

# progressiveMauve: Multiple Genome Alignment with G

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Pan-genome sequence analysis using Panseq; an online tool for the rapid analysis of core and accessory genomic regions. BMC Bioinformatics, 2010, 11, 461.	2.6	249
2	Inference of Homologous Recombination in Bacteria Using Whole-Genome Sequences. Genetics, 2010, 186, 1435-1449.	2.9	155
3	Inferring Transcript Phylogenies. , 2011, , .		3
4	Genomic and Proteomic Characterization of the Broad-Host-Range Salmonella Phage PVP-SE1: Creation of a New Phage Genus. Journal of Virology, 2011, 85, 11265-11273.	3.4	80
5	Complete Genome Sequence of Rickettsia heilongjiangensis, an Emerging Tick-Transmitted Human Pathogen. Journal of Bacteriology, 2011, 193, 5564-5565.	2.2	22
6	Two New Complete Genome Sequences Offer Insight into Host and Tissue Specificity of Plant Pathogenic Xanthomonas spp. Journal of Bacteriology, 2011, 193, 5450-5464.	2.2	189
7	Design of multiple sequence alignment algorithms on parallel, distributed memory supercomputers. , 2011, 2011, 924-7.		9
8	Exploring the common molecular basis for the universal DNA mutation bias: Revival of LÃ¶wdin mutation model. Biochemical and Biophysical Research Communications, 2011, 409, 367-371.	2.1	24
9	The pathogenic potential of Yersinia enterocolitica 1A. International Journal of Medical Microbiology, 2011, 301, 556-561.	3.6	44
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20	Identification of Salmonella enterica species- and subgroup-specific genomic regions using Panseq 2.0. Infection, Genetics and Evolution, 2011, 11, 2151-2161.	2.3	10
21	Everything at once: Comparative analysis of the genomes of bacterial pathogens. Veterinary Microbiology, 2011, 153, 13-26.	1.9	12
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108	Characterization of the <i>Salmonella</i> bacteriophage vB_SenS-Ent1. <i>Journal of General Virology</i> , 2012, 93, 2046-2056.	2.9	30
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111	Multifractal analysis of HIV-1 genomes. <i>Molecular Phylogenetics and Evolution</i> , 2012, 62, 756-763.	2.7	15
112	Transforming clinical microbiology with bacterial genome sequencing. <i>Nature Reviews Genetics</i> , 2012, 13, 601-612.	16.3	684
113	Ribosomal multilocus sequence typing: universal characterization of bacteria from domain to strain. <i>Microbiology (United Kingdom)</i> , 2012, 158, 1005-1015.	1.8	497
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117	An Evolutionary Link between Natural Transformation and CRISPR Adaptive Immunity. <i>MBio</i> , 2012, 3, .	4.1	70
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119	Genome characterisation of the genus <i>Francisella</i> reveals insight into similar evolutionary paths in pathogens of mammals and fish. <i>BMC Genomics</i> , 2012, 13, 268.	2.8	121
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121	Analysis of the <i>Lactobacillus casei</i> supragenome and its influence in species evolution and lifestyle adaptation. <i>BMC Genomics</i> , 2012, 13, 533.	2.8	144
122	Comparative genomics of the classical <i>Bordetella</i> subspecies: the evolution and exchange of virulence-associated diversity amongst closely related pathogens. <i>BMC Genomics</i> , 2012, 13, 545.	2.8	99
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138	Comparative Genomics of Plant-Associated <i>Pseudomonas</i> spp.: Insights into Diversity and Inheritance of Traits Involved in Multitrophic Interactions. <i>PLoS Genetics</i> , 2012, 8, e1002784.	3.5	578
139	Molecular tracing of the emergence, adaptation, and transmission of hospital-associated methicillin-resistant <i>Staphylococcus aureus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 9107-9112.	7.1	174
140	Genome sequence of temperate bacteriophage <i>Psymv2</i> from Antarctic Dry Valley soil isolate <i>Psychrobacter</i> sp. MV2. <i>Extremophiles</i> , 2012, 16, 715-726.	2.3	30
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142	Whole-genome analysis of diverse <i>Chlamydia trachomatis</i> strains identifies phylogenetic relationships masked by current clinical typing. <i>Nature Genetics</i> , 2012, 44, 413-419.	21.4	279
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1078	Comparative analysis of the mitochondrial genomes of <i>Colletotrichum gloeosporioides sensu lato</i> : insights into the evolution of a fungal species complex interacting with diverse plants. <i>BMC Genomics</i> , 2017, 18, 171.	2.8	35
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1080	Comparative genome and transcriptome analysis reveals distinctive surface characteristics and unique physiological potentials of <i>Pseudomonas aeruginosa</i> ATCC 27853. <i>BMC Genomics</i> , 2017, 18, 459.	2.8	33
1081	Comparative genomics of <i>Enterococcus</i> spp. isolated from bovine feces. <i>BMC Microbiology</i> , 2017, 17, 52.	3.3	83
1082	High-quality draft genome sequence of <i>Rhizobium mesoamericanum</i> strain STM6155, a <i>Mimosa pudica</i> microsymbiont from New Caledonia. <i>Standards in Genomic Sciences</i> , 2017, 12, 7.	1.5	2
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1084	Chromosomal features of <i>Escherichia coli</i> serotype O2:K2, an avian pathogenic <i>E. coli</i> . <i>Standards in Genomic Sciences</i> , 2017, 12, 33.	1.5	5
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1092	The use of Oxford Nanopore native barcoding for complete genome assembly. <i>GigaScience</i> , 2017, 6, 1-6.	6.4	19
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1096	Resequencing of the <i>Leishmania infantum</i> (strain JPCM5) genome and de novo assembly into 36 contigs. <i>Scientific Reports</i> , 2017, 7, 18050.	3.3	47
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1099	Computational Methods in Microbial Population Genomics. <i>Population Genomics</i> , 2017, , 3-29.	0.5	2
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1101	Development of Chloroplast and Nuclear DNA Markers for Chinese Oaks ( <i>Quercus</i> Subgenus <i>Quercus</i> ) and Assessment of Their Utility as DNA Barcodes. <i>Frontiers in Plant Science</i> , 2017, 8, 816.	3.6	64
1102	Phenotypic and Genotypic Features of a <i>Salmonella</i> Heidelberg Strain Isolated in Broilers in Brazil and Their Possible Association to Antibiotics and Short-Chain Organic Acids Resistance and Susceptibility. <i>Frontiers in Veterinary Science</i> , 2017, 4, 184.	2.2	7
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1106	The Complete Chloroplast Genome Sequences of Six Rehmannia Species. Genes, 2017, 8, 103.	2.4	78
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1117	Comparative Genomic Characterization of the Highly Persistent and Potentially Virulent Cronobacter sakazakii ST83, CC65 Strain H322 and Other ST83 Strains. Frontiers in Microbiology, 2017, 8, 1136.	3.5	31
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1119	Comparative Analysis of the Flavobacterium columnare Genomovar I and II Genomes. Frontiers in Microbiology, 2017, 8, 1375.	3.5	37
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1121	Comparative Sequence Analysis of Multidrug-Resistant IncA/C Plasmids from Salmonella enterica. Frontiers in Microbiology, 2017, 8, 1459.	3.5	50

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1123	Adaptation of Surface-Associated Bacteria to the Open Ocean: A Genomically Distinct Subpopulation of <i>Phaeobacter gallaeciensis</i> Colonizes Pacific Mesozooplankton. <i>Frontiers in Microbiology</i> , 2017, 8, 1659.	3.5	28
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1128	Genomic Comparisons Reveal Microevolutionary Differences in <i>Mycobacterium abscessus</i> Subspecies. <i>Frontiers in Microbiology</i> , 2017, 8, 2042.	3.5	16
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1130	Delineating the Origins of <i>Vibrio parahaemolyticus</i> Isolated from Outbreaks of Acute Hepatopancreatic Necrosis Disease in Asia by the Use of Whole Genome Sequencing. <i>Frontiers in Microbiology</i> , 2017, 8, 2354.	3.5	15
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1134	Genomic divergence and cohesion in a species of pelagic freshwater bacteria. <i>BMC Genomics</i> , 2017, 18, 794.	2.8	14
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1136	Draft Genome Sequence of <i>Lactobacillus curvatus</i> FLECO3, a Meat-Borne Isolate from Beef Carpaccio Packaged in a Modified Atmosphere. <i>Genome Announcements</i> , 2017, 5, .	0.8	5
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1143	Comparative genomic analysis between <i>Corynebacterium pseudotuberculosis</i> strains isolated from buffalo. PLoS ONE, 2017, 12, e0176347.	2.5	30
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1150	Genomics-enabled analysis of the emergent disease cotton bacterial blight. PLoS Genetics, 2017, 13, e1007003.	3.5	36
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1156	Genome characterization of a novel binary toxin-positive strain of <i>Clostridium difficile</i> and comparison with the epidemic O27 and O78 strains. Gut Pathogens, 2017, 9, 42.	3.4	15
1157	Draft genome sequences of <i>Bradyrhizobium shewense</i> sp. nov. ERR11T and <i>Bradyrhizobium yuanmingense</i> CCBAU 10071T. Standards in Genomic Sciences, 2017, 12, 74.	1.5	29

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1159	Draft genome sequence of <i>Pseudomonas extremaustralis</i> strain USBA-GBX 515 isolated from Superparamo soil samples in Colombian Andes. <i>Standards in Genomic Sciences</i> , 2017, 12, 78.	1.5	7
1160	Draft genome sequence of <i>Dethiosulfovibrio salsuginis</i> DSM 21565T an anaerobic, slightly halophilic bacterium isolated from a Colombian saline spring. <i>Standards in Genomic Sciences</i> , 2017, 12, 86.	1.5	0
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1162	Fatal Outbreak in Tonkean Macaques Caused by Possibly Novel Orthopoxvirus, Italy, January 20151. <i>Emerging Infectious Diseases</i> , 2017, 23, 1941-1949.	4.3	27
1163	Whole-Genome Comparative Analysis of <i>Salmonella enterica</i> Serovar Newport Strains Reveals Lineage-Specific Divergence. <i>Genome Biology and Evolution</i> , 2017, 9, 1047-1050.	2.5	46
1164	Whole-Genome Analysis of <i>Bartonella ancashensis</i> , a Novel Pathogen Causing Verruga Peruana, Rural Ancash Region, Peru. <i>Emerging Infectious Diseases</i> , 2017, 23, 430-438.	4.3	21
1165	Coccolithoviruses: A Review of Cross-Kingdom Genomic Thievery and Metabolic Thuggery. <i>Viruses</i> , 2017, 9, 52.	3.3	27
1166	Isolation and Characterization of a <i>Shewanella</i> Phage–Host System from the Gut of the Tunicate, <i>Ciona intestinalis</i> . <i>Viruses</i> , 2017, 9, 60.	3.3	18
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1173	Culture-Facilitated Comparative Genomics of the Facultative Symbiont <i>Hamiltonella defensa</i> . <i>Genome Biology and Evolution</i> , 2018, 10, 786-802.	2.5	37
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1180	First Description in Greece of <i>Staphylococcus</i> -Positive <i>Staphylococci</i> Causing Subclinical Mastitis in Ewes. <i>Microbial Drug Resistance</i> , 2018, 24, 1050-1053.	2.0	1
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1183	Draft Genome Sequences of Four Clinical <i>Legionella pneumophila</i> Isolates from Ontario, Canada. <i>Genome Announcements</i> , 2018, 6, .	0.8	0
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1188	Retrospective genome-wide comparisons of <i>Salmonella enterica</i> serovar Enteritidis from suspected outbreaks in Singapore. <i>Infection, Genetics and Evolution</i> , 2018, 61, 229-233.	2.3	5
1189	Sequence Analysis of IncA/C and Inc11 Plasmids Isolated from Multidrug-Resistant <i>Salmonella</i> Newport Using Single-Molecule Real-Time Sequencing. <i>Foodborne Pathogens and Disease</i> , 2018, 15, 361-371.	1.8	16
1190	The reduced genome of <i>Candidatus</i> Kinetoplastibacterium sorsogonicus, the endosymbiont of <i>Kentomonas sorsogonicus</i> (Trypanosomatidae): loss of the haem-synthesis pathway. <i>Parasitology</i> , 2018, 145, 1287-1293.	1.5	20
1191	<i>In Situ</i> Analyses Directly in Diarrheal Stool Reveal Large Variations in Bacterial Load and Active Toxin Expression of Enterotoxigenic <i>Escherichia coli</i> and <i>Vibrio cholerae</i> . <i>MSphere</i> , 2018, 3, .	2.9	14
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1193	Complete sequence of the tumor-inducing plasmid pTiChry5 from the hypervirulent <i>Agrobacterium tumefaciens</i> strain Chry5. <i>Plasmid</i> , 2018, 96-97, 1-6.	1.4	15



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1195	The Birth and Demise of the IS <i>&lt;i&gt;Apl1&lt;/i&gt;</i> - <i>&lt;i&gt;mcr-1&lt;/i&gt;</i> -IS <i>&lt;i&gt;Apl1&lt;/i&gt;</i> Composite Transposon: the Vehicle for Transferable Colistin Resistance. <i>MBio</i> , 2018, 9, .	4.1	103
1196	Genomic and functional characterisation of two <i>Enterococcus</i> strains isolated from Cotija cheese and their potential role in ripening. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 2251-2267.	3.6	14
1197	Draft Genome Sequences of Four <i>&lt;i&gt;Salmonella enterica&lt;/i&gt;</i> subsp. <i>&lt;i&gt;enterica&lt;/i&gt;</i> Serovar Enteritidis Strains Implicated in Infections of Avian and Human Hosts. <i>Genome Announcements</i> , 2018, 6, .	0.8	1
1198	Screening and Genomic Characterization of Filamentous Hemagglutinin-Deficient <i>Bordetella pertussis</i> . <i>Infection and Immunity</i> , 2018, 86, .	2.2	27
1199	Biochemical and genetic characterization of a novel metallo- $\beta$ -lactamase from marine bacterium <i>Erythrobacter litoralis</i> HTCC 2594. <i>Scientific Reports</i> , 2018, 8, 803.	3.3	13
1200	Draft genome of the fungicidal biological control agent <i>Burkholderia anthina</i> strain XXVI. <i>Archives of Microbiology</i> , 2018, 200, 803-810.	2.2	14
1201	Comparative genomics reveals new single-nucleotide polymorphisms that can assist in identification of adherent-invasive <i>Escherichia coli</i> . <i>Scientific Reports</i> , 2018, 8, 2695.	3.3	46
1202	The mycobiota of the sand fly <i>&lt;i&gt;Phlebotomus perniciosus&lt;/i&gt;</i> : Involvement of yeast symbionts in uric acid metabolism. <i>Environmental Microbiology</i> , 2018, 20, 1064-1077.	3.8	14
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1206	Sequence-Based Synteny Analysis of Multiple Large Genomes. <i>Methods in Molecular Biology</i> , 2018, 1704, 317-329.	0.9	2
1207	<i>Elizabethkingia anophelis</i> Is the Dominant <i>Elizabethkingia</i> Species Found in Blood Cultures in Singapore. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	3.9	51
1208	Aureo Wiki Ìµ The repository of the <i>Staphylococcus aureus</i> research and annotation community. <i>International Journal of Medical Microbiology</i> , 2018, 308, 558-568.	3.6	99
1209	Characterization of KPC-Encoding Plasmids from <i>Enterobacteriaceae</i> Isolated in a Czech Hospital. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	3.2	13
1210	Transmission and persistence of IncF conjugative plasmids in the gut microbiota of full-term infants. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	2.7	15
1211	Genomic characterization of key bacteriophages to formulate the potential biocontrol agent to combat enteric pathogenic bacteria. <i>Archives of Microbiology</i> , 2018, 200, 611-622.	2.2	10



#	ARTICLE	IF	CITATIONS
1212	Complete genome sequence of <i>Tsukamurella</i> sp. MH1: A wide-chain length alkane-degrading actinomycete. <i>Journal of Biotechnology</i> , 2018, 268, 1-5.	3.8	5
1213	Genetic Competence Drives Genome Diversity in <i>Bacillus subtilis</i> . <i>Genome Biology and Evolution</i> , 2018, 10, 108-124.	2.5	67
1214	Organellar phylogenomics inform systematics in the green algal family Hydrodictyaceae (Chlorophyceae) and provide clues to the complex evolutionary history of plastid genomes in the green algal tree of life. <i>American Journal of Botany</i> , 2018, 105, 315-329.	1.7	23
1215	Draft Genome Sequence of <i>Bacillus pumilus</i> SCAL1, an Endophytic Heat-Tolerant Plant Growth-Promoting Bacterium. <i>Genome Announcements</i> , 2018, 6, .	0.8	12
1216	ClustAGE: a tool for clustering and distribution analysis of bacterial accessory genomic elements. <i>BMC Bioinformatics</i> , 2018, 19, 150.	2.6	40
1217	Analysis of <i>Theileria orientalis</i> draft genome sequences reveals potential species-level divergence of the Ikeda, Chitose and Buffeli genotypes. <i>BMC Genomics</i> , 2018, 19, 298.	2.8	24
1218	A hybrid reference-guided de novo assembly approach for generating <i>Cyclospora</i> mitochondrion genomes. <i>Gut Pathogens</i> , 2018, 10, 15.	3.4	17
1219	Ancient DNA study reveals HLA susceptibility locus for leprosy in medieval Europeans. <i>Nature Communications</i> , 2018, 9, 1569.	12.8	67
1220	Male-killing toxin in a bacterial symbiont of <i>Drosophila</i> . <i>Nature</i> , 2018, 557, 252-255.	27.8	111
1221	A new strategy to infer circularity applied to four new complete frog mitogenomes. <i>Ecology and Evolution</i> , 2018, 8, 4011-4018.	1.9	15
1222	Whole-genome comparison of high and low virulent <i>Staphylococcus aureus</i> isolates inducing implant-associated bone infections. <i>International Journal of Medical Microbiology</i> , 2018, 308, 505-513.	3.6	15
1223	Genomic characterization of endemic <i>Salmonella enterica</i> serovar Typhimurium and <i>Salmonella enterica</i> serovar I 4,[5],12:i:- isolated in Malaysia. <i>Infection, Genetics and Evolution</i> , 2018, 62, 109-121.	2.3	6
1224	Comparison of the first whole genome sequence of <i>Haemophilus quentini</i> ™ with two new strains of <i>Haemophilus quentini</i> ™ and other species of <i>Haemophilus</i> . <i>Genome</i> , 2018, 61, 379-385.	2.0	4
1225	A Single-Nucleotide Insertion in a Drug Transporter Gene Induces a Thermotolerance Phenotype in <i>Gluconobacter frateurii</i> by Increasing the NADPH/NADP + Ratio via Metabolic Change. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	15
1226	Hitting with a BAM: Selective Killing by Lectin-Like Bacteriocins. <i>MBio</i> , 2018, 9, .	4.1	48
1227	Resolving the complete genome of <i>Kuenenia stuttgartiensis</i> from a membrane bioreactor enrichment using Single-Molecule Real-Time sequencing. <i>Scientific Reports</i> , 2018, 8, 4580.	3.3	48
1228	<i>Exiguobacterium</i> : an overview of a versatile genus with potential in industry and agriculture. <i>Critical Reviews in Biotechnology</i> , 2018, 38, 141-156.	9.0	120
1229	The discovery of the virulence gene <i>ToxA</i> in the wheat and barley pathogen <i>Bipolaris sorokiniana</i> . <i>Molecular Plant Pathology</i> , 2018, 19, 432-439.	4.2	122

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1231	Genomic Analysis of <i>Bacillus</i> sp. Strain B25, a Biocontrol Agent of Maize Pathogen <i>Fusarium verticillioides</i> . <i>Current Microbiology</i> , 2018, 75, 247-255.	2.2	40
1232	Organization of plastid genomes in the freshwater red algal order Batrachospermales (Rhodophyta). <i>Journal of Phycology</i> , 2018, 54, 25-33.	2.3	8
1233	Tropical soils are a reservoir for fluorescent <i>Pseudomonas</i> spp. biodiversity. <i>Environmental Microbiology</i> , 2018, 20, 62-74.	3.8	28
1234	The repeat structure of two paralogous genes, <i>Yersinia ruckeri</i> invasin (yrlnv) and a <i>Y. ruckeri</i> invasin-like molecule (yrlm) sheds light on the evolution of adhesive capacities of a fish pathogen. <i>Journal of Structural Biology</i> , 2018, 201, 171-183.	2.8	22
1235	Prospects on the evolutionary mitogenomics of plants: A case study on the olive family (Oleaceae). <i>Molecular Ecology Resources</i> , 2018, 18, 407-423.	4.8	49
1236	<i>In silico</i> analysis of the competition between <i>Streptococcus sanguinis</i> and <i>Streptococcus mutans</i> in the dental biofilm. <i>Molecular Oral Microbiology</i> , 2018, 33, 168-180.	2.7	24
1237	Challenges of <i>Francisella</i> classification exemplified by an atypical clinical isolate. <i>Diagnostic Microbiology and Infectious Disease</i> , 2018, 90, 241-247.	1.8	3
1238	Acquisition of the Phosphate Transporter NptA Enhances <i>Staphylococcus aureus</i> Pathogenesis by Improving Phosphate Uptake in Divergent Environments. <i>Infection and Immunity</i> , 2018, 86, .	2.2	20
1239	The gut virome of the protochordate model organism, <i>Ciona intestinalis</i> subtype A. <i>Virus Research</i> , 2018, 244, 137-146.	2.2	17
1240	Bacteriophage Taxonomy: An Evolving Discipline. <i>Methods in Molecular Biology</i> , 2018, 1693, 57-71.	0.9	34
1241	Mutualism between <i>Klebsiella</i> SGM 81 and <i>Dianthus caryophyllus</i> in modulating root plasticity and rhizospheric bacterial density. <i>Plant and Soil</i> , 2018, 424, 273-288.	3.7	22
1242	Essential Steps in Characterizing Bacteriophages: Biology, Taxonomy, and Genome Analysis. <i>Methods in Molecular Biology</i> , 2018, 1681, 197-215.	0.9	20
1243	Draft Genome Sequence of <i>Thermaerobacter</i> sp. Strain PB12/4term, a Thermophilic Facultative Anaerobic Bacterium from Bottom Sediments of Lake Baikal, Russia. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	1
1244	Complete Genome Sequences of <i>Bordetella pertussis</i> Clinical Isolate FR5810 and Reference Strain Tohama from Combined Oxford Nanopore and Illumina Sequencing. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	11
1245	<i>Thermosiphon</i> spp. immune system differences affect variation in genome size and geographical distributions. <i>Genome Biology and Evolution</i> , 2018, 10, 2853-2866.	2.5	4
1246	New Reference Genome Sequences for 17 Bacterial Strains of the Honey Bee Gut Microbiota. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	14
1247	Complete Genome Sequence of <i>Ferriphaselus amnicola</i> Strain OYT1, a Neutrophilic, Stalk-Forming, Iron-Oxidizing Bacterium. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	4

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1249	Visualization-assisted binning of metagenome assemblies reveals potential new pathogenic profiles in idiopathic travelers' diarrhea. <i>Microbiome</i> , 2018, 6, 201.	11.1	20
1250	Genomic surveillance of <i>Neisseria gonorrhoeae</i> to investigate the distribution and evolution of antimicrobial-resistance determinants and lineages. <i>Microbial Genomics</i> , 2018, 4, .	2.0	47
1251	The <i>Enterococcus</i> Cassette Chromosome, a Genomic Variation Enabler in <i>Enterococci</i> . <i>MSphere</i> , 2018, 3, .	2.9	7
1252	Complete mitochondrial genomes of six species of the freshwater red algal order <i>Batrachospermales</i> (Rhodophyta). <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 607-610.	0.4	4
1253	Genomic organization and role of SPI-13 in nutritional fitness of <i>Salmonella</i> . <i>International Journal of Medical Microbiology</i> , 2018, 308, 1043-1052.	3.6	9
1254	Comparative genomic and methylome analysis of non-virulent D74 and virulent Nagasaki <i>Haemophilus parasuis</i> isolates. <i>PLoS ONE</i> , 2018, 13, e0205700.	2.5	6
1255	Assembly of <i>Schizosaccharomyces cryophilus</i> chromosomes and their comparative genomic analyses revealed principles of genome evolution of the haploid fission yeasts. <i>Scientific Reports</i> , 2018, 8, 14629.	3.3	8
1256	Community-acquired methicillin-resistant <i>Staphylococcus aureus</i> from ST1 lineage harboring a new SCC <sub>mec</sub> IV subtype (SCC <sub>mec</sub> IVm) containing the <i>tetK</i> gene. <i>Infection and Drug Resistance</i> , 2018, Volume 11, 2583-2592.	2.7	13
1257	Whole genome sequencing of <i>Moraxella bovoculi</i> reveals high genetic diversity and evidence for interspecies recombination at multiple loci. <i>PLoS ONE</i> , 2018, 13, e0209113.	2.5	19
1258	Genetic Loci Associated With Fluoride Resistance in <i>Streptococcus mutans</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 3093.	3.5	16
1259	High-Quality Draft Genome Sequence of <i>Xanthomonas</i> sp. Strain CPBF 424, a Walnut-Pathogenic Strain with Atypical Features. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	7
1260	Complete Genome Sequence of <i>Klebsiella pneumoniae</i> Siphophage Sugarland. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	4
1261	High-Quality Draft Genome Sequence of <i>Xanthomonas arboricola</i> pv. <i>juglandis</i> CPBF 1521, Isolated from Leaves of a Symptomatic Walnut Tree in Portugal without a Past of Phytosanitary Treatment. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	5
1262	Novel Hybrid of Typical Enteropathogenic <i>Escherichia coli</i> and Shiga-Toxin-Producing <i>E. coli</i> (tEPEC/STEC) Emerging From Pet Birds. <i>Frontiers in Microbiology</i> , 2018, 9, 2975.	3.5	21
1263	Genome-Guided Analysis of <i>Clostridium ultunense</i> and Comparative Genomics Reveal Different Strategies for Acetate Oxidation and Energy Conservation in Syntrophic Acetate-Oxidising Bacteria. <i>Genes</i> , 2018, 9, 225.	2.4	27
1264	Complete Genome Sequence of <i>Sinorhizobium</i> Phage $\phi$ M6, the First Terrestrial Phage of a Marine Phage Group. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	8
1265	Loss of Bacitracin Resistance Due to a Large Genomic Deletion among <i>Bacillus anthracis</i> Strains. <i>MSystems</i> , 2018, 3, .	3.8	9

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1267	Complete and Draft Genome Sequences of Nine <i>Lactobacillus sakei</i> Strains Selected from the Three Known Phylogenetic Lineages and Their Main Clonal Complexes. <i>Genome Announcements</i> , 2018, 6, .	0.8	2
1268	Genomic and Virulence Characterization of Intrauterine Pathogenic <i>Escherichia coli</i> With Multi-Drug Resistance Isolated From Cow Uteri With Metritis. <i>Frontiers in Microbiology</i> , 2018, 9, 3137.	3.5	17
1269	Comparative genome analysis of marine purple sulfur bacterium <i>Marichromatium gracile</i> YL28 reveals the diverse nitrogen cycle mechanisms and habitat-specific traits. <i>Scientific Reports</i> , 2018, 8, 17803.	3.3	12
1270	The mitochondrial genome of <i>Endoconidiophora resinifera</i> is intron rich. <i>Scientific Reports</i> , 2018, 8, 17591.	3.3	56
1271	A Strain of an Emerging Indian <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> Pathotype Defeats the Rice Bacterial Blight Resistance Gene xa13 Without Inducing a Clade III SWEET Gene and Is Nearly Identical to a Recent Thai Isolate. <i>Frontiers in Microbiology</i> , 2018, 9, 2703.	3.5	17
1272	Genome Analysis of Haplotype D of <i>Candidatus Liberibacter Solanacearum</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 2933.	3.5	10
1273	Comparative Genomic Analysis and Characterization of Two <i>Salmonella enterica</i> Serovar Enteritidis Isolates From Poultry With Notably Different Survival Abilities in Egg Whites. <i>Frontiers in Microbiology</i> , 2018, 9, 2111.	3.5	11
1274	Development of a genome-informed loop-mediated isothermal amplification assay for rapid and specific detection of <i>Xanthomonas euvesicatoria</i> . <i>Scientific Reports</i> , 2018, 8, 14298.	3.3	43
1275	Comparative genome analysis provides deep insights into <i>Aeromonas hydrophila</i> taxonomy and virulence-related factors. <i>BMC Genomics</i> , 2018, 19, 712.	2.8	26
1276	Genome-wide analysis of <i>Borrelia turcica</i> and <i>Candidatus Borrelia tachyglossi</i> ™ shows relapsing fever-like genomes with unique genomic links to Lyme disease <i>Borrelia</i> . <i>Infection, Genetics and Evolution</i> , 2018, 66, 72-81.	2.3	28
1277	Complete Genome Sequence of <i>Escherichia coli</i> ME8067, an Azide-Resistant Laboratory Strain Used for Conjugation Experiments. <i>Genome Announcements</i> , 2018, 6, .	0.8	2
1278	A non-coding region near Follistatin controls head colour polymorphism in the Gouldian finch. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018, 285, 20181788.	2.6	39
1279	Transcriptional and Functional Analysis of <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> Exposure to Tetracycline. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	22
1280	Genomic characterisation of <i>Leptospira inadai</i> serogroup Lyme isolated from captured rat in Brazil and comparative analysis with human reference strain. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2018, 113, e170444.	1.6	0
1281	Comparison of Highly and Weakly Virulent <i>Dickeya solani</i> Strains, With a View on the Pangenome and Panregulon of This Species. <i>Frontiers in Microbiology</i> , 2018, 9, 1940.	3.5	50
1282	S-plot2: Rapid Visual and Statistical Analysis of Genomic Sequences. <i>Evolutionary Bioinformatics</i> , 2018, 14, 117693431879735.	1.2	8
1283	Plastid genome analysis of three <i>Nemaliophycidae</i> red algal species suggests environmental adaptation for iron limited habitats. <i>PLoS ONE</i> , 2018, 13, e0196995.	2.5	9

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1284	A Mechanism for Genome Size Reduction Following Genomic Rearrangements. <i>Frontiers in Genetics</i> , 2018, 9, 454.	2.3	23
1285	Achieving Accurate Sequence and Annotation Data for <i>Caulobacter vibrioides</i> CB13. <i>Current Microbiology</i> , 2018, 75, 1642-1648.	2.2	6
1286	Function of BriC peptide in the pneumococcal competence and virulence portfolio. <i>PLoS Pathogens</i> , 2018, 14, e1007328.	4.7	44
1287	Comparative Genomics of the First and Complete Genome of <i>Actinobacillus porcitonisillorum</i> Supports the Novel Species Hypothesis. <i>International Journal of Genomics</i> , 2018, 2018, 1-8.	1.6	10
1288	Comparative Genomics of <i>Aspergillus flavus</i> S and L Morphotypes Yield Insights into Niche Adaptation. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3915-3930.	1.8	23
1289	Insight Into Metabolic Versatility of an Aromatic Compounds-Degrading <i>Arthrobacter</i> sp. YC-RL1. <i>Frontiers in Microbiology</i> , 2018, 9, 2438.	3.5	31
1290	Prophage-driven genomic structural changes promote <i>Bartonella</i> vertical evolution. <i>Genome Biology and Evolution</i> , 2018, 10, 3089-3103.	2.5	13
1291	Genome sequence of <i>Shigella sonnei</i> 4303. <i>Gut Pathogens</i> , 2018, 10, 47.	3.4	2
1292	Comparative study on mitogenomes of green tide algae. <i>Genetica</i> , 2018, 146, 529-540.	1.1	12
1293	Comparative genomics of clinical strains of <i>Pseudomonas aeruginosa</i> strains isolated from different geographic sites. <i>Scientific Reports</i> , 2018, 8, 15668.	3.3	61
1294	Phylogenomic evidence for ancient recombination between plastid genomes of the <i>Cupressus-Juniperus-Xanthocyparis</i> complex (Cupressaceae). <i>BMC Evolutionary Biology</i> , 2018, 18, 137.	3.2	17
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1296	pYR4 From a Norwegian Isolate of <i>Yersinia ruckeri</i> Is a Putative Virulence Plasmid Encoding Both a Type IV Pilus and a Type IV Secretion System. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 373.	3.9	9
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1298	In vivo competition and horizontal gene transfer among distinct <i>Staphylococcus aureus</i> lineages as major drivers for adaptational changes during long-term persistence in humans. <i>BMC Microbiology</i> , 2018, 18, 152.	3.3	24
1299	Comparative Genomics of <i>Wolbachia</i> "Cardinium Dual Endosymbiosis in a Plant-Parasitic Nematode. <i>Frontiers in Microbiology</i> , 2018, 9, 2482.	3.5	36
1300	Comparative Genomics and in vitro Infection of Field Clonal Isolates of <i>Brucella melitensis</i> Biovar 3 Did Not Identify Signature of Host Adaptation. <i>Frontiers in Microbiology</i> , 2018, 9, 2505.	3.5	6
1301	<i>Cupriavidus metallidurans</i> Strains with Different Mobilomes and from Distinct Environments Have Comparable Phenomes. <i>Genes</i> , 2018, 9, 507.	2.4	21

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1303	Lessons learnt from a porcine epidemic diarrhea (PED) case in France in 2014: Descriptive epidemiology and control measures implemented. <i>Veterinary Microbiology</i> , 2018, 226, 9-14.	1.9	3
1304	To B or Not to B: Comparative Genomics Suggests <i>Arsenophonus</i> as a Source of B Vitamins in Whiteflies. <i>Frontiers in Microbiology</i> , 2018, 9, 2254.	3.5	49
1305	Complete genome sequencing of sixteen <i>Francisella noatunensis</i> subsp. <i>orientalis</i> isolates: A genomic approach for molecular characterization and spread dynamics of this clonal population. <i>Genomics</i> , 2018, 110, 442-449.	2.9	2
1306	Coordinate systems for supergenomes. <i>Algorithms for Molecular Biology</i> , 2018, 13, 15.	1.2	10
1307	Homology Search and Multiple Alignment. <i>Computational Biology</i> , 2018, , 325-360.	0.2	0
1308	Evaluating the origin and virulence of a <i>Helicobacter pylori</i> cagA-positive strain isolated from a non-human primate. <i>Scientific Reports</i> , 2018, 8, 15981.	3.3	11
1309	Dynamic evolution of inverted repeats in Euglenophyta plastid genomes. <i>Scientific Reports</i> , 2018, 8, 16071.	3.3	25
1310	The Complete Genome and Physiological Analysis of the Microbialite-Dwelling <i>Agrococcus pavilionensis</i> sp. nov; Reveals Genetic Promiscuity and Predicted Adaptations to Environmental Stress. <i>Frontiers in Microbiology</i> , 2018, 9, 2180.	3.5	22
1311	Antagonistic Pleiotropy in the Bifunctional Surface Protein FadL (OmpP1) during Adaptation of <i>Haemophilus influenzae</i> to Chronic Lung Infection Associated with Chronic Obstructive Pulmonary Disease. <i>MBio</i> , 2018, 9, .	4.1	39
1312	Mutations in Peptidoglycan Synthesis Gene <i>ponA</i> Improve Electrotransformation Efficiency of <i>Corynebacterium glutamicum</i> ATCC 13869. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	7
1313	Complete Genome of the <i>Xanthomonas euvesicatoria</i> Specific Bacteriophage $\phi$ 1, Its Survival and Potential in Control of Pepper Bacterial Spot. <i>Frontiers in Microbiology</i> , 2018, 9, 2021.	3.5	43
1314	Spread of Carbapenem Resistance by Transposition and Conjugation Among <i>Pseudomonas aeruginosa</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 2057.	3.5	38
1315	Comparative genomics of Czech vaccine strains of <i>Bordetella pertussis</i> . <i>Pathogens and Disease</i> , 2018, 76, .	2.0	7
1316	Genomic and biological characterization of a new member of the genus <i>Phikmvirus</i> infecting phytopathogenic <i>Ralstonia</i> bacteria. <i>Archives of Virology</i> , 2018, 163, 3275-3290.	2.1	12
1317	Using phylogenomics to reconstruct phylogenetic relationships within tribe Polygonateae (Asparagaceae), with a special focus on <i>Polygonatum</i> . <i>Molecular Phylogenetics and Evolution</i> , 2018, 129, 202-213.	2.7	29
1318	Attack of the clones: whole genome-based characterization of two closely related enterohemorrhagic <i>Escherichia coli</i> O26 epidemic lineages. <i>BMC Genomics</i> , 2018, 19, 647.	2.8	7
1319	Whole genome sequencing reveals the emergence of a <i>Pseudomonas aeruginosa</i> shared strain sub-lineage among patients treated within a single cystic fibrosis centre. <i>BMC Genomics</i> , 2018, 19, 644.	2.8	16



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1321	Approximate, simultaneous comparison of microbial genome architectures via syntenic anchoring of quiver representations. <i>Bioinformatics</i> , 2018, 34, i732-i742.	4.1	7
1322	Metagenomic analysis with strain-level resolution reveals fine-scale variation in the human pregnancy microbiome. <i>Genome Research</i> , 2018, 28, 1467-1480.	5.5	117
1323	First Genome Sequence of <i>Pasteurella multocida</i> Type B Strain BAUTB2, a Major Pathogen Responsible for Mortality of Bovines in Bangladesh. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	1
1324	Reconfiguration of the plastid genome in <i>Lamprocapnos spectabilis</i> : IR boundary shifting, inversion, and intraspecific variation. <i>Scientific Reports</i> , 2018, 8, 13568.	3.3	43
1325	Pushing the limits of de novo genome assembly for complex prokaryotic genomes harboring very long, near identical repeats. <i>Nucleic Acids Research</i> , 2018, 46, 8953-8965.	14.5	104
1326	High and Variable Rates of Repeat-Mediated Mitochondrial Genome Rearrangement in a Genus of Plants. <i>Molecular Biology and Evolution</i> , 2018, 35, 2773-2785.	8.9	60
1327	PGAweb: A Web Server for Bacterial Pan-Genome Analysis. <i>Frontiers in Microbiology</i> , 2018, 9, 1910.	3.5	24
1328	PGAP-X: extension on pan-genome analysis pipeline. <i>BMC Genomics</i> , 2018, 19, 36.	2.8	29
1329	Genomic repeats, misassembly and reannotation: a case study with long-read resequencing of <i>Porphyromonas gingivalis</i> reference strains. <i>BMC Genomics</i> , 2018, 19, 54.	2.8	28
1330	Evolution of the U.S. Biological Select Agent <i>Rathayibacter toxicus</i> . <i>MBio</i> , 2018, 9, .	4.1	10
1331	Comparative genome and phenotypic analysis of three <i>Clostridioides difficile</i> strains isolated from a single patient provide insight into multiple infection of <i>C. difficile</i> . <i>BMC Genomics</i> , 2018, 19, 1.	2.8	725
1332	Hotspot mutations and ColE1 plasmids contribute to the fitness of <i>Salmonella</i> Heidelberg in poultry litter. <i>PLoS ONE</i> , 2018, 13, e0202286.	2.5	34
1333	Whole-genome sequencing enabling the detection of a colistin-resistant hypermutating <i>Citrobacter werkmanii</i> strain harbouring a novel metallo- $\beta$ -lactamase VIM-48. <i>International Journal of Antimicrobial Agents</i> , 2018, 51, 867-874.	2.5	12
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1335	Complete Genome Sequences of Two Bioluminescent <i>Vibrio campbellii</i> Strains Isolated from Biofouling Communities in the Bay of Bengal. <i>Genome Announcements</i> , 2018, 6, .	0.8	4
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1466	A Novel Alphabaculovirus from the Soybean Looper, <i>Chrysodeixis includens</i> , that Produces Tetrahedral Occlusion Bodies and Encodes Two Copies of he65. <i>Viruses</i> , 2019, 11, 579.	3.3	3
1467	Plastome phylogenomics of <i>Saussurea</i> (Asteraceae: Cardueae). <i>BMC Plant Biology</i> , 2019, 19, 290.	3.6	34
1468	Systematic Identification and Analysis of <i>Acinetobacter baumannii</i> Type VI Secretion System Effector and Immunity Components. <i>Frontiers in Microbiology</i> , 2019, 10, 2440.	3.5	32
1469	Next Generation Sequencing and Bioinformatics Methodologies for Infectious Disease Research and Public Health: Approaches, Applications, and Considerations for Development of Laboratory Capacity. <i>Journal of Infectious Diseases</i> , 2020, 221, S292-S307.	4.0	64
1470	Large Plasmid Complement Resolved: Complete Genome Sequencing of <i>Lactobacillus plantarum</i> MF1298, a Candidate Probiotic Strain Associated with Unfavorable Effect. <i>Microorganisms</i> , 2019, 7, 262.	3.6	9
1471	Development and Implementation of Multiplex TaqMan Array Cards for Specimen Testing at Child Health and Mortality Prevention Surveillance Site Laboratories. <i>Clinical Infectious Diseases</i> , 2019, 69, S311-S321.	5.8	39
1472	Molecular epidemiology of <i>Mycoplasma hyorhinis</i> porcine field isolates in the United States. <i>PLoS ONE</i> , 2019, 14, e0223653.	2.5	12
1473	The PATRIC Bioinformatics Resource Center: expanding data and analysis capabilities. <i>Nucleic Acids Research</i> , 2020, 48, D606-D612.	14.5	552
1474	First complete genome sequence and comparative analysis of <i>Salmonella enterica</i> subsp. <i>diarizonae</i> serovar 61:k:1,5,(7) indicates host adaptation traits to sheep. <i>Gut Pathogens</i> , 2019, 11, 48.	3.4	8
1475	Red-Brown Pigmentation of <i>Acidipropionibacterium jensenii</i> Is Tied to Haemolytic Activity and <i>cyl</i> -Like Gene Cluster. <i>Microorganisms</i> , 2019, 7, 512.	3.6	10
1476	Organelle genome composition and candidate gene identification for Nsa cytoplasmic male sterility in <i>Brassica napus</i> . <i>BMC Genomics</i> , 2019, 20, 813.	2.8	9
1477	Cultivation-assisted genome of <i>Candidatus Fukatsuia symbiotica</i> ; the enigmatic “X-type” symbiont of aphids. <i>Genome Biology and Evolution</i> , 2019, 11, 3510-3522.	2.5	23
1478	Phylogenetic Analyses of <i>Xanthomonas</i> Causing Bacterial Leaf Spot of Tomato and Pepper: <i>Xanthomonas euvesicatoria</i> Revealed Homologous Populations Despite Distant Geographical Distribution. <i>Microorganisms</i> , 2019, 7, 462.	3.6	10
1479	Multiplex PCR for genotyping <i>Flavobacterium columnare</i> . <i>Journal of Fish Diseases</i> , 2019, 42, 1531-1542.	1.9	17
1480	GenGraph: a python module for the simple generation and manipulation of genome graphs. <i>BMC Bioinformatics</i> , 2019, 20, 519.	2.6	4
1481	Isolation of <i>Legionella pneumophila</i> by Co-culture with Local Ameba, Canada. <i>Emerging Infectious Diseases</i> , 2019, 25, 2104-2107.	4.3	7

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1483	The complete chloroplast genomes of two species in threatened monocot genus <i>Caldesia</i> in China. <i>Genetica</i> , 2019, 147, 381-390.	1.1	4
1484	Origin and Evolution of Hybrid Shiga Toxin-Producing and Uropathogenic <i>Escherichia coli</i> Strains of Sequence Type 141. <i>Journal of Clinical Microbiology</i> , 2019, 58, .	3.9	31
1485	Origin and diversification of <i>Xanthomonas citri</i> subsp. <i>citri</i> pathotypes revealed by inclusive phylogenomic, dating, and biogeographic analyses. <i>BMC Genomics</i> , 2019, 20, 700.	2.8	33
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1487	Complete genome analysis of a novel temperate bacteriophage induced from <i>Corynebacterium striatum</i> . <i>Archives of Virology</i> , 2019, 164, 2877-2880.	2.1	7
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1490	<i>Pasteurella multocida</i> : Genotypes and Genomics. <i>Microbiology and Molecular Biology Reviews</i> , 2019, 83, .	6.6	100
1491	CRISPR-Cas System of a Prevalent Human Gut Bacterium Reveals Hyper-targeting against Phages in a Human Virome Catalog. <i>Cell Host and Microbe</i> , 2019, 26, 325-335.e5.	11.0	53
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1496	Genomic epidemiology of Iranian <i>Bordetella pertussis</i> : 50 years after the implementation of whole cell vaccine. <i>Emerging Microbes and Infections</i> , 2019, 8, 1416-1427.	6.5	23
1497	Bacteriophage Application for Difficult-to-treat Musculoskeletal Infections: Development of a Standardized Multidisciplinary Treatment Protocol. <i>Viruses</i> , 2019, 11, 891.	3.3	98
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1501	Population Genomics Insights into Adaptive Evolution and Ecological Differentiation in <i>Streptomyces</i> . <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	16
1502	A comparative analysis of complete plastid genomes from <i>Prangos fedtschenkoi</i> and <i>Prangos lipskyi</i> (Apiaceae). <i>Ecology and Evolution</i> , 2019, 9, 364-377.	1.9	13
1503	Impact of Homologous Recombination on the Evolution of Prokaryotic Core Genomes. <i>MBio</i> , 2019, 10, .	4.1	60
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1505	<i>Lactococcus lactis</i> subsp. <i>lactis</i> as a natural anti-listerial agent in the mushroom industry. <i>Food Microbiology</i> , 2019, 82, 30-35.	4.2	19
1506	Uncoupled Quorum Sensing Modulates the Interplay of Virulence and Resistance in a Multidrug-Resistant Clinical <i>Pseudomonas aeruginosa</i> Isolate Belonging to the MLST550 Clonal Complex. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	17
1507	Comparative analysis reveals the Genomic Islands in <i>Pasteurella multocida</i> population genetics: on Symbiosis and adaptability. <i>BMC Genomics</i> , 2019, 20, 63.	2.8	9
1508	Analysis of genetic diversity of <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> populations in Taiwan. <i>Scientific Reports</i> , 2019, 9, 316.	3.3	11
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1510	Metabolic diversity within the globally abundant Marine Group II Euryarchaea offers insight into ecological patterns. <i>Nature Communications</i> , 2019, 10, 271.	12.8	66
1511	Development of a PCR test for detection of <i>Xanthomonas campestris</i> pv. <i>raphani</i> . <i>Australasian Plant Pathology</i> , 2019, 48, 179-182.	1.0	4
1512	Compositional assessment of bacterial communities in probiotic supplements by means of metagenomic techniques. <i>International Journal of Food Microbiology</i> , 2019, 294, 1-9.	4.7	26
1513	<i>In Silico</i> Serotyping Based on Whole-Genome Sequencing Improves the Accuracy of <i>Shigella</i> Identification. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	37
1514	Dissecting the Evolutionary Development of the Species <i>Bifidobacterium animalis</i> through Comparative Genomics Analyses. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	11
1515	Evolution and Diversification of FRUITFULL Genes in Solanaceae. <i>Frontiers in Plant Science</i> , 2019, 10, 43.	3.6	13
1516	Complete Genome Sequence of <i>Klebsiella pneumoniae</i> Myophage May. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	2
1517	Complete Genome Sequence of <i>Serratia marcescens</i> Siphophage Serbin. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	4

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1519	Hybrid Genome Assembly of a Major Quantitative Disease Resistance Locus in Soybean Toward <i>Fusarium graminearum</i> . <i>Plant Genome</i> , 2019, 12, 180102.	2.8	8
1520	Molecular evolution of <i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Gallinarum</i> biovar <i>Gallinarum</i> in the field. <i>Veterinary Microbiology</i> , 2019, 235, 63-70.	1.9	14
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1522	Diversity patterns of bacteriophages infecting <i>Aggregatibacter</i> and <i>Haemophilus</i> species across clades and niches. <i>ISME Journal</i> , 2019, 13, 2500-2522.	9.8	20
1523	Complete Genome Sequence of <i>Serratia marcescens</i> Phage MTx. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	2
1524	A genome-wide scan for genes under balancing selection in the plant pathogen <i>Ralstonia solanacearum</i> . <i>BMC Evolutionary Biology</i> , 2019, 19, 123.	3.2	24
1525	Comparative Chloroplast Genomics at Low Taxonomic Levels: A Case Study Using <i>Amphilophium</i> (Bignoniaceae, Bignoniaceae). <i>Frontiers in Plant Science</i> , 2019, 10, 796.	3.6	55
1526	<i>Cuscuta</i> Species Identification Based on the Morphology of Reproductive Organs and Complete Chloroplast Genome Sequences. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2726.	4.1	16
1527	Plasmid analysis of <i>Escherichia coli</i> isolates from South Korea co-producing NDM-5 and OXA-181 carbapenemases. <i>Plasmid</i> , 2019, 104, 102417.	1.4	25
1528	Two <i>Pseudomonas aeruginosa</i> clonal groups belonging to the PA14 clade are indigenous to the Churince system in Cuatro Ci�negas Coahuila, M�xico. <i>Environmental Microbiology</i> , 2019, 21, 2964-2976.	3.8	10
1529	Draft Genome Sequences of Type VI Secretion System-Encoding <i>Vibrio fischeri</i> Strains FQ-A001 and ES401. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	11
1530	Variable Carbon Source Utilization, Stress Resistance, and Virulence Profiles Among <i>Listeria monocytogenes</i> Strains Responsible for Listeriosis Outbreaks in Switzerland. <i>Frontiers in Microbiology</i> , 2019, 10, 957.	3.5	30
1531	Unprecedented Parallel Photosynthetic Losses in a Heterotrophic Orchid Genus. <i>Molecular Biology and Evolution</i> , 2019, 36, 1884-1901.	8.9	38
1532	Novel Genes and Metabolite Trends in <i>Bifidobacterium longum</i> subsp. <i>infantis</i> Bi-26 Metabolism of Human Milk Oligosaccharide �-fucosyllactose. <i>Scientific Reports</i> , 2019, 9, 7983.	3.3	45
1533	Caught in action: fine-scale plastome evolution in the parasitic plants of <i>Cuscuta</i> section <i>Ceratophorae</i> (Convolvulaceae). <i>Plant Molecular Biology</i> , 2019, 100, 621-634.	3.9	17
1534	Complete Genome Sequence of <i>Klebsiella pneumoniae</i> Podophage Patroon. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	1
1535	Construction of restorer lines and molecular mapping for restorer gene of <i>hau</i> cytoplasmic male sterility in <i>Brassica napus</i> . <i>Theoretical and Applied Genetics</i> , 2019, 132, 2525-2539.	3.6	6



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1538	Genomic determinants of speciation and spread of the <i>Mycobacterium tuberculosis</i> complex. Science Advances, 2019, 5, eaaw3307.	10.3	61
1539	Genomic erosion and extensive horizontal gene transfer in gut-associated Acetobacteraceae. BMC Genomics, 2019, 20, 472.	2.8	32
1540	Complete Genome Sequence of <i>Escherichia coli</i> Myophage Minorna. Microbiology Resource Announcements, 2019, 8, .	0.6	0
1541	Patterns of inter- and intrasubspecific homologous recombination inform eco-evolutionary dynamics of <i>Xylella fastidiosa</i> . ISME Journal, 2019, 13, 2319-2333.	9.8	55
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1543	Long-read sequencing reveals intra-species tolerance of substantial structural variations and new subtelomere formation in <i>C. elegans</i> . Genome Research, 2019, 29, 1023-1035.	5.5	67
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1548	Genomic characterization of four novel <i>Staphylococcus myoviruses</i> . Archives of Virology, 2019, 164, 2171-2173.	2.1	9
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1555	Complete Genome Sequence of <i>Klebsiella pneumoniae</i> Myophage Mineola. Microbiology Resource Announcements, 2019, 8, .	0.6	1
1556	Draft Genome Sequence of <i>Lactobacillus paraplantarum</i> OSY-TC318, a Producer of the Novel Lantibiotic Paraplantaracin TC318. Microbiology Resource Announcements, 2019, 8, .	0.6	4
1557	Complete Genome Sequence of <i>Serratia marcescens</i> Siphophage Scapp. Microbiology Resource Announcements, 2019, 8, .	0.6	2
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1564	Genomic Diversity and Recombination among <i>Xylella fastidiosa</i> Subspecies. Applied and Environmental Microbiology, 2019, 85, .	3.1	63
1565	Complete Genome Sequence of <i>Klebsiella pneumoniae</i> Myophage Menlow. Microbiology Resource Announcements, 2019, 8, .	0.6	2
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1574	Complete Genome Sequences of <i>Xanthomonas axonopodis</i> pv. <i>glycines</i> Isolates from the United States and Thailand Reveal Conserved Transcription Activator-Like Effectors. <i>Genome Biology and Evolution</i> , 2019, 11, 1380-1384.	2.5	11
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1581	Molecular and phenotypic characterization of <i>Leptospira johnsonii</i> sp. nov., <i>Leptospira ellinghauseni</i> sp. nov. and <i>Leptospira ryugeni</i> sp. nov. isolated from soil and water in Japan. <i>Microbiology and Immunology</i> , 2019, 63, 89-99.	1.4	22
1582	Draft Genome Sequence of <i>Sinorhizobium meliloti</i> Strain CXM1-105. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	2
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1588	Aneuploidy and Ethanol Tolerance in <i>Saccharomyces cerevisiae</i> . <i>Frontiers in Genetics</i> , 2019, 10, 82.	2.3	71
1589	Uncovering the Mechanisms of Halotolerance in the Extremely Acidophilic Members of the <i>Acidihalobacter</i> Genus Through Comparative Genome Analysis. <i>Frontiers in Microbiology</i> , 2019, 10, 155.	3.5	24

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1591	Chloroplast and mitochondrial genomes of <i>Balbiania investiens</i> (Balbianiales, Nemaliophycidae). <i>Phycologia</i> , 2019, 58, 310-318.	1.4	6
1592	Pathogenic potential of non-typhoidal <i>Salmonella</i> serovars isolated from aquatic environments in Mexico. <i>Genes and Genomics</i> , 2019, 41, 767-779.	1.4	2
1593	Bioinformatics applied to biotechnology: A review towards bioenergy research. <i>Biomass and Bioenergy</i> , 2019, 123, 195-224.	5.7	17
1594	Genome analysis of <i>Pseudomonas syringae</i> pv. <i>actinidiae</i> biovar 6, which produces the phytotoxins, phaseolotoxin and coronatine. <i>Scientific Reports</i> , 2019, 9, 3836.	3.3	35
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1601	Evolution of the human cold/menthol receptor, TRPM8. <i>Molecular Phylogenetics and Evolution</i> , 2019, 136, 104-118.	2.7	13
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1603	Cumulative acquisition of pathogenicity islands has shaped virulence potential and contributed to the emergence of LEE-negative Shiga toxin-producing <i>Escherichia coli</i> strains. <i>Emerging Microbes and Infections</i> , 2019, 8, 486-502.	6.5	39
1604	Complete plastome sequences of 14 African yam species ( <i>Dioscorea</i> spp.). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 74-76.	0.4	4
1605	Closely related viruses of the marine picoeukaryotic alga <i>Ostreococcus lucimarinus</i> exhibit different ecological strategies. <i>Environmental Microbiology</i> , 2019, 21, 2148-2170.	3.8	15
1606	Variation among human, veterinary and environmental <i>Mycobacterium chelonae-abscessus</i> complex isolates observed using core genome phylogenomic analysis, targeted gene comparison, and anti-microbial susceptibility patterns. <i>PLoS ONE</i> , 2019, 14, e0214274.	2.5	12
1607	WGS of 1058 <i>Enterococcus faecium</i> from Copenhagen, Denmark, reveals rapid clonal expansion of vancomycin-resistant clone ST80 combined with widespread dissemination of a vanA-containing plasmid and acquisition of a heterogeneous accessory genome. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 1776-1785.	3.0	43

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1609	Plasmids contribute to food processing environment-associated stress survival in three <i>Listeria monocytogenes</i> ST121, ST8, and ST5 strains. <i>International Journal of Food Microbiology</i> , 2019, 299, 39-46.	4.7	52
1610	Draft genome sequence of <i>Enterococcus faecium</i> SP15, a potential probiotic strain isolated from spring water. <i>BMC Research Notes</i> , 2019, 12, 99.	1.4	3
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1624	Prevalence of isomeric plastomes and effectiveness of plastome super-barcodes in yews ( <i>Taxus</i> ) worldwide. <i>Scientific Reports</i> , 2019, 9, 2773.	3.3	54
1625	Integrated mobile genetic elements in Thaumarchaeota. <i>Environmental Microbiology</i> , 2019, 21, 2056-2078.	3.8	38

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1645	First report of <i>Klebsiella quasipneumoniae</i> harboring blaKPC-2 in Saudi Arabia. <i>Antimicrobial Resistance and Infection Control</i> , 2019, 8, 203.	4.1	15
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1659	RNAdetect: efficient computational detection of novel non-coding RNAs. <i>Bioinformatics</i> , 2019, 35, 1133-1141.	4.1	7
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1661	Genomic analyses of a novel bacteriophage (VB_PmIS-Isfahan) within Siphoviridae family infecting <i>Proteus mirabilis</i> . <i>Genomics</i> , 2019, 111, 1283-1291.	2.9	13

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1663	Phoenix phylogeny, and analysis of genetic variation in a diverse collection of date palm ( <i>Phoenix</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock	3.7	27
1664	Expansion and Diversification of MFS Transporters in <i>Kluyveromyces marxianus</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 3330.	3.5	17
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1677	Persistence and Microevolution of <i>Pseudomonas aeruginosa</i> in the Cystic Fibrosis Lung: A Single-Patient Longitudinal Genomic Study. <i>Frontiers in Microbiology</i> , 2018, 9, 3242.	3.5	27
1678	Comparative genomic analysis of <i>Pseudomonas amygdali</i> pv. <i>lachrymans</i> NM002: Insights into its potential virulence genes and putative invasion determinants. <i>Genomics</i> , 2019, 111, 1493-1503.	2.9	7
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1681	Genome Comparisons of Wild Isolates of <i>Caulobacter crescentus</i> Reveal Rates of Inversion and Horizontal Gene Transfer. <i>Current Microbiology</i> , 2019, 76, 159-167.	2.2	11
1682	Enlarged and highly repetitive plastome of <i>Lagarostrobos</i> and plastid phylogenomics of Podocarpaceae. <i>Molecular Phylogenetics and Evolution</i> , 2019, 133, 24-32.	2.7	8
1683	Alignment-free inference of hierarchical and reticulate phylogenomic relationships. <i>Briefings in Bioinformatics</i> , 2019, 20, 426-435.	6.5	74
1684	Comparative genomic analysis of <i>Lactobacillus mucosae</i> LM1 identifies potential niche-specific genes and pathways for gastrointestinal adaptation. <i>Genomics</i> , 2019, 111, 24-33.	2.9	47
1685	Investigation of putative invasion determinants of <i>Actinobacillus</i> species using comparative genomics. <i>Genomics</i> , 2019, 111, 59-66.	2.9	4
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1690	Complete plastome sequencing of <i>Allium paradoxum</i> reveals unusual rearrangements and the loss of the <i>ndh</i> genes as compared to <i>Allium ursinum</i> and other onions. <i>Gene</i> , 2020, 726, 144154.	2.2	11
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1700	Computational Framework for High-Quality Production and Large-Scale Evolutionary Analysis of Metagenome Assembled Genomes. <i>Molecular Biology and Evolution</i> , 2020, 37, 593-598.	8.9	11
1701	Living Trees: High-Quality Reproducible and Reusable Construction of Bacterial Phylogenetic Trees. <i>Molecular Biology and Evolution</i> , 2020, 37, 563-575.	8.9	17
1702	Comparative genomics of three clinical <i>Ureaplasma</i> species: analysis of their core genomes and multiple-banded antigen locus. <i>Future Microbiology</i> , 2020, 15, 49-61.	2.0	0
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1704	A Bioinformatic Analysis of Integrative Mobile Genetic Elements Highlights Their Role in Bacterial Adaptation. <i>Cell Host and Microbe</i> , 2020, 27, 140-153.e9.	11.0	119
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1706	TonB-dependent uptake of $\beta$ -lactam antibiotics in the opportunistic human pathogen <i>Stenotrophomonas maltophilia</i> . <i>Molecular Microbiology</i> , 2020, 113, 492-503.	2.5	17
1707	Genome of an iconic Australian bird: High-quality assembly and linkage map of the superb fairywren ( <i>Malurus cyaneus</i> ). <i>Molecular Ecology Resources</i> , 2020, 20, 560-578.	4.8	24
1708	Genomic analyses reveal moderate levels of ploidy, high heterozygosity and structural variations in a Colombian isolate of <i>Leishmania</i> ( <i>Leishmania</i> ) <i>amazonensis</i> . <i>Acta Tropica</i> , 2020, 203, 105296.	2.0	13
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1713	Epigenomic characterization of <i>Clostridioides difficile</i> finds a conserved DNA methyltransferase that mediates sporulation and pathogenesis. <i>Nature Microbiology</i> , 2020, 5, 166-180.	13.3	75
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1717	Phylogeographical Analysis Reveals the Historic Origin, Emergence, and Evolutionary Dynamics of Methicillin-Resistant <i>Staphylococcus aureus</i> ST228. <i>Frontiers in Microbiology</i> , 2020, 11, 2063.	3.5	6
1718	Genomic Epidemiology of <i>Salmonella</i> Infantis in Ecuador: From Poultry Farms to Human Infections. <i>Frontiers in Veterinary Science</i> , 2020, 7, 547891.	2.2	29
1719	Molecular Epidemiology of <i>Escherichia coli</i> Producing CTX-M and pAmpC $\beta$ -Lactamases from Dairy Farms Identifies a Dominant Plasmid Encoding CTX-M-32 but No Evidence for Transmission to Humans in the Same Geographical Region. <i>Applied and Environmental Microbiology</i> , 2020, 87, .	3.1	17
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1723	Comparative genomics of ocular <i>Pseudomonas aeruginosa</i> strains from keratitis patients with different clinical outcomes. <i>Genomics</i> , 2020, 112, 4769-4776.	2.9	12
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1727	Characterization of lactic acid bacteria isolated from a traditional Ivorian beer process to develop starter cultures for safe sorghum-based beverages. <i>International Journal of Food Microbiology</i> , 2020, 322, 108547.	4.7	16
1728	An xa5 Resistance Gene-Breaking Indian Strain of the Rice Bacterial Blight Pathogen <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> Is Nearly Identical to a Thai Strain. <i>Frontiers in Microbiology</i> , 2020, 11, 579504.	3.5	8
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1730	Comparative Genomics Analysis Provides New Strategies for Bacteriostatic Ability of <i>Bacillus velezensis</i> HAB-2. <i>Frontiers in Microbiology</i> , 2020, 11, 594079.	3.5	12
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1743	Limited Genetic Diversity of bla <sub>CMY-2</sub> -Containing Inc11-pST12 Plasmids from Enterobacteriaceae of Human and Broiler Chicken Origin in The Netherlands. <i>Microorganisms</i> , 2020, 8, 1755.	3.6	1
1744	Mitochondrial and plastid genome variability of <i>Corallina officinalis</i> (Corallinales). <i>Tj ETQq0 0 0 rgBT /Overlock,10 Tf 5Q 342 Td (R</i>	1.3	1
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1751	A Repertory of Rearrangements and the Loss of an Inverted Repeat Region in <i>Passiflora</i> Chloroplast Genomes. <i>Genome Biology and Evolution</i> , 2020, 12, 1841-1857.	2.5	49



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1754	Insights into the phylogenetic relationships and drug targets of <i>Babesia</i> isolates infective to small ruminants from the mitochondrial genomes. Parasites and Vectors, 2020, 13, 378.	2.5	9
1755	A novel community-acquired MRSA clone, USA300-LV/J, uniquely evolved in Japan. Journal of Antimicrobial Chemotherapy, 2020, 75, 3131-3134.	3.0	12
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1761	Taxonomy and Phylogenetic Research on <i>Ralstonia solanacearum</i> Species Complex: A Complex Pathogen with Extraordinary Economic Consequences. Pathogens, 2020, 9, 886.	2.8	44
1762	Pangenomics in Crop Plants. Population Genomics, 2020, , 1.	0.5	1
1763	Comparative Genome Analysis of <i>Bifidobacterium longum</i> subsp. <i>infantis</i> Strains Reveals Variation in Human Milk Oligosaccharide Utilization Genes among Commercial Probiotics. Nutrients, 2020, 12, 3247.	4.1	46
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1765	Comparative genomic analysis of a Shiga toxin-producing <i>Escherichia coli</i> (STEC) O145:H25 associated with a severe pediatric case of hemolytic uremic syndrome in Davidson County, Tennessee, US. BMC Genomics, 2020, 21, 564.	2.8	3
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1767	Improved <i>De Novo</i> Draft Genome Sequence of the Nocavionin-Producing Type Strain <i>Nocardia terpenica</i> IFM 0706 and Comparative Genomics with the Closely Related Strain <i>Nocardia terpenica</i> IFM 0406. Microbiology Resource Announcements, 2020, 9, .	0.6	6
1768	A persistently replicating SARS-CoV-2 variant derived from an asymptomatic individual. Journal of Translational Medicine, 2020, 18, 362.	4.4	46
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1771	Draft genome sequence of <i>scale drop disease virus</i> (SDDV) retrieved from metagenomic investigation of infected barramundi, <i>Lates calcarifer</i> (Bloch, 1790). Journal of Fish Diseases, 2020, 43, 1287-1298.	1.9	7
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1778	New insights into the biodiversity of coliphages in the intestine of poultry. Scientific Reports, 2020, 10, 15220.	3.3	13
1779	Genomic Signatures of Honey Bee Association in an Acetic Acid Symbiont. Genome Biology and Evolution, 2020, 12, 1882-1894.	2.5	18
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1782	Cryptic speciation of a pelagic <i>Roseobacter</i> population varying at a few thousand nucleotide sites. ISME Journal, 2020, 14, 3106-3119.	9.8	11
1783	Tracking of Antibiotic Resistance Transfer and Rapid Plasmid Evolution in a Hospital Setting by Nanopore Sequencing. MSphere, 2020, 5, .	2.9	51
1784	Scalable multiple whole-genome alignment and locally collinear block construction with SibeliaZ. Nature Communications, 2020, 11, 6327.	12.8	39
1785	Pandemic <i>Vibrio cholerae</i> shuts down site-specific recombination to retain an interbacterial defence mechanism. Nature Communications, 2020, 11, 6246.	12.8	17
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1787	Biological and Genomic Characterization of a Novel Jumbo Bacteriophage, vB_VhaM_pir03 with Broad Host Lytic Activity against <i>Vibrio harveyi</i> . Pathogens, 2020, 9, 1051.	2.8	20

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1789	Genomic differences between the new <i>Fusarium oxysporum</i> f. sp. <i>apii</i> (Foa) race 4 on celery, the less virulent Foa races 2 and 3, and the avirulent on celery f. sp. <i>coriandrii</i> . <i>BMC Genomics</i> , 2020, 21, 730.	2.8	12
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1792	Comparative Evolutionary Patterns of <i>Burkholderia cenocepacia</i> and <i>B. multivorans</i> During Chronic Co-infection of a Cystic Fibrosis Patient Lung. <i>Frontiers in Microbiology</i> , 2020, 11, 574626.	3.5	7
1793	Whole genome analysis of the koa wilt pathogen ( <i>Fusarium oxysporum</i> f. sp. <i>koae</i> ) and the development of molecular tools for early detection and monitoring. <i>BMC Genomics</i> , 2020, 21, 764.	2.8	11
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1795	Comparative Genomics of Pathogenic <i>Clavibacter michiganensis</i> subsp. <i>michiganensis</i> Strains from Chile Reveals Potential Virulence Features for Tomato Plants. <i>Microorganisms</i> , 2020, 8, 1679.	3.6	14
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1797	Amino Acid k-mer Feature Extraction for Quantitative Antimicrobial Resistance (AMR) Prediction by Machine Learning and Model Interpretation for Biological Insights. <i>Biology</i> , 2020, 9, 365.	2.8	21
1798	Complete Genome Sequence of <i>Serratia marcescens</i> Podophage Pila. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	1
1799	Complete genome sequencing and comparative genomic analyses of <i>Bacillus</i> sp. S3, a novel hyper Sb(III)-oxidizing bacterium. <i>BMC Microbiology</i> , 2020, 20, 106.	3.3	11
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1801	Complete Genome Sequence of <i>Moraxella osloensis</i> Strain YV1, Isolated from an Australian Wastewater Treatment Plant. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	2
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1804	Complete Genome Sequence of <i>Stenotrophomonas</i> Phage Mendera. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	5
1805	Genomic Differences between <i>Listeria monocytogenes</i> EGDe Isolates Reveal Crucial Roles for SigB and Wall Rhamnosylation in Biofilm Formation. <i>Journal of Bacteriology</i> , 2020, 202, .	2.2	16

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1807	Complete Mitochondrial Genome of the Fungal Biocontrol Agent <i>Trichoderma atroviride</i> : Genomic Features, Comparative Analysis and Insight Into the Mitochondrial Evolution in <i>Trichoderma</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 785.	3.5	11
1808	Isolation and Characterization of Two <i>Klebsiella pneumoniae</i> Phages Encoding Divergent Depolymerases. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3160.	4.1	21
1809	Draft genome of five <i>Cupriavidus plantarum</i> strains: agave, maize and sorghum plant-associated bacteria with resistance to metals. <i>3 Biotech</i> , 2020, 10, 242.	2.2	1
1810	The loss of photosynthesis pathway and genomic locations of the lost plastid genes in a holoparasitic plant <i>Aeginetia indica</i> . <i>BMC Plant Biology</i> , 2020, 20, 199.	3.6	16
1811	Past and ongoing adaptation of human cytomegalovirus to its host. <i>PLoS Pathogens</i> , 2020, 16, e1008476.	4.7	19
1812	Assessment of a Potential Role of <i>Dickeya dadantii</i> DSM 18020 as a Pectinase Producer for Utilization in Poultry Diets Based on in silico Analyses. <i>Frontiers in Microbiology</i> , 2020, 11, 751.	3.5	4
1813	Isolation, Characterization and Genomic Analysis of a Novel Bacteriophage VB_EcoS-Golestan Infecting Multidrug-Resistant <i>Escherichia coli</i> Isolated from Urinary Tract Infection. <i>Scientific Reports</i> , 2020, 10, 7690.	3.3	45
1814	Comparison of Two Multilocus Sequence Typing Schemes for <i>Mycoplasma bovis</i> and Revision of the PubMLST Reference Method. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	3.9	22
1815	Two new bacilladnaviruses associated with the diatom <i>Haslea ostrearia</i> . <i>European Journal of Phycology</i> , 2020, 55, 444-453.	2.0	1
1816	Unprecedented Intraindividual Structural Heteroplasmy in <i>Eleocharis</i> (Cyperaceae, Poales) Plastomes. <i>Genome Biology and Evolution</i> , 2020, 12, 641-655.	2.5	22
1817	Complete Genome Sequence of an Alphabaculovirus from <i>Choristoneura diversana</i> . <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	0
1818	Discovery of thermophilic Bacillales using reduced-representation genotyping for identification. <i>BMC Microbiology</i> , 2020, 20, 114.	3.3	4
1819	High Synteny and Sequence Identity between Genomes of <i>Nitrosococcus oceani</i> Strains Isolated from Different Oceanic Gyres Reveals Genome Economization and Autochthonous Clonal Evolution. <i>Microorganisms</i> , 2020, 8, 693.	3.6	4
1820	Dataset on phenotypic characterization, on protein and genome analysis of three fluorescent <i>Pseudomonas</i> strains from mid-mountain water. <i>Data in Brief</i> , 2020, 30, 105466.	1.0	0
1821	Fatal <i>Clostridium sordellii</i> -mediated hemorrhagic and necrotizing gastroenteropathy in a dog: case report. <i>BMC Veterinary Research</i> , 2020, 16, 152.	1.9	2
1822	The Concerted Action of Two B3-Like Prophage Genes Excludes Superinfecting Bacteriophages by Blocking DNA Entry into <i>Pseudomonas aeruginosa</i> . <i>Journal of Virology</i> , 2020, 94, .	3.4	5
1823	Pan-CWAS of <i>Streptococcus agalactiae</i> Highlights Lineage-Specific Genes Associated with Virulence and Niche Adaptation. <i>MBio</i> , 2020, 11, .	4.1	47

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1825	Unexpected conservation and global transmission of agrobacterial virulence plasmids. <i>Science</i> , 2020, 368, .	12.6	56
1826	Lactic acid bacterial diversity in Brie cheese focusing on salt concentration and pH of isolation medium and characterisation of halophilic and alkaliphilic lactic acid bacterial isolates. <i>International Dairy Journal</i> , 2020, 109, 104757.	3.0	15
1827	Complete plastome sequencing resolves taxonomic relationships among species of <i>Calligonum</i> L. ( <i>Polygonaceae</i> ) in China. <i>BMC Plant Biology</i> , 2020, 20, 261.	3.6	30
1828	Analysis of 1321 <i>Eubacterium rectale</i> genomes from metagenomes uncovers complex phylogeographic population structure and subspecies functional adaptations. <i>Genome Biology</i> , 2020, 21, 138.	8.8	72
1829	Genetic and Functional Analyses of Virulence Potential of an <i>Escherichia coli</i> O157:H7 Strain Isolated From Super-Shedder Cattle. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 271.	3.9	14
1830	Diversity of Mobile Genetic Elements in the Mitogenomes of Closely Related <i>Fusarium culmorum</i> and <i>F. graminearum sensu stricto</i> Strains and Its Implication for Diagnostic Purposes. <i>Frontiers in Microbiology</i> , 2020, 11, 1002.	3.5	11
1831	<i>Moraxella catarrhalis</i> phase-variable loci show differences in expression during conditions relevant to disease. <i>PLoS ONE</i> , 2020, 15, e0234306.	2.5	5
1832	Characterization of Extremely Drug-Resistant and Hypervirulent <i>Acinetobacter baumannii</i> ABO30. <i>Antibiotics</i> , 2020, 9, 328.	3.7	11
1833	Rapid diversification of wild social groups driven by toxin-immunity loci on mobile genetic elements. <i>ISME Journal</i> , 2020, 14, 2474-2487.	9.8	15
1834	Comparative Genomics of <i>Pediococcus pentosaceus</i> Isolated From Different Niches Reveals Genetic Diversity in Carbohydrate Metabolism and Immune System. <i>Frontiers in Microbiology</i> , 2020, 11, 253.	3.5	36
1835	Outbreak of <i>Dirkmeia churashimaensis</i> Fungemia in a Neonatal Intensive Care Unit, India. <i>Emerging Infectious Diseases</i> , 2020, 26, 764-768.	4.3	7
1836	Novel heavy metal resistance gene clusters are present in the genome of <i>Cupriavidus neocaledonicus</i> STM 6070, a new species of <i>Mimosa pudica</i> microsymbiont isolated from heavy-metal-rich mining site soil. <i>BMC Genomics</i> , 2020, 21, 214.	2.8	18
1837	Emergence of OXA-232-producing hypervirulent <i>Klebsiella pneumoniae</i> ST23 causing neonatal sepsis. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 2004-2006.	3.0	22
1838	Plastome Evolution and Phylogeny of <i>Orchidaceae</i> , With 24 New Sequences. <i>Frontiers in Plant Science</i> , 2020, 11, 22.	3.6	62
1839	<i>Chlamydia psittaci</i> in fulmars on the Faroe Islands: a causative link to South American psittacines eight decades after a severe epidemic. <i>Microbes and Infection</i> , 2020, 22, 356-359.	1.9	9
1840	<i>Streptomyces</i> spp. From the Marine Sponge <i>Antho dichotoma</i> : Analyses of Secondary Metabolite Biosynthesis Gene Clusters and Some of Their Products. <i>Frontiers in Microbiology</i> , 2020, 11, 437.	3.5	25
1841	<i>Zygnema circumcarinatum</i> UTEX 1559 chloroplast and mitochondrial genomes provide insight into land plant evolution. <i>Journal of Experimental Botany</i> , 2020, 71, 3361-3373.	4.8	9

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1843	Population structure and adaptation of a bacterial pathogen in California grapevines. <i>Environmental Microbiology</i> , 2020, 22, 2625-2638.	3.8	26
1844	A survey of extended-spectrum beta-lactamase-producing <i>Enterobacteriaceae</i> in urban wetlands in southwestern Nigeria as a step towards generating prevalence maps of antimicrobial resistance. <i>PLoS ONE</i> , 2020, 15, e0229451.	2.5	19
1845	Genome analysis of <i>Lactobacillus plantarum</i> subsp. <i>plantarum</i> KCCP11226 reveals a well-conserved C30 carotenoid biosynthetic pathway. <i>3 Biotech</i> , 2020, 10, 150.	2.2	8
1846	Taxonomic scheme of the order Chaetophorales (Chlorophyceae, Chlorophyta) based on chloroplast genomes. <i>BMC Genomics</i> , 2020, 21, 442.	2.8	13
1847	An Avirulence Gene Cluster in the Wheat Stripe Rust Pathogen ( <i>Puccinia striiformis</i> f. sp. <i>tritici</i> ) Tj ETQq1 1 0.784314 rgBT /Overl 2020, 5, .	2.9	18
1848	Draft genome sequence of antimicrobial producing <i>Paenibacillus alvei</i> strain MP1 reveals putative novel antimicrobials. <i>BMC Research Notes</i> , 2020, 13, 280.	1.4	7
1849	Introducing Lu-1, a Novel <i>Lactobacillus jensenii</i> Phage Abundant in the Urogenital Tract. <i>PLoS ONE</i> , 2020, 15, e0234159.	2.5	10
1850	The Loss of the Inverted Repeat in the Putranjivoid Clade of Malpighiales. <i>Frontiers in Plant Science</i> , 2020, 11, 942.	3.6	22
1851	IMP-38-Producing High-Risk Sequence Type 307 <i>Klebsiella pneumoniae</i> Strains from a Neonatal Unit in China. <i>MSphere</i> , 2020, 5, .	2.9	6
1852	The Genome Sequence of the Jean-Talon Strain, an Archeological Beer Yeast from QuÃ©bec, Reveals Traces of Adaptation to Specific Brewing Conditions. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3087-3097.	1.8	3
1853	Plastome Structural Conservation and Evolution in the Clusioid Clade of Malpighiales. <i>Scientific Reports</i> , 2020, 10, 9091.	3.3	22
1854	The Origin and Evolution of Plastid Genome Downsizing in Southern Hemispheric Cypresses (Cupressaceae). <i>Frontiers in Plant Science</i> , 2020, 11, 901.	3.6	6
1855	Genomics analysis of the steroid estrogen-degrading bacterium <i>Serratia nematodiphila</i> DH-S01. <i>Biotechnology and Biotechnological Equipment</i> , 2020, 34, 430-440.	1.3	10
1856	Genomic Analysis and Antimicrobial Resistance of <i>Aliarcobacter cryaerophilus</i> Strains From German Water Poultry. <i>Frontiers in Microbiology</i> , 2020, 11, 1549.	3.5	10
1857	Population genomics of <i>Vibrionaceae</i> isolated from an endangered oasis reveals local adaptation after an environmental perturbation. <i>BMC Genomics</i> , 2020, 21, 418.	2.8	6
1858	Highâ€contiguity genome assembly of the chemosynthetic gammaproteobacterial endosymbiont of the cold seep tubeworm <i>Lamellibrachia barhami</i> . <i>Molecular Ecology Resources</i> , 2020, 20, 1432-1444.	4.8	6
1859	Complete genome sequence and epigenetic profile of <i>Bacillus velezensis</i> UCMB5140 used for plant and crop protection in comparison with other plant-associated <i>Bacillus</i> strains. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 7643-7656.	3.6	10



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1860	Experimental infection of the white snook <i>Centropomus viridis</i> Lockington (1877) with <i>Vibrio ponticus</i> : Histopathological manifestations and screening for putative virulence genes. <i>Aquaculture</i> , 2020, 528, 735599.	3.5	2
1861	Evolutionary epidemiology of <i>Streptococcus iniae</i> : Linking mutation rate dynamics with adaptation to novel immunological landscapes. <i>Infection, Genetics and Evolution</i> , 2020, 85, 104435.	2.3	11
1862	Fine mapping and candidate gene analysis of qKW7b, a major QTL for kernel width in maize. <i>Molecular Breeding</i> , 2020, 40, 1.	2.1	4
1863	CRISPR-Cas9-Mediated Carbapenemase Gene and Plasmid Curing in Carbapenem-Resistant <i>Enterobacteriaceae</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	3.2	50
1864	Phylogeographical Analyses and Antibiotic Resistance Genes of <i>Acinetobacter johnsonii</i> Highlight Its Clinical Relevance. <i>MSphere</i> , 2020, 5, .	2.9	13
1865	Characterization of Bacteriophages against <i>Pseudomonas Syringae</i> pv. <i>Actinidiae</i> with Potential Use as Natural Antimicrobials in Kiwifruit Plants. <i>Microorganisms</i> , 2020, 8, 974.	3.6	33
1866	Comparative genomics of multidrug-resistant <i>Enterococcus</i> spp. isolated from wastewater treatment plants. <i>BMC Microbiology</i> , 2020, 20, 20.	3.3	31
1867	<p><Consequences Of Long-Term Bacteriaâ€™s Exposure To Silver Nanoformulations With Different PhysicoChemical Properties</p>. <i>International Journal of Nanomedicine</i> , 2020, Volume 15, 199-213.	6.7	14
1868	Comparative Analysis of <i>Actaea</i> Chloroplast Genomes and Molecular Marker Development for the Identification of Authentic <i>Cimicifuga</i> Rhizoma. <i>Plants</i> , 2020, 9, 157.	3.5	4
1869	Characterization of <i>Staphylococcus intermedius</i> Group Isolates Associated with Animals from Antarctica and Emended Description of <i>Staphylococcus delphini</i> . <i>Microorganisms</i> , 2020, 8, 204.	3.6	19
1870	Complete genome sequence and genome-scale metabolic modelling of <i>Acinetobacter baumannii</i> type strain ATCC 19606. <i>International Journal of Medical Microbiology</i> , 2020, 310, 151412.	3.6	11
1871	Integrated Genome-Wide Analysis of an Isogenic Pair of <i>Pseudomonas aeruginosa</i> Clinical Isolates with Differential Antimicrobial Resistance to Ceftolozane/Tazobactam, Ceftazidime/Avibactam, and Piperacillin/Tazobactam. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1026.	4.1	11
1872	Characterization of blaCTX-M-14 transposition from plasmid to chromosome in <i>Escherichia coli</i> experimental strain. <i>International Journal of Medical Microbiology</i> , 2020, 310, 151395.	3.6	11
1873	Data of de novo genome assembly of the <i>Chlamydia psittaci</i> strain isolated from the livestock in Volga Region, Russian Federation. <i>Data in Brief</i> , 2020, 29, 105190.	1.0	4
1874	Organelle inheritance and genome architecture variation in isogamous brown algae. <i>Scientific Reports</i> , 2020, 10, 2048.	3.3	12
1875	Characterization and Genome Analysis of a Novel <i>Salmonella</i> Phage vB_SenS_SE1. <i>Current Microbiology</i> , 2020, 77, 1308-1315.	2.2	18
1876	Whole genome sequencing of carbapenem-resistant <i>Klebsiella pneumoniae</i> : evolutionary analysis for outbreak investigation. <i>Future Microbiology</i> , 2020, 15, 203-212.	2.0	7
1877	Comparative genomic analysis of <i>Bordetella bronchiseptica</i> isolates from the lungs of pigs with porcine respiratory disease complex (PRDC). <i>Infection, Genetics and Evolution</i> , 2020, 81, 104258.	2.3	6

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1878	Comparative genetic and physiological characterisation of <i>Pectinatus</i> species reveals shared tolerance to beer-associated stressors but halotolerance specific to pickle-associated strains. <i>Food Microbiology</i> , 2020, 90, 103462.	4.2	6
1879	An Extended-Spectrum Beta-Lactamase-Producing Hybrid Shiga-Toxigenic and Enterotoxigenic <i>Escherichia coli</i> Strain Isolated from a Piglet with Diarrheal Disease in Northeast China. <i>Foodborne Pathogens and Disease</i> , 2020, 17, 382-387.	1.8	3
1880	Genomic insight into the origins and evolution of symbiosis genes in <i>Phaseolus vulgaris</i> microsymbionts. <i>BMC Genomics</i> , 2020, 21, 186.	2.8	24
1881	Fluorescent <i>Pseudomonas</i> strains from mid-mountain water able to release antioxidant proteins directly into water. <i>Microbiological Research</i> , 2020, 236, 126444.	5.3	0
1882	Complete organelle genomes of <i>Sinapis arvensis</i> and their evolutionary implications. <i>Crop Journal</i> , 2020, 8, 505-514.	5.2	12
1883	Comparative genome characterization of the periodontal pathogen <i>Tannerella forsythia</i> . <i>BMC Genomics</i> , 2020, 21, 150.	2.8	9
1884	Comparative Genomic Analysis Reveals the Mechanism Driving the Diversification of Plastomic Structure in <i>Taxaceae</i> Species. <i>Frontiers in Genetics</i> , 2019, 10, 1295.	2.3	4
1885	Phylogenetic Analysis and Substitution Rate Estimation of Colonial Volvocine Algae Based on Mitochondrial Genomes. <i>Genes</i> , 2020, 11, 115.	2.4	5
1886	Comparative genomics reveals signature regions used to develop a robust and sensitive multiplex TaqMan real-time qPCR assay to detect the genus <i>Dickeya</i> and <i>Dickeya dianthicola</i> . <i>Journal of Applied Microbiology</i> , 2020, 128, 1703-1719.	3.1	19
1887	Comparative genomic analysis and identification of pathogenicity islands of hypervirulent ST-17 <i>Streptococcus agalactiae</i> Brazilian strain. <i>Infection, Genetics and Evolution</i> , 2020, 80, 104195.	2.3	9
1888	Isolation of Four Lytic Phages Infecting <i>Klebsiella pneumoniae</i> K22 Clinical Isolates from Spain. <i>International Journal of Molecular Sciences</i> , 2020, 21, 425.	4.1	19
1889	Isolation and Characterization of vB_PagP-SK1, a T7-Like Phage Infecting <i>Pantoea agglomerans</i> . <i>Phage</i> , 2020, 1, 45-56.	1.7	7
1890	Complete Chloroplast Genome Sequence of Chinese Lacquer Tree ( <i>Toxicodendron vernicifluum</i> ), Tj ETQq0 0.0rgBT /Overlock 10	1.9	15
1891	Genome-Based Comparison of All Species of the Genus <i>Moorella</i> , and Status of the Species <i>Moorella thermoacetica</i> and <i>Moorella thermoautotrophica</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 3070.	3.5	12
1892	Discovery of <i>Paenibacillus larvae</i> ERIC V: Phenotypic and genomic comparison to genotypes ERIC I-IV reveal different inventories of virulence factors which correlate with epidemiological prevalences of American Foulbrood. <i>International Journal of Medical Microbiology</i> , 2020, 310, 151394.	3.6	47
1893	Pathogenomes of Atypical Non-shigatoxigenic <i>Escherichia coli</i> NSF/SF O157:H7/NM: Comprehensive Phylogenomic Analysis Using Closed Genomes. <i>Frontiers in Microbiology</i> , 2020, 11, 619.	3.5	11
1894	Evolution and Genetic Diversity of Primate Cytomegaloviruses. <i>Microorganisms</i> , 2020, 8, 624.	3.6	11
1895	Complete Chloroplast Genome Sequence and Phylogenetic Inference of the Canary Islands Dragon Tree ( <i>Dracaena draco</i> L.). <i>Forests</i> , 2020, 11, 309.	2.1	14

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1896	Bioinformatics approaches applied in pan-genomics and their challenges. , 2020, , 43-64.		1
1897	Assembly and Analysis of the Complete Mitochondrial Genome of <i>Capsella bursa-pastoris</i> . <i>Plants</i> , 2020, 9, 469.	3.5	14
1898	Parallel Evolution in the Integration of a Co-obligate Aphid Symbiosis. <i>Current Biology</i> , 2020, 30, 1949-1957.e6.	3.9	54
1899	The complete genome sequence of <i>Mycobacterium bovis</i> Mb3601, a SB0120 spoligotype strain representative of a new clonal group. <i>Infection, Genetics and Evolution</i> , 2020, 82, 104309.	2.3	22
1900	Complete Genome Sequence of <i>Stenotrophomonas maltophilia</i> Myophage Moby. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	5
1901	Comparative Genome Analysis of Hungarian and Global Strains of <i>Salmonella</i> <i>Infantis</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 539.	3.5	19
1902	Severe Plastid Genome Size Reduction in a Mycoheterotrophic Orchid, <i>Danxiaorchis singchiana</i> , Reveals Heavy Gene Loss and Gene Relocations. <i>Plants</i> , 2020, 9, 521.	3.5	4
1903	Complete Genome Sequence of <i>Serratia</i> Phage Muldoon. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	4
1904	Comparative Genomic Analysis of Closely Related <i>Acetobacter pasteurianus</i> Strains Provides Evidence of Horizontal Gene Transfer and Reveals Factors Necessary for Thermotolerance. <i>Journal of Bacteriology</i> , 2020, 202, .	2.2	17
1905	Mutation of <i>kvxA</i> Causes OmpK35 and OmpK36 Porin Downregulation and Reduced Meropenem-Vaborbactam Susceptibility in KPC-Producing <i>Klebsiella pneumoniae</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	3.2	20
1906	A soil bacterial catabolic pathway on the move: Transfer of nicotine catabolic genes between <i>Arthrobacter</i> genus megaplasmids and invasion by mobile elements. <i>Journal of Biosciences</i> , 2020, 45, 1.	1.1	4
1907	Complete Genome Sequence of <i>Escherichia coli</i> BL21-AI. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	8
1908	Complete Genome Sequence of <i>Serratia marcescens</i> Siphophage Slocum. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	3
1909	Complete Genome Sequence of Myophage Ec_Makalu_002, Which Infects Uropathogenic <i>Escherichia coli</i> . <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	2
1910	Wide crossing diversify mitogenomes of rice. <i>BMC Plant Biology</i> , 2020, 20, 159.	3.6	5
1911	Human intestinal enteroids as a model of <i>Clostridioides difficile</i> -induced enteritis. <i>American Journal of Physiology - Renal Physiology</i> , 2020, 318, G870-G888.	3.4	23
1912	Evolution of Predicted Acid Resistance Mechanisms in the Extremely Acidophilic <i>Leptospirillum</i> Genus. <i>Genes</i> , 2020, 11, 389.	2.4	23
1913	The First Glimpse of <i>Streptocarpus ionanthus</i> (Gesneriaceae) Phylogenomics: Analysis of Five Subspecies' Chloroplast Genomes. <i>Plants</i> , 2020, 9, 456.	3.5	13

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1914	Complete Genome Sequencing Provides Novel Insight Into the Virulence Repertoires and Phylogenetic Position of Dry Beans Pathogen <i>Curtobacterium flaccumfaciens</i> pv. <i>flaccumfaciens</i> . <i>Phytopathology</i> , 2021, 111, 268-280.	2.2	26
1915	Genome analysis of <i>Streptococcus suis</i> serotype 2 revealed genomic diversity among strains of different virulence. <i>Transboundary and Emerging Diseases</i> , 2021, 68, 637-647.	3.0	19
1916	Plastid phylogenomic insights into the evolution of subfamily Dialioideae (Leguminosae). <i>Plant Diversity</i> , 2021, 43, 27-34.	3.7	16
1917	Foliose <i>Ulva</i> Species Show Considerable Inter-specific Genetic Diversity, Low Intra-specific Genetic Variation, and the Rare Occurrence of Inter-specific Hybrids in the Wild. <i>Journal of Phycology</i> , 2021, 57, 219-233.	2.3	24
1918	Evolution and dissemination of L and M plasmid lineages carrying antibiotic resistance genes in diverse Gram-negative bacteria. <i>Plasmid</i> , 2021, 113, 102528.	1.4	10
1919	Deciphering the origin of <i>Aspergillus flavus</i> NRRL21882, the active biocontrol agent of <i>Afla-Guard</i> <sup>®</sup> . <i>Letters in Applied Microbiology</i> , 2021, 72, 509-516.	2.2	11
1920	Evolutionary History of Mitochondrial Genomes in <i>Discoba</i> , Including the Extreme Halophile <i>Pleurostomum flabellatum</i> (Heterolobosea). <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	6
1921	Plastome phylogenomics of <i>Cephalotaxus</i> (Cephalotaxaceae) and allied genera. <i>Annals of Botany</i> , 2021, 127, 697-708.	2.9	14
1922	ICEHpsaHPS7, a Novel Multiple Drug Resistance Integrative Conjugative Element in <i>Glaesserella parasuis</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, .	3.2	7
1923	Diversification of methanogens into hyperalkaline serpentinizing environments through adaptations to minimize oxidant limitation. <i>ISME Journal</i> , 2021, 15, 1121-1135.	9.8	37
1924	Comparative Omics Analysis of Historic and Recent Isolates of <i>Bordetella pertussis</i> and Effects of Genome Rearrangements on Evolution. <i>Emerging Infectious Diseases</i> , 2021, 27, 57-68.	4.3	10
1925	De novo assembly and comparative analysis of the complete mitochondrial genome sequence of the pistachio psyllid, <i>Agonoscyta pistaciae</i> (Hemiptera: Aphalaridae). <i>International Journal of Tropical Insect Science</i> , 2021, 41, 1387-1396.	1.0	1
1926	<i>Bradyrhizobium campsiandrae</i> sp. nov., a nitrogen-fixing bacterial strain isolated from a native leguminous tree from the Amazon adapted to flooded conditions. <i>Archives of Microbiology</i> , 2021, 203, 233-240.	2.2	8
1927	Genome Analysis of <i>Erwinia amylovora</i> Strains Responsible for a Fire Blight Outbreak in Korea. <i>Plant Disease</i> , 2021, 105, 1143-1152.	1.4	12
1928	Repeats in mitochondrial and chloroplast genomes characterize the ecotypes of the <i>Oryza</i> . <i>Molecular Breeding</i> , 2021, 41, 1.	2.1	1
1929	Complete Genome Sequence of <i>Francisella</i> sp. Strain LA11-2445 (FDC406), a Novel <i>Francisella</i> Species Isolated from a Human Skin Lesion. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	0
1930	Evolutionary Rescue of an Environmental <i>Pseudomonas otitidis</i> in Response to Anthropogenic Perturbation. <i>Frontiers in Microbiology</i> , 2020, 11, 563885.	3.5	5
1931	Comparative Virulence and Genomic Analysis of <i>Streptococcus suis</i> Isolates. <i>Frontiers in Microbiology</i> , 2020, 11, 620843.	3.5	11

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1932	Complete Genome Sequence of <i>Rhizobium japonicum</i> Podophage Pasto. Microbiology Resource Announcements, 2021, 10, .	0.6	2
1933	Complete Genome Sequence of <i>Streptomyces</i> Siphophage Sycamore. Microbiology Resource Announcements, 2021, 10, .	0.6	0
1934	Increasing New Delhi metallo- $\beta$ -lactamase-positive <i>Escherichia coli</i> among carbapenem non-susceptible Enterobacteriaceae in Taiwan during 2016 to 2018. Scientific Reports, 2021, 11, 2609.	3.3	16
1935	Genome-wide comparison of four MRSA clinical isolates from Germany and Hungary. PeerJ, 2021, 9, e10185.	2.0	6
1936	Genetic diversification of persistent <i>Mycobacterium abscessus</i> within cystic fibrosis patients. Virulence, 2021, 12, 2415-2429.	4.4	14
1937	Plastid Genomes of Flowering Plants: Essential Principles. Methods in Molecular Biology, 2021, 2317, 3-47.	0.9	16
1938	Holocene chloroplast genetic variation of shrubs ( <i>Alnus alnobetula</i> , <i>Betula nana</i> ,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 50 assembly and sedimentary ancient DNA analyses. Ecology and Evolution, 2021, 11, 2173-2193.	1.9	9
1939	Complete Genome Sequence of <i>Rhizobium phaseoli</i> Podophage Palo. Microbiology Resource Announcements, 2021, 10, .	0.6	1
1940	Complete Genome Sequence of <i>Streptomyces</i> Siphophage Sitrop. Microbiology Resource Announcements, 2021, 10, .	0.6	0
1941	Comparative Genomics, from the Annotated Genome to Valuable Biological Information: A Case Study. Methods in Molecular Biology, 2021, 2242, 91-112.	0.9	0
1942	Genome Analysis of a Historical <i>Shigella dysenteriae</i> Serotype 1 Strain Carrying a Conserved Stx Prophage Region. Frontiers in Microbiology, 2020, 11, 614793.	3.5	1
1943	Type <i>IV</i> pili are widespread among non-pathogenic Gram-positive gut bacteria with diverse carbohydrate utilization patterns. Environmental Microbiology, 2021, 23, 1527-1540.	3.8	3
1944	Identification and Characterization of Mycobacterial Species Using Whole-Genome Sequences. Methods in Molecular Biology, 2021, 2314, 399-457.	0.9	0
1945	One is not enough: On the effects of reference genome for the mapping and subsequent analyses of short-reads. PLoS Computational Biology, 2021, 17, e1008678.	3.2	46
1946	Genomic Analysis of a Newly Isolated <i>Acidithiobacillus ferridurans</i> JAGS Strain Reveals Its Adaptation to Acid Mine Drainage. Minerals (Basel, Switzerland), 2021, 11, 74.	2.0	15
1947	Complete Genome Sequence of <i>Streptomyces</i> Phage Shady. Microbiology Resource Announcements, 2021, 10, .	0.6	0
1948	Complete Genome Sequence of <i>Klebsiella aerogenes</i> Siphophage Solomon. Microbiology Resource Announcements, 2021, 10, .	0.6	0
1949	Complete Genome Sequence of <i>Klebsiella pneumoniae</i> Myophage Muenster. Microbiology Resource Announcements, 2021, 10, .	0.6	3

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1950	Complete Genome Sequence of <i>Klebsiella pneumoniae</i> Jumbo Phage Miami. Microbiology Resource Announcements, 2021, 10, .	0.6	4
1951	Reorganized Genomic Taxonomy of Francisellaceae Enables Design of Robust Environmental PCR Assays for Detection of <i>Francisella tularensis</i> . Microorganisms, 2021, 9, 146.	3.6	19
1952	Mitochondrial genome of the harmful algal bloom species <i>Odontella regia</i> (Mediophyceae,) Tj ETQq0 0 0 rgBT /Overclock 10 Tf 50 662 To	2.8	9
1953	Phylogenetic Methods for Genome-Wide Association Studies in Bacteria. Methods in Molecular Biology, 2021, 2242, 205-220.	0.9	5
1954	Complete Genome Sequence of <i>Streptomyces</i> Phage Sentinel. Microbiology Resource Announcements, 2021, 10, .	0.6	0
1955	Complete Genome Sequence of <i>Streptomyces</i> Phage Salutena. Microbiology Resource Announcements, 2021, 10, .	0.6	0
1956	Whole genomic comparative analysis of <i>Streptococcus pneumoniae</i> serotype 1 isolates causing invasive and non-invasive infections among children under 5 years in Casablanca, Morocco. BMC Genomics, 2021, 22, 39.	2.8	2
1958	Mitochondrial Genome Evolution in Pelagophyte Algae. Genome Biology and Evolution, 2021, 13, .	2.5	10
1959	Examination of <i>Staphylococcus aureus</i> Prophages Circulating in Egypt. Viruses, 2021, 13, 337.	3.3	5
1960	Comparative plastome genomics and phylogenetic analyses of Liliaceae. Botanical Journal of the Linnean Society, 2021, 196, 279-293.	1.6	19
1961	Essential Amino Acid Enrichment and Positive Selection Highlight Endosymbiont's Role in a Global Virus-Vectoring Pest. MSystems, 2021, 6, .	3.8	3
1962	Assessing <i>Trypanosoma cruzi</i> Parasite Diversity through Comparative Genomics: Implications for Disease Epidemiology and Diagnostics. Pathogens, 2021, 10, 212.	2.8	24
1963	Complete Genome Sequence of <i>Klebsiella aerogenes</i> Myophage Metamorpho. Microbiology Resource Announcements, 2021, 10, .	0.6	0
1965	Comparative genomics of MRSA strains from human and canine origins reveals similar virulence gene repertoire. Scientific Reports, 2021, 11, 4724.	3.3	13
1966	Temporal Stability and Genetic Diversity of 48-Year-Old T-Series Phages. MSystems, 2021, 6, .	3.8	9
1967	Genomic analysis of a functional haloacid-degrading gene of <i>Bacillus megaterium</i> strain BHS1 isolated from Blue Lake (Mavi Gölü, Turkey). Annals of Microbiology, 2021, 71, .	2.6	5
1968	Complete Genome Sequence of <i>Burkholderia cenocepacia</i> Phage Mica. Microbiology Resource Announcements, 2021, 10, .	0.6	1
1969	Point mutation in the stop codon of MAV_RS14660 increases the growth rate of <i>Mycobacterium avium</i> subspecies <i>hominissuis</i> . Microbiology (United Kingdom), 2021, 167, .	1.8	0



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1970	Extremely low nucleotide diversity among thirty-six new chloroplast genome sequences from <i>Aldama</i> (Heliantheae, Asteraceae) and comparative chloroplast genomics analyses with closely related genera. <i>PeerJ</i> , 2021, 9, e10886.	2.0	15
1971	Complete Genome Sequence of <i>Bradyrhizobium japonicum</i> Podophage Paso. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	0
1972	Assessing the Involvement of Selected Phenotypes of <i>Pseudomonas simiae</i> PICF7 in Olive Root Colonization and Biological Control of <i>Verticillium dahliae</i> . <i>Plants</i> , 2021, 10, 412.	3.5	20
1973	Comparative analysis of <i>Phytophthora</i> genomes reveals oomycete pathogenesis in crops. <i>Heliyon</i> , 2021, 7, e06317.	3.2	3
1974	Evolution of genome structure in the <i>Drosophila simulans</i> species complex. <i>Genome Research</i> , 2021, 31, 380-396.	5.5	55
1975	Continental-Scale Gene Flow Prevents Allopatric Divergence of Pelagic Freshwater Bacteria. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	50
1976	Comparative genomics of two <i>Shewanella xiamenensis</i> strains isolated from a pilgrim before and during travels to the Hajj. <i>Gut Pathogens</i> , 2021, 13, 9.	3.4	5
1978	Complete Genome Sequence of <i>Burkholderia cenocepacia</i> Phage Magia. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	0
1980	Chloroplast genomes and phylogenetic analysis of two species of <i>Oedocladium</i> (Oedogoniales.) <i>Tj ETQq0 0 0 rgBT /Qverlock_10 Tf 50 42</i>	2.0	5
1981	Genomic analysis of the diversity, antimicrobial resistance and virulence potential of clinical <i>Campylobacter jejuni</i> and <i>Campylobacter coli</i> strains from Chile. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009207.	3.0	23
1982	A <i>Sarcina</i> bacterium linked to lethal disease in sanctuary chimpanzees in Sierra Leone. <i>Nature Communications</i> , 2021, 12, 763.	12.8	17
1983	Whole-genome comparative analysis of Malaysian <i>Burkholderia pseudomallei</i> clinical isolates. <i>Microbial Genomics</i> , 2021, 7, .	2.0	7
1984	Pangenome analysis reveals genetic isolation in <i>Campylobacter hyointestinalis</i> subspecies adapted to different mammalian hosts. <i>Scientific Reports</i> , 2021, 11, 3431.	3.3	7
1985	An Efficient, Counter-Selection-Based Method for Prophage Curing in <i>Pseudomonas aeruginosa</i> Strains. <i>Viruses</i> , 2021, 13, 336.	3.3	2
1987	A Novel Group of Promiscuous Podophages Infecting Diverse Gammaproteobacteria from River Communities Exhibits Dynamic Intergenous Host Adaptation. <i>MSystems</i> , 2021, 6, .	3.8	17
1988	Improved multiplex TaqMan qPCR assay with universal internal control offers reliable and accurate detection of <i>Clavibacter michiganensis</i> . <i>Journal of Applied Microbiology</i> , 2021, 131, 1405-1416.	3.1	6
1989	Improving the Inhibitory Effect of Phages against <i>Pseudomonas aeruginosa</i> Isolated from a Burn Patient Using a Combination of Phages and Antibiotics. <i>Viruses</i> , 2021, 13, 334.	3.3	25
1990	The genomic content and context of auxiliary metabolic genes in roseophages. <i>Environmental Microbiology</i> , 2021, 23, 3743-3757.	3.8	18

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1991	Unraveling the emergence and population diversity of <i>Listeria monocytogenes</i> in a newly built meat facility through whole genome sequencing. <i>International Journal of Food Microbiology</i> , 2021, 340, 109043.	4.7	28
1992	Lineage-specific plastid degradation in subtribe <i>Gentianinae</i> ( <i>Gentianaceae</i> ). <i>Ecology and Evolution</i> , 2021, 11, 3286-3299.	1.9	21
1993	Complete Genome Sequence of <i>Burkholderia gladioli</i> Phage Maja. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	1
1994	Chloroplast Genomes of Two Species of <i>Cypripedium</i> : Expanded Genome Size and Proliferation of AT-Biased Repeat Sequences. <i>Frontiers in Plant Science</i> , 2021, 12, 609729.	3.6	30
1995	Characterization and complete genome sequence of <i>Privateer</i> , a highly prolate <i>Proteus mirabilis</i> podophage. <i>PeerJ</i> , 2021, 9, e10645.	2.0	6
1996	Overview of bioinformatic methods for analysis of antibiotic resistome from genome and metagenome data. <i>Journal of Microbiology</i> , 2021, 59, 270-280.	2.8	16
1997	A Novel Antidipteran <i>Bacillus thuringiensis</i> Strain: Unusual Cry Toxin Genes in a Highly Dynamic Plasmid Environment. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	3.1	3
1998	Triclosan Tolerance Is Driven by a Conserved Mechanism in Diverse <i>Pseudomonas</i> Species. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	3.1	8
2000	Community spread and acquisition of clinically relevant <i>Escherichia coli</i> harbouring <i>bla</i> NDM among healthy Japanese residents of Yangon, Myanmar. <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 1448-1454.	3.0	6
2001	Genomic insights into the host specific adaptation of the <i>Pneumocystis</i> genus. <i>Communications Biology</i> , 2021, 4, 305.	4.4	23
2003	A new symbiotic lineage related to <i>Neisseria</i> and <i>Snodgrassella</i> arises from the dynamic and diverse microbiomes in sucking lice. <i>Molecular Ecology</i> , 2021, 30, 2178-2196.	3.9	16
2005	Genomic Insights Into the Pathogenicity of a Novel Biofilm-Forming <i>Enterococcus</i> sp. <i>Bacteria</i> ( <i>Enterococcus lacertideformus</i> ) Identified in Reptiles. <i>Frontiers in Microbiology</i> , 2021, 12, 635208.	3.5	6
2006	Apparent nosocomial adaptation of <i>Enterococcus faecalis</i> predates the modern hospital era. <i>Nature Communications</i> , 2021, 12, 1523.	12.8	69
2007	Dissecting the molecular diversity and commonality of bovine and human treponemes identifies key survival and adhesion mechanisms. <i>PLoS Pathogens</i> , 2021, 17, e1009464.	4.7	7
2008	Epidemic <i>HI2</i> Plasmids Mobilising the Carbapenemase Gene <i>bla</i> IMP-4 in Australian Clinical Samples Identified in Multiple Sublineages of <i>Escherichia coli</i> ST216 Colonising Silver Gulls. <i>Microorganisms</i> , 2021, 9, 567.	3.6	21
2009	Definition of a High-Resolution Molecular Marker for Tracking the Genetic Diversity of the Harmful Algal Species <i>Eucampia zodiacus</i> Through Comparative Analysis of Mitochondrial Genomes. <i>Frontiers in Microbiology</i> , 2021, 12, 631144.	3.5	7
2011	Comparison of MiSeq, MinION, and hybrid genome sequencing for analysis of <i>Campylobacter jejuni</i> . <i>Scientific Reports</i> , 2021, 11, 5676.	3.3	24
2012	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.	3.3	16

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2013	Draft Genome of <i>Proteus mirabilis</i> Serogroup O18 Elaborating Phosphocholine-Decorated O Antigen. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 620010.	3.9	3
2014	Gene disruption by structural mutations drives selection in US rice breeding over the last century. <i>PLoS Genetics</i> , 2021, 17, e1009389.	3.5	6
2015	Engineered yeast genomes accurately assembled from pure and mixed samples. <i>Nature Communications</i> , 2021, 12, 1485.	12.8	11
2017	Draft Genome Sequence of <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Enteritidis ODA 99-30581-13, a Heat-Resistant Strain Isolated from Shell Eggs. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	1
2018	Complete Genome Sequence of <i>Stenotrophomonas maltophilia</i> Siphophage Salva. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	2
2020	Genomic analysis revealed a novel genotype of methicillin-susceptible <i>Staphylococcus aureus</i> isolated from a fatal sepsis case in dengue patient. <i>Scientific Reports</i> , 2021, 11, 4228.	3.3	5
2021	Genome Sequence and Characterization of <i>Acinetobacter</i> Phage DMU1. <i>Phage</i> , 2021, 2, 50-56.	1.7	2
2022	A Large-Scale Sequencing-Based Survey of Plasmids in <i>Listeria monocytogenes</i> Reveals Global Dissemination of Plasmids. <i>Frontiers in Microbiology</i> , 2021, 12, 653155.	3.5	21
2025	Development of a high-resolution molecular marker for tracking <i>Pseudo-nitzschia pungens</i> genetic diversity through comparative analysis of mitochondrial genomes. <i>Journal of Applied Phycology</i> , 2021, 33, 2283-2298.	2.8	5
2026	Complete Genome Sequence of <i>Bifidobacterium longum</i> subsp. <i>longum</i> JCM7052. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	1
2027	Genome and Pangenome Analysis of <i>Lactobacillus hilgardii</i> FLUBA New Strain Isolated from Mead. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3780.	4.1	2
2028	Isolation and Characterization of a Virulent Bacteriophage for Controlling <i>Salmonella</i> Enteritidis Growth in Ready-to-Eat Mixed-Ingredient Salads. <i>Journal of Food Protection</i> , 2021, 84, 1629-1639.	1.7	8
2029	The complete genome sequence of <i>Listeria monocytogenes</i> strain S2542 and expression of selected genes under high-pressure processing. <i>BMC Research Notes</i> , 2021, 14, 137.	1.4	1
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2033	Bacteriophages against <i>Vibrio coralliilyticus</i> and <i>Vibrio tubiashii</i> : Isolation, Characterization, and Remediation of Larval Oyster Mortalities. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	3.1	13
2034	Genomic Characterization of <i>Salmonella typhimurium</i> DT104 Strains Associated with Cattle and Beef Products. <i>Pathogens</i> , 2021, 10, 529.	2.8	7
2035	Comparative genomics of the ADA clade within the Nostocales. <i>Harmful Algae</i> , 2021, 104, 102037.	4.8	11

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2037	JD419, a <i>Staphylococcus aureus</i> Phage With a Unique Morphology and Broad Host Range. <i>Frontiers in Microbiology</i> , 2021, 12, 602902.	3.5	20
2038	Building a cluster of NLR genes conferring resistance to pests and pathogens: the story of the Vat gene cluster in cucurbits. <i>Horticulture Research</i> , 2021, 8, 72.	6.3	14
2039	Multiple internal controls enhance reliability for PCR and real time PCR detection of <i>Rathayibacter toxicus</i> . <i>Scientific Reports</i> , 2021, 11, 8365.	3.3	9
2040	Long-read-sequenced reference genomes of the seven major lineages of enterotoxigenic <i>Escherichia coli</i> (ETEC) circulating in modern time. <i>Scientific Reports</i> , 2021, 11, 9256.	3.3	12
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2044	The genome sequence of hairy root <i>Rhizobium</i> strain LBA9402: Bioinformatics analysis suggests the presence of a new opine system in the agropine Ri plasmid. <i>MicrobiologyOpen</i> , 2021, 10, e1180.	3.0	10
2045	Cocultivation of an ultrasmall environmental parasitic bacterium with lytic ability against bacteria associated with wastewater foams. <i>Nature Microbiology</i> , 2021, 6, 703-711.	13.3	43
2046	Horsing Around: <i>Escherichia coli</i> ST1250 of Equine Origin Harboring Epidemic IncHI1/ST9 Plasmid with CTX-M-1 and an Operon for Short-Chain Fructooligosaccharide Metabolism. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, .	3.2	5
2047	Genome sequence, transcriptome, and annotation of rodent malaria parasite <i>Plasmodium yoelii</i> nigeriensis N67. <i>BMC Genomics</i> , 2021, 22, 303.	2.8	7
2049	<i>Haslea silbo</i> , A Novel Cosmopolitan Species of Blue Diatoms. <i>Biology</i> , 2021, 10, 328.	2.8	12
2050	Silent spread of mobile colistin resistance gene mcr-9.1 on IncHI2 superplasmids in clinical carbapenem-resistant Enterobacterales. <i>Clinical Microbiology and Infection</i> , 2021, 27, 1856.e7-1856.e13.	6.0	37
2051	Fundamental evolution of all Orthocoronavirinae including three deadly lineages descendent from Chiroptera-hosted coronaviruses: SARS-CoV, MERS-CoV and SARS-CoV-2. <i>Cladistics</i> , 2021, 37, 461-488.	3.3	16
2052	Sequence analysis of tyrosine recombinases allows annotation of mobile genetic elements in prokaryotic genomes. <i>Molecular Systems Biology</i> , 2021, 17, e9880.	7.2	33
2053	Essential Gene Analysis in <i>Acinetobacter baumannii</i> by High-Density Transposon Mutagenesis and CRISPR Interference. <i>Journal of Bacteriology</i> , 2021, 203, e0056520.	2.2	25
2054	Complete Genome Sequence of <i>Burkholderia gladioli</i> Myophage Mana. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	1
2056	Comparison of mitochondrial genomes provides insights into intron dynamics and evolution in <i>Botryosphaeria dothidea</i> and <i>B. kuwatsukai</i> . <i>Environmental Microbiology</i> , 2021, 23, 5320-5333.	3.8	4
2057	Unraveling the Central Role of Sulfur-Oxidizing <i>Acidiphilium multivorum</i> LMS in Industrial Bioprocessing of Gold-Bearing Sulfide Concentrates. <i>Microorganisms</i> , 2021, 9, 984.	3.6	12

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2059	Genomic GC content drifts downward in most bacterial genomes. <i>PLoS ONE</i> , 2021, 16, e0244163.	2.5	7
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2062	Whole-Genome Analysis of <i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> IS900 Insertions Reveals Strain Type-Specific Modalities. <i>Frontiers in Microbiology</i> , 2021, 12, 660002.	3.5	7
2063	Four Complete Genome Sequences for <i>Bradyrhizobium</i> sp. Strains Isolated from an Endemic Australian <i>Acacia</i> Legume Reveal Structural Variation. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	2
2064	Characterization of bla NDM-5-harboring <i>Klebsiella pneumoniae</i> sequence type 11 international high-risk clones isolated from clinical samples in Yangon General Hospital, a tertiary-care hospital in Myanmar. <i>Journal of Medical Microbiology</i> , 2021, 70, .	1.8	4
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2069	Complete Genome Sequence of <i>Klebsiella pneumoniae</i> Podophage Pune. <i>Microbiology Resource Announcements</i> , 2021, 10, e0140520.	0.6	0
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2071	Genomic analysis of novel <i>Yarrowia</i> -like yeast symbionts associated with the carrion-feeding burying beetle <i>Nicrophorus vespilloides</i> . <i>BMC Genomics</i> , 2021, 22, 323.	2.8	3
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2075	Genomic analysis of the lectotype specimens of European <i>Ulva rigida</i> and <i>Ulva lacinulata</i> (Ulvaceae, Chlorophyta) reveals the ongoing misapplication of names. <i>European Journal of Phycology</i> , 2022, 57, 143-153.	2.0	35
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2092	New Insight into Taxonomy of European Mountain Pines, Pinus mugo Complex, Based on Complete Chloroplast Genomes Sequencing. Plants, 2021, 10, 1331.	3.5	10
2093	Molecular Evolution and Adaptation of Livestock-Associated Methicillin-Resistant Staphylococcus aureus (LA-MRSA) Sequence Type 9. MSys, 2021, 6, e0049221.	3.8	36
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2099	Comparative genome analysis revealed gene inversions, boundary expansions and contractions, and gene loss in the <i>Stemona sessilifolia</i> (Miq.) Miq. chloroplast genome. <i>PLoS ONE</i> , 2021, 16, e0247736.	2.5	7
2100	The complete mitogenome assemblies of 10 diploid potato clones reveal recombination and overlapping variants. <i>DNA Research</i> , 2021, 28, .	3.4	4
2101	Molecular characterization of a <i>Bacillus thuringiensis</i> strain from Argentina, toxic against <i>Lepidoptera</i> and <i>Coleoptera</i> , based on its whole-genome and Cry protein analysis. <i>Journal of Invertebrate Pathology</i> , 2021, 183, 107563.	3.2	8
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2103	<i>Pseudomonas aeruginosa</i> PAO 1 In Vitro Timeâ€“Kill Kinetics Using Single Phages and Phage Formulationsâ€“Modulating Death, Adaptation, and Resistance. <i>Antibiotics</i> , 2021, 10, 877.	3.7	5
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2106	Extreme Enlargement of the Inverted Repeat Region in the Plastid Genomes of Diatoms from the Genus <i>Climaconeis</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 7155.	4.1	8
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2109	Differential insecticidal properties of <i>Spodoptera frugiperda</i> multiple nucleopolyhedrovirus isolates against corn-strain and rice-strain fall armyworm, and genomic analysis of three isolates. <i>Journal of Invertebrate Pathology</i> , 2021, 183, 107561.	3.2	10
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2115	Complete genome sequence and phylogenomic analysis of the first N4-like lytic bacteriophage vB_Ppp_A38 (Î•A38) infecting <i>Pectobacterium parmentieri</i> . <i>European Journal of Plant Pathology</i> , 2021, 161, 483-489.	1.7	2
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2120	Large Differences in the Haptophyte <i>Phaeocystis globosa</i> Mitochondrial Genomes Driven by Repeat Amplifications. <i>Frontiers in Microbiology</i> , 2021, 12, 676447.	3.5	7
2121	Unveiling the Virulent Genotype and Unusual Biochemical Behavior of <i>Escherichia coli</i> ST59. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0074321.	3.1	5
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2126	Harmonization of whole-genome sequencing for outbreak surveillance of Enterobacteriaceae and Enterococci. <i>Microbial Genomics</i> , 2021, 7, .	2.0	6
2128	Repeated exposure of nosocomial pathogens to silver does not select for silver resistance but does impact ciprofloxacin susceptibility. <i>Acta Biomaterialia</i> , 2021, 134, 760-773.	8.3	1
2129	In Silico Analysis of Potential Outer Membrane Beta-Barrel Proteins in <i>Aeromonas hydrophila</i> Pangenome. <i>International Journal of Peptide Research and Therapeutics</i> , 2021, , 1-9.	1.9	1
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2134	Genomic and Phenotypic Biology of Novel Strains of <i>Dickeya zeae</i> Isolated From Pineapple and Taro in Hawaii: Insights Into Genome Plasticity, Pathogenicity, and Virulence Determinants. <i>Frontiers in Plant Science</i> , 2021, 12, 663851.	3.6	15
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2137	BnaA02.YTG1, encoding a tetratricopeptide repeat protein, is required for early chloroplast biogenesis in <i>Brassica napus</i> . <i>Crop Journal</i> , 2022, 10, 597-610.	5.2	3

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2139	Molecular evidence for homologous strains of infectious spleen and kidney necrosis virus (ISKNV) genotype I infecting inland freshwater cultured Asian sea bass ( <i>Lates calcarifer</i> ) in Thailand. <i>Archives of Virology</i> , 2021, 166, 3061-3074.	2.1	8
2140	High-Quality Complete Genome Resource of Tomato Rhizosphere Strain <i>Pseudomonas donghuensis</i> P482, a Representative of a Species with Biocontrol Activity Against Plant Pathogens. <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 1450-1454.	2.6	3
2141	Safe and easy in vitro evaluation of tmRNA-SmpB-mediated trans-translation from ESKAPE pathogenic bacteria. <i>Rna</i> , 2021, 27, 1390-1399.	3.5	2
2142	Tailed Lytic Bacteriophages of Soft Rot Pectobacteriaceae. <i>Microorganisms</i> , 2021, 9, 1819.	3.6	7
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2153	Equine Intestinal O-Seroconverting Temperate Coliphage Hf4s: Genomic and Biological Characterization. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0112421.	3.1	4
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2167	Extensive genomic rearrangements mediated by repetitive sequences in plastomes of <i>Medicago</i> and its relatives. <i>BMC Plant Biology</i> , 2021, 21, 421.	3.6	25
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2227	Bayesian identification of bacterial strains from sequencing data. <i>Microbial Genomics</i> , 2016, 2, e000075.	2.0	19
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2230	Comparative analysis of the <i>Burkholderia cenocepacia</i> K56-2 essential genome reveals cell envelope functions that are uniquely required for survival in species of the genus <i>Burkholderia</i> . <i>Microbial Genomics</i> , 2017, 3, .	2.0	27
2231	Comparative genomics of <i>Salmonella enterica</i> serovar Montevideo reveals lineage-specific gene differences that may influence ecological niche association. <i>Microbial Genomics</i> , 2018, 4, .	2.0	19
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2243	Acquisition of plasmids conferring carbapenem and aminoglycoside resistance and loss of surface-exposed macromolecule structures as strategies for the adaptation of <i>Acinetobacter baumannii</i> CC104O/CC15P strains to the clinical setting. <i>Microbial Genomics</i> , 2020, 6, .	2.0	6
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2251	Phylogenetic diversity, antimicrobial susceptibility and virulence characteristics of phylogroup F <i>Escherichia coli</i> in Australia. <i>Microbiology (United Kingdom)</i> , 2016, 162, 1904-1912.	1.8	59
2252	<i>Xylella fastidiosa</i> CoDiRO strain associated with the olive quick decline syndrome in southern Italy belongs to a clonal complex of the subspecies <i>pauca</i> that evolved in Central America. <i>Microbiology (United Kingdom)</i> , 2016, 162, 2087-2098.	1.8	26

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2254	Broad-spectrum antimicrobial activity by <i>Burkholderia cenocepacia</i> TATl-371, a strain isolated from the tomato rhizosphere. <i>Microbiology (United Kingdom)</i> , 2018, 164, 1072-1086.	1.8	24
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2315	Phylogeny and Comparative Genomics: the Shifting Landscape in the Genomics Era. , 0, , 84-141.		23
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2318	Complete Genome Sequence of <i>Stenotrophomonas maltophilia</i> Podophage Ponderosa. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	8
2319	Complete Genome Sequence of <i>Escherichia coli</i> Myophage Mangalitsa. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	4
2320	Complete Genome Sequence of <i>Serratia marcescens</i> Myophage MyoSmar. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	2
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2322	Complete Genome Sequence of <i>Staphylococcus aureus</i> Myophage Maine. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	2
2323	Complete Genome Sequence of <i>Escherichia coli</i> Siphophage Snoko. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	1
2324	Complete Genome Sequence of <i>Escherichia coli</i> Phage Pisces. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	2
2325	Complete Genome Sequence of <i>Escherichia coli</i> Phage Paul. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	4
2326	Complete Genome Sequence of <i>Stenotrophomonas</i> Phage Pokken. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	7
2327	Detection of Five <i>mcr-9</i> -Carrying <i>Enterobacterales</i> Isolates in Four Czech Hospitals. <i>MSphere</i> , 2020, 5, .	2.9	26
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2331	The Harvest suite for rapid core-genome alignment and visualization of thousands of intraspecific microbial genomes. <i>Genome Biology</i> , 2014, 15, 524.	9.6	76
2332	Choice of assembly software has a critical impact on virome characterisation. <i>Microbiome</i> , 2019, 7, 12.	11.1	106
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2334	C-Sibelia: an easy-to-use and highly accurate tool for bacterial genome comparison. <i>F1000Research</i> , 2013, 2, 258.	1.6	29
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2340	MLST and Whole-Genome-Based Population Analysis of <i>Cryptococcus gattii</i> VGIII Links Clinical, Veterinary and Environmental Strains, and Reveals Divergent Serotype Specific Sub-populations and Distant Ancestors. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004861.	3.0	49
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2637	Resolving the structure of phage-bacteria interactions in the context of natural diversity. <i>Nature Communications</i> , 2022, 13, 372.	12.8	48
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2651	Long-Read Sequencing Reveals Genetic Adaptation of <i>Bartonella Adhesin A</i> Among Different <i>Bartonella henselae</i> Isolates. <i>Frontiers in Microbiology</i> , 2022, 13, 838267.	3.5	9

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2662	Population structure of <i>bla</i> KPC-harboring IncN plasmids at a New York City medical centre and evidence for multi-species horizontal transmission. <i>Journal of Antimicrobial Chemotherapy</i> , 2022, 77, 1873-1882.	3.0	7
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2675	Complete Genome Sequence of <i>Stenotrophomonas maltophilia</i> Siphophage Suzuki. <i>Microbiology Resource Announcements</i> , 2022, , e0013622.	0.6	0
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2681	Complete Genome Sequence of <i>Enterococcus faecalis</i> Siphophage Sigurd. <i>Microbiology Resource Announcements</i> , 2022, , e0012322.	0.6	0
2682	Complete Genome Sequence of <i>Stenotrophomonas maltophilia</i> Podophage Ptah. <i>Microbiology Resource Announcements</i> , 2022, , e0013722.	0.6	1
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2697	Complete Genome Sequence of <i>Stenotrophomonas maltophilia</i> Podophage Piffle. Microbiology Resource Announcements, 2022, , e0015922.	0.6	0
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2717	Surveillance of multi-drug resistance phenotypes in <i>Staphylococcus aureus</i> in Japan and correlation with whole-genome sequence findings. <i>Journal of Hospital Infection</i> , 2022, 123, 34-42.	2.9	5
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2724	Phage Annotation Guide: Guidelines for Assembly and High-Quality Annotation. <i>Phage</i> , 2021, 2, 170-182.	1.7	24
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2727	Advances in Biosynthesis of Natural Products from Marine Microorganisms. <i>Microorganisms</i> , 2021, 9, 2551.	3.6	11
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2731	Full Issue PDF. <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 1336-1464.	2.6	0
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3473	Whole-genome sequencing analysis of two heat-evolved <i>Escherichia coli</i> strains. <i>BMC Genomics</i> , 2023, 24, .	2.8	1
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3478	High level of novelty under the hood of convergent evolution. <i>Science</i> , 2023, 379, 1043-1049.	12.6	17
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3489	Novel insights into chloroplast genome evolution in the green macroalgal genus <i>Ulva</i> (Ulvophyceae), Tj ETQq0 0 0 rgBT <sub>0</sub> /Overlock 3.6	3.6	3
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3501	<i>Schizosaccharomyces lindneri</i> sp. nov., a fission yeast occurring in honey. <i>Yeast</i> , 2023, 40, 237-253.	1.7	7
3502	Comparative Genomic Analysis of Multi-Drug Resistant <i>Pseudomonas aeruginosa</i> Sequence Type 235 Isolated from Sudan. <i>Microorganisms</i> , 2023, 11, 1432.	3.6	0
3503	Phylogenetic Analysis of Bacterial Pathogen Genomes. <i>Methods in Molecular Biology</i> , 2023, , 87-99.	0.9	0
3504	Isolation, Characterization, and Comparative Genomic Analysis of Bacteriophage Ec_MI-02 from Pigeon Feces Infecting <i>Escherichia coli</i> O157:H7. <i>International Journal of Molecular Sciences</i> , 2023, 24, 9506.	4.1	0
3505	Comparative plastomes of <i>Pueraria montana</i> var. <i>lobata</i> (Leguminosae: Phaseoleae) and closely related taxa: insights into phylogenomic implications and evolutionary divergence. <i>BMC Genomics</i> , 2023, 24, .	2.8	1
3506	Detecting gene breakpoints in noisy genome sequences using position-annotated colored de-Bruijn graphs. <i>BMC Bioinformatics</i> , 2023, 24, .	2.6	0
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3508	PanGraph: scalable bacterial pan-genome graph construction. <i>Microbial Genomics</i> , 2023, 9, .	2.0	4
3509	Three Novel Marine Species of <i>Paracoccus</i> , <i>P. aerodenitrificans</i> sp. nov., <i>P. sediminicola</i> sp. nov. and <i>P. albus</i> sp. nov., and the Characterization of Their Capability to Perform Heterotrophic Nitrification and Aerobic Denitrification. <i>Microorganisms</i> , 2023, 11, 1532.	3.6	2
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3519	Fim3-dependent autoagglutination of <i>Bordetella pertussis</i> . <i>Scientific Reports</i> , 2023, 13, .	3.3	1

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