8	37
1547	The chloroplast genome of a unicellular green alga strain isolated from the rubber processing wastewater. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 15-16.	0.2	2
1550	Whole genome characterization of strains belonging to the <i>Ralstonia solanacearum</i> species complex and in silico analysis of TaqMan assays for detection in this heterogenous species complex. <i>European Journal of Plant Pathology</i> , 2021, 159, 593-613.	0.8	2

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1552	Whole-Genome Sequence of Synthesized Allopolyploids in <i>Cucumis</i> Reveals Insights into the Genome Evolution of Allopolyploidization. <i>Advanced Science</i> , 2021, 8, 2004222.	5.6	24
1553	Pathogenomic analyses of <i>Mycobacterium microti</i> , an ESX-1-deleted member of the <i>Mycobacterium tuberculosis</i> complex causing disease in various hosts. <i>Microbial Genomics</i> , 2021, 7, .	1.0	11
1554	Hidden genomic features of an invasive malaria vector, <i>Anopheles stephensi</i> , revealed by a chromosome-level genome assembly. <i>BMC Biology</i> , 2021, 19, 28.	1.7	77
1555	Chromosome-Level Genome Assembly and Annotation of a Sciaenid Fish, <i>Argyrosomus japonicus</i> . <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	6
1556	Critical evaluation of short, long, and hybrid assembly for contextual analysis of antibiotic resistance genes in complex environmental metagenomes. <i>Scientific Reports</i> , 2021, 11, 3753.	1.6	53
1557	Application of computational approaches to analyze metagenomic data. <i>Journal of Microbiology</i> , 2021, 59, 233-241.	1.3	9
1559	Current status and impending progress for cassava structural genomics. <i>Plant Molecular Biology</i> , 2022, 109, 177-191.	2.0	11
1560	Genes Influencing Phage Host Range in <i>Staphylococcus aureus</i> on a Species-Wide Scale. <i>MSphere</i> , 2021, 6, .	1.3	19
1562	Evolutionary and genomic comparisons of hybrid uninucleate and nonhybrid <i>Rhizoctonia</i> fungi. <i>Communications Biology</i> , 2021, 4, 201.	2.0	16
1563	Genome assembly and population genomic analysis provide insights into the evolution of modern sweet corn. <i>Nature Communications</i> , 2021, 12, 1227.	5.8	37
1565	Hologenome analysis reveals dual symbiosis in the deep-sea hydrothermal vent snail <i>Gigantopelta aegis</i> . <i>Nature Communications</i> , 2021, 12, 1165.	5.8	38
1566	Potential of whole-genome sequencing-based pharmacogenetic profiling. <i>Pharmacogenomics</i> , 2021, 22, 177-190.	0.6	18
1567	Insight Into the Virulence Related Secretion Systems, Fimbriae, and Toxins in O2:K1 <i>Escherichia coli</i> Isolated From Bovine Mastitis. <i>Frontiers in Veterinary Science</i> , 2021, 8, 622725.	0.9	3
1569	Generating long-read sequences using Oxford Nanopore Technology from <i>Diospyros celebica</i> genomic DNA. <i>BMC Research Notes</i> , 2021, 14, 75.	0.6	5
1570	Behavioral and Genomic Sensory Adaptations Underlying the Pest Activity of <i>Drosophila suzukii</i> . <i>Molecular Biology and Evolution</i> , 2021, 38, 2532-2546.	3.5	31
1571	Identification and elimination of genomic regions irrelevant for magnetosome biosynthesis by large-scale deletion in <i>Magnetospirillum gryphiswaldense</i> . <i>BMC Microbiology</i> , 2021, 21, 65.	1.3	8
1572	Characterization of the genomic sequence data around common cutworm resistance genes in soybean (<i>Glycine max</i>) using short- and long-read sequencing methods. <i>Data in Brief</i> , 2021, 34, 106577.	0.5	2

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1574	Spread of Multidrug-Resistant <i>Rhodococcus equi</i> , United States. <i>Emerging Infectious Diseases</i> , 2021, 27, 529-537.	2.0	24
1575	Comparative genomics of <i>Chlamydomonas</i> . <i>Plant Cell</i> , 2021, 33, 1016-1041.	3.1	46
1576	The novel pathogenic <i>Citrobacter freundii</i> (CFC202) isolated from diseased crucian carp (<i>Carassius</i>) Tj ETQq1 1 0.784314 rgBT /Overlaid 533, 736190.	1.7	10
1577	<i>Pseudodesulfovibrio cashew</i> sp. Nov., a Novel Deep-Sea Sulfate-Reducing Bacterium, Linking Heavy Metal Resistance and Sulfur Cycle. <i>Microorganisms</i> , 2021, 9, 429.	1.6	9
1578	A Reference Genome Assembly of American Bison, <i>Bison bison bison</i> . <i>Journal of Heredity</i> , 2021, 112, 174-183.	1.0	14
1579	First complete genome characterization of swinepox virus directly from a clinical sample indicates divergence of a Eurasian-lineage virus. <i>Archives of Virology</i> , 2021, 166, 1217-1225.	0.9	2
1580	Characterization of JEN family carboxylate transporters from the acid-tolerant yeast <i>Pichia kudriavzevii</i> and their applications in succinic acid production. <i>Microbial Biotechnology</i> , 2021, 14, 1130-1147.	2.0	23
1581	A New <i>Micromonospora</i> Strain with Antibiotic Activity Isolated from the Microbiome of a Mid-Atlantic Deep-Sea Sponge. <i>Marine Drugs</i> , 2021, 19, 105.	2.2	25
1584	A long reads-based <i>de-novo</i> assembly of the genome of the Arlee homozygous line reveals chromosomal rearrangements in rainbow trout. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	40
1585	Evolution of genome structure in the <i>Drosophila simulans</i> species complex. <i>Genome Research</i> , 2021, 31, 380-396.	2.4	55
1586	Towards a 'chassis' for bacterial magnetosome biosynthesis: genome streamlining of <i>Magnetospirillum gryphiswaldense</i> by multiple deletions. <i>Microbial Cell Factories</i> , 2021, 20, 35.	1.9	16
1587	Haplotype-resolved <i>de novo</i> assembly using phased assembly graphs with hifiasm. <i>Nature Methods</i> , 2021, 18, 170-175.	9.0	1,675
1588	<i>Brassica carinata</i> genome characterization clarifies U TM s triangle model of evolution and polyploidy in <i>Brassica</i> . <i>Plant Physiology</i> , 2021, 186, 388-406.	2.3	75
1589	Chromosome-level assembly of the brown planthopper genome with a characterized Y chromosome. <i>Molecular Ecology Resources</i> , 2021, 21, 1287-1298.	2.2	26
1593	Chromosome-level genome assembly and structural variant analysis of two laboratory yeast strains from the Peterhof Genetic Collection lineage. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	7
1594	Serine-glycine betaine, a novel dipeptide from an endophyte <i>Macrophomina phaseolina</i> : isolation, bioactivity and biosynthesis. <i>Journal of Applied Microbiology</i> , 2021, 131, 756-767.	1.4	7
1595	Microbiome-based environmental monitoring of a dairy processing facility highlights the challenges associated with low microbial-load samples. <i>Npj Science of Food</i> , 2021, 5, 4.	2.5	18

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1597	Accurate haplotype-resolved assembly reveals the origin of structural variants for human trios. <i>Bioinformatics</i> , 2021, 37, 2095-2102.	1.8	4
1598	Pentadecaibins –V: 15-Residue Peptaibols Produced by a Marine-Derived <i>Trichoderma</i> sp. of the <i>Harzianum</i> Clade. <i>Journal of Natural Products</i> , 2021, 84, 1271-1282.	1.5	22
1599	A new <i>Cannabis</i> genome assembly associates elevated cannabidiol (CBD) with hemp introgressed into marijuana. <i>New Phytologist</i> , 2021, 230, 1665-1679.	3.5	87
1601	Degradation of 1,4-Dioxane by <i>Xanthobacter</i> sp. YN2. <i>Current Microbiology</i> , 2021, 78, 992-1005.	1.0	13
1603	Complete chloroplast genome sequence of <i>Populus euphratica</i> from PacBio Sequel platform. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 378-380.	0.2	0
1604	Benchmarking of next and third generation sequencing technologies and their associated algorithms for <i>deNovo</i> genome assembly. <i>Molecular Medicine Reports</i> , 2021, 23, .	1.1	18
1606	Complete Genome Sequence of <i>Sphingomonas paucimobilis</i> Strain Kira, Isolated from Human Neuroblastoma SH-SY5Y Cell Cultures Supplemented with Retinoic Acid. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	2
1608	Genomic insight into diet adaptation in the biological control agent <i>Cryptolaemus montrouzieri</i> . <i>BMC Genomics</i> , 2021, 22, 135.	1.2	7
1609	<i>Novakomyces olei</i> sp. nov., the First Member of a Novel Taphrinomycotina Lineage. <i>Microorganisms</i> , 2021, 9, 301.	1.6	3
1610	Genome sequencing and annotation and phylogenomic analysis of the medicinal mushroom <i>Amauroderma rugosum</i> , a traditional medicinal species in the family Ganodermataceae. <i>Mycologia</i> , 2021, 113, 268-277.	0.8	7
1611	The genomic structure of a human chromosome 22 nucleolar organizer region determined by TAR cloning. <i>Scientific Reports</i> , 2021, 11, 2997.	1.6	13
1612	<i>Pseudomonas paracarnis</i> sp. nov., isolated from refrigerated beef. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	8
1613	Chromosome-Level Genome Assembly of the American Cranberry (<i>Vaccinium macrocarpon</i> Ait.) and Its Wild Relative <i>Vaccinium microcarpum</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 633310.	1.7	29
1615	Comparative chloroplast genomes: insights into the evolution of the chloroplast genome of <i>Camellia sinensis</i> and the phylogeny of <i>Camellia</i> . <i>BMC Genomics</i> , 2021, 22, 138.	1.2	46
1619	Insights into triterpene synthesis and unsaturated fatty-acid accumulation provided by chromosomal-level genome analysis of <i>Akebia trifoliata</i> subsp. <i>australis</i> . <i>Horticulture Research</i> , 2021, 8, 33.	2.9	23
1620	A Circular Chloroplast Genome of <i>Fagus sylvatica</i> Reveals High Conservation between Two Individuals from Germany and One Individual from Poland and an Alternate Direction of the Small Single-Copy Region. <i>Forests</i> , 2021, 12, 180.	0.9	8
1621	Topologically associating domains and their role in the evolution of genome structure and function in <i>Drosophila</i> . <i>Genome Research</i> , 2021, 31, 397-410.	2.4	36

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1623	SARS-CoV-2 Genomes From Oklahoma, United States. <i>Frontiers in Genetics</i> , 2020, 11, 612571.	1.1	5
1624	AlignGraph2: similar genome-assisted reassembly pipeline for PacBio long reads. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	3
1625	Benchmarking of long-read assemblers for prokaryote whole genome sequencing. <i>F1000Research</i> , 2019, 8, 2138.	0.8	128
1626	Whole Genome Analysis of Sugarcane Root-Associated Endophyte <i>Pseudomonas aeruginosa</i> B18â€”A Plant Growth-Promoting Bacterium With Antagonistic Potential Against <i>Sporisorium scitamineum</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 628376.	1.5	53
1627	Complete Genome Sequence of <i>Rhodococcus</i> sp. Strain M8, a Platform Strain for Acrylic Monomer Production. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	2
1628	Genome editing reveals fitness effects of a gene for sexual dichromatism in Sulawesian fishes. <i>Nature Communications</i> , 2021, 12, 1350.	5.8	36
1629	Cell wall protein variation, breakâ€”induced replication, and subtelomere dynamics in <i>Candida glabrata</i> . <i>Molecular Microbiology</i> , 2021, 116, 260-276.	1.2	16
1631	The completed genome sequence of the pathogenic ascomycete fungus <i>Penicillium digitatum</i> . <i>Genomics</i> , 2021, 113, 439-446.	1.3	10
1632	Long-read sequencing and <i>de novo</i> genome assemblies reveal complex chromosome end structures caused by telomere dysfunction at the single nucleotide level. <i>Nucleic Acids Research</i> , 2021, 49, 3338-3353.	6.5	12
1633	Telomere-to-telomere assembly of the genome of an individual <i>Oikopleura dioica</i> from Okinawa using Nanopore-based sequencing. <i>BMC Genomics</i> , 2021, 22, 222.	1.2	18
1635	The complete mitochondrial genome of <i>Trematomus loennbergii</i> (Perciformes, Nototheniidae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1032-1033.	0.2	3
1636	Chromosome-level assembly of the mangrove plant <i>Aegiceras corniculatum</i> genome generated through Illumina, PacBio and Hiâ€”C sequencing technologies. <i>Molecular Ecology Resources</i> , 2021, 21, 1593-1607.	2.2	16
1637	Genome sequence and genetic diversity analysis of an under-domesticated orphan crop, white fonio (<i>Digitaria exilis</i>). <i>GigaScience</i> , 2021, 10, .	3.3	23
1638	SMARTdenovo: a de novo assembler using long noisy reads. <i>GigaByte</i> , 0, 2021, 1-9.	0.0	109
1639	Clade-specific chromosomal rearrangements and loss of subtelomeric adhesins in <i>Candida auris</i> . <i>Genetics</i> , 2021, 218, .	1.2	54
1640	Transcriptomic analysis reveals resistance mechanisms of <i>Klebsiella michiganensis</i> to copper toxicity under acidic conditions. <i>Ecotoxicology and Environmental Safety</i> , 2021, 211, 111919.	2.9	11
1641	Compact and evenly distributed <i>k</i> -mer binning for genomic sequences. <i>Bioinformatics</i> , 2021, 37, 2563-2569.	1.8	15

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1644	Genomic insights into the host specific adaptation of the Pneumocystis genus. Communications Biology, 2021, 4, 305.	2.0	23
1646	Genomic analysis of <i>Medicago ruthenica</i> provides insights into its tolerance to abiotic stress and demographic history. Molecular Ecology Resources, 2021, 21, 1641-1657.	2.2	17
1647	Most Genomic Loci Misrepresent the Phylogeny of an Avian Radiation Because of Ancient Gene Flow. Systematic Biology, 2021, 70, 961-975.	2.7	45
1648	SLR-superscaffolder: a de novo scaffolding tool for synthetic long reads using a top-to-bottom scheme. BMC Bioinformatics, 2021, 22, 158.	1.2	7
1649	Additional description and genome analyses of <i>Caenorhabditis auriculariae</i> representing the basal lineage of genus <i>Caenorhabditis</i> . Scientific Reports, 2021, 11, 6720.	1.6	10
1651	Comparative Genomics Reveals Prophylactic and Catabolic Capabilities of <i>Actinobacteria</i> within the Fungus-Farming Termite Symbiosis. MSphere, 2021, 6, .	1.3	17
1652	A new symbiotic lineage related to <i>Neisseria</i> and <i>Snodgrassella</i> arises from the dynamic and diverse microbiomes in sucking lice. Molecular Ecology, 2021, 30, 2178-2196.	2.0	16
1653	Ubiquitous Selfish Toxin-Antidote Elements in <i>Caenorhabditis</i> Species. Current Biology, 2021, 31, 990-1001.e5.	1.8	27
1655	The complete mitochondrial genome of <i>Aconitum kusnezoffii</i> Rchb. (Ranales, Ranunculaceae). Mitochondrial DNA Part B: Resources, 2021, 6, 779-781.	0.2	6
1656	Choice of library preparation affects sequence quality, genome assembly, and precise in silico prediction of virulence genes in shiga toxin-producing <i>Escherichia coli</i> . PLoS ONE, 2021, 16, e0242294.	1.1	8
1657	Deeply Altered Genome Architecture in the Endoparasitic Flowering Plant <i>Sapria himalayana</i> Griff. (Rafflesiaceae). Current Biology, 2021, 31, 1002-1011.e9.	1.8	63
1658	A chromosome-level genome assembly for the Pacific oyster <i>Crassostrea gigas</i> . GigaScience, 2021, 10, .	3.3	88
1659	Comprehensive Pathogen Identification, Antibiotic Resistance, and Virulence Genes Prediction Directly From Simulated Blood Samples and Positive Blood Cultures by Nanopore Metagenomic Sequencing. Frontiers in Genetics, 2021, 12, 620009.	1.1	16
1661	SCRaMBLE: A Study of Its Robustness and Challenges through Enhancement of Hygromycin B Resistance in a Semi-Synthetic Yeast. Bioengineering, 2021, 8, 42.	1.6	10
1663	A New Zebrafish Model for Pseudoxanthoma Elasticum. Frontiers in Cell and Developmental Biology, 2021, 9, 628699.	1.8	2
1665	Effective Identification and Annotation of Fungal Genomes. Journal of Computer Science and Technology, 2021, 36, 248-260.	0.9	0
1668	Complete Genome Sequence of a Type III Ovine Strain of <i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> . Microbiology Resource Announcements, 2021, 10, .	0.3	1

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1670	Chromosome-scale assembly of the genome of <i>Salix dunnii</i> reveals a male heterogametic sex determination system on chromosome 7. <i>Molecular Ecology Resources</i> , 2021, 21, 1966-1982.	2.2	28
1671	Chromosome-length genome assembly and structural variations of the primal Basenji dog (<i>Canis lupus</i>) Tj ETQq0 0,0 rgBT /Overlock 10	1.2	22
1672	Complete Genome and Plasmid Sequences of Three <i>Fluviibacter phosphoraccumulans</i> Polyphosphate-Accumulating Bacterioplankton Strains Isolated from Surface River Water. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	1
1674	Robust Benchmark Structural Variant Calls of An Asian Using State-of-the-art Long-read Sequencing Technologies. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 192-204.	3.0	6
1675	Comparative in silico genome analysis of <i>Clostridium perfringens</i> unravels stable phylogroups with different genome characteristics and pathogenic potential. <i>Scientific Reports</i> , 2021, 11, 6756.	1.6	16
1676	A route to de novo domestication of wild allotetraploid rice. <i>Cell</i> , 2021, 184, 1156-1170.e14.	13.5	259
1677	Long-read assembly of a Great Dane genome highlights the contribution of GC-rich sequence and mobile elements to canine genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	25
1678	A chromosome level genome assembly of <i>Propiloscerus akamusi</i> to understand its response to heavy metal exposure. <i>Molecular Ecology Resources</i> , 2021, 21, 1996-2012.	2.2	11
1680	Gene disruption by structural mutations drives selection in US rice breeding over the last century. <i>PLoS Genetics</i> , 2021, 17, e1009389.	1.5	6
1682	Engineered yeast genomes accurately assembled from pure and mixed samples. <i>Nature Communications</i> , 2021, 12, 1485.	5.8	11
1683	Assembly and comparative analysis of the complete mitochondrial genome of <i>Suaeda glauca</i> . <i>BMC Genomics</i> , 2021, 22, 167.	1.2	67
1684	Complete Genome Sequence of <i>Mycobacterium heckeshornense</i> JCM 15655 T, Closely Related to a Pathogenic Nontuberculous Mycobacterial Species, <i>Mycobacterium xenopi</i> . <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	0
1686	Comparison of different sequencing strategies for assembling chromosome-level genomes of extremophiles with variable GC content. <i>IScience</i> , 2021, 24, 102219.	1.9	3
1687	Signs of biofilm formation in the genome of <i>Labrenzia</i> sp. PO1. <i>Saudi Journal of Biological Sciences</i> , 2021, 28, 1900-1912.	1.8	9
1688	Aerobic Denitrification and Heterotrophic Sulfur Oxidation in the Genus <i>Halomonas</i> Revealed by Six Novel Species Characterizations and Genome-Based Analysis. <i>Frontiers in Microbiology</i> , 2021, 12, 652766.	1.5	19
1689	Two-component spike nanoparticle vaccine protects macaques from SARS-CoV-2 infection. <i>Cell</i> , 2021, 184, 1188-1200.e19.	13.5	154
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1693	Genome Sequence and Characterization of <i>Acinetobacter</i> Phage DMU1. Phage, 2021, 2, 50-56.	0.8	2
1694	Complete Whole Genome Sequences of Escherichia coli Surrogate Strains and Comparison of Sequence Methods with Application to the Food Industry. Microorganisms, 2021, 9, 608.	1.6	3
1695	Characterization of novel zebrafish MHC class I U lineage genes and their haplotype. Developmental and Comparative Immunology, 2021, 116, 103952.	1.0	2
1696	Recovery of complete genomes and non-chromosomal replicons from activated sludge enrichment microbial communities with long read metagenome sequencing. Npj Biofilms and Microbiomes, 2021, 7, 23.	2.9	29
1697	Chromosome-level genome assemblies of the malaria vectors <i>Anopheles coluzzii</i> and <i>Anopheles arabiensis</i> . GigaScience, 2021, 10, .	3.3	12
1698	Complete Genome Analysis of Campylobacter jejuni subsp. <i>jejuni</i> Isolated from Bloodstream Infection. Microbiology Resource Announcements, 2021, 10, .	0.3	0
1700	GenomicsBench: A Benchmark Suite for Genomics. , 2021, , .		6
1701	Reconstruction of the Origin of a Neo-Y Sex Chromosome and Its Evolution in the Spotted Knifejaw, <i>Oplegnathus punctatus</i> . Molecular Biology and Evolution, 2021, 38, 2615-2626.	3.5	21
1702	Genome Assembly of Salicaceae <i>Populus deltoides</i> (Eastern Cottonwood) <i>l-69</i> Based on Nanopore Sequencing and Hi-C Technologies. Journal of Heredity, 2021, 112, 303-310.	1.0	13
1703	Chromosome-scale genome assembly of <i>Cucumis hystrix</i> a wild species interspecifically cross-compatible with cultivated cucumber. Horticulture Research, 2021, 8, 40.	2.9	18
1704	Metagenomic Data Assembly – The Way of Decoding Unknown Microorganisms. Frontiers in Microbiology, 2021, 12, 613791.	1.5	67
1705	A Vernalization Response in a Winter Safflower (<i>Carthamus tinctorius</i>) Involves the Upregulation of Homologs of FT, FUL, and MAF. Frontiers in Plant Science, 2021, 12, 639014.	1.7	5
1708	Nutrient-driven genome evolution revealed by comparative genomics of chryomonad flagellates. Communications Biology, 2021, 4, 328.	2.0	7
1709	DIAMOND+MEGAN: Fast and Easy Taxonomic and Functional Analysis of Short and Long Microbiome Sequences. Current Protocols, 2021, 1, e59.	1.3	55
1710	Methylation analysis of Klebsiella pneumoniae from Portuguese hospitals. Scientific Reports, 2021, 11, 6491.	1.6	10
1711	Hybrid genome de novo assembly with methylome analysis of the anaerobic thermophilic subsurface bacterium Thermanaerosceptum fracticalcis strain DRI-13T. BMC Genomics, 2021, 22, 209.	1.2	3
1713	Draft genome sequence resource for the orange rust pathogen of sugarcane Puccinia kuehnii. Phytopathology, 2021, , PHYTO01210008A.	1.1	1

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1715	Homopolish: a method for the removal of systematic errors in nanopore sequencing by homologous polishing. <i>Genome Biology</i> , 2021, 22, 95.	3.8	79
1716	The genome of <i>Magnolia biondii</i> Pamp. provides insights into the evolution of Magnoliales and biosynthesis of terpenoids. <i>Horticulture Research</i> , 2021, 8, 38.	2.9	32
1717	The complete mitochondrial and plastid genomes of <i>Rhododendron simsii</i> , an important parent of widely cultivated azaleas. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1197-1199.	0.2	6
1718	Different kinetoplast degradation patterns in American <i>Trypanosoma vivax</i> strains: Multiple independent origins or fast evolution?. <i>Genomics</i> , 2021, 113, 843-853.	1.3	5
1719	Connecting structure to function with the recovery of over 1000 high-quality metagenome-assembled genomes from activated sludge using long-read sequencing. <i>Nature Communications</i> , 2021, 12, 2009.	5.8	177
1723	Reevaluation of the <i>Toxoplasma gondii</i> and <i>Neospora caninum</i> genomes reveals misassembly, karyotype differences, and chromosomal rearrangements. <i>Genome Research</i> , 2021, 31, 823-833.	2.4	18
1724	Complete Genome Sequence of an Antimicrobial-Producing <i>Bacillus velezensis</i> Sam8H1 Isolate from the Makgadikgadi Salt pans of Botswana. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	0
1725	Comparison of long-read sequencing technologies in interrogating bacteria and fly genomes. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	26
1726	Insights into salvianolic acid B biosynthesis from chromosome-scale assembly of the <i>Salvia bowleyana</i> genome. <i>Journal of Integrative Plant Biology</i> , 2021, 63, 1309-1323.	4.1	18
1727	Structure and biosynthesis of sorangipyranone – a new β -dihydropyrone from the myxobacterial strain MSr12020. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2021, 48, .	1.4	5
1728	A Chromosome-Level Genome Assembly of the Spotted Scat (<i>Scatophagus argus</i>). <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	17
1730	Accessory Genome Dynamics and Structural Variation of <i>Shigella</i> from Persistent Infections. <i>MBio</i> , 2021, 12, .	1.8	7
1731	The chromosome-scale reference genome of safflower (<i>Carthamus tinctorius</i>) provides insights into linoleic acid and flavonoid biosynthesis. <i>Plant Biotechnology Journal</i> , 2021, 19, 1725-1742.	4.1	60
1732	Nanopore Sequencing Is a Credible Alternative to Recover Complete Genomes of Geminiviruses. <i>Microorganisms</i> , 2021, 9, 903.	1.6	18
1733	<i>Serratia rhizosphaerae</i> sp. nov., a novel plant resistance inducer against soft rot disease in tobacco. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	7
1734	Improved de novo chromosome-level genome assembly of the vulnerable walnut tree <i>Juglans mandshurica</i> reveals gene family evolution and possible genome basis of resistance to lesion nematode. <i>Molecular Ecology Resources</i> , 2021, 21, 2063-2076.	2.2	20
1735	Comparative genome analyses of four rice-infecting <i>Rhizoctonia solani</i> isolates reveal extensive enrichment of homogalacturonan modification genes. <i>BMC Genomics</i> , 2021, 22, 242.	1.2	18

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1736	Complete Genome Sequence of <i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> Strain 42-13-1, Isolated in Japan. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	1
1737	Full-Genome Sequence of <i>Bacillus safensis</i> Strain IDN1, Isolated from Commercially Available Natto in Indonesia. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	0
1739	Characterization of Two Unique Cold-Active Lipases Derived from a Novel Deep-Sea Cold Seep Bacterium. <i>Microorganisms</i> , 2021, 9, 802.	1.6	7
1742	<i>Polyrhizophydium stewartii</i> , the first known rhizomycelial genus and species in the Rhizophydiales, is closely related to <i>Batrachochytrium</i> . <i>Mycologia</i> , 2021, 113, 684-690.	0.8	5
1743	The genomic basis of geographic differentiation and fiber improvement in cultivated cotton. <i>Nature Genetics</i> , 2021, 53, 916-924.	9.4	75
1744	Sequencing, assembly and annotation of the whole-insect genome of <i>Lymantria dispar dispar</i> , the European gypsy moth. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	5
1745	Third-generation sequencing revises the molecular karyotype for <i>Toxoplasma gondii</i> and identifies emerging copy number variants in sexual recombinants. <i>Genome Research</i> , 2021, 31, 834-851.	2.4	19
1746	Discovering multiple types of DNA methylation from bacteria and microbiome using nanopore sequencing. <i>Nature Methods</i> , 2021, 18, 491-498.	9.0	83
1747	Raw pacific biosciences and illumina sequencing reads and assembled genome data for the cattle ticks <i>Rhipicephalus microplus</i> and <i>Rhipicephalus annulatus</i> . <i>Data in Brief</i> , 2021, 35, 106852.	0.5	6
1749	Genome of the destructive oomycete <i>Phytophthora cinnamomi</i> provides insights into its pathogenicity and adaptive potential. <i>BMC Genomics</i> , 2021, 22, 302.	1.2	24
1751	Genome sequencing and comparative genomic analysis of highly and weakly aggressive strains of <i>Sclerotium rolfsii</i> , the causal agent of peanut stem rot. <i>BMC Genomics</i> , 2021, 22, 276.	1.2	20
1752	Complete Genome Sequence of a Novel Bacteriophage RpY1 Infecting <i>Ralstonia solanacearum</i> Strains. <i>Current Microbiology</i> , 2021, 78, 2044-2050.	1.0	9
1756	A novel fragmented mitochondrial genome in the protist pathogen <i>Toxoplasma gondii</i> and related tissue coccidia. <i>Genome Research</i> , 2021, 31, 852-865.	2.4	17
1757	Comparative Genomics Supports That Brazilian Bioethanol <i>Saccharomyces cerevisiae</i> Comprise a Unified Group of Domesticated Strains Related to Cachaça Spirit Yeasts. <i>Frontiers in Microbiology</i> , 2021, 12, 644089.	1.5	16
1758	Chromosome-level genome reference and genome editing of the tea geometrid. <i>Molecular Ecology Resources</i> , 2021, 21, 2034-2049.	2.2	8
1760	Insights into genomic evolution from the chromosomal and mitochondrial genomes of <i>Ustilaginoidea virens</i> . <i>Phytopathology Research</i> , 2021, 3, .	0.9	9
1761	Microbial community characterization of shrimp survivors to AHPND challenge test treated with an effective shrimp probiotic (<i>Vibrio diabolicus</i>). <i>Microbiome</i> , 2021, 9, 88.	4.9	36
1762	The <i>Gossypium stocksii</i> genome as a novel resource for cotton improvement. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	8

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1764	Genome Sequence of Sulfide-Dependent Denitrification Bacterium <i>Thermomonas</i> sp. Strain XSG, Isolated from Marine Sediment. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	4
1765	Construction of a chromosome-level genome and variation map for the Pacific oyster <i>Crassostrea gigas</i> . <i>Molecular Ecology Resources</i> , 2021, 21, 1670-1685.	2.2	45
1766	The reference genome and transcriptome of the limestone langur, <i>Trachypithecus leucocephalus</i> , reveal expansion of genes related to alkali tolerance. <i>BMC Biology</i> , 2021, 19, 67.	1.7	3
1767	Deciphering the <i>Monilinia fructicola</i> Genome to Discover Effector Genes Possibly Involved in Virulence. <i>Genes</i> , 2021, 12, 568.	1.0	23
1768	Benchmarking Oxford Nanopore read assemblers for high-quality molluscan genomes. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2021, 376, 20200160.	1.8	22
1769	Differential expression pattern of pathogenicity-related genes of <i>Ralstonia pseudosolanacearum</i> YQ responding to tissue debris of <i>Casuarina equisetifolia</i> . <i>Phytopathology</i> , 2021, , PHYTO11200490R.	1.1	0
1772	Genome Sequence Resource for the Plant Pathogen <i>Sclerotinia sclerotiorum</i> WH6 Isolated in China. <i>Plant Disease</i> , 2021, 105, 3720-3722.	0.7	4
1773	Complete Chromosome-Scale Genome Sequence Resource for <i>Sporisorium panici-leucophaei</i> , the Causal Agent of Sorghum Smut Disease. <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 448-452.	1.4	3
1774	Engineered sex ratio distortion by X-shredding in the global agricultural pest <i>Ceratitis capitata</i> . <i>BMC Biology</i> , 2021, 19, 78.	1.7	29
1775	Complete Genome Sequence of <i>Shewanella</i> sp. Strain Lzh-2, an Algicidal Bacterial Strain Isolated from Lake Taihu, People's Republic of China. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	2
1776	Occurrence and Transmission of bla _{NDM} -Carrying <i>Enterobacteriaceae</i> from Geese and the Surrounding Environment on a Commercial Goose Farm. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	13
1777	The contributions from the progenitor genomes of the mesopolyploid Brassicaceae are evolutionarily distinct but functionally compatible. <i>Genome Research</i> , 2021, 31, 799-810.	2.4	21
1778	Computational methods for chromosome-scale haplotype reconstruction. <i>Genome Biology</i> , 2021, 22, 101.	3.8	49
1779	A plasmid locus associated with <i>Klebsiella</i> clinical infections encodes a microbiome-dependent gut fitness factor. <i>PLoS Pathogens</i> , 2021, 17, e1009537.	2.1	20
1781	<i>Vibrio nitrifigilis</i> sp. nov., a marine nitrogen-fixing bacterium isolated from the lagoon sediment of an islet inside an atoll. <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 933-945.	0.7	12
1782	Nanopore sequencing reveals TACC2 locus complexity and diversity of isoforms transcribed from an intronic promoter. <i>Scientific Reports</i> , 2021, 11, 9355.	1.6	2
1783	The <i>Pectobacterium</i> pangenome, with a focus on <i>Pectobacterium brasiliense</i> , shows a robust core and extensive exchange of genes from a shared gene pool. <i>BMC Genomics</i> , 2021, 22, 265.	1.2	27

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1785	Complete vertebrate mitogenomes reveal widespread repeats and gene duplications. <i>Genome Biology</i> , 2021, 22, 120.	3.8	69
1786	Chromosome-scale assembly and analysis of biomass crop <i>Miscanthus lutarioriparius</i> genome. <i>Nature Communications</i> , 2021, 12, 2458.	5.8	25
1787	Biocontrol of Soft Rot Caused by <i>Pectobacterium odoriferum</i> with Bacteriophage phiPccP-1 in Kimchi Cabbage. <i>Microorganisms</i> , 2021, 9, 779.	1.6	14
1788	<i>Dissulfurispira thermophila</i> gen. nov., sp. nov., a thermophilic chemolithoautotroph growing by sulfur disproportionation, and proposal of novel taxa in the phylum Nitrospirota to reclassify the genus <i>Thermodesulfobivrio</i> . <i>Systematic and Applied Microbiology</i> , 2021, 44, 126184.	1.2	48
1789	Sequencing of SARS-CoV-2 genome using different nanopore chemistries. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 3225-3234.	1.7	21
1790	Genetic features of the <i>poxtA</i> linezolid resistance gene in human enterococci from France. <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 1978-1985.	1.3	14
1792	High-Level Aminoglycoside Resistance in Human Clinical <i>Klebsiella pneumoniae</i> Complex Isolates and Characteristics of <i>armA</i> -Carrying <i>InchI5</i> Plasmids. <i>Frontiers in Microbiology</i> , 2021, 12, 636396.	1.5	8
1793	Identification of polycistronic transcriptional units and non-canonical introns in green algal chloroplasts based on long-read RNA sequencing data. <i>BMC Genomics</i> , 2021, 22, 298.	1.2	2
1796	Genome and transcriptome of a pathogenic yeast, <i>Candida nivariensis</i> . <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	1
1797	A Primer on the Analysis of High-Throughput Sequencing Data for Detection of Plant Viruses. <i>Microorganisms</i> , 2021, 9, 841.	1.6	36
1799	Insight into the denitrification mechanism of <i>Bacillus subtilis</i> JD-014 and its application potential in bioremediation of nitrogen wastewater. <i>Process Biochemistry</i> , 2021, 103, 78-86.	1.8	23
1800	Rapid evolution and host immunity drive the rise and fall of carbapenem resistance during an acute <i>Pseudomonas aeruginosa</i> infection. <i>Nature Communications</i> , 2021, 12, 2460.	5.8	47
1801	Balancing selection maintains hyper-divergent haplotypes in <i>Caenorhabditis elegans</i> . <i>Nature Ecology and Evolution</i> , 2021, 5, 794-807.	3.4	89
1802	Draft Genome Sequence of <i>Xylaria grammica</i> EL000614, a Strain Producing Grammicin, a Potent Nematicidal Compound. <i>Mycobiology</i> , 2021, 49, 1-3.	0.6	0
1806	Complete Genome Sequences of Four Canadian <i>Mycoplasma bovis</i> Strains Isolated from Bison and Cattle. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	4
1807	A chromosome-level reference genome of the hazelnut, <i>Corylus heterophylla</i> Fisch. <i>GigaScience</i> , 2021, 10, .	3.3	13
1808	Complete Genome Sequence of <i>Geobacter</i> sp. Strain SVR, an Antimonate-Reducing Bacterium Isolated from Antimony-Rich Mine Soil. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	1

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1810	Long-read genome sequencing for the molecular diagnosis of neurodevelopmental disorders. <i>Human Genetics and Genomics Advances</i> , 2021, 2, 100023.	1.0	20
1811	De novo assembly of a new <i>Olea europaea</i> genome accession using nanopore sequencing. <i>Horticulture Research</i> , 2021, 8, 64.	2.9	41
1812	Towards complete and error-free genome assemblies of all vertebrate species. <i>Nature</i> , 2021, 592, 737-746.	13.7	1,139
1813	Big Data in Conservation Genomics: Boosting Skills, Hedging Bets, and Staying Current in the Field. <i>Journal of Heredity</i> , 2021, 112, 313-327.	1.0	10
1814	Chromosome-level genome assembly of the hard-shelled mussel <i>Mytilus coruscus</i> , a widely distributed species from the temperate areas of East Asia. <i>GigaScience</i> , 2021, 10, .	3.3	45
1815	Mobile Type VI secretion system loci of the gut Bacteroidales display extensive intra-ecosystem transfer, multi-species spread and geographical clustering. <i>PLoS Genetics</i> , 2021, 17, e1009541.	1.5	32
1816	Identification and Characterization of a Novel SXT/R391 Integrative and Conjugative Element in a <i>Proteus mirabilis</i> Food Isolate. <i>Foodborne Pathogens and Disease</i> , 2021, 18, 727-732.	0.8	4
1818	Stable Recombinant-Gene Expression from a <i>Ligilactobacillus</i> Live Bacterial Vector via Chromosomal Integration. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	4
1819	Nanopore/Illumina hybrid genome sequence resource for <i>Corynespora cassicola</i> strain XJ infecting rubber tree in China. <i>Plant Disease</i> , 2021, , PDIS03210458A.	0.7	1
1820	A high-quality carabid genome assembly provides insights into beetle genome evolution and cold adaptation. <i>Molecular Ecology Resources</i> , 2021, 21, 2145-2165.	2.2	13
1821	Comparative genome sequencing reveals insights into the dynamics of <i>Wolbachia</i> in native and invasive cherry fruit flies. <i>Molecular Ecology</i> , 2021, 30, 6259-6272.	2.0	17
1822	Chromosomal-Level Reference Genome of the Neotropical Tree <i>Jacaranda mimosifolia</i> D. Don. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	7
1823	Complete Genome Sequence of <i>Longicatena caecimuris</i> Strain 3BBH23, Isolated from Healthy Japanese Feces. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	1
1824	High-quality chromosome-level genomes of <i>Cucumis metuliferus</i> and <i>Cucumis melo</i> provide insight into <i>Cucumis</i> genome evolution. <i>Plant Journal</i> , 2021, 107, 136-148.	2.8	20
1825	Dog10K_Boxer_Tasha_1.0: A Long-Read Assembly of the Dog Reference Genome. <i>Genes</i> , 2021, 12, 847.	1.0	19
1826	Characterization of gross genome rearrangements in <i>Deinococcus radiodurans</i> recA mutants. <i>Scientific Reports</i> , 2021, 11, 10939.	1.6	1
1827	Extensive variation within the pan-genome of cultivated and wild sorghum. <i>Nature Plants</i> , 2021, 7, 766-773.	4.7	94

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1828	The identification of a transposon affecting the asexual reproduction of the wheat pathogen <i>Zymoseptoria tritici</i> . <i>Molecular Plant Pathology</i> , 2021, 22, 800-816.	2.0	17
1829	Time- and memory-efficient genome assembly with Raven. <i>Nature Computational Science</i> , 2021, 1, 332-336.	3.8	173
1830	Comparative Genome Analyses Highlight Transposon-Mediated Genome Expansion and the Evolutionary Architecture of 3D Genomic Folding in Cotton. <i>Molecular Biology and Evolution</i> , 2021, 38, 3621-3636.	3.5	41
1831	Genome of the butterfly hillstream loach provides insights into adaptations to torrential mountain stream life. <i>Molecular Ecology Resources</i> , 2021, 21, 1922-1935.	2.2	1
1832	Complete Multipartite Genome Sequence of the <i>Cupriavidus basilensis</i> Type Strain, a 2,6-Dichlorophenol-Degrading Bacterium. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	5
1833	Complete Genome Sequences of <i>Pseudomonas atacamensis</i> Strain SM1 and <i>Pseudomonas toyotomiensis</i> Strain SM2, Isolated from the Date Palm Rhizosphere. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	4
1834	Multiplex PCR-Based Nanopore Sequencing and Epidemiological Surveillance of Hantaan orthohantavirus in <i>Apodemus agrarius</i> , Republic of Korea. <i>Viruses</i> , 2021, 13, 847.	1.5	8
1835	PthAW1, a transcription activator-like effector of <i>Xanthomonas citri</i> subsp. <i>citri</i> , promotes host specific immune responses. <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 1033-1047.	1.4	4
1836	Genomic Resources for <i>Pseudomonas savastanoi</i> pv. <i>phaseolicola</i> Races 5 and 8. <i>Phytopathology</i> , 2021, 111, 893-895.	1.1	3
1837	Re-examination of two diatom reference genomes using long-read sequencing. <i>BMC Genomics</i> , 2021, 22, 379.	1.2	22
1838	Evaluating the accuracy of <i>Listeria monocytogenes</i> assemblies from quasimetagenomic samples using long and short reads. <i>BMC Genomics</i> , 2021, 22, 389.	1.2	9
1841	Introgressing the <i>Aegilops tauschii</i> genome into wheat as a basis for cereal improvement. <i>Nature Plants</i> , 2021, 7, 774-786.	4.7	65
1842	<i>Pseudomonas lalucatii</i> sp. nov. isolated from Vallgornera, a karstic cave in Mallorca, Western Mediterranean. <i>Systematic and Applied Microbiology</i> , 2021, 44, 126205.	1.2	13
1844	Physiological and Genomic Analysis of <i>Bacillus pumilus</i> UAMX Isolated from the Gastrointestinal Tract of Overweight Individuals. <i>Microorganisms</i> , 2021, 9, 1076.	1.6	2
1846	The Assembled and Annotated Genome of the Fairy-Ring Fungus <i>Marasmius oreades</i> . <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	13
1848	Genome analysis of <i>Spiroplasma citri</i> strains from different host plants and its leafhopper vectors. <i>BMC Genomics</i> , 2021, 22, 373.	1.2	8
1849	Genomic features of humoral immunity support tolerance model in Egyptian rousette bats. <i>Cell Reports</i> , 2021, 35, 109140.	2.9	19
1850	Complete Genome Sequence of <i>Tsuneonella flava</i> SS-21NJ, a Potential Oil Sludge Bioremediation Agent. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	1

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1851	Adaptive laboratory evolution accelerated glutarate production by <i>Corynebacterium glutamicum</i> . <i>Microbial Cell Factories</i> , 2021, 20, 97.	1.9	19
1852	Subtelomeric assembly of a multi-gene pathway for antimicrobial defense compounds in cereals. <i>Nature Communications</i> , 2021, 12, 2563.	5.8	51
1853	Characterising Foot-and-Mouth Disease Virus in Clinical Samples Using Nanopore Sequencing. <i>Frontiers in Veterinary Science</i> , 2021, 8, 656256.	0.9	6
1854	The genome of <i>Nautilus pompilius</i> illuminates eye evolution and biomineralization. <i>Nature Ecology and Evolution</i> , 2021, 5, 927-938.	3.4	40
1855	Complete Genome Sequence of <i>Buttiauxella agrestis</i> DSM 9389. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	1
1856	Complete Genome Sequence of <i>Bacillus coagulans</i> BC01, a Promising Human Probiotic Strain Isolated from Thick Broad Bean Sauce. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	5
1857	The Whole Genome Sequence of <i>Fusarium redolens</i> strain YP04, a Pathogen that Causes Root Rot of American Ginseng. <i>Phytopathology</i> , 2021, , PHYTO03210084A.	1.1	2
1858	Novel chromosomal insertions of ISEcp1-blaCTX-M-15 and diverse antimicrobial resistance genes in Zambian clinical isolates of <i>Enterobacter cloacae</i> and <i>Escherichia coli</i> . <i>Antimicrobial Resistance and Infection Control</i> , 2021, 10, 79.	1.5	24
1859	Macrosynteny analysis between <i>Lentinula edodes</i> and <i>Lentinula novae-zelandiae</i> reveals signals of domestication in <i>Lentinula edodes</i> . <i>Scientific Reports</i> , 2021, 11, 9845.	1.6	3
1862	Genomics-Enabled Novel Insight Into the Pathovar-Specific Population Structure of the Bacterial Leaf Streak Pathogen <i>Xanthomonas translucens</i> in Small Grain Cereals. <i>Frontiers in Microbiology</i> , 2021, 12, 674952.	1.5	31
1863	Long-read metagenomics retrieves complete single-contig bacterial genomes from canine feces. <i>BMC Genomics</i> , 2021, 22, 330.	1.2	41
1864	Antifungal mechanism of <i>Bacillus amyloliquefaciens</i> strain GKT04 against <i>Fusarium</i> wilt revealed using genomic and transcriptomic analyses. <i>MicrobiologyOpen</i> , 2021, 10, e1192.	1.2	13
1865	Characterization of the Complete Mitochondrial Genome of Basidiomycete Yeast <i>Hannaella oryzae</i> : Intron Evolution, Gene Rearrangement, and Its Phylogeny. <i>Frontiers in Microbiology</i> , 2021, 12, 646567.	1.5	25
1866	A Comparison of Three Circular Mitochondrial Genomes of <i>Fagus sylvatica</i> from Germany and Poland Reveals Low Variation and Complete Identity of the Gene Space. <i>Forests</i> , 2021, 12, 571.	0.9	4
1867	A Chromosome-Level Genome Assembly of the Parasitoid Wasp, <i>Cotesia glomerata</i> (Hymenoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.0	11
1868	Molecular characterization of two novel NDM-1-producing atypical enteroaggregative <i>Escherichia coli</i> isolates from patients. <i>Plasmid</i> , 2021, 115, 102568.	0.4	2
1869	Complete Genome Sequence of <i>Adlercreutzia equolifaciens</i> subsp. <i>celatus</i> DSM 18785. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	5
1870	Complete Genome Sequences of <i>Francisella marina</i> Strains E95-16 and E103-15, Isolated from Maricultured Spotted Rose Snapper (<i>Lutjanus guttatus</i>) on the Pacific Coast of Central America. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	0

#	ARTICLE	IF	CITATIONS
1871	Complete Genome Sequence of <i>Bacillus</i> sp. Strain V3, Isolated from Mangrove Sediments in Wenzhou, China. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	0
1872	Complete Genome Sequence of <i>Pseudomonas taiwanensis</i> WRS8, a Plant Growth-Promoting and Biotite-Weathering Strain. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	0
1873	Chromosome-level genome assembly and manually-curated proteome of model necrotroph <i>Parastagonospora nodorum</i> Sn15 reveals a genome-wide trove of candidate effector homologs, and redundancy of virulence-related functions within an accessory chromosome. <i>BMC Genomics</i> , 2021, 22, 382.	1.2	12
1875	Genetic variation, environment and demography intersect to shape <i>Arabidopsis</i> defense metabolite variation across Europe. <i>ELife</i> , 2021, 10, .	2.8	33
1876	ARAMIS: From systematic errors of NGS long reads to accurate assemblies. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	9
1877	Parallel String Graph Construction and Transitive Reduction for De Novo Genome Assembly. , 2021, , .		5
1879	Evolution of virulence in a novel family of transmissible megaplasmids. <i>Environmental Microbiology</i> , 2021, 23, 5289-5304.	1.8	5
1881	Polyploidy underlies co-option and diversification of biosynthetic triterpene pathways in the apple tribe. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	37
1884	NeuralPolish: a novel Nanopore polishing method based on alignment matrix construction and orthogonal Bi-GRU Networks. <i>Bioinformatics</i> , 2021, 37, 3120-3127.	1.8	13
1885	Metaviromes Reveal the Dynamics of <i>Pseudomonas</i> Host-Specific Phages Cultured and Uncultured by Plaque Assay. <i>Viruses</i> , 2021, 13, 959.	1.5	7
1886	The Genomic Signature of Allopatric Speciation in a Songbird Is Shaped by Genome Architecture (Aves: <i>Turdus philomelos</i>). <i>Genome Biology and Evolution</i> , 2021, 13, 1000.	1.1	10
1887	<i>Bacillus velezensis</i> WLYS23 strain possesses antagonistic activity against hybrid snakehead bacterial pathogens. <i>Journal of Applied Microbiology</i> , 2021, 131, 3056-3068.	1.4	19
1888	First draft genome assembly of the desert locust, <i>Schistocerca gregaria</i> . <i>F1000Research</i> , 2020, 9, 775.	0.8	24
1889	Automated improvement of stickleback reference genome assemblies with <i>LepAnch</i> software. <i>Molecular Ecology Resources</i> , 2021, 21, 2166-2176.	2.2	21
1890	Genome Sequences of Equine Herpesvirus 1 Strains from a European Outbreak of Neurological Disorders Linked to a Horse Gathering in Valencia, Spain, in 2021. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	14
1892	<i>Peteryoungia</i> gen. nov. with four new species combinations and description of <i>Peteryoungia desertarenae</i> sp. nov., and taxonomic revision of the genus <i>Ciceribacter</i> based on phylogenomics of Rhizobiaceae. <i>Archives of Microbiology</i> , 2021, 203, 3591-3604.	1.0	51
1893	The domestication of <i>Cucurbita argyrosperma</i> as revealed by the genome of its wild relative. <i>Horticulture Research</i> , 2021, 8, 109.	2.9	21
1894	Cas9-targeted nanopore sequencing reveals epigenetic heterogeneity after de novo assembly of native full-length hepatitis B virus genomes. <i>Microbial Genomics</i> , 2021, 7, .	1.0	7

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1895	Whole genome sequencing of a snailfish from the Yap Trench (~7,000 m) clarifies the molecular mechanisms underlying adaptation to the deep sea. <i>PLoS Genetics</i> , 2021, 17, e1009530.	1.5	26
1896	Comparative genome analysis reveals the presence of multiple quorum-sensing systems in plant pathogenic bacterium, <i>Erwinia rhapontici</i> . <i>Bioscience, Biotechnology and Biochemistry</i> , 2021, 85, 1910-1914.	0.6	2
1897	WeFaceNano: a user-friendly pipeline for complete ONT sequence assembly and detection of antibiotic resistance in multi-plasmid bacterial isolates. <i>BMC Microbiology</i> , 2021, 21, 171.	1.3	1
1898	Morphological stasis masks ecologically divergent coral species on tropical reefs. <i>Current Biology</i> , 2021, 31, 2286-2298.e8.	1.8	39
1899	Integrated genomic, epidemiologic investigation of <i>Candida auris</i> skin colonization in a skilled nursing facility. <i>Nature Medicine</i> , 2021, 27, 1401-1409.	15.2	73
1900	Genomic signatures of adaptation to natural settings in non-typhoidal <i>Salmonella enterica</i> Serovars Saintpaul, Thompson and Weltevreden. <i>Infection, Genetics and Evolution</i> , 2021, 90, 104771.	1.0	5
1902	Genomic Analysis of <i>Delftia tsuruhatensis</i> Strain TR1180 Isolated From A Patient From China With In4-Like Integron-Associated Antimicrobial Resistance. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 663933.	1.8	12
1903	Annotated Genome Sequence of the High-Biomass-Producing Yellow-Green Alga <i>Tribonema minus</i> . <i>Microbiology Resource Announcements</i> , 2021, 10, e0032721.	0.3	4
1904	Population-scale peach genome analyses unravel selection patterns and biochemical basis underlying fruit flavor. <i>Nature Communications</i> , 2021, 12, 3604.	5.8	31
1907	Identification of floR Variants Associated With a Novel Tn4371-Like Integrative and Conjugative Element in Clinical <i>Pseudomonas aeruginosa</i> Isolates. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 685068.	1.8	5
1908	Evolution of VIM-1-Producing <i>Klebsiella pneumoniae</i> Isolates from a Hospital Outbreak Reveals the Genetic Bases of the Loss of the Urease-Positive Identification Character. <i>MSystems</i> , 2021, 6, e0024421.	1.7	5
1909	Insights into the ancestry evolution of the <i>Mycobacterium tuberculosis</i> complex from analysis of <i>Mycobacterium riyadhense</i> . <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab070.	1.5	3
1910	Nanopore and Illumina Genome Sequencing of <i>Fusarium oxysporum</i> f. sp. lini Strains of Different Virulence. <i>Frontiers in Genetics</i> , 2021, 12, 662928.	1.1	8
1911	Pan-genome analysis of 33 genetically diverse rice accessions reveals hidden genomic variations. <i>Cell</i> , 2021, 184, 3542-3558.e16.	13.5	237
1912	<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
1913	Genomic Analysis of the Mycoparasite <i>Pestalotiopsis</i> sp. PG52. <i>Polish Journal of Microbiology</i> , 2021, 70, 189-199.	0.6	5
1914	Cotton D genome assemblies built with long-read data unveil mechanisms of centromere evolution and stress tolerance divergence. <i>BMC Biology</i> , 2021, 19, 115.	1.7	14
1915	Wolfberry genomes and the evolution of <i>Lycium</i> (Solanaceae). <i>Communications Biology</i> , 2021, 4, 671.	2.0	40

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1916	Whole genome data from <i>Curtobacterium flaccumfaciens</i> pv. <i>flaccumfaciens</i> strains associated with tan spot of mungbean and soybean reveal diverse plasmid profiles. <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 1216-1222.	1.4	7
1918	A de novo transcriptional atlas in <i>Danaus plexippus</i> reveals variability in dosage compensation across tissues. <i>Communications Biology</i> , 2021, 4, 791.	2.0	9
1919	High-quality genome assembly of Huazhan and Tianfeng, the parents of an elite rice hybrid Tian-you-hua-zhan. <i>Science China Life Sciences</i> , 2022, 65, 398-411.	2.3	15
1920	Nanopore Sequencing Indicates That Tandem Amplification of Chromosome 20q11.21 in Human Pluripotent Stem Cells Is Driven by Break-Induced Replication. <i>Stem Cells and Development</i> , 2021, 30, 578-586.	1.1	4
1921	Machine-learning predicts genomic determinants of meiosis-driven structural variation in a eukaryotic pathogen. <i>Nature Communications</i> , 2021, 12, 3551.	5.8	21
1922	Overcoming uncollapsed haplotypes in long-read assemblies of non-model organisms. <i>BMC Bioinformatics</i> , 2021, 22, 303.	1.2	32
1923	Genomic insights of <i>optrA</i> -carrying linezolid-resistant <i>Enterococcus faecium</i> using hybrid assembly: first report from India. <i>Journal of Global Antimicrobial Resistance</i> , 2021, 25, 331-336.	0.9	9
1925	Horizontal Gene Transfer of Genes Encoding Copper-Containing Membrane-Bound Monooxygenase (CuMMO) and Soluble Di-iron Monooxygenase (SDIMO) in Ethane- and Propane-Oxidizing <i>Rhodococcus</i> Bacteria. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0022721.	1.4	5
1926	Analysis of the <i>Coptis chinensis</i> genome reveals the diversification of protoberberine-type alkaloids. <i>Nature Communications</i> , 2021, 12, 3276.	5.8	68
1928	<i>Oryza</i> pan-genomics: A new foundation for future rice research and improvement. <i>Crop Journal</i> , 2021, 9, 622-632.	2.3	7
1929	Chromosome assembled and annotated genome sequence of <i>Aspergillus flavus</i> NRRL 3357. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	19
1930	Transition From PCR-Ribotyping to Whole Genome Sequencing Based Typing of <i>Clostridioides difficile</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 681518.	1.8	14
1931	Concerted evolution reveals co-adapted amino acid substitutions in Na ⁺ K ⁺ -ATPase of frogs that prey on toxic toads. <i>Current Biology</i> , 2021, 31, 2530-2538.e10.	1.8	20
1932	Dissemination of IncFII plasmids carrying <i>fos</i> A3 and <i>bla</i> CTX β 55 in clinical isolates of <i>Salmonella</i> enteritidis. <i>Zoonoses and Public Health</i> , 2021, 68, 760-768.	0.9	9
1933	Genomic and Phenotypic Characterization of <i>Chloracidobacterium</i> Isolates Provides Evidence for Multiple Species. <i>Frontiers in Microbiology</i> , 2021, 12, 704168.	1.5	3
1934	Adaptive evolution of sulfite tolerance in <i>Brettanomyces bruxellensis</i> . <i>FEMS Yeast Research</i> , 2021, 21, .	1.1	6
1935	Genome assembly using quantum and quantum-inspired annealing. <i>Scientific Reports</i> , 2021, 11, 13183.	1.6	24
1936	The chromosome-level <i>Stevia</i> genome provides insights into steviol glycoside biosynthesis. <i>Horticulture Research</i> , 2021, 8, 129.	2.9	35

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1937	Development of polymorphic markers in the immune gene complex loci of cattle. <i>Journal of Dairy Science</i> , 2021, 104, 6897-6908.	1.4	2
1938	Genomic Characteristics and Comparative Genomics Analysis of Two Chinese <i>Corynespora cassiicola</i> Strains Causing <i>Corynespora</i> Leaf Fall (CLF) Disease. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 485.	1.5	5
1939	Genome mining <i>Streptomyces</i> sp. KCTC 0041BP as a producer of dihydrochalcomycin. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 5023-5037.	1.7	4
1940	Genomic analyses provide comprehensive insights into the domestication of bast fiber crop ramie (<i>Boehmeria nivea</i>). <i>Plant Journal</i> , 2021, 107, 787-800.	2.8	18
1941	Two gap-free reference genomes and a global view of the centromere architecture in rice. <i>Molecular Plant</i> , 2021, 14, 1757-1767.	3.9	133
1942	Genomic insights into the fast growth of paulownias and the formation of Paulownia witches' broom. <i>Molecular Plant</i> , 2021, 14, 1668-1682.	3.9	39
1943	The Evolution of Interdependence in a Four-Way Mealybug Symbiosis. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	9
1944	LazyB: fast and cheap genome assembly. <i>Algorithms for Molecular Biology</i> , 2021, 16, 8.	0.3	4
1945	Complete Genome Sequence of <i>Escherichia coli</i> Antibiotic Resistance Isolate Bank Number 0346. <i>Microbiology Resource Announcements</i> , 2021, 10, e0030521.	0.3	0
1946	Complete Genome Sequence of <i>Paradevosia shaoguanensis</i> Type Strain J5-3, Obtained Using Nanopore and Illumina Sequencing Technologies. <i>Microbiology Resource Announcements</i> , 2021, 10, e0009921.	0.3	3
1948	Interpreting nature's finest insect silks (Order Embioptera): hydrophobicity, interrupted repetitive motifs, and fiber-to-film transformation for two neotropical species. <i>Zoology</i> , 2021, 146, 125923.	0.6	3
1949	MicroPIPE: validating an end-to-end workflow for high-quality complete bacterial genome construction. <i>BMC Genomics</i> , 2021, 22, 474.	1.2	25
1950	<i>Trueperella pecoris</i> sp. nov. isolated from bovine and porcine specimens. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	7
1952	Chromosome-level genome assembly of the bean bug <i>Riptortus pedestris</i> . <i>Molecular Ecology Resources</i> , 2021, 21, 2423-2436.	2.2	24
1953	Cas9 targeted enrichment of mobile elements using nanopore sequencing. <i>Nature Communications</i> , 2021, 12, 3586.	5.8	33
1954	Wide Genetic Diversity of <i>Blastocystis</i> in White-Tailed Deer (<i>Odocoileus virginianus</i>) from Maryland, USA. <i>Microorganisms</i> , 2021, 9, 1343.	1.6	54
1956	The <i>Dryas iulia</i> Genome Supports Multiple Gains of a W Chromosome from a B Chromosome in Butterflies. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	24
1957	Comparison of Primary Virus Isolation in Pulmonary Alveolar Macrophages and Four Different Continuous Cell Lines for Type 1 and Type 2 Porcine Reproductive and Respiratory Syndrome Virus. <i>Vaccines</i> , 2021, 9, 594.	2.1	4

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1959	Complete genome sequence data of a novel <i>Streptomyces</i> sp. strain A2-16, a potential biological control agent for potato late blight. <i>Plant Disease</i> , 2021, . .	0.7	0
1961	Genomic diversity, chromosomal rearrangements, and interspecies hybridization in the <i>Ogataea polymorpha</i> species complex. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	2
1962	Chromosome-level genome assembly of a regenerable maize inbred line A188. <i>Genome Biology</i> , 2021, 22, 175.	3.8	32
1963	Comparative Genomics Reveals Potential Mechanisms of Plant Beneficial Effects of a Novel Bamboo-Endophytic Bacterial Isolate <i>Paraburkholderia sacchari</i> Suichang626. <i>Frontiers in Microbiology</i> , 2021, 12, 686998.	1.5	5
1964	An exploration of assembly strategies and quality metrics on the accuracy of the rewarewa (<i>Knightsia excelsa</i>) genome. <i>Molecular Ecology Resources</i> , 2021, 21, 2125-2144.	2.2	9
1965	Differences in the genome, methylome, and transcriptome do not differentiate isolates of <i>Streptococcus equi</i> subsp. <i>equi</i> from horses with acute clinical signs from isolates of inapparent carriers. <i>PLoS ONE</i> , 2021, 16, e0252804.	1.1	4
1966	Enhancer Hijacking Drives Oncogenic <i>BCL11B</i> Expression in Lineage-Ambiguous Stem Cell Leukemia. <i>Cancer Discovery</i> , 2021, 11, 2846-2867.	7.7	83
1967	Chromosome Fusion Affects Genetic Diversity and Evolutionary Turnover of Functional Loci but Consistently Depends on Chromosome Size. <i>Molecular Biology and Evolution</i> , 2021, 38, 4449-4462.	3.5	51
1968	Enteric viruses evoke broad host immune responses resembling those elicited by the bacterial microbiome. <i>Cell Host and Microbe</i> , 2021, 29, 1014-1029.e8.	5.1	35
1969	Comparison of whole genome sequences of three <i>Bacillus cereus</i> strains reveals the food safety risks of <i>Apostichopus japonicus</i> in China. <i>Aquaculture Reports</i> , 2021, 20, 100649.	0.7	2
1970	Genomic architecture constrained placental mammal X Chromosome evolution. <i>Genome Research</i> , 2021, 31, 1353-1365.	2.4	16
1971	Reference genomes of the two cultivated jute species. <i>Plant Biotechnology Journal</i> , 2021, 19, 2235-2248.	4.1	25
1973	Chromosome-Scale Genome for a Red-Fruited, Perpetual Flowering and Runnerless Woodland Strawberry (<i>Fragaria vesca</i>). <i>Frontiers in Genetics</i> , 2021, 12, 671371.	1.1	8
1974	Dissecting the chromosome-level genome of the Asian Clam (<i>Corbicula fluminea</i>). <i>Scientific Reports</i> , 2021, 11, 15021.	1.6	5
1975	Genomic insights into methicillin-resistant <i>Staphylococcus pseudintermedius</i> isolates from dogs and humans of the same sequence types reveals diversity in prophages and pathogenicity islands. <i>PLoS ONE</i> , 2021, 16, e0254382.	1.1	8
1976	Chromosome-Level Genome Sequence of the Black Koji Fungus <i>Aspergillus luchuensis</i> RIB2601. <i>Microbiology Resource Announcements</i> , 2021, 10, e0038421.	0.3	4
1977	Oncogenic cooperation between TCF7-SPI1 and NRAS(G12D) requires β -catenin activity to drive T-cell acute lymphoblastic leukemia. <i>Nature Communications</i> , 2021, 12, 4164.	5.8	9
1978	<i>Wolbachia</i> in the spittlebug <i>Prosapia ignipectus</i> : Variable infection frequencies, but no apparent effect on host reproductive isolation. <i>Ecology and Evolution</i> , 2021, 11, 10054-10065.	0.8	5

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1979	The complete mitogenome assemblies of 10 diploid potato clones reveal recombination and overlapping variants. <i>DNA Research</i> , 2021, 28, .	1.5	4
1981	Comparison of Two <i>Aspergillus oryzae</i> Genomes From Different Clades Reveals Independent Evolution of Alpha-Amylase Duplication, Variation in Secondary Metabolism Genes, and Differences in Primary Metabolism. <i>Frontiers in Microbiology</i> , 2021, 12, 691296.	1.5	7
1982	Optimizing experimental design for genome sequencing and assembly with Oxford Nanopore Technologies. <i>GigaByte</i> , 0, 2021, 1-26.	0.0	10
1983	DNA transposons mediate duplications via transposition-independent and -dependent mechanisms in metazoans. <i>Nature Communications</i> , 2021, 12, 4280.	5.8	9
1984	Highly Replicated Evolution of Parapatric Ecotypes. <i>Molecular Biology and Evolution</i> , 2021, 38, 4805-4821.	3.5	17
1985	Identification of Three Clf-Sdr Subfamily Proteins in <i>Staphylococcus warneri</i> , and Comparative Genomics Analysis of a Locus Encoding CWA Proteins in <i>Staphylococcus</i> Species. <i>Frontiers in Microbiology</i> , 2021, 12, 691087.	1.5	0
1987	Highly contiguous assemblies of 101 drosophilid genomes. <i>ELife</i> , 2021, 10, .	2.8	108
1988	A genome sequence resource for the genus <i>Passiflora</i> , the genome of the wild diploid species <i>Passiflora organensis</i> . <i>Plant Genome</i> , 2021, 14, e20117.	1.6	8
1989	Comparative Analysis of Host-Associated Variation in <i>Phytophthora cactorum</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 679936.	1.5	10
1991	Complete Genome Sequence of the Ammonia-Oxidizing Bacterium <i>Nitrosospira</i> sp. Strain NRS527, Isolated from the Rhizoplane of Paddy Rice. <i>Microbiology Resource Announcements</i> , 2021, 10, e0042021.	0.3	1
1992	Complete Genome Sequence of Atopobiaceae Bacterium Strain P1, Isolated from Mouse Feces. <i>Microbiology Resource Announcements</i> , 2021, 10, e0062721.	0.3	1
1993	Complete Genome Sequence of <i>Streptococcus oralis</i> SF100, Isolated from Blood Cultures from a Patient with Infective Endocarditis. <i>Microbiology Resource Announcements</i> , 2021, 10, e0017621.	0.3	1
1994	Diploidy within a Haploid Genus of Entomopathogenic Fungi. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	5
1995	The first draft genome of feather grasses using SMRT sequencing and its implications in molecular studies of <i>Stipa</i> . <i>Scientific Reports</i> , 2021, 11, 15345.	1.6	6
1996	Root Endophytes and <i>Ginkgo biloba</i> Are Likely to Share and Compensate Secondary Metabolic Processes, and Potentially Exchange Genetic Information by LTR-RTs. <i>Frontiers in Plant Science</i> , 2021, 12, 704985.	1.7	12
1997	Strainberry: automated strain separation in low-complexity metagenomes using long reads. <i>Nature Communications</i> , 2021, 12, 4485.	5.8	25
1999	Exploration of the <i>Ixodes ricinus</i> virosphere unveils an extensive virus diversity including novel coltiviruses and other reoviruses. <i>Virus Evolution</i> , 2021, 7, veab066.	2.2	8
2000	Comparative genomics of <i>Edwardsiella ictaluri</i> revealed four distinct host-specific genotypes and thirteen potential vaccine candidates. <i>Genomics</i> , 2021, 113, 1976-1987.	1.3	10

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2001	Identification and characteristics of a novel aminoglycoside phosphotransferase, APH(3â€²)-IId, from an MDR clinical isolate of <i>Brucella intermedia</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 2787-2794.	1.3	5
2004	Actinomycosis in a gray four-eyed opossum (<i>Philander opossum</i>) caused by a novel species of <i>Schaalia</i> . <i>BMC Veterinary Research</i> , 2021, 17, 243.	0.7	3
2005	Characterization and identification of SFDC-1, a novel AmpC-type β -lactamase in <i>Serratia fonticola</i> . <i>Environmental Microbiology</i> , 2021, , .	1.8	0
2006	Comparison of De Novo Assembly Strategies for Bacterial Genomes. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7668.	1.8	22
2007	A chromosome-level genome assembly of the miiuy croaker (<i>Miichthys miiuy</i>) using nanopore sequencing and Hi-C. <i>Aquaculture and Fisheries</i> , 2024, 9, 218-225.	1.2	4
2008	Transcriptional response to host chemical cues underpins the expansion of host range in a fungal plant pathogen lineage. <i>ISME Journal</i> , 2022, 16, 138-148.	4.4	17
2009	Parallel evolution of trehalose production machinery in anhydrobiotic animals via recurrent gene loss and horizontal transfer. <i>Open Biology</i> , 2021, 11, 200413.	1.5	17
2010	Sequence of the Mitochondrial Genome of <i>Lactuca virosa</i> Suggests an Unexpected Role in <i>Lactuca sativa</i> 's Evolution. <i>Frontiers in Plant Science</i> , 2021, 12, 697136.	1.7	4
2012	Genomic insights into molecular adaptation to intertidal environments in the mangrove <i>Aegiceras corniculatum</i> . <i>New Phytologist</i> , 2021, 231, 2346-2358.	3.5	32
2013	Chromosomal-level genome assembly of the semi-dwarf rice Taichung Native 1, an initiator of Green Revolution. <i>Genomics</i> , 2021, 113, 2656-2674.	1.3	11
2014	<i>Gossypium tomentosum</i> genome and interspecific ultra-dense genetic maps reveal genomic structures, recombination landscape and flowering depression in cotton. <i>Genomics</i> , 2021, 113, 1999-2009.	1.3	8
2015	Identification of <i>qnrE3</i> and <i>qnrE4</i> , New Transferable Quinolone Resistance <i>qnrE</i> Family Genes Originating from <i>Enterobacter mori</i> and <i>Enterobacter asburiae</i> , Respectively. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, e0045621.	1.4	6
2016	Empirical evaluation of methods for <i>de novo</i> genome assembly. <i>PeerJ Computer Science</i> , 2021, 7, e636.	2.7	15
2020	A Chromosome-level Genome Assembly of Wild Castor Provides New Insights into its Adaptive Evolution in Tropical Desert. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 42-59.	3.0	18
2021	The first draft genome of <i>Picrorhiza kurroa</i> , an endangered medicinal herb from Himalayas. <i>Scientific Reports</i> , 2021, 11, 14944.	1.6	10
2022	Improving Common Bacterial Blight Phenotyping by Using Rub Inoculation and Machine Learning: Cheaper, Better, Faster, Stronger. <i>Phytopathology</i> , 2022, 112, 691-699.	1.1	2
2023	Complete Genome Resources for <i>Ralstonia</i> Bacterial Wilt Strains UW763 (Phylotype I); Rs5 and UW700 (Phylotype II); and UW386, RUN2474, and RUN2279 (Phylotype III). <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 1212-1215.	1.4	6
2024	Mitochondrial genome of <i>Geomydoecus aurei</i> , a pocket-gopher louse. <i>PLoS ONE</i> , 2021, 16, e0254138.	1.1	3

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2025	Transmission dynamics of a linear vanA-plasmid during a nosocomial multiclonal outbreak of vancomycin-resistant enterococci in a non-endemic area, Japan. <i>Scientific Reports</i> , 2021, 11, 14780.	1.6	11
2026	Antimicrobial Resistance Profiling and Phylogenetic Analysis of <i>Neisseria gonorrhoeae</i> Clinical Isolates From Kenya in a Resource-Limited Setting. <i>Frontiers in Microbiology</i> , 2021, 12, 647565.	1.5	8
2029	Complete Genome Sequence of the Biocontrol Agent <i>Pseudomonas chlororaphis</i> subsp. <i>aureofaciens</i> SPS-41. <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 839-841.	1.4	2
2030	Using Combined Methods of Genetic Mapping and Nanopore-Based Sequencing Technology to Analyze the Insertion Positions of G10evo-EPSPS and Cry1Ab/Cry2Aj Transgenes in Maize. <i>Frontiers in Plant Science</i> , 2021, 12, 690951.	1.7	6
2031	Global high-throughput genotyping of organellar genomes reveals insights into the origin and spread of invasive starry stonewort (<i>Nitellopsis obtusa</i>). <i>Biological Invasions</i> , 2021, 23, 3471-3482.	1.2	5
2032	Complete Genome Sequences of Two <i>Lysobacter</i> Strains, Isolated from Seawater (<i>Lysobacter</i> Tj ETQq1 1 0.784314 rgBT / 0.3 Announcements, 2021, 10, e0033721.	0.3	0
2035	Long-read genome assembly and genetic architecture of fruit shape in the bottle gourd. <i>Plant Journal</i> , 2021, 107, 956-968.	2.8	23
2037	Haplotype-resolved genome assembly provides insights into evolutionary history of the tea plant <i>Camellia sinensis</i> . <i>Nature Genetics</i> , 2021, 53, 1250-1259.	9.4	157
2038	Plasmid analysis of NDM metallo-β-lactamase-producing Enterobacterales isolated in Vietnam. <i>PLoS ONE</i> , 2021, 16, e0231119.	1.1	10
2039	Evolutionarily recent dual obligatory symbiosis among adelgids indicates a transition between fungus- and insect-associated lifestyles. <i>ISME Journal</i> , 2022, 16, 247-256.	4.4	16
2040	Isolation and characterization of a novel bacteriophage WO from <i>Allonemobius socius</i> crickets in Missouri. <i>PLoS ONE</i> , 2021, 16, e0250051.	1.1	8
2041	Complete Genome Sequence of <i>Pasteurella multocida</i> HuN001, a Capsular Type A Strain from a Human. <i>Microbiology Resource Announcements</i> , 2021, 10, e0039521.	0.3	7
2042	Draft Genome Assembly and Transcriptome Dataset for European Turnip (<i>Brassica rapa</i> L. ssp. <i>rapifera</i>), ECD4 Carrying Clubroot Resistance. <i>Frontiers in Genetics</i> , 2021, 12, 651298.	1.1	5
2043	Eight soybean reference genome resources from varying latitudes and agronomic traits. <i>Scientific Data</i> , 2021, 8, 164.	2.4	13
2044	Evolution of the MLO gene families in octoploid strawberry (<i>Fragaria</i> and <i>Ananassa</i>) and progenitor diploid species identified potential genes for strawberry powdery mildew resistance. <i>Horticulture Research</i> , 2021, 8, 153.	2.9	11
2046	Improving the Utilization of Isomaltose and Panose by Lager Yeast <i>Saccharomyces pastorianus</i> . <i>Fermentation</i> , 2021, 7, 107.	1.4	0
2047	A shotgun metagenomics approach to detect and characterize unauthorized genetically modified microorganisms in microbial fermentation products. <i>Food Chemistry Molecular Sciences</i> , 2021, 2, 100023.	0.9	5
2048	Genome archaeology of two laboratory <i>Salmonella enterica enterica</i> sv Typhimurium. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	4

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2049	Coupling of the engineered DNA "emulator" to a biosensor as a new paradigm for activation of silent biosynthetic gene clusters in <i>Streptomyces</i> . <i>Nucleic Acids Research</i> , 2021, 49, 8396-8405.	6.5	5
2050	Positive Selection of Transcription Factors Is a Prominent Feature of the Evolution of a Plant Pathogenic Genus Originating in the Miocene. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	3
2051	Development of the yeast and lactic acid bacteria co-culture agent for atmospheric ammonia removing: Genomic features and on-site applications. <i>Ecotoxicology and Environmental Safety</i> , 2021, 218, 112287.	2.9	5
2052	Whole genome sequencing and bulked segregant analysis suggest a new mechanism of amitraz resistance in the citrus red mite, <i>Panonychus citri</i> (Acari: Tetranychidae). <i>Pest Management Science</i> , 2021, 77, 5032-5048.	1.7	6
2053	Screening of intestinal probiotics and the effects of feeding probiotics on the digestive enzyme activity, immune, intestinal flora and WSSV resistance of <i>Procambarus clarkii</i> . <i>Aquaculture</i> , 2021, 540, 736748.	1.7	18
2054	Global patterns in genomic diversity underpinning the evolution of insecticide resistance in the aphid crop pest <i>Myzus persicae</i> . <i>Communications Biology</i> , 2021, 4, 847.	2.0	55
2055	Profiling variable-number tandem repeat variation across populations using repeat-pangenome graphs. <i>Nature Communications</i> , 2021, 12, 4250.	5.8	27
2056	<i>De novo</i> genome assembly of the marine teleost, bluefin trevally (<i>Caranx melampygus</i>). <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	2
2059	A reference-grade genome identifies salt-tolerance genes from the salt-secreting mangrove species <i>Avicennia marina</i> . <i>Communications Biology</i> , 2021, 4, 851.	2.0	32
2060	Identification of structural variation and polymorphisms of a sex co-segregating scaffold in spinach. <i>Plant Reproduction</i> , 2021, , 1.	1.3	1
2061	Mobilization of the nonconjugative virulence plasmid from hypervirulent <i>Klebsiella pneumoniae</i> . <i>Genome Medicine</i> , 2021, 13, 119.	3.6	60
2063	Genome assembly of <i>Scorias spongiosa</i> and comparative genomics provide insights into ecological adaptation of honeydew-dependent sooty mould fungi. <i>Genomics</i> , 2021, 113, 2189-2198.	1.3	2
2064	Comparative genome and transcriptome analyses reveal innate differences in response to host plants by two color forms of the two-spotted spider mite <i>Tetranychus urticae</i> . <i>BMC Genomics</i> , 2021, 22, 569.	1.2	4
2065	Genomic Analysis and Stability Evaluation of the Phenol-Degrading Bacterium <i>Acinetobacter</i> sp. DW-1 During Water Treatment. <i>Frontiers in Microbiology</i> , 2021, 12, 687511.	1.5	6
2066	Genetic variability of <i>Edwardsiella piscicida</i> isolates from Mississippi catfish aquaculture with an assessment of virulence in channel and channel-blue hybrid catfish. <i>Journal of Fish Diseases</i> , 2021, 44, 0.9 1725-1751.		7
2067	Genome of the world's smallest flowering plant, <i>Wolffia australiana</i> , helps explain its specialized physiology and unique morphology. <i>Communications Biology</i> , 2021, 4, 900.	2.0	16
2068	Genome Analysis of <i>Streptomycesnojiriensis</i> JCM 3382 and Distribution of Gene Clusters for Three Antibiotics and an Azasugar across the Genus <i>Streptomyces</i> . <i>Microorganisms</i> , 2021, 9, 1802.	1.6	5
2069	Comparative Analysis of PacBio and Oxford Nanopore Sequencing Technologies for Transcriptomic Landscape Identification of <i>Penaeus monodon</i> . <i>Life</i> , 2021, 11, 862.	1.1	7

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2071	The genome of a daddy-long-legs (Opiliones) illuminates the evolution of arachnid appendages. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2021, 288, 20211168.	1.2	17
2072	Telomere Roles in Fungal Genome Evolution and Adaptation. <i>Frontiers in Genetics</i> , 2021, 12, 676751.	1.1	12
2073	Technology dictates algorithms: recent developments in read alignment. <i>Genome Biology</i> , 2021, 22, 249.	3.8	51
2074	Large scale genomic rearrangements in selected <i>Arabidopsis thaliana</i> T-DNA lines are caused by T-DNA insertion mutagenesis. <i>BMC Genomics</i> , 2021, 22, 599.	1.2	42
2075	Telomere to telomere genome assembly of <i>Fusarium musae</i> F31, causal agent of crown rot disease of banana.. <i>Molecular Plant-Microbe Interactions</i> , 2021, , MPMI05210127A.	1.4	8
2077	Novel quality metrics allow identifying and generating high-quality assemblies of piRNA clusters. <i>Molecular Ecology Resources</i> , 2022, 22, 102-121.	2.2	13
2078	The first genome assembly of fungal pathogen <i>Pyrenophora tritici-repentis</i> race 1 isolate using Oxford Nanopore MinION sequencing. <i>BMC Research Notes</i> , 2021, 14, 334.	0.6	3
2079	The Genome of the Haptophyte <i>Diacronema lutheri</i> (<i>Pavlova lutheri</i> , Pavlovales): A Model for Lipid Biosynthesis in Eukaryotic Algae. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	7
2080	SWALO: scaffolding with assembly likelihood optimization. <i>Nucleic Acids Research</i> , 2021, 49, e117-e117.	6.5	3
2081	Laboratory Stock Variants of the Archetype Silver Resistance Plasmid pMG101 Demonstrate Plasmid Fusion, Loss of Transmissibility, and Transposition of Tn7/pco/sil Into the Host Chromosome. <i>Frontiers in Microbiology</i> , 2021, 12, 723322.	1.5	13
2082	Genome-wide analysis of butterfly bush (<i>Buddleja alternifolia</i>) in three uplands provides insights into biogeography, demography and speciation. <i>New Phytologist</i> , 2021, 232, 1463-1476.	3.5	21
2083	In situ role of extracellular polymeric substances in microbial electron transfer by <i>Methylomonas</i> sp. LW13. <i>Fundamental Research</i> , 2021, 1, 735-741.	1.6	10
2084	Formation of artificial chromosomes in <i>Caenorhabditis elegans</i> and analyses of their segregation in mitosis, DNA sequence composition and holocentromere organization. <i>Nucleic Acids Research</i> , 2021, 49, 9174-9193.	6.5	13
2085	<i>Streptomonospora litoralis</i> sp. nov., a halophilic thiopeptides producer isolated from sand collected at Cuxhaven beach. <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 1483-1496.	0.7	6
2086	Identification and Characterization of a Novel Aminoglycoside 3'-Nucleotidyltransferase, ANT(3'')-IId, From <i>Acinetobacter Iwoffii</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 728216.	1.5	0
2087	Gene expression profiling reveals candidate genes for defining spider silk gland types. <i>Insect Biochemistry and Molecular Biology</i> , 2021, 135, 103594.	1.2	9
2088	The Resistome and Mobilome of Multidrug-Resistant <i>Staphylococcus sciuri</i> C2865 Unveil a Transferable Trimethoprim Resistance Gene, Designated <i>dfrE</i> , Spread Unnoticed. <i>MSystems</i> , 2021, 6, e0051121.	1.7	7

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2090	The genome of the thin-necked bladder worm <i>Taenia hydatigena</i> reveals evolutionary strategies for helminth survival. <i>Communications Biology</i> , 2021, 4, 1004.	2.0	2
2091	<i>Prevotella copri</i> increases fat accumulation in pigs fed with formula diets. <i>Microbiome</i> , 2021, 9, 175.	4.9	100
2093	Systematic Comparison of the Performances of De Novo Genome Assemblers for Oxford Nanopore Technology Reads From Piroplasm. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 696669.	1.8	16
2094	Quinoa genome assembly employing genomic variation for guided scaffolding. <i>Theoretical and Applied Genetics</i> , 2021, 134, 3577-3594.	1.8	4
2095	Haplotype-resolved genome assembly and allele-specific gene expression in cultivated ginger. <i>Horticulture Research</i> , 2021, 8, 188.	2.9	31
2096	Distinctive Mobile Genetic Elements Observed in the Clonal Expansion of Carbapenem-Resistant <i>Klebsiella pneumoniae</i> in India. <i>Microbial Drug Resistance</i> , 2021, 27, 1096-1104.	0.9	14
2097	<i>Ruminococcus bovis</i> sp. nov., a novel species of amyolytic <i>Ruminococcus</i> isolated from the rumen of a dairy cow. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	17
2098	Using de novo assembly to identify structural variation of eight complex immune system gene regions. <i>PLoS Computational Biology</i> , 2021, 17, e1009254.	1.5	22
2099	A high-quality draft genome for <i>Melaleuca alternifolia</i> (tea tree): a new platform for evolutionary genomics of myrtaceous terpene-rich species. <i>CigaByte</i> , 0, 2021, 1-15.	0.0	11
2100	High-quality genome assembly of the soybean fungal pathogen <i>Cercospora kikuchii</i> . <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	5
2102	Complete chloroplast genome of the medicinal plant <i>Evolvulus alsinoides</i> : comparative analysis, identification of mutational hotspots and evolutionary dynamics with species of Solanales. <i>Physiology and Molecular Biology of Plants</i> , 2021, 27, 1867-1884.	1.4	3
2103	Transcriptome Analyses of Barley Roots Inoculated with Novel <i>Paenibacillus</i> sp. and <i>Erwinia gerundensis</i> Strains Reveal Beneficial Early-Stage Plant-Bacteria Interactions. <i>Plants</i> , 2021, 10, 1802.	1.6	10
2104	Diploid genomic architecture of <i>Nitzschia inconspicua</i> , an elite biomass production diatom. <i>Scientific Reports</i> , 2021, 11, 15592.	1.6	12
2105	A conserved role of the duplicated Masculinizer gene in sex determination of the Mediterranean flour moth, <i>Ephestia kuehniella</i> . <i>PLoS Genetics</i> , 2021, 17, e1009420.	1.5	14
2108	A reference genome for the nectar-robbing Black-throated Flowerpiercer (<i>Diglossa</i>) Tj ETQq1 1 0.784314 rgBT / Overlock 10 Tf 50 142 0,8		
2109	Clinical and Histopathologic Features of a Feline SARS-CoV-2 Infection Model Are Analogous to Acute COVID-19 in Humans. <i>Viruses</i> , 2021, 13, 1550.	1.5	20
2111	Complete Genome Sequence of <i>Gelria</i> sp. Strain Kuro-4, a Thermophilic Anaerobe Isolated from a Thermophilic Anaerobic Digestion Reactor Treating Poly(L-Lactic Acid). <i>Microbiology Resource Announcements</i> , 2021, 10, e0054421.	0.3	0

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2113	Mitotic recombination between homologous chromosomes drives genomic diversity in diatoms. <i>Current Biology</i> , 2021, 31, 3221-3232.e9.	1.8	29
2114	Apicidin biosynthesis is linked to accessory chromosomes in <i>Fusarium poae</i> isolates. <i>BMC Genomics</i> , 2021, 22, 591.	1.2	7
2115	Long-read nanopore sequencing enables accurate confirmation of a recurrent PMS2 insertionâ€“deletion variant located in a region of complex genomic architecture. <i>Cancer Genetics</i> , 2021, 256-257, 122-126.	0.2	4
2117	Gene Annotation and Transcriptome Delineation on a De Novo Genome Assembly for the Reference <i>Leishmania major</i> Friedlin Strain. <i>Genes</i> , 2021, 12, 1359.	1.0	7
2118	A chromosomeâ€“scale assembly of the bilberry genome identifies a complex locus controlling berry anthocyanin composition. <i>Molecular Ecology Resources</i> , 2022, 22, 345-360.	2.2	28
2119	Gradual evolution of allopolyploidy in <i>Arabidopsis suecica</i> . <i>Nature Ecology and Evolution</i> , 2021, 5, 1367-1381.	3.4	64
2120	Amino acid substitutions in ribosomal protein RpsU enable switching between high fitness and multiple-stress resistance in <i>Listeria monocytogenes</i> . <i>International Journal of Food Microbiology</i> , 2021, 351, 109269.	2.1	7
2121	Antimicrobial Activity and Identification of the Biosynthetic Gene Cluster of X-14952B From <i>Streptomyces</i> sp. 135. <i>Frontiers in Microbiology</i> , 2021, 12, 703093.	1.5	7
2123	In-/Near-Memory Computing. <i>Synthesis Lectures on Computer Architecture</i> , 2021, 16, 1-140.	1.3	2
2124	Unraveling the Genome of a High Yielding Colombian Sugarcane Hybrid. <i>Frontiers in Plant Science</i> , 2021, 12, 694859.	1.7	13
2126	Genomic and Experimental Investigations of <i>Auriscalpium</i> and <i>Strobilurus</i> Fungi Reveal New Insights into Pinecone Decomposition. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 679.	1.5	1
2127	Genome Sequence Resource for <i>Erysiphe necator</i> NAFU1, a Grapevine Powdery Mildew Isolate Identified in Shaanxi Province of China (Retracted). <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 1446-1449.	1.4	2
2128	Transposable elements and introgression introduce genetic variation in the invasive ant <i>Cardiocondyla obscurior</i> . <i>Molecular Ecology</i> , 2021, 30, 6211-6228.	2.0	20
2129	Improved Whole-Genome Sequence of <i>Phytophthora capsici</i> Generated by Long-Read Sequencing. <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 866-869.	1.4	9
2130	Comparative Genomic and Transcriptomic Analysis of <i>Naegleria fowleri</i> Clinical and Environmental Isolates. <i>MSphere</i> , 2021, 6, e0063721.	1.3	8
2131	Complete Genome Sequence of <i>Caballeronia</i> sp. Strain NK8 (MAFF311271), a Chlorobenzoate-Degrading Bacterium. <i>Microbiology Resource Announcements</i> , 2021, 10, e0041621.	0.3	2
2133	New highâ€“quality peach (<i>Prunus persica</i> L. Batsch) genome assembly to analyze the molecular evolutionary mechanism of volatile compounds in peach fruits. <i>Plant Journal</i> , 2021, 108, 281-295.	2.8	31

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2135	Genomic selection in salmonids: new discoveries and future perspectives. <i>Aquaculture International</i> , 2021, 29, 2259-2289.	1.1	13
2136	De novo assembly, annotation, and comparative analysis of 26 diverse maize genomes. <i>Science</i> , 2021, 373, 655-662.	6.0	282
2137	Generalizable characteristics of false-positive bacterial variant calls. <i>Microbial Genomics</i> , 2021, 7, .	1.0	11
2140	A chromosome-anchored genome assembly for Lake Trout (<i>Salvelinus namaycush</i>). <i>Molecular Ecology Resources</i> , 2022, 22, 679-694.	2.2	16
2141	Complete Genome Sequence of the plant pathogenic fungus <i>Colletotrichum lupini</i> . <i>Molecular Plant-Microbe Interactions</i> , 2021, , MPMI07210173A.	1.4	9
2142	Chromosome Genome Assembly and Annotation of the <i>Capitulum mitella</i> With PacBio and Hi-C Sequencing Data. <i>Frontiers in Genetics</i> , 2021, 12, 707546.	1.1	1
2143	Complete and Circularized Genome Sequences of Three <i>Xanthomonas</i> Strains Pathogenic on Soybean and Alfalfa. <i>Microbiology Resource Announcements</i> , 2021, 10, e0053721.	0.3	1
2146	Comparative genomics of two inbred lines of the potato cyst nematode <i>Globodera rostochiensis</i> reveals disparate effector family-specific diversification patterns. <i>BMC Genomics</i> , 2021, 22, 611.	1.2	6
2147	Complete and Circularized Genome Sequences of 17 <i>Xanthomonas</i> Strains Responsible for Common Bacterial Blight of Bean. <i>Microbiology Resource Announcements</i> , 2021, 10, e0037121.	0.3	1
2148	High-Quality Genome Sequence Resource for <i>Fusarium andiyazi</i> Causing Pokkah Boeng Disease of Sugarcane in China. <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, MPMI-11-20-0331.	1.4	2
2150	Characterization and Clonal Diffusion of Ceftaroline Non-Susceptible MRSA in Two Hospitals in Central Italy. <i>Antibiotics</i> , 2021, 10, 1026.	1.5	1
2154	Multi-omics of the esophageal microenvironment identifies signatures associated with progression of Barrett's esophagus. <i>Genome Medicine</i> , 2021, 13, 133.	3.6	11
2155	Characterisation of Early Positive <i>mcr-1</i> Resistance Gene and Plasmidome in <i>Escherichia coli</i> Pathogenic Strains Associated with Variable Phylogroups under Colistin Selection. <i>Antibiotics</i> , 2021, 10, 1041.	1.5	7
2157	The whale shark genome reveals patterns of vertebrate gene family evolution. <i>ELife</i> , 2021, 10, .	2.8	19
2158	A chromosome-scale genome assembly and karyotype of the ctenophore <i>Hormiphora californensis</i> . <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	18
2159	<i>Thermococcus aciditolerans</i> sp. nov., a piezotolerant, hyperthermophilic archaeon isolated from a deep-sea hydrothermal vent chimney in the Southwest Indian Ridge. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	9
2160	Classification of three corynebacterial strains isolated from a small paddock in North Rhine-Westphalia: proposal of <i>Corynebacterium kalinowskii</i> sp. nov., <i>Corynebacterium comes</i> sp. nov. and <i>Corynebacterium occultum</i> sp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	13

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2161	The Interspecific Fungal Hybrid <i>Verticillium longisporum</i> Displays Subgenome-Specific Gene Expression. <i>MBio</i> , 2021, 12, e0149621.	1.8	8
2162	Pan-genome of <i>Raphanus</i> highlights genetic variation and introgression among domesticated, wild, and weedy radishes. <i>Molecular Plant</i> , 2021, 14, 2032-2055.	3.9	56
2163	Recovery of small plasmid sequences via Oxford Nanopore sequencing. <i>Microbial Genomics</i> , 2021, 7, .	1.0	44
2164	A Y-linked anti-M β 4lllerian hormone type-II receptor is the sex-determining gene in ayu, <i>Plecoglossus altivelis</i> . <i>PLoS Genetics</i> , 2021, 17, e1009705.	1.5	25
2166	Species-Specific Humoral Immune Responses in Sheep and Goats upon Small Ruminant Lentivirus Infections Inversely Correlate with Protection against Virus Replication and Pathological Lesions. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9824.	1.8	3
2167	High-quality genome assembly of 'Cuiguan' pear (<i>Pyrus pyrifolia</i>) as a reference genome for identifying regulatory genes and epigenetic modifications responsible for bud dormancy. <i>Horticulture Research</i> , 2021, 8, 197.	2.9	44
2168	<i>Pengzhenrongella sicca</i> gen. nov., sp. nov., a new member of suborder Micrococccineae isolated from High Arctic tundra soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	8
2169	Genome Assembly and Sex-Determining Region of Male and Female <i>Populus sibirica</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 625416.	1.7	9
2170	Chromosome-scale genome assembly and population genomics provide insights into the adaptation, domestication, and flavonoid metabolism of Chinese plum. <i>Plant Journal</i> , 2021, 108, 1174-1192.	2.8	16
2171	A chromosome-level genome of <i>Antechinus flavipes</i> provides a reference for an Australian marsupial genus with male death after mating. <i>Molecular Ecology Resources</i> , 2022, 22, 740-754.	2.2	12
2172	Chromosome-scale assembly of the <i>Dendrobium chrysotoxum</i> genome enhances the understanding of orchid evolution. <i>Horticulture Research</i> , 2021, 8, 183.	2.9	41
2176	Genome Sequencing and Functional Characterization of <i>Xanthomonas cucurbitae</i> , the Causal Agent of Bacterial Spot Disease of Cucurbits. <i>Phytopathology</i> , 2021, 111, PHYTO-06-20-022.	1.1	2
2178	Activation of Cryptic Antibiotic Biosynthetic Gene Clusters Guided by RNA-seq Data from Both <i>Streptomyces ansochromogenes</i> and <i>Streptomyces wblA</i> . <i>Antibiotics</i> , 2021, 10, 1097.	1.5	4
2179	Tricycler: consensus long-read assemblies for bacterial genomes. <i>Genome Biology</i> , 2021, 22, 266.	3.8	175
2180	The Biocontrol and Plant Growth-Promoting Properties of <i>Streptomyces alfalfae</i> XN-04 Revealed by Functional and Genomic Analysis. <i>Frontiers in Microbiology</i> , 2021, 12, 745766.	1.5	13
2181	The mitogenome of <i>Halotydeus destructor</i> (Tucker) and its relationships with other trombidiform mites as inferred from nucleotide sequences and gene arrangements. <i>Ecology and Evolution</i> , 2021, 11, 14162-14174.	0.8	5
2183	Incipient diploidization of the medicinal plant <i>Perilla</i> within 10,000 years. <i>Nature Communications</i> , 2021, 12, 5508.	5.8	35
2184	Genome-Wide Transcriptional Changes of <i>Rhodosporidium kratochvilovae</i> at Low Temperature. <i>Frontiers in Microbiology</i> , 2021, 12, 727105.	1.5	5

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2185	High-Quality Genome Resource of <i>Clonostachys rosea</i> Strain CanS41 by Oxford Nanopore Long-Read Sequencing. <i>Plant Disease</i> , 2021, 105, 2231-2234.	0.7	8
2186	Complete genome sequence of <i>Microbulbifer</i> sp. YPW1 from mangrove sediments in Yanpu harbor, China. <i>Archives of Microbiology</i> , 2021, 203, 6143-6151.	1.0	1
2187	Whole-Genome and Transcriptome Sequencing of <i>Phlebopus portentosus</i> Reveals Its Associated Ectomycorrhizal Niche and Conserved Pathways Involved in Fruiting Body Development. <i>Frontiers in Microbiology</i> , 2021, 12, 732458.	1.5	8
2188	High quality haplotype-resolved genome assemblies of <i>Populus tomentosa</i> Carr., a stabilized interspecific hybrid species widespread in Asia. <i>Molecular Ecology Resources</i> , 2022, 22, 786-802.	2.2	19
2189	Haploid Genome Analysis Reveals a Tandem Cluster of Four HSP20 Genes Involved in the High-Temperature Adaptation of <i>Coriopsis trogii</i> . <i>Microbiology Spectrum</i> , 2021, 9, e0028721.	1.2	7
2191	Characterization of Shiga Toxin 2a Encoding Bacteriophages Isolated From High-Virulent O145:H25 Shiga Toxin-Producing <i>Escherichia coli</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 728116.	1.5	1
2192	Chromosome-Level Genome Sequence of <i>Aspergillus chevalieri</i> M1, Isolated from Katsuoobushi. <i>Microbiology Resource Announcements</i> , 2021, 10, e0038521.	0.3	1
2193	The <i>Gossypium anomalum</i> genome as a resource for cotton improvement and evolutionary analysis of hybrid incompatibility. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	13
2194	An Improved Assembly of the <i>Albugo candida</i> Ac2V Genome Reveals the Expansion of the CCG Class of Effectors. <i>Molecular Plant-Microbe Interactions</i> , 2022, 35, 39-48.	1.4	6
2196	<i>Dyella telluris</i> sp. nov. and <i>Dyella acidiphila</i> sp. nov., isolated from forest soil of Dinghushan Biosphere Reserve, China. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	16
2197	Engineering the thermotolerant industrial yeast <i>Kluyveromyces marxianus</i> for anaerobic growth. <i>Metabolic Engineering</i> , 2021, 67, 347-364.	3.6	14
2198	Comparative Mitogenomic Analysis and the Evolution of <i>Rhizoctonia solani</i> Anastomosis Groups. <i>Frontiers in Microbiology</i> , 2021, 12, 707281.	1.5	5
2199	Genomic anatomy of male-specific microchromosomes in a gynogenetic fish. <i>PLoS Genetics</i> , 2021, 17, e1009760.	1.5	17
2200	Precise Characterization of <i>Bombyx mori</i> Fibroin Heavy Chain Gene Using Cpf1-Based Enrichment and Oxford Nanopore Technologies. <i>Insects</i> , 2021, 12, 832.	1.0	3
2202	A chromosome-level reference genome of red swamp crayfish <i>Procambarus clarkii</i> provides insights into the gene families regarding growth or development in crustaceans. <i>Genomics</i> , 2021, 113, 3274-3284.	1.3	20
2203	Rapid identification and metagenomics analysis of the adenovirus type 55 outbreak in Hubei using real-time and high-throughput sequencing platforms. <i>Infection, Genetics and Evolution</i> , 2021, 93, 104939.	1.0	8
2204	Molecular and FISH analysis of 45S rDNA on BAC molecule of <i>Saccharina japonica</i> . <i>Aquaculture and Fisheries</i> , 2023, 8, 103-107.	1.2	1
2205	High-Efficiency Genome Editing Based on Endogenous CRISPR-Cas System Enhances Cell Growth and Lactic Acid Production in <i>Pediococcus acidilactici</i> . <i>Applied and Environmental Microbiology</i> , 2021, 87, e0094821.	1.4	20

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2206	The chromosome-scale genome of <i>Magnolia officinalis</i> provides insight into the evolutionary position of magnoliids. <i>IScience</i> , 2021, 24, 102997.	1.9	14
2207	Draft Genome Sequence of a Diploid and Hybrid <i>Candida</i> Strain, <i>Candida sanyaensis</i> UCD423, Isolated from Compost in Ireland. <i>Microbiology Resource Announcements</i> , 2021, 10, e0076121.	0.3	2
2208	Chromosome-scale assembly reveals asymmetric paleo-subgenome evolution and targets for the acceleration of fungal resistance breeding in the nut crop, pecan. <i>Plant Communications</i> , 2021, 2, 100247.	3.6	10
2209	Neofunctionalization of an ancient domain allows parasites to avoid intraspecific competition by manipulating host behaviour. <i>Nature Communications</i> , 2021, 12, 5489.	5.8	15
2210	Modulation of bioelectric cues in the evolution of flying fishes. <i>Current Biology</i> , 2021, 31, 5052-5061.e8.	1.8	16
2212	A high-quality chromosome-level genome of wild <i>Rosa rugosa</i> . <i>DNA Research</i> , 2021, 28, .	1.5	10
2213	Genome assembly and annotation of the tambaqui (<i>Colossoma macropomum</i>): an emblematic fish of the Amazon River Basin. <i>GigaByte</i> , 0, 2021, 1-14.	0.0	3
2214	Long-read metagenomics of multiple displacement amplified DNA of low-biomass human gut phageomes by SACRA preprocessing chimeric reads. <i>DNA Research</i> , 2021, 28, .	1.5	11
2215	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> . <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	7
2216	Characterisation of the whole genome sequence of an avian hepatitis E virus directly from clinical specimens reveals possible recombination events between European and USA strains. <i>Infection, Genetics and Evolution</i> , 2021, 96, 105095.	1.0	5
2218	Genome Sequence Resource for <i>Stagonosporopsis cucurbitacearum</i> , a Cause of Gummy Stem Blight Disease of Watermelon. <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 977-980.	1.4	3
2219	MetaPlatanus: a metagenome assembler that combines long-range sequence links and species-specific features. <i>Nucleic Acids Research</i> , 2021, 49, e130-e130.	6.5	6
2220	Gramtools enables multiscale variation analysis with genome graphs. <i>Genome Biology</i> , 2021, 22, 259.	3.8	15
2221	Genome Evolution of Filamentous Cyanobacterium <i>Nostoc</i> Species: From Facultative Symbiosis to Free Living. <i>Microorganisms</i> , 2021, 9, 2015.	1.6	4
2222	Mitochondrial genome divergence supports an ancient origin of circatidal behaviour in the Anurida <i>maritima</i> (Collembola: Neanuridae) species group. <i>Organisms Diversity and Evolution</i> , 0, , 1.	0.7	1
2223	Downregulated expression of <i>S²-RNase</i> attenuates self-incompatibility in 'Guiyou No. 1' pummelo. <i>Horticulture Research</i> , 2021, 8, 199.	2.9	12
2225	Organelle Genomes and Transcriptomes of Nymphaea Reveal the Interplay between Intron Splicing and RNA Editing. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9842.	1.8	7
2226	Prowler: a novel trimming algorithm for Oxford Nanopore sequence data. <i>Bioinformatics</i> , 2021, 37, 3936-3937.	1.8	11

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2229	Evaluation of probiotic characteristics and whole genome analysis of <i>Pediococcus pentosaceus</i> MR001 for use as probiotic bacteria in shrimp aquaculture. <i>Scientific Reports</i> , 2021, 11, 18334.	1.6	20
2230	NanoHIV: A Bioinformatics Pipeline for Producing Accurate, Near Full-Length HIV Proviral Genomes Sequenced Using the Oxford Nanopore Technology. <i>Cells</i> , 2021, 10, 2577.	1.8	7
2231	The genome sequence provides insights into salt tolerance of <i>Achnatherum splendens</i> (Gramineae), a constructive species of alkaline grassland. <i>Plant Biotechnology Journal</i> , 2022, 20, 116-128.	4.1	18
2233	High contiguity de novo genome assembly and DNA modification analyses for the fungus fly, <i>Sciara coprophila</i> , using single-molecule sequencing. <i>BMC Genomics</i> , 2021, 22, 643.	1.2	17
2234	Nanopore sequencing approach for immunoglobulin gene analysis in chronic lymphocytic leukemia. <i>Scientific Reports</i> , 2021, 11, 17668.	1.6	6
2235	Whole genome sequencing of <i>Enterobacter mori</i> , an emerging pathogen of kiwifruit and the potential genetic adaptation to pathogenic lifestyle. <i>AMB Express</i> , 2021, 11, 129.	1.4	4
2236	Aerobactin Seems To Be a Promising Marker Compared With Unstable RmpA2 for the Identification of Hypervirulent Carbapenem-Resistant <i>Klebsiella pneumoniae</i> : In Silico and In Vitro Evidence. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 709681.	1.8	30
2237	Chromosome-Level Genome Sequence of <i>Aspergillus puulauensis</i> MK2, a Fungus Isolated from a Dead Hard Tick. <i>Microbiology Resource Announcements</i> , 2021, 10, e0037221.	0.3	1
2238	Characterization of the Radiation Desiccation Response Regulon of the Radioresistant Bacterium <i>Deinococcus radiodurans</i> by Integrative Genomic Analyses. <i>Cells</i> , 2021, 10, 2536.	1.8	7
2239	Highly integrated adaptive mechanisms in <i>Spiribacter halalkaliphilus</i> , a bacterium abundant in Chinese soda saline lakes. <i>Environmental Microbiology</i> , 2021, 23, 6463-6482.	1.8	4
2240	Chromosome-scale reference genome assembly of a diploid potato clone derived from an elite variety. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	12
2241	Developmental changes and metabolic reprogramming during establishment of infection and progression of <i>Trypanosoma brucei brucei</i> through its insect host. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009504.	1.3	16
2242	Genomic insights on DNase production in <i>Streptococcus agalactiae</i> ST17 and ST19 strains. <i>Infection, Genetics and Evolution</i> , 2021, 93, 104969.	1.0	2
2243	Rambutan genome revealed gene networks for spine formation and aril development. <i>Plant Journal</i> , 2021, 108, 1037-1052.	2.8	7
2245	Whole Genome Sequence of <i>Alternaria alternata</i> , the Causal Agent of Black Spot of Kiwifruit. <i>Frontiers in Microbiology</i> , 2021, 12, 713462.	1.5	7
2246	<i>Pseudonocardia abyssalis</i> sp. nov. and <i>Pseudonocardia oceani</i> sp. nov., two novel actinomycetes isolated from the deep Southern Ocean. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	11
2248	Genomic basis of high-altitude adaptation in Tibetan <i>Prunus</i> fruit trees. <i>Current Biology</i> , 2021, 31, 3848-3860.e8.	1.8	41
2249	The complete genome sequence of <i>Eimeria tenella</i> (Tyzzer 1929), a common gut parasite of chickens. <i>Wellcome Open Research</i> , 2021, 6, 225.	0.9	14

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2251	The Genome of the CTG(Ser1) Yeast <i>Scheffersomyces stipitis</i> Is Plastic. <i>MBio</i> , 2021, 12, e0187121.	1.8	1
2252	Laccase Directed Lignification Is One of the Major Processes Associated With the Defense Response Against <i>Pythium ultimum</i> Infection in Apple Roots. <i>Frontiers in Plant Science</i> , 2021, 12, 629776.	1.7	12
2253	Phylogeographic reconstruction of the marbled crayfish origin. <i>Communications Biology</i> , 2021, 4, 1096.	2.0	8
2254	Complete mitochondrial genomes of three reef forming <i>Acropora</i> corals (Acroporidae, Scleractinia) from Chagos Archipelago, Indian Ocean. <i>Biodiversity Data Journal</i> , 2021, 9, e72762.	0.4	5
2255	The first case of <i>Planococcus glaciei</i> found in blood, a report from the Czech Republic. <i>Folia Microbiologica</i> , 2022, 67, 121-127.	1.1	2
2256	Genomic and biochemical characterization of antifungal compounds produced by <i>Bacillus subtilis</i> PMB102 against <i>Alternaria brassicicola</i> . <i>Microbiological Research</i> , 2021, 251, 126815.	2.5	18
2257	Heterologous expression of bacterial cytochrome P450 from <i>Microbacterium keratanolyticum</i> ZY and its application in dichloromethane dechlorination. <i>Environmental Pollution</i> , 2021, 287, 117597.	3.7	6
2258	Complete genome of <i>Pelagovum pacificum</i> SM1903T isolated from the marine surface oligotrophic environment. <i>Marine Genomics</i> , 2021, 59, 100874.	0.4	0
2259	Human commensal gut Proteobacteria withstand type VI secretion attacks through immunity protein-independent mechanisms. <i>Nature Communications</i> , 2021, 12, 5751.	5.8	34
2260	The Complete Mitochondrial Genome of One Breeding Strain of Asian Swamp Eel (<i>Monopterus albus</i> ,) Tj ETQq0 0 0 rgBT /Overlock 10 T Synbranchiformes. <i>Genes</i> , 2021, 12, 1567.	1.0	0
2261	In silico comparative genomics analysis of <i>Lactiplantibacillus plantarum</i> DW12, a potential gamma-aminobutyric acid (GABA)-producing strain. <i>Microbiological Research</i> , 2021, 251, 126833.	2.5	11
2262	Comparative genomics of bovine mastitis-origin <i>Staphylococcus aureus</i> strains classified into prevalent human genotypes. <i>Research in Veterinary Science</i> , 2021, 139, 67-77.	0.9	4
2264	Characterization of antibiotic resistance and virulence genes of ocular methicillin-resistant <i>Staphylococcus aureus</i> strains through complete genome analysis. <i>Experimental Eye Research</i> , 2021, 212, 108764.	1.2	4
2265	A haploid diamondback moth (<i>Plutella xylostella</i> L.) genome assembly resolves 31 chromosomes and identifies a diamide resistance mutation. <i>Insect Biochemistry and Molecular Biology</i> , 2021, 138, 103622.	1.2	19
2266	Applications and potentials of nanopore sequencing in the (epi)genome and (epi)transcriptome era. <i>Innovation(China)</i> , 2021, 2, 100153.	5.2	15
2267	Rapidly fatal infection with <i>Bacillus cereus/thuringiensis</i> : genome assembly of the responsible pathogen and consideration of possibly contributing toxins. <i>Diagnostic Microbiology and Infectious Disease</i> , 2021, 101, 115534.	0.8	1
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2271	Characterization of florfenicol resistance genes in the coagulase-negative <i>Staphylococcus</i> (CoNS) isolates and genomic features of a multidrug-resistant <i>Staphylococcus lentus</i> strain H29. <i>Antimicrobial Resistance and Infection Control</i> , 2021, 10, 9.	1.5	14
2272	Complete Genome Sequences of Four Atrazine-Degrading Bacterial Strains, <i>Pseudomonas</i> sp. Strain ADPe, <i>Arthrobacter</i> sp. Strain TES, <i>Variovorax</i> sp. Strain 38R, and <i>Chelatobacter</i> sp. Strain SR38. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	8
2273	Specialized Metabolites Reveal Evolutionary History and Geographic Dispersion of a Multilateral Symbiosis. <i>ACS Central Science</i> , 2021, 7, 292-299.	5.3	23
2274	<i>De novo</i> genome assembly of the tobacco hornworm moth (<i>Manduca sexta</i>). <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	20
2275	<i>Amyntas corticis</i> genome reveals molecular mechanisms behind global distribution. <i>Communications Biology</i> , 2021, 4, 135.	2.0	6
2276	Benchmarking of single-virus genomics: a new tool for uncovering the virosphere. <i>Environmental Microbiology</i> , 2021, 23, 1584-1593.	1.8	7
2277	A new emu genome illuminates the evolution of genome configuration and nuclear architecture of avian chromosomes. <i>Genome Research</i> , 2021, 31, 497-511.	2.4	30
2278	Estimation of pathogenic potential of an environmental <i>Pseudomonas aeruginosa</i> isolate using comparative genomics. <i>Scientific Reports</i> , 2021, 11, 1370.	1.6	5
2279	Complete sequences of <i>Schizosaccharomyces pombe</i> subtelomeres reveal multiple patterns of genome variation. <i>Nature Communications</i> , 2021, 12, 611.	5.8	19
2280	Comprehensive genomic resources related to domestication and crop improvement traits in Lima bean. <i>Nature Communications</i> , 2021, 12, 702.	5.8	39
2282	Catalase impairs <i>Leishmania mexicana</i> development and virulence. <i>Virulence</i> , 2021, 12, 852-867.	1.8	10
2283	PacBio-Based Protocol for Bacterial Genome Assembly. <i>Methods in Molecular Biology</i> , 2021, 2242, 3-14.	0.4	1
2284	Comparative genomics of opportunistic <i>Phialophora</i> species involved in divergent disease types. <i>Mycoses</i> , 2021, 64, 555-568.	1.8	7
2285	HapSolo: an optimization approach for removing secondary haplotigs during diploid genome assembly and scaffolding. <i>BMC Bioinformatics</i> , 2021, 22, 9.	1.2	9
2287	Intraspecies plasmid and genomic variation of <i>Mycobacterium kansasii</i> revealed by the complete genome sequences of two clinical isolates. <i>Microbial Genomics</i> , 2021, 7, .	1.0	7
2288	Telomere length <i>de novo</i> assembly of all 7 chromosomes and mitogenome sequencing of the model entomopathogenic fungus, <i>Metarhizium brunneum</i> , by means of a novel assembly pipeline. <i>BMC Genomics</i> , 2021, 22, 87.	1.2	10
2289	Pursuing Advances in DNA Sequencing Technology to Solve a Complex Genomic Jigsaw Puzzle: The Agglutinin-Like Sequence (ALS) Genes of <i>Candida tropicalis</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 594531.	1.5	9

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2291	Complete Genome Sequences for 36 Canadian <i>Salmonella enterica</i> Serovar Typhimurium and I 1,4,[5],12:i:â€“ Isolates from Clinical and Animal Sources. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	2
2292	Population Genomics of Filamentous Plant Pathogensâ€”A Brief Overview of Research Questions, Approaches, and Pitfalls. <i>Phytopathology</i> , 2021, 111, 12-22.	1.1	6
2294	Draft Genome Sequence of a Highly Pigmented Bacterium <i>Paracoccus marcusii</i> KGP Capable of Producing Galacto-oligosaccharides Synthesising Enzyme. <i>Current Microbiology</i> , 2021, 78, 634-641.	1.0	5
2296	Nanopore Long Read DNA Sequencing of Protozoan Parasites: Hybrid Genome Assembly of <i>Trypanosoma cruzi</i> . <i>Methods in Molecular Biology</i> , 2021, 2369, 3-13.	0.4	5
2297	Integrated hybrid <i>de novo</i> assembly technologies to obtain high-quality pig genome using short and long reads. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	3
2298	Sequencing of the <i>Arabidopsis</i> NOR2 reveals its distinct organization and tissue-specific rRNA ribosomal variants. <i>Nature Communications</i> , 2021, 12, 387.	5.8	32
2299	Construction and integration of three <i>de novo</i> Japanese human genome assemblies toward a population-specific reference. <i>Nature Communications</i> , 2021, 12, 226.	5.8	31
2300	The Mobilome: Metagenomic Analysis of Circular Plasmids, Viruses, and Other Extrachromosomal Elements. <i>Methods in Molecular Biology</i> , 2020, 2075, 253-264.	0.4	6
2301	Haplotype and Repeat Separation in Long Reads. <i>Lecture Notes in Computer Science</i> , 2019, , 103-114.	1.0	1
2302	Strategies for Sequencing and Assembling Grapevine Genomes. <i>Compendium of Plant Genomes</i> , 2019, , 77-88.	0.3	14
2303	Genomics and Transcriptomics Advance in Plant Sciences. <i>Energy, Environment, and Sustainability</i> , 2019, , 419-448.	0.6	5
2304	Complete genome sequence of a boxwood endophyte <i>Burkholderia</i> sp. SSG with broad biotechnological application potential. <i>Biotechnology Reports (Amsterdam, Netherlands)</i> , 2020, 26, e00455.	2.1	8
2305	A chromosome-level reference genome of non-heading Chinese cabbage [<i>Brassica campestris</i> (syn.) <i>Tj</i> ETQq1 1 0.784314 rgBT /Overlaid	2.9	51
2306	A chromosome-scale genome assembly of <i>Isatis indigotica</i> , an important medicinal plant used in traditional Chinese medicine. <i>Horticulture Research</i> , 2020, 7, 18.	2.9	58
2307	The evolutionary origin and domestication history of goldfish (<i>Carassius auratus</i>). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 29775-29785.	3.3	47
2308	<i>Mycena</i> genomes resolve the evolution of fungal bioluminescence. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 31267-31277.	3.3	30
2309	Impact of lossy compression of nanopore raw signal data on basecalling and consensus accuracy. <i>Bioinformatics</i> , 2021, 36, 5313-5321.	1.8	5

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2310	Assembly Graph Browser: interactive visualization of assembly graphs. <i>Bioinformatics</i> , 2019, 35, 3476-3478.	1.8	12
2311	Genome sequence of the oyster mushroom <i>Pleurotus ostreatus</i> strain PC9. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	20
2312	<i>Austropuccinia psidii</i> , causing myrtle rust, has a gigabase-sized genome shaped by transposable elements. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	22
2313	Chromosomal assembly of the nuclear genome of the endosymbiont-bearing trypanosomatid <i>Angomonas deanei</i> . <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, 1-7.	0.8	12
2314	A high-quality <i>de novo</i> genome assembly of one swamp eel (<i>Monopterus albus</i>) strain with PacBio and Hi-C sequencing data. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, 1-9.	0.8	15
2315	Genome analysis of <i>Salmonella enterica</i> serovar Typhimurium bacteriophage L, indicator for StySA (StyLT2III) restriction-modification system action. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	7
2316	Symbiotic and Nonsymbiotic Members of the Genus <i>Ensifer</i> (syn. <i>Sinorhizobium</i>) Are Separated into Two Clades Based on Comparative Genomics and High-Throughput Phenotyping. <i>Genome Biology and Evolution</i> , 2020, 12, 2521-2534.	1.1	30
2317	Chromosomal-Level Genome Assembly of Silver Sillago (<i>Sillago sihama</i>). <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	6
2318	Comparison of long-read methods for sequencing and assembly of a plant genome. <i>GigaScience</i> , 2020, 9, .	3.3	62
2319	Ultracontinuous Single Haplotype Genome Assemblies for the Domestic Cat (<i>Felis catus</i>) and Asian Leopard Cat (<i>Prionailurus bengalensis</i>). <i>Journal of Heredity</i> , 2021, 112, 165-173.	1.0	28
2320	The Genomes of the Livebearing Fish Species <i>Poeciliopsis retropinna</i> and <i>Poeciliopsis turrubarensis</i> Reflect Their Different Reproductive Strategies. <i>Molecular Biology and Evolution</i> , 2020, 37, 1376-1386.	3.5	8
2321	NanoSPC: a scalable, portable, cloud compatible viral nanopore metagenomic data processing pipeline. <i>Nucleic Acids Research</i> , 2020, 48, W366-W371.	6.5	14
2322	First hybrid complete genome of <i>Aeromonas veronii</i> reveals chromosome-mediated novel structural variant mcr-3.30 from a human clinical sample. <i>Access Microbiology</i> , 2020, 2, acmi000103.	0.2	14
2323	Insights into the complete genomes of carbapenem-resistant <i>Acinetobacter baumannii</i> harbouring bla OXA-23, bla OXA-420 and bla NDM-1 genes using a hybrid-assembly approach. <i>Access Microbiology</i> , 2020, 2, acmi000140.	0.2	12
2324	Classification of three corynebacterial strains isolated from the Northern Bald Ibis (<i>Geronticus tinnuncius</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 192. <i>Corynebacterium gerontici</i> sp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 2928-2935.	0.8	21
2325	<i>Corynebacterium endometrii</i> sp. nov., isolated from the uterus of a cow with endometritis. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 146-152.	0.8	12
2326	Description of <i>Erysipelothrix piscisicarius</i> sp. nov., an emergent fish pathogen, and assessment of virulence using a tiger barb (<i>Puntigrus tetrazona</i>) infection model. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 857-867.	0.8	28
2327	<i>Roseovarius arcticus</i> sp. nov., a bacterium isolated from Arctic marine sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 2072-2078.	0.8	8

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2328	Cultivation and description of <i>Duncaniella dubosii</i> sp. nov., <i>Duncaniella freteri</i> sp. nov. and emended description of the species <i>Duncaniella muris</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 3105-3110.	0.8	23
2329	<i>Jeotgalibaca ciconiae</i> sp. nov., isolated from the faeces of an Oriental stork. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 3247-3254.	0.8	12
2330	<i>Chitinimonas arctica</i> sp. nov., isolated from Arctic tundra soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 3455-3461.	0.8	6
2331	<i>Corynebacterium urogenitale</i> sp. nov. isolated from the genital tract of a cow. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 3625-3632.	0.8	9
2332	<i>Muribaculum gordoncarteri</i> sp. nov., an anaerobic bacterium from the faeces of C57BL/6J mice. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 4725-4729.	0.8	19
2333	<i>Sphingosinithalassobacter tenebrarum</i> sp. nov., isolated from a deep-sea cold seep. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 5561-5566.	0.8	11
2334	<i>Sporofaciens musculi</i> gen. nov., sp. nov., a novel bacterium isolated from the caecum of an obese mouse. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 71, .	0.8	15
2335	Virulence genes in isolates of <i>Klebsiella pneumoniae</i> from the UK during 2016, including among carbapenemase gene-positive hypervirulent K1-ST23 and "non-hypervirulent"™ types ST147, ST15 and ST383. <i>Journal of Medical Microbiology</i> , 2018, 67, 118-128.	0.7	94
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2777	TipToft: detecting plasmids contained in uncorrected long read sequencing data. <i>Journal of Open Source Software</i> , 2019, 4, 1021.	2.0	1
2782	Draft genome assembly and transcriptome sequencing of the golden algae <i>Hydrurus foetidus</i> (Chrysophyceae). <i>F1000Research</i> , 2019, 8, 401.	0.8	3
2790	<i>Kaistella flava</i> sp. nov., isolated from Antarctic tundra soil, and emended descriptions of <i>Kaistella yonginensis</i> , <i>Kaistella jeonii</i> , <i>Kaistella antarctica</i> and <i>Kaistella chaponensis</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 71, .	0.8	11
2794	<i>Pseudomonas bijjeensis</i> sp. nov., isolated from cornfield soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 71, .	0.8	8

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2915	MosaicFlye: Resolving Long Mosaic Repeats Using Long Reads. <i>Lecture Notes in Computer Science</i> , 2020, , 226-228.	1.0	1
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3014	Characterization of nuclear mitochondrial insertions in the whole genomes of primates. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa089.	1.5	14
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3034	Identification of Two Myrosinases from a <i>Leclercia adecarboxylata</i> Strain and Investigation of Its Tolerance Mechanism to Glucosinolate Hydrolysate. <i>Journal of Agricultural and Food Chemistry</i> , 2021, 69, 14151-14164.	2.4	8
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3057	Genome-Guided Discovery of Natural Products through Multiplexed Low-Coverage Whole-Genome Sequencing of Soil Actinomycetes on Oxford Nanopore Flongle. <i>MSystems</i> , 2021, 6, e0102021.	1.7	6
3058	A draft genome assembly of "Cas" (<i>Psidium friedrichsthalianum</i> (O. Berg) Nied.): an indigenous crop of Costa Rica untapped. <i>Genetic Resources and Crop Evolution</i> , 2022, 69, 39-47.	0.8	3
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3081	Telomere-to-telomere genome assembly of asparaginase-producing <i>Trichoderma simmonsii</i> . <i>BMC Genomics</i> , 2021, 22, 830.	1.2	9
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3085	Chromosome-Scale Genome Assembly for Chinese Sour Jujube and Insights Into Its Genome Evolution and Domestication Signature. <i>Frontiers in Plant Science</i> , 2021, 12, 773090.	1.7	20
3086	Efficient iterative Hi-C scaffolder based on N-best neighbors. <i>BMC Bioinformatics</i> , 2021, 22, 569.	1.2	12
3088	Complete Genome Sequence of <i>Megamonas funiformis</i> Strain 1CBH44, Isolated from Human Feces. <i>Microbiology Resource Announcements</i> , 2021, 10, e0078521.	0.3	0
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3090	Aerobiology from an Inactive Pyrite Mine: the Genome Sequence of the Airborne <i>Pseudomonas</i> sp. Strain L5B5. <i>Microbiology Resource Announcements</i> , 2021, 10, e0102921.	0.3	2
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3100	Rapid Genome Evolution and Adaptation of <i>Thlaspi arvense</i> Mediated by Recurrent RNA-Based and Tandem Gene Duplications. <i>Frontiers in Plant Science</i> , 2021, 12, 772655.	1.7	8
3101	Genome sequences of five <i>Sitopsis</i> species of <i>Aegilops</i> and the origin of polyploid wheat B subgenome. <i>Molecular Plant</i> , 2022, 15, 488-503.	3.9	84
3102	Whole Genome Assembly of Human Papillomavirus by Nanopore Long-Read Sequencing. <i>Frontiers in Genetics</i> , 2021, 12, 798608.	1.1	5
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3910	Biodegradation of polyester polyurethane by the marine fungus <i>Cladosporium halotolerans</i> 6UPA1. <i>Journal of Hazardous Materials</i> , 2022, 437, 129406.	6.5	21
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3913	Characterization and Genomic Analysis of a Nitrate Reducing Bacterium from Shale Oil in the Ordos Basin and the Associated Biosurfactant Production. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
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3920	Comparative genomics of <i>Acinetobacter baumannii</i> and therapeutic bacteriophages from a patient undergoing phage therapy. <i>Nature Communications</i> , 2022, 13, .	5.8	20
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3928	Identification of a Stable Chromosomal Tandem Multicopy of <i>bla</i> _{VIM-63} , a New <i>bla</i> _{VIM-2} Carbapenemase. <i>Journal of Bacteriology</i> , 2022, 204, .	1.0	1
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3937	Emergence of plasmid-mediated tigecycline, β -lactam and florfenicol resistance genes tet(X), blaOXA-347 and floR in <i>Riemerella anatipestifer</i> isolated in China. <i>Poultry Science</i> , 2022, 101, 102057.	1.5	7

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4076	Genomic Analysis Reveals Adaptation of <i>Vibrio campbellii</i> to the Hadal Ocean. <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	5
4077	Chromosome-Level Genome Assembly of <i>Callitettix versicolor</i> (Rice Spittlebug). <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	2
4078	Assembly of high-quality genomes of the locoweed <i>Oxytropis ochrocephala</i> and its endophyte <i>Alternaria oxytropis</i> provides new evidence for their symbiotic relationship and swainsonine biosynthesis. <i>Molecular Ecology Resources</i> , 2023, 23, 253-272.	2.2	4
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4081	Draft Genome Sequence of the Freshwater Diatom <i>Fragilaria crotonensis</i> SAG 28.96. <i>Microbiology Resource Announcements</i> , 2022, 11, .	0.3	2
4082	The isolation of a novel <i>Streptomyces</i> <i>termitum</i> and identification its active substance against fish pathogens. <i>Reproduction and Breeding</i> , 2022, 2, 95-105.	0.8	5
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4086	Safety evaluation and comparative genomics analysis of the industrial strain <i>Aspergillus flavus</i> SU-16 used for Huangjiu brewing. <i>International Journal of Food Microbiology</i> , 2022, 380, 109859.	2.1	5
4087	A novel <i>Diaphorobacter</i> sp. strain isolated from saponification wastewater shows highly efficient phenanthrene degradation. <i>Environmental Research</i> , 2022, 214, 114047.	3.7	5
4088	JACC-FPGA: A hardware accelerator for Jaccard similarity estimation using FPGAs in the cloud. <i>Future Generation Computer Systems</i> , 2023, 138, 26-42.	4.9	3
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4091	Functional genomics analysis reveals the evolutionary adaptation and demographic history of pygmy lorises. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	5
4092	A chromosome-level genome assembly of the highly heterozygous sea urchin <i>Echinometra</i> sp. EZ reveals adaptation in the regulatory regions of stress response genes. <i>Genome Biology and Evolution</i> , 0, , .	1.1	1
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4096	The chromosome-scale genome of the raccoon dog: Insights into its evolutionary characteristics. <i>IScience</i> , 2022, 25, 105117.	1.9	6
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4098	The genetic adaptations of <i>Toxoptera aurantii</i> facilitated its rapid multiple plant hosts dispersal and invasion. <i>Genomics</i> , 2022, 114, 110472.	1.3	2
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4101	Novel Methods for Studying the Structure and Function of Hot Desert Microorganisms and Their Communities. <i>Ecological Studies</i> , 2022, , 37-63.	0.4	0
4102	Development of Abiotic Stress Resistant Grapevine Varieties. , 2022, , 61-159.		2
4103	Nanopore quality score resolution can be reduced with little effect on downstream analysis. <i>Bioinformatics Advances</i> , 2022, 2, .	0.9	3
4104	Advances in antimicrobial resistance testing. <i>Advances in Clinical Chemistry</i> , 2022, , 1-68.	1.8	2
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4106	<i>>De novo</i> assembly of plant complete genomes. , 2022, 1, 1-8.		4
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4117	The genus <i>Serratia</i> revisited by genomics. <i>Nature Communications</i> , 2022, 13, .	5.8	21
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4119	Prokaryotes of renowned Karlovy Vary (Carlsbad) thermal springs: phylogenetic and cultivation analysis. <i>Environmental Microbiomes</i> , 2022, 17, .	2.2	7
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4123	Isolation, Identification and Characterization of Growth Parameters of <i>Pseudomonas putida</i> HSM-C2 with Coumarin-Degrading Bacteria. <i>Molecules</i> , 2022, 27, 6007.	1.7	2
4124	Complete Genome Sequence of <i>Burkholderia gladioli</i> BK04 with Biocontrol Potential Against Cotton Verticillium Wilt (<i>Verticillium dahliae</i>). <i>Molecular Plant-Microbe Interactions</i> , 0, , .	1.4	2
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4132	Nebulous without <i>white</i> : annotated long-read genome assembly and CRISPR/Cas9 genome engineering in <i>Drosophila nebulosa</i> . <i>G3: Genes, Genomes, Genetics</i> , 0, , .	0.8	3
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4138	Isolation and characterization of piezotolerant fungi from Mariana Trench sediment. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2022, 190, 103873.	0.6	4
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4144	Blue Light-Dependent Pre-mRNA Splicing Controls Pigment Biosynthesis in the Mushroom <i>Terana caerulea</i> . <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	5
4145	A High-quality genome assembly of <i>Lactarius hatsudake</i> strain JH5. <i>G3: Genes, Genomes, Genetics</i> , 0, , .	0.8	0
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4148	NanoCoV19: An analytical pipeline for rapid detection of severe acute respiratory syndrome coronavirus 2. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	2
4149	Dynamic genome evolution in a model fern. <i>Nature Plants</i> , 2022, 8, 1038-1051.	4.7	56
4151	<i>Moraxella nasovis</i> sp. nov., isolated from a sheep with respiratory disease. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	5
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4157	Development of a stable semi-continuous lipid production system of an oleaginous <i>Chlamydomonas</i> sp. mutant using multi-omics profiling. , 2022, 15, .		1
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4159	Genome sequence assembly algorithms and misassembly identification methods. <i>Molecular Biology Reports</i> , 2022, 49, 11133-11148.	1.0	2
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4161	The genome of <i>Areca catechu</i> provides insights into sex determination of monoecious plants. <i>New Phytologist</i> , 2022, 236, 2327-2343.	3.5	12
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4167	A genome for <i>Cissus</i> illustrates features underlying its evolutionary success in dry savannas. <i>Horticulture Research</i> , 2022, 9, .	2.9	3
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4170	Chromosome-level genome assembly and resequencing of camphor tree (<i>Cinnamomum</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tj biosynthesis of <i>Cinnamomum</i> . <i>Horticulture Research</i> , 2022, 9, .	2.9	5
4171	Comparative Genomic Analysis of Agarolytic <i>Flavobacterium faecale</i> WV33T. <i>International Journal of Molecular Sciences</i> , 2022, 23, 10884.	1.8	2
4172	Top-Down, Knowledge-Based Genetic Reduction of Yeast Central Carbon Metabolism. <i>MBio</i> , 2022, 13, .	1.8	2
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4177	Whole-Genome Sequence Resource of <i>Phytophthora pini</i> , the Causal Pathogen of Foliage Blight and Shoot Dieback of <i>Rhododendron pulchrum</i> . <i>Molecular Plant-Microbe Interactions</i> , 0, .	1.4	3
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4181	Genome Sequence of <i>Halomonas</i> sp. Strain MS1, a Metallophore-Producing, Algal Growth-Promoting Marine Bacterium Isolated from the Green Seaweed <i>Ulva mutabilis</i> (Chlorophyta). <i>Microbiology Resource Announcements</i> , 2022, 11, .	0.3	1
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4183	The plasmid-encoded lactose operon plays a vital role in the acid production rate of <i>Lactocaseibacillus casei</i> during milk beverage fermentation. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
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4186	Phylogenomics of a <i>Saccharomyces cerevisiae</i> cocoa strain reveals adaptation to a West African fermented food population. <i>IScience</i> , 2022, 25, 105309.	1.9	1
4187	A highly contiguous, scaffold-level nuclear genome assembly for the fever tree (<i>Cinchona pubescens</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 0.0		
4189	The complex genome and adaptive evolution of polyploid Chinese pepper (<i>Zanthoxylum armatum</i>) Tj ETQq1 1 0.784314 rgBT 0 4.1 10		
4190	MSIM: A Highly Parallel Near-Memory Accelerator for MinHash Sketch. , 2022, , .		1
4191	Whole genome analysis of <i>Enterobacter cloacae</i> Rs-2 and screening of genes related to plant-growth promotion. <i>Environmental Science and Pollution Research</i> , 2023, 30, 21548-21564.	2.7	2
4192	Phylogenomics provides insights into the evolution of cactophily and host plant shifts in <i>Drosophila</i> . <i>Molecular Phylogenetics and Evolution</i> , 2023, 178, 107653.	1.2	4
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4197	Three Distinct Annotation Platforms Differ in Detection of Antimicrobial Resistance Genes in Long-Read, Short-Read, and Hybrid Sequences Derived from Total Genomic DNA or from Purified Plasmid DNA. <i>Antibiotics</i> , 2022, 11, 1400.	1.5	1
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4201	Draft Genome Sequence of the Yeast <i>Torulaspota quercuum</i> Strain UCD657, Isolated from Soil in Ireland. <i>Microbiology Resource Announcements</i> , 0, , .	0.3	0
4202	Draft Whole-Genome Sequence of <i>Penicillium simplicissimum</i> A4, a Putative Endophyte from <i>Echium plantagineum</i> . <i>Microbiology Resource Announcements</i> , 0, , .	0.3	0
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4211	Ancient homomorphy of molluscan sex chromosomes sustained by reversible sex-biased genes and sex determiner translocation. <i>Nature Ecology and Evolution</i> , 2022, 6, 1891-1906.	3.4	23
4214	The chromosome-level genome of <i>Akebia trifoliata</i> as an important resource to study plant evolution and environmental adaptation in the Cretaceous. <i>Plant Journal</i> , 2022, 112, 1316-1330.	2.8	14
4215	Mirubactin C rescues the lethal effect of cell wall biosynthesis mutations in <i>Bacillus subtilis</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
4216	Whole-Genome Sequence of <i>Sediminibacterium</i> sp. Strain TEGAF015, Isolated from a Shallow Eutrophic Freshwater Lake in Japan. <i>Microbiology Resource Announcements</i> , 2022, 11, .	0.3	1
4217	The genome and lifestage-specific transcriptomes of a plant-parasitic nematode and its host reveal susceptibility genes involved in trans-kingdom synthesis of vitamin B5. <i>Nature Communications</i> , 2022, 13, .	5.8	28
4220	HaploDMF: viral haplotype reconstruction from long reads via deep matrix factorization. <i>Bioinformatics</i> , 2022, 38, 5360-5367.	1.8	1
4222	<i>Vibrio ostreae</i> sp. nov., a novel gut bacterium isolated from a Yellow Sea oyster. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	4

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4224	Karyotype variation, spontaneous genome rearrangements affecting chemical insensitivity, and expression level polymorphisms in the plant pathogen <i>Phytophthora infestans</i> revealed using its first chromosome-scale assembly. <i>PLoS Pathogens</i> , 2022, 18, e1010869.	2.1	4
4225	Molecular mechanisms of plant growth promotion for methylotrophic <i>Bacillus aryabhatai</i> LAD. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
4226	Endophytic Bacteria Associated with <i>Origanumâheracleoticum</i> L. (Lamiaceae) Seeds. <i>Microorganisms</i> , 2022, 10, 2086.	1.6	3
4227	A rapid bacterial pathogen and antimicrobial resistance diagnosis workflow using Oxford nanopore adaptive sequencing method. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	16
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4230	Genome sequence of the entomopathogenic <i>Serratia entomophila</i> isolate 626 and characterisation of the species specific itaconate degradation pathway. <i>BMC Genomics</i> , 2022, 23, .	1.2	4
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