

# progressiveMauve: Multiple Genome Alignment with G

PLoS ONE

5, e11147

DOI: [10.1371/journal.pone.0011147](https://doi.org/10.1371/journal.pone.0011147)

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.	1.2	249
2	Inference of Homologous Recombination in Bacteria Using Whole-Genome Sequences. Genetics, 2010, 186, 1435-1449.	1.2	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.	1.5	80
5	Complete Genome Sequence of Rickettsia heilongjiangensis, an Emerging Tick-Transmitted Human Pathogen. Journal of Bacteriology, 2011, 193, 5564-5565.	1.0	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.	1.0	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.	1.0	24
9	The pathogenic potential of Yersinia enterocolitica 1A. International Journal of Medical Microbiology, 2011, 301, 556-561.	1.5	44
10	Comparative Genomics of Vibrio cholerae from Haiti, Asia, and Africa. Emerging Infectious Diseases, 2011, 17, 2113-21.	2.0	136
11	Genome-Wide Sequence Variation among Mycobacterium avium Subspecies paratuberculosis Isolates: A Better Understanding of Johne?s Disease Transmission Dynamics. Frontiers in Microbiology, 2011, 2, 236.	1.5	25
12	Substoichiometrically Different Mitotypes Coexist in Mitochondrial Genomes of Brassica napus L. PLoS ONE, 2011, 6, e17662.	1.1	99
13	Evolutionary Genomics of a Temperate Bacteriophage in an Obligate Intracellular Bacteria (Wolbachia). PLoS ONE, 2011, 6, e24984.	1.1	45
14	A Very Early-Branching Staphylococcus aureus Lineage Lacking the Carotenoid Pigment Staphyloxanthin. Genome Biology and Evolution, 2011, 3, 881-895.	1.1	142
15	Positional Information Resolves Structural Variations and Uncovers an Evolutionarily Divergent Genetic Locus in Accessions of Arabidopsis thaliana. Genome Biology and Evolution, 2011, 3, 627-640.	1.1	6
16	The -omics Era- Toward a Systems-Level Understanding of Streptomyces. Current Genomics, 2011, 12, 404-416.	0.7	24
17	Francisella halioticida sp. nov., a pathogen of farmed giant abalone (Haliotis gigantea) in Japan. Journal of Applied Microbiology, 2011, 111, 1044-1056.	1.4	55
18	A central metabolic circuit controlled by QseC in pathogenic Escherichia coli. Molecular Microbiology, 2011, 80, 1516-1529.	1.2	107

#	ARTICLE	IF	CITATIONS
19	Analysis of antibiotic resistance regions in Gram-negative bacteria. <i>FEMS Microbiology Reviews</i> , 2011, 35, 820-855.	3.9	290
20	Identification of <i>Salmonella enterica</i> species- and subgroup-specific genomic regions using Panseq 2.0. <i>Infection, Genetics and Evolution</i> , 2011, 11, 2151-2161.	1.0	10
21	Everything at once: Comparative analysis of the genomes of bacterial pathogens. <i>Veterinary Microbiology</i> , 2011, 153, 13-26.	0.8	12
22	Genome sequence analyses of two isolates from the recent <i>Escherichia coli</i> outbreak in Germany reveal the emergence of a new pathotype: Entero-Aggregative-Haemorrhagic <i>Escherichia coli</i> (EAHEC). <i>Archives of Microbiology</i> , 2011, 193, 883-891.	1.0	238
23	A genomic island provides <i>Acidithiobacillus ferrooxidans</i> ATCC 53993 additional copper resistance: a possible competitive advantage. <i>Applied Microbiology and Biotechnology</i> , 2011, 92, 761-767.	1.7	69
24	Interplay of recombination and selection in the genomes of <i>Chlamydia trachomatis</i> . <i>Biology Direct</i> , 2011, 6, 28.	1.9	70
25	Improving pan-genome annotation using whole genome multiple alignment. <i>BMC Bioinformatics</i> , 2011, 12, 272.	1.2	38
26	nocoRNAc: Characterization of non-coding RNAs in prokaryotes. <i>BMC Bioinformatics</i> , 2011, 12, 40.	1.2	39
27	STELLAR: fast and exact local alignments. <i>BMC Bioinformatics</i> , 2011, 12, S15.	1.2	28
28	Genome-level homology and phylogeny of <i>Shewanella</i> (Gammaproteobacteria: Iteromonadales): Tj ETQq1 1 0.784314 rgBT /Overlock 40	1.2	40
29	<i>Yersinia enterocolitica</i> palearctica serobiotyp O:3/4 - a successful group of emerging zoonotic pathogens. <i>BMC Genomics</i> , 2011, 12, 348.	1.2	21
30	Mitochondrial genome sequencing helps show the evolutionary mechanism of mitochondrial genome formation in <i>Brassica</i> . <i>BMC Genomics</i> , 2011, 12, 497.	1.2	99
31	Comparative genomic analysis of <i>Streptococcus suis</i> reveals significant genomic diversity among different serotypes. <i>BMC Genomics</i> , 2011, 12, 523.	1.2	71
32	Within-species lateral genetic transfer and the evolution of transcriptional regulation in <i>Escherichia coli</i> and <i>Shigella</i> . <i>BMC Genomics</i> , 2011, 12, 532.	1.2	28
33	Whole genome sequencing of peach ( <i>Prunus persica</i> L.) for SNP identification and selection. <i>BMC Genomics</i> , 2011, 12, 569.	1.2	65
34	Comparative analysis and supragenome modeling of twelve <i>Moraxella catarrhalis</i> clinical isolates. <i>BMC Genomics</i> , 2011, 12, 70.	1.2	50
35	Genome organization of epidemic <i>Acinetobacter baumannii</i> strains. <i>BMC Microbiology</i> , 2011, 11, 224.	1.3	115
36	Evidence of a Dominant Lineage of <i>Vibrio cholerae</i> -Specific Lytic Bacteriophages Shed by Cholera Patients over a 10-Year Period in Dhaka, Bangladesh. <i>MBio</i> , 2011, 2, e00334-10.	1.8	115

#	ARTICLE	IF	CITATIONS
37	Genome of Multidrug-Resistant Uropathogenic <i>Escherichia coli</i> Strain NA114 from India. <i>Journal of Bacteriology</i> , 2011, 193, 4272-4273.	1.0	63
38	Mauve Assembly Metrics. <i>Bioinformatics</i> , 2011, 27, 2756-2757.	1.8	108
39	Positional orthology: putting genomic evolutionary relationships into context. <i>Briefings in Bioinformatics</i> , 2011, 12, 401-412.	3.2	78
40	Genome Analysis of a <i>Mycoplasma hyorhinis</i> Strain Derived from a Primary Human Melanoma Cell Line. <i>Journal of Bacteriology</i> , 2011, 193, 4543-4544.	1.0	17
41	Complete Genome Sequence of the Commensal <i>Enterococcus faecalis</i> 62, Isolated from a Healthy Norwegian Infant. <i>Journal of Bacteriology</i> , 2011, 193, 2377-2378.	1.0	46
42	The Comprehensive Phytopathogen Genomics Resource: a web-based resource for data-mining plant pathogen genomes. <i>Database: the Journal of Biological Databases and Curation</i> , 2011, 2011, bar053-bar053.	1.4	26
43	An alternative approach to multiple genome comparison. <i>Nucleic Acids Research</i> , 2011, 39, e101-e101.	6.5	3
44	The <i>Xylella fastidiosa</i> Biocontrol Strain EB92-1 Genome Is Very Similar and Syntenic to Pierce's Disease Strains. <i>Journal of Bacteriology</i> , 2011, 193, 5576-5577.	1.0	34
45	Assemblathon 1: A competitive assessment of de novo short read assembly methods. <i>Genome Research</i> , 2011, 21, 2224-2241.	2.4	443
46	Whole-Genome Sequence of <i>Streptococcus pseudopneumoniae</i> Isolate IS7493. <i>Journal of Bacteriology</i> , 2011, 193, 6102-6103.	1.0	20
47	Genome of a Novel Isolate of <i>Paracoccus denitrificans</i> Capable of Degrading N , N -Dimethylformamide. <i>Journal of Bacteriology</i> , 2011, 193, 5598-5599.	1.0	42
48	Easyfig: a genome comparison visualizer. <i>Bioinformatics</i> , 2011, 27, 1009-1010.	1.8	2,861
49	Novel Metabolic Attributes of the Genus <i>Cyanothece</i> , Comprising a Group of Unicellular Nitrogen-Fixing Cyanobacteria. <i>MBio</i> , 2011, 2, .	1.8	93
50	ORIGINAL RESEARCH: Comparative constraint-based model development for thermophilic hydrogen production. <i>Industrial Biotechnology</i> , 2011, 7, 63-82.	0.5	4
51	PGAT: a multistrain analysis resource for microbial genomes. <i>Bioinformatics</i> , 2011, 27, 2429-2430.	1.8	74
52	A Comparative Genomic Analysis of Diverse Clonal Types of Enterotoxigenic <i>Escherichia coli</i> Reveals Pathovar-Specific Conservation. <i>Infection and Immunity</i> , 2011, 79, 950-960.	1.0	122
53	Complete Genome Sequences of Four Mammalian Isolates of <i>Chlamydomonas psittaci</i> . <i>Journal of Bacteriology</i> , 2011, 193, 4258-4258.	1.0	24
54	Genome Sequence of <i>Neisseria meningitidis</i> Serogroup B Strain H44/76. <i>Journal of Bacteriology</i> , 2011, 193, 2371-2372.	1.0	30

#	ARTICLE	IF	CITATIONS
55	Recombination and Population Structure in <i>Salmonella enterica</i> . <i>PLoS Genetics</i> , 2011, 7, e1002191.	1.5	135
56	Sequence Conservation and Functional Constraint on Intergenic Spacers in Reduced Genomes of the Obligate Symbiont <i>Buchnera</i> . <i>PLoS Genetics</i> , 2011, 7, e1002252.	1.5	47
57	Cactus: Algorithms for genome multiple sequence alignment. <i>Genome Research</i> , 2011, 21, 1512-1528.	2.4	245
58	Mugsy: fast multiple alignment of closely related whole genomes. <i>Bioinformatics</i> , 2011, 27, 334-342.	1.8	444
59	Comparative Genomic Analysis of <i>Xanthomonas axonopodis</i> pv. <i>citrumelo</i> F1, Which Causes Citrus Bacterial Spot Disease, and Related Strains Provides Insights into Virulence and Host Specificity. <i>Journal of Bacteriology</i> , 2011, 193, 6342-6357.	1.0	82
60	Virus Pathogen Database and Analysis Resource (ViPR): A Comprehensive Bioinformatics Database and Analysis Resource for the Coronavirus Research Community. <i>Viruses</i> , 2012, 4, 3209-3226.	1.5	156
61	Genomic and Transcriptomic Studies of an RDX (Hexahydro-1,3,5-Trinitro-1,3,5-Triazine)-Degrading Actinobacterium. <i>Applied and Environmental Microbiology</i> , 2012, 78, 7798-7800.	1.4	20
62	Nucleoid-Associated Proteins Affect Mutation Dynamics in <i>E. coli</i> in a Growth Phase-Specific Manner. <i>PLoS Computational Biology</i> , 2012, 8, e1002846.	1.5	21
64	Insights from Genomics into Bacterial Pathogen Populations. <i>PLoS Pathogens</i> , 2012, 8, e1002874.	2.1	87
65	Opposing Regulation of PROX1 by Interleukin-3 Receptor and NOTCH Directs Differential Host Cell Fate Reprogramming by Kaposi Sarcoma Herpes Virus. <i>PLoS Pathogens</i> , 2012, 8, e1002770.	2.1	25
66	Patterns of Gene Flow Define Species of Thermophilic Archaea. <i>PLoS Biology</i> , 2012, 10, e1001265.	2.6	214
67	Revised Phylogeny and Novel Horizontally Acquired Virulence Determinants of the Model Soft Rot Phytopathogen <i>Pectobacterium wasabiae</i> SCC3193. <i>PLoS Pathogens</i> , 2012, 8, e1003013.	2.1	93
68	Genomic analysis uncovers a phenotypically diverse but genetically homogeneous <i>Escherichia coli</i> ST131 clone circulating in unrelated urinary tract infections. <i>Journal of Antimicrobial Chemotherapy</i> , 2012, 67, 868-877.	1.3	47
69	Complete Genome Sequence of <i>Lactococcus lactis</i> subsp. <i>cremoris</i> A76. <i>Journal of Bacteriology</i> , 2012, 194, 1241-1242.	1.0	26
70	Genome Sequence of the Bacteriocin-Producing Strain <i>Lactococcus garvieae</i> DCC43. <i>Journal of Bacteriology</i> , 2012, 194, 6976-6977.	1.0	15
71	Whole-Genome Shotgun Sequence of <i>Rhodococcus</i> Species Strain JVH1. <i>Journal of Bacteriology</i> , 2012, 194, 5492-5493.	1.0	7
72	Directional Evolution of <i>Chlamydia trachomatis</i> towards Niche-Specific Adaptation. <i>Journal of Bacteriology</i> , 2012, 194, 6143-6153.	1.0	41
73	Complete Genome Sequence of <i>Actinobacillus suis</i> H91-0380, a Virulent Serotype O2 Strain. <i>Journal of Bacteriology</i> , 2012, 194, 6686-6687.	1.0	13

#	ARTICLE	IF	CITATIONS
74	Pangenomic Study of <i>Corynebacterium diphtheriae</i> That Provides Insights into the Genomic Diversity of Pathogenic Isolates from Cases of Classical Diphtheria, Endocarditis, and Pneumonia. <i>Journal of Bacteriology</i> , 2012, 194, 3199-3215.	1.0	142
75	Complete Genome Sequence of the Porcine Isolate <i>Enterococcus faecalis</i> D32. <i>Journal of Bacteriology</i> , 2012, 194, 5490-5491.	1.0	16
76	Genomic epidemiology of the <i>Escherichia coli</i> O104:H4 outbreaks in Europe, 2011. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 3065-3070.	3.3	262
77	High-throughput genomic sequencing of cassava bacterial blight strains identifies conserved effectors to target for durable resistance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E1972-9.	3.3	128
78	Characterization of the ELPhiS Prophage from <i>Salmonella enterica</i> Serovar Enteritidis Strain LK5. <i>Applied and Environmental Microbiology</i> , 2012, 78, 1785-1793.	1.4	23
79	Draft Genome Sequence of <i>Vibrio fischeri</i> SR5, a Strain Isolated from the Light Organ of the Mediterranean Squid <i>Sepiola robusta</i> . <i>Journal of Bacteriology</i> , 2012, 194, 1639-1639.	1.0	15
80	MupB, a New High-Level Mupirocin Resistance Mechanism in <i>Staphylococcus aureus</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2012, 56, 1916-1920.	1.4	94
81	Candidate Targets of Balancing Selection in the Genome of <i>Staphylococcus aureus</i> . <i>Molecular Biology and Evolution</i> , 2012, 29, 1175-1186.	3.5	26
82	A <i>Rickettsia</i> Genome Overrun by Mobile Genetic Elements Provides Insight into the Acquisition of Genes Characteristic of an Obligate Intracellular Lifestyle. <i>Journal of Bacteriology</i> , 2012, 194, 376-394.	1.0	152
83	Comparative Genomics and Systems Biology of Malaria Parasites <i>Plasmodium</i> . <i>Current Bioinformatics</i> , 2012, 7, 478-489.	0.7	8
84	Genome Sequence of the Swine Pathogen <i>Streptococcus suis</i> Serotype 2 Strain S735. <i>Journal of Bacteriology</i> , 2012, 194, 6343-6344.	1.0	10
85	Bacteriophage cocktail significantly reduces <i>Escherichia coli</i> O157. <i>Bacteriophage</i> , 2012, 2, 178-185.	1.9	118
86	GenomeRing: alignment visualization based on SuperGenome coordinates. <i>Bioinformatics</i> , 2012, 28, i7-i15.	1.8	41
87	Draft Genome Sequence of <i>Bacillus pumilus</i> BA06, a Producer of Alkaline Serine Protease with Leather-Dehairing Function. <i>Journal of Bacteriology</i> , 2012, 194, 6668-6669.	1.0	17
88	Impact of Loci Nature on Estimating Recombination and Mutation Rates in <i>Chlamydia trachomatis</i> . G3: Genes, Genomes, Genetics, 2012, 2, 761-768.	0.8	12
89	Evolutionary dynamics of <i>Staphylococcus aureus</i> during progression from carriage to disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 4550-4555.	3.3	244
90	Complete Genome Sequence of <i>Bacillus subtilis</i> Strain QB928, a Strain Widely Used in <i>B. subtilis</i> Genetic Studies. <i>Journal of Bacteriology</i> , 2012, 194, 6308-6309.	1.0	10
91	Complete genome sequence of <i>Liberibacter crescens</i> BT-1. <i>Standards in Genomic Sciences</i> , 2012, 7, 271-283.	1.5	96

#	ARTICLE	IF	CITATIONS
92	Selection of Marker Genes Using Whole-Genome DNA Polymorphism Analysis. <i>Evolutionary Bioinformatics</i> , 2012, 8, EBO.S8989.	0.6	7
93	Horizontal Transfer and Death of a Fungal Secondary Metabolic Gene Cluster. <i>Genome Biology and Evolution</i> , 2012, 4, 289-293.	1.1	108
94	Draft Genome Sequences of <i>Staphylococcus aureus</i> Sequence Type 34 (ST34) and ST42 Hybrids. <i>Journal of Bacteriology</i> , 2012, 194, 2740-2741.	1.0	13
95	The Novel Kasugamycin 2- <i>N</i> -Acetyltransferase Gene <i>aac(2)-IIa</i> , Carried by the IncP Island, Confers Kasugamycin Resistance to Rice-Pathogenic Bacteria. <i>Applied and Environmental Microbiology</i> , 2012, 78, 5555-5564.	1.4	21
96	Evolutionary Dynamics of Small RNAs in 27 <i>Escherichia coli</i> and <i>Shigella</i> Genomes. <i>Genome Biology and Evolution</i> , 2012, 4, 330-345.	1.1	43
97	Recent Acceleration of Plastid Sequence and Structural Evolution Coincides with Extreme Mitochondrial Divergence in the Angiosperm Genus <i>Silene</i> . <i>Genome Biology and Evolution</i> , 2012, 4, 294-306.	1.1	111
98	Rapid divergence and expansion of the X chromosome in papaya. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 13716-13721.	3.3	52
99	Complete Genome Sequences of Probiotic Strains <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> B420 and Bi-07. <i>Journal of Bacteriology</i> , 2012, 194, 4131-4132.	1.0	22
100	Characterization of Novel Phages Isolated in Coagulase-Negative Staphylococci Reveals Evolutionary Relationships with <i>Staphylococcus aureus</i> Phages. <i>Journal of Bacteriology</i> , 2012, 194, 5829-5839.	1.0	50
101	Complete Genome Sequence of <i>Paenibacillus</i> strain Y4.12MC10, a Novel <i>Paenibacillus lautus</i> strain Isolated from Obsidian Hot Spring in Yellowstone National Park. <i>Standards in Genomic Sciences</i> , 2012, 6, 381-400.	1.5	32
102	Phylogeny rather than ecology or lifestyle biases the construction of <i>Escherichia coli</i> and <i>Shigella</i> genetic exchange communities. <i>Open Biology</i> , 2012, 2, 120112.	1.5	42
103	Comparative Genomics and stx Phage Characterization of LEE-Negative Shiga Toxin-Producing <i>Escherichia coli</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2012, 2, 133.	1.8	84
104	Pathogenomics of <i>Pasteurella multocida</i> . <i>Current Topics in Microbiology and Immunology</i> , 2012, 361, 23-38.	0.7	38
105	Comparative analysis of mitochondrial genomes of <i>Rhizophagus irregularis</i> syn. <i>Glomus irregulare</i> reveals a polymorphism induced by variability generating elements. <i>New Phytologist</i> , 2012, 196, 1217-1227.	3.5	66
106	Intraspecific variation in mitochondrial genome sequence, structure, and gene content in <i>Silene vulgaris</i> , an angiosperm with pervasive cytoplasmic male sterility. <i>New Phytologist</i> , 2012, 196, 1228-1239.	3.5	108
107	Targeted genome enrichment for efficient purification of endosymbiont DNA from host DNA. <i>Symbiosis</i> , 2012, 58, 201-207.	1.2	31
108	Characterization of the <i>Salmonella</i> bacteriophage vB_SenS-Ent1. <i>Journal of General Virology</i> , 2012, 93, 2046-2056.	1.3	30
109	Evolution and Virulence Contributions of the Autotransporter Proteins YapJ and YapK of <i>Yersinia pestis</i> CO92 and Their Homologs in <i>Y. pseudotuberculosis</i> IP32953. <i>Infection and Immunity</i> , 2012, 80, 3693-3705.	1.0	8

#	ARTICLE	IF	CITATIONS
110	Analysis of a <i>Streptococcus pyogenes</i> Puerperal Sepsis Cluster by Use of Whole-Genome Sequencing. <i>Journal of Clinical Microbiology</i> , 2012, 50, 2224-2228.	1.8	55
111	Multifractal analysis of HIV-1 genomes. <i>Molecular Phylogenetics and Evolution</i> , 2012, 62, 756-763.	1.2	15
112	Transforming clinical microbiology with bacterial genome sequencing. <i>Nature Reviews Genetics</i> , 2012, 13, 601-612.	7.7	684
113	Ribosomal multilocus sequence typing: universal characterization of bacteria from domain to strain. <i>Microbiology (United Kingdom)</i> , 2012, 158, 1005-1015.	0.7	497
114	Population Genomics of <i>Chlamydia trachomatis</i> : Insights on Drift, Selection, Recombination, and Population Structure. <i>Molecular Biology and Evolution</i> , 2012, 29, 3933-3946.	3.5	94
115	Magnetic capture hybridization of <i>Batrachochytrium dendrobatidis</i> genomic DNA. <i>Journal of Microbiological Methods</i> , 2012, 90, 156-159.	0.7	5
116	The mitochondrial genome of <i>Moniliophthora roreri</i> , the frosty pod rot pathogen of cacao. <i>Fungal Biology</i> , 2012, 116, 551-562.	1.1	29
117	An Evolutionary Link between Natural Transformation and CRISPR Adaptive Immunity. <i>MBio</i> , 2012, 3, .	1.8	70
118	Impact of homologous and non-homologous recombination in the genomic evolution of <i>Escherichia coli</i> . <i>BMC Genomics</i> , 2012, 13, 256.	1.2	141
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.	1.2	121
120	Tracing genomic variations in two highly virulent <i>Yersinia enterocolitica</i> strains with unequal ability to compete for host colonization. <i>BMC Genomics</i> , 2012, 13, 467.	1.2	18
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.	1.2	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.	1.2	99
123	Comparative genomics of bacteria in the genus <i>Providencia</i> isolated from wild <i>Drosophila melanogaster</i> . <i>BMC Genomics</i> , 2012, 13, 612.	1.2	32
124	The large universal <i>Pantoea</i> plasmid LPP-1 plays a major role in biological and ecological diversification. <i>BMC Genomics</i> , 2012, 13, 625.	1.2	76
125	Genomic basis of broad host range and environmental adaptability of <i>Rhizobium tropici</i> CIAT 899 and <i>Rhizobium</i> sp. PRF 81 which are used in inoculants for common bean ( <i>Phaseolus vulgaris</i> L.). <i>BMC Genomics</i> , 2012, 13, 735.	1.2	118
126	Genome sequencing of ovine isolates of <i>Mycobacterium avium</i> subspecies paratuberculosis offers insights into host association. <i>BMC Genomics</i> , 2012, 13, 89.	1.2	54
127	Complete genome sequence of <i>Enterococcus faecium</i> strain TX16 and comparative genomic analysis of <i>Enterococcus faecium</i> genomes. <i>BMC Microbiology</i> , 2012, 12, 135.	1.3	126



#	ARTICLE	IF	CITATIONS
128	Extensive remodeling of the <i>Pseudomonas syringae</i> pv. <i>avellanae</i> type III secretome associated with two independent host shifts onto hazelnut. <i>BMC Microbiology</i> , 2012, 12, 141.	1.3	67
129	Genome sequence of <i>Desulfitobacterium hafniense</i> DCB-2, a Gram-positive anaerobe capable of dehalogenation and metal reduction. <i>BMC Microbiology</i> , 2012, 12, 21.	1.3	84
130	Genomes-based phylogeny of the genus <i>Xanthomonas</i> . <i>BMC Microbiology</i> , 2012, 12, 43.	1.3	71
131	Genome and proteome analysis of 7-7-1, a flagellotropic phage infecting <i>Agrobacterium</i> sp H13-3. <i>Virology Journal</i> , 2012, 9, 102.	1.4	23
132	A sliding window and keyword tree based algorithm for multiple sequence alignment. , 2012, , .		0
133	Replacing and Additive Horizontal Gene Transfer in <i>Streptococcus</i> . <i>Molecular Biology and Evolution</i> , 2012, 29, 3309-3320.	3.5	33
134	Evolutionary Dynamics of the <i>Yersinia enterocolitica</i> Complex. <i>Advances in Experimental Medicine and Biology</i> , 2012, 954, 15-22.	0.8	5
135	Comparative Genomics of Two Independently Enriched "Candidate" <i>Kuenenia stuttgartiensis</i> Anammox Bacteria. <i>Frontiers in Microbiology</i> , 2012, 3, 307.	1.5	51
136	Whole-Genome Alignment. <i>Methods in Molecular Biology</i> , 2012, 855, 237-257.	0.4	27
137	Genomic, Proteomic and Physiological Characterization of a T5-like Bacteriophage for Control of Shiga Toxin-Producing <i>Escherichia coli</i> O157:H7. <i>PLoS ONE</i> , 2012, 7, e34585.	1.1	64
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.	1.5	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.	3.3	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.	0.9	30
141	Comparing Fungal Genomes: Insight into Functional and Evolutionary Processes. <i>Methods in Molecular Biology</i> , 2012, 835, 531-548.	0.4	7
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.	9.4	279
143	Molecular Signatures Identify a Candidate Target of Balancing Selection in an <i>arcD</i> -Like Gene of <i>Staphylococcus epidermidis</i> . <i>Journal of Molecular Evolution</i> , 2012, 75, 43-54.	0.8	10
144	Normalized N50 assembly metric using gap-restricted co-linear chaining. <i>BMC Bioinformatics</i> , 2012, 13, 255.	1.2	17
145	Increased knowledge of <i>Francisella</i> genus diversity highlights the benefits of optimised DNA-based assays. <i>BMC Microbiology</i> , 2012, 12, 220.	1.3	16

#	ARTICLE	IF	CITATIONS
146	A Comparison of Shiga-Toxin 2 Bacteriophage from Classical Enterohemorrhagic <i>Escherichia coli</i> Serotypes and the German <i>E. coli</i> O104:H4 Outbreak Strain. <i>PLoS ONE</i> , 2012, 7, e37362.	1.1	47
147	Molecular Characterization of Podoviral Bacteriophages Virulent for <i>Clostridium perfringens</i> and Their Comparison with Members of the Picovirinae. <i>PLoS ONE</i> , 2012, 7, e38283.	1.1	37
148	Gegenees: Fragmented Alignment of Multiple Genomes for Determining Phylogenomic Distances and Genetic Signatures Unique for Specified Target Groups. <i>PLoS ONE</i> , 2012, 7, e39107.	1.1	238
149	Identification and Characterization of Novel <i>Salmonella</i> Mobile Elements Involved in the Dissemination of Genes Linked to Virulence and Transmission. <i>PLoS ONE</i> , 2012, 7, e41247.	1.1	61
150	Two Different Secondary Metabolism Gene Clusters Occupied the Same Ancestral Locus in Fungal Dermatophytes of the Arthrodermataceae. <i>PLoS ONE</i> , 2012, 7, e41903.	1.1	9
151	Molecular Evolution of Trehalose-6-Phosphate Synthase (TPS) Gene Family in <i>Populus</i> , <i>Arabidopsis</i> and Rice. <i>PLoS ONE</i> , 2012, 7, e42438.	1.1	64
152	Nontypeable <i>Haemophilus influenzae</i> Genetic Islands Associated with Chronic Pulmonary Infection. <i>PLoS ONE</i> , 2012, 7, e44730.	1.1	25
153	Pan-Genomic Analysis Provides Insights into the Genomic Variation and Evolution of <i>Salmonella</i> Paratyphi A. <i>PLoS ONE</i> , 2012, 7, e45346.	1.1	26
154	Sequence Features Contributing to Chromosomal Rearrangements in <i>Neisseria gonorrhoeae</i> . <i>PLoS ONE</i> , 2012, 7, e46023.	1.1	12
155	Optimization of dengue virus genome assembling using GSFLX 454 pyrosequencing data: evaluation of assembling strategies. <i>Genetics and Molecular Research</i> , 2012, 11, 3688-3695.	0.3	22
156	A Gene-By-Gene Approach to Bacterial Population Genomics: Whole Genome MLST of <i>Campylobacter</i> . <i>Genes</i> , 2012, 3, 261-277.	1.0	135
157	Unidirectional Evolutionary Transitions in Fungal Mating Systems and the Role of Transposable Elements. <i>Molecular Biology and Evolution</i> , 2012, 29, 3215-3226.	3.5	96
158	In vitro and in vivo characterization and strain safety of <i>Lactobacillus reuteri</i> NCIMB 30253 for probiotic applications. <i>Canadian Journal of Microbiology</i> , 2012, 58, 776-787.	0.8	12
159	Plastid Genomes of Seed Plants. <i>Advances in Photosynthesis and Respiration</i> , 2012, , 103-126.	1.0	268
160	Comparative genomics of rhizobia nodulating soybean suggests extensive recruitment of lineage-specific genes in adaptations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 8629-8634.	3.3	234
161	Phylomark, a Tool To Identify Conserved Phylogenetic Markers from Whole-Genome Alignments. <i>Applied and Environmental Microbiology</i> , 2012, 78, 4884-4892.	1.4	39
162	Proteomic and physiological experiments to test <i>Thermotoga neapolitana</i> constraint-based model hypotheses of carbon source utilization. <i>Biotechnology Progress</i> , 2012, 28, 312-318.	1.3	2
163	Optical mapping and sequencing of the <i>Escherichia coli</i> KO11 genome reveal extensive chromosomal rearrangements, and multiple tandem copies of the <i>Zymomonas mobilis</i> <i>pdC</i> and <i>adhB</i> genes. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2012, 39, 629-639.	1.4	40

#	ARTICLE	IF	CITATIONS
164	Metagenomic analysis of a complex marine planktonic thaumarchaeal community from the Gulf of Maine. <i>Environmental Microbiology</i> , 2012, 14, 254-267.	1.8	56
165	Exposing the third chromosome of <i>Burkholderia cepacia</i> complex strains as a virulence plasmid. <i>Molecular Microbiology</i> , 2012, 83, 362-378.	1.2	90
166	Characterization of a mobile and multiple resistance plasmid isolated from swine manure and its detection in soil after manure application. <i>Journal of Applied Microbiology</i> , 2012, 112, 1123-1133.	1.4	30
167	Inheritance of the <i>Salmonella</i> virulence plasmids: Mostly vertical and rarely horizontal. <i>Infection, Genetics and Evolution</i> , 2012, 12, 1058-1063.	1.0	43
168	Polyphyly of non-bioluminescent <i>Vibrio fischeri</i> sharing a lux locus deletion. <i>Environmental Microbiology</i> , 2012, 14, 655-668.	1.8	17
169	Genome plasticity and systems evolution in <i>Streptomyces</i> . <i>BMC Bioinformatics</i> , 2012, 13, S8.	1.2	61
170	Inferring transcript phylogenies. <i>BMC Bioinformatics</i> , 2012, 13, S1.	1.2	14
171	The genome and proteome of a <i>Campylobacter coli</i> bacteriophage vB_CcoM-IBB_35 reveal unusual features. <i>Virology Journal</i> , 2012, 9, 35.	1.4	19
172	The complete genome sequence of <i>Pantoea ananatis</i> AJ13355, an organism with great biotechnological potential. <i>Applied Microbiology and Biotechnology</i> , 2012, 93, 331-341.	1.7	55
173	The host-range, genomics and proteomics of <i>Escherichia coli</i> O157:H7 bacteriophage rV5. <i>Virology Journal</i> , 2013, 10, 76.	1.4	55
174	Genome sequence and analysis of a broad-host range lytic bacteriophage that infects the <i>Bacillus cereus</i> group. <i>Virology Journal</i> , 2013, 10, 48.	1.4	44
175	Beginner's guide to comparative bacterial genome analysis using next-generation sequence data. <i>Microbial Informatics and Experimentation</i> , 2013, 3, 2.	7.6	113
176	Comparative genome characterization of <i>Achromobacter</i> members reveals potential genetic determinants facilitating the adaptation to a pathogenic lifestyle. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 6413-6425.	1.7	45
177	Global Aspects of pacC Regulation of Pathogenicity Genes in <i>Colletotrichum gloeosporioides</i> as Revealed by Transcriptome Analysis. <i>Molecular Plant-Microbe Interactions</i> , 2013, 26, 1345-1358.	1.4	94
178	Genomic analysis of the biocontrol strain <i>Pseudomonas fluorescens</i> Pf-29 with evidence of <i>T3SS</i> and <i>T6SS</i> gene expression on plant roots. <i>Environmental Microbiology Reports</i> , 2013, 5, 393-403.	1.0	62
179	Comparisons of infant <i>Escherichia coli</i> isolates link genomic profiles with adaptation to the ecological niche. <i>BMC Genomics</i> , 2013, 14, 81.	1.2	12
180	Genome sequence reveals that <i>Pseudomonas fluorescens</i> F113 possesses a large and diverse array of systems for rhizosphere function and host interaction. <i>BMC Genomics</i> , 2013, 14, 54.	1.2	78
181	Genome-level homology and phylogeny of <i>Vibrionaceae</i> (Gammaproteobacteria: Vibrionales) with three new complete genome sequences. <i>BMC Microbiology</i> , 2013, 13, 80.	1.3	11

#	ARTICLE	IF	CITATIONS
182	Complete plastid genome sequence of <i>Vaccinium macrocarpon</i> : structure, gene content, and rearrangements revealed by next generation sequencing. <i>Tree Genetics and Genomes</i> , 2013, 9, 489-498.	0.6	97
183	Repeated loss of an anciently horizontally transferred gene cluster in <i>Botrytis</i> . <i>Mycologia</i> , 2013, 105, 1126-1134.	0.8	39
184	Comparative genomic analysis of twelve <i>Streptococcus suis</i> (pro)phages. <i>Genomics</i> , 2013, 101, 336-344.	1.3	41
185	Long-term strain improvements accumulate mutations in regulatory elements responsible for hyper-production of cellulolytic enzymes. <i>Scientific Reports</i> , 2013, 3, 1569.	1.6	104
186	Genomic impact of CRISPR immunization against bacteriophages. <i>Biochemical Society Transactions</i> , 2013, 41, 1383-1391.	1.6	54
187	Description of <i>Bacillus toyonensis</i> sp. nov., a novel species of the <i>Bacillus cereus</i> group, and pairwise genome comparisons of the species of the group by means of ANI calculations. <i>Systematic and Applied Microbiology</i> , 2013, 36, 383-391.	1.2	217
188	Recombinational Switching of the <i>Clostridium difficile</i> S-Layer and a Novel Glycosylation Gene Cluster Revealed by Large-Scale Whole-Genome Sequencing. <i>Journal of Infectious Diseases</i> , 2013, 207, 675-686.	1.9	93
189	<i>Bifidobacterium animalis</i> subsp. <i>lactis</i> ATCC 27673 Is a Genomically Unique Strain within Its Conserved Subspecies. <i>Applied and Environmental Microbiology</i> , 2013, 79, 6903-6910.	1.4	30
190	Comparative genomics of two <i>Candidatus</i> <i>Accumulibacter</i> ™ clades performing biological phosphorus removal. <i>ISME Journal</i> , 2013, 7, 2301-2314.	4.4	101
191	The <i>Sinorhizobium meliloti</i> Essential Porin RopA1 Is a Target for Numerous Bacteriophages. <i>Journal of Bacteriology</i> , 2013, 195, 3663-3671.	1.0	20
192	Heterogeneity in the entire genome for three genotypes of peach [ <i>Prunus persica</i> (L.) Batsch] as distinguished from sequence analysis of genomic variants. <i>BMC Genomics</i> , 2013, 14, 750.	1.2	19
193	Phylogenetic relationship and virulence inference of <i>Streptococcus Anginosus</i> Group: curated annotation and whole-genome comparative analysis support distinct species designation. <i>BMC Genomics</i> , 2013, 14, 895.	1.2	51
194	A typing scheme for the honeybee pathogen <i>Melissococcus plutonius</i> allows detection of disease transmission events and a study of the distribution of variants. <i>Environmental Microbiology Reports</i> , 2013, 5, 525-529.	1.0	33
195	Recent Diversification of a Marine Genus ( <i>Tursiops</i> spp.) Tracks Habitat Preference and Environmental Change. <i>Systematic Biology</i> , 2013, 62, 865-877.	2.7	84
196	Genomic diversity and adaptation of <i>Salmonella enterica</i> serovar Typhimurium from analysis of six genomes of different phage types. <i>BMC Genomics</i> , 2013, 14, 718.	1.2	34
197	Isolation, characterization and comparative genomics of bacteriophage SfiV: a novel serotype converting phage from <i>Shigella flexneri</i> . <i>BMC Genomics</i> , 2013, 14, 677.	1.2	37
198	SynTView™ an interactive multi-view genome browser for next-generation comparative microorganism genomics. <i>BMC Bioinformatics</i> , 2013, 14, 277.	1.2	31
199	Comparative analysis of the complete genome of an epidemic hospital sequence type 203 clone of vancomycin-resistant <i>Enterococcus faecium</i> . <i>BMC Genomics</i> , 2013, 14, 595.	1.2	50

#	ARTICLE	IF	CITATIONS
200	inTB - a data integration platform for molecular and clinical epidemiological analysis of tuberculosis. BMC Bioinformatics, 2013, 14, 264.	1.2	7
201	Genetic variability of mutans streptococci revealed by wide whole-genome sequencing. BMC Genomics, 2013, 14, 430.	1.2	31
202	Single-cell genomics reveal low recombination frequencies in freshwater bacteria of the SAR11 clade. Genome Biology, 2013, 14, R130.	13.9	74
203	Genome anatomy of the gastrointestinal pathogen, <i>Vibrio parahaemolyticus</i> of crustacean origin. Gut Pathogens, 2013, 5, 37.	1.6	7
204	Two Rapidly Evolving Genes Contribute to Male Fitness in <i>Drosophila</i> . Journal of Molecular Evolution, 2013, 77, 246-259.	0.8	6
205	Genome sequence of <i>Xanthomonas fuscans</i> subsp. <i>fuscans</i> strain 4834-R reveals that flagellar motility is not a general feature of xanthomonads. BMC Genomics, 2013, 14, 761.	1.2	55
206	Genomic analysis of smooth tubercle bacilli provides insights into ancestry and pathoadaptation of <i>Mycobacterium tuberculosis</i> . Nature Genetics, 2013, 45, 172-179.	9.4	264
207	Computing the Joint Distribution of Tree Shape and Tree Distance for Gene Tree Inference and Recombination Detection. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 1-1.	1.9	3
208	Complete Genome Sequence of the Frog Pathogen <i>Mycobacterium ulcerans</i> Ecovar <i>Liflandii</i> . Journal of Bacteriology, 2013, 195, 556-564.	1.0	44
209	Comparative Genomic Analysis and Benzene, Toluene, Ethylbenzene, and <i>m</i> -Xylene, and <i>p</i> -Xylene (BTEX) Degradation Pathways of <i>Pseudoxanthomonas spadix</i> BD-a59. Applied and Environmental Microbiology, 2013, 79, 663-671.	1.4	73
210	Genomic analysis and secondary metabolite production in <i>Bacillus amyloliquefaciens</i> AS 43.3: A biocontrol antagonist of <i>Fusarium</i> head blight. Biological Control, 2013, 64, 166-175.	1.4	88
211	Phylogenomics of Brazilian epidemic isolates of <i>Mycobacterium abscessus</i> subsp. <i>bolletii</i> reveals relationships of global outbreak strains. Infection, Genetics and Evolution, 2013, 20, 292-297.	1.0	44
212	The Mitochondrial Genome of <i>Raphanus sativus</i> and Gene Evolution of Cruciferous Mitochondrial Types. Journal of Genetics and Genomics, 2013, 40, 117-126.	1.7	9
213	Entire sequence of the colonization factor coli surface antigen 6-encoding plasmid pC <sub>ss</sub> 165 from an enterotoxigenic <i>Escherichia coli</i> clinical isolate. Plasmid, 2013, 70, 343-352.	0.4	15
214	First case of <i>E. anophelis</i> outbreak in an intensive-care unit. Lancet, The, 2013, 382, 855-856.	6.3	78
215	The IncF plasmid pRSB225 isolated from a municipal wastewater treatment plant's on-site preflooder combining antibiotic resistance and putative virulence functions is highly related to virulence plasmids identified in pathogenic <i>E. coli</i> isolates. Plasmid, 2013, 69, 127-137.	0.4	35
216	Activation of <i>R</i> -mediated innate immunity and disease susceptibility is affected by mutations in a cytosolic <i>O</i> -acetylserine (thiol) lyase in <i>A</i> -rabidopsis. Plant Journal, 2013, 73, 118-130.	2.8	36
217	The phylogeographic pattern of <i>F</i> <i>rancisella tularensis</i> in <i>S</i> <i>weden</i> indicates a <i>S</i> <i>candinavian</i> origin of <i>E</i> <i>urosiberian tularaemia</i> . Environmental Microbiology, 2013, 15, 634-645.	1.8	68

#	ARTICLE	IF	CITATIONS
218	Life in the dark: metagenomic evidence that a microbial slime community is driven by inorganic nitrogen metabolism. ISME Journal, 2013, 7, 1227-1236.	4.4	63
219	Chromosome 10 in the tomato plant carries clusters of genes responsible for field resistance/defence to <i>Phytophthora infestans</i> . Genomics, 2013, 101, 249-255.	1.3	7
220	Evolutionary potential, cross-stress behavior and the genetic basis of acquired stress resistance in <i>Escherichia coli</i> . Molecular Systems Biology, 2013, 9, 643.	3.2	115
221	Type 1 and type 2 strains of <i>Mycoplasma pneumoniae</i> form different biofilms. Microbiology (United Kingdom), 2013, 153, 1071-1079.	0.7	59
222	New Linear Lipopeptides Produced by <i>Pseudomonas cichorii</i> SF1-54 Are Involved in Virulence, Swarming Motility, and Biofilm Formation. Molecular Plant-Microbe Interactions, 2013, 26, 585-598.	1.4	47
223	Comparative Genomics of a Plant-Pathogenic Fungus, <i>Pyrenophora tritici-repentis</i> , Reveals Transduplication and the Impact of Repeat Elements on Pathogenicity and Population Divergence. G3: Genes, Genomes, Genetics, 2013, 3, 41-63.	0.8	167
224	Genome-Wide Comparison of Medieval and Modern <i>Mycobacterium leprae</i> . Science, 2013, 341, 179-183.	6.0	313
225	Pathogen typing in the genomics era: MLST and the future of molecular epidemiology. Infection, Genetics and Evolution, 2013, 16, 38-53.	1.0	157
226	A genome-wide analysis of multidrug-resistant and extensively drug-resistant strains of <i>Mycobacterium tuberculosis</i> Beijing genotype. Molecular Genetics and Genomics, 2013, 288, 425-436.	1.0	12
227	Complete genome sequences provide a case study for the evaluation of gene tree thinking. Cladistics, 2013, 29, 672-682.	1.5	5
228	RNA-Seq of <i>Bacillus licheniformis</i> : active regulatory RNA features expressed within a productive fermentation. BMC Genomics, 2013, 14, 667.	1.2	40
229	Combining de novo and reference-guided assembly with scaffold_builder. Source Code for Biology and Medicine, 2013, 8, 23.	1.7	59
230	Effects of DNA Size on Transformation and Recombination Efficiencies in <i>Xylella fastidiosa</i> . Applied and Environmental Microbiology, 2013, 79, 1712-1717.	1.4	62
231	Evolution of a Self-Inducible Cytolethal Distending Toxin Type V-Encoding Bacteriophage from <i>Escherichia coli</i> O157:H7 to <i>Shigella sonnei</i> . Journal of Virology, 2013, 87, 13665-13675.	1.5	18
232	Candidate phylum TM6 genome recovered from a hospital sink biofilm provides genomic insights into this uncultivated phylum. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E2390-9.	3.3	192
233	STAR: ultrafast universal RNA-seq aligner. Bioinformatics, 2013, 29, 15-21.	1.8	35,376
234	Draft Genome Sequences for Ten <i>Salmonella enterica</i> Serovar Typhimurium Phage Type 135 Variants. Genome Announcements, 2013, 1, .	0.8	3
235	Draft Genome Sequence of <i>Curtobacterium flaccumfaciens</i> Strain UCD-AKU (Phylum Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 62	0.8	7



#	ARTICLE	IF	CITATIONS
236	Genome Sequence of <i>Salmonella bongori</i> Strain N268-08, a Rare Clinical Isolate. <i>Genome Announcements</i> , 2013, 1, .	0.8	2
237	Draft Genome Sequence of <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Manhattan Strain 111113, from an Outbreak of Human Infections in Northern Italy. <i>Genome Announcements</i> , 2013, 1, .	0.8	2
238	Draft Genome Sequence of <i>Bacillus subtilis</i> Strain S1-4, Which Degrades Feathers Efficiently. <i>Genome Announcements</i> , 2013, 1, .	0.8	5
239	Complete Genome Sequence of <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Thompson Strain RM6836. <i>Genome Announcements</i> , 2013, 1, .	0.8	2
240	Complete Genome Sequence of <i>Streptococcus pneumoniae</i> Strain A026, a Clinical Multidrug-Resistant Isolate Carrying Tn <i>2010</i> . <i>Genome Announcements</i> , 2013, 1, .	0.8	5
241	Complete Genome Sequence of <i>Bacillus toyonensis</i> BCT-7112 <sup>T</sup> , the Active Ingredient of the Feed Additive Preparation Toyocerin. <i>Genome Announcements</i> , 2013, 1, .	0.8	30
242	Evolutionary Genomics of <i>Salmonella enterica</i> Subspecies. <i>MBio</i> , 2013, 4, .	1.8	106
243	Livestock Origin for a Human Pandemic Clone of Community-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> . <i>MBio</i> , 2013, 4, .	1.8	177
244	Genome Sequencing of <i>Ralstonia solanacearum</i> FQY_4, Isolated from a Bacterial Wilt Nursery Used for Breeding Crop Resistance. <i>Genome Announcements</i> , 2013, 1, .	0.8	26
245	Comparative Genomic Analysis of Rapid Evolution of an Extreme-Drug-Resistant <i>Acinetobacter baumannii</i> Clone. <i>Genome Biology and Evolution</i> , 2013, 5, 807-818.	1.1	42
246	Whole-Genome Sequence of the Microcin E492-Producing Strain <i>Klebsiella pneumoniae</i> RYC492. <i>Genome Announcements</i> , 2013, 1, .	0.8	12
247	Genome Sequences of Three hpAfrica2 Strains of <i>Helicobacter pylori</i> . <i>Genome Announcements</i> , 2013, 1, .	0.8	11
248	Complete Genome Sequence of <i>Lactococcus lactis</i> subsp. <i>lactis</i> KLDS4.0325. <i>Genome Announcements</i> , 2013, 1, .	0.8	18
249	Proteomic and Transcriptomic Analyses of <i>Candidatus</i> <i>Pelagibacter ubique</i> —Describe the First P <sub>II</sub> -Independent Response to Nitrogen Limitation in a Free-Living Alphaproteobacterium. <i>MBio</i> , 2013, 4, e00133-12.	1.8	54
250	Conservation of Meningococcal Antigens in the Genus <i>Neisseria</i> . <i>MBio</i> , 2013, 4, e00163-13.	1.8	50
251	Within-Host Evolution of <i>Burkholderia pseudomallei</i> over a Twelve-Year Chronic Carriage Infection. <i>MBio</i> , 2013, 4, .	1.8	121
252	Comparative Genomics of Recent Shiga Toxin-Producing <i>Escherichia coli</i> O104:H4: Short-Term Evolution of an Emerging Pathogen. <i>MBio</i> , 2013, 4, e00452-12.	1.8	68
253	Complete Genome Sequence of <i>Staphylococcus aureus</i> Tager 104, a Sequence Type 49 Ancestor. <i>Genome Announcements</i> , 2013, 1, .	0.8	8

#	ARTICLE	IF	CITATIONS
254	The Epidemic of Extended-Spectrum-β-Lactamase-Producing <i>Escherichia coli</i> ST131 Is Driven by a Single Highly Pathogenic Subclone, <i>H30-Rx</i> . <i>MBio</i> , 2013, 4, e00377-13.	1.8	380
255	Comparative Analysis of <i>Chlamydia psittaci</i> Genomes Reveals the Recent Emergence of a Pathogenic Lineage with a Broad Host Range. <i>MBio</i> , 2013, 4, .	1.8	90
256	Comparative Genomics of <i>Wolbachia</i> and the Bacterial Species Concept. <i>PLoS Genetics</i> , 2013, 9, e1003381.	1.5	164
257	Genome Sequence of a Plant-Associated Bacterium, <i>Bacillus amyloliquefaciens</i> Strain UCMB5036. <i>Genome Announcements</i> , 2013, 1, e0011113.	0.8	14
258	Mechanisms of Functional and Physical Genome Reduction in Photosynthetic and Nonphotosynthetic Parasitic Plants of the Broomrape Family. <i>Plant Cell</i> , 2013, 25, 3711-3725.	3.1	289
259	Secondary Evolution of a Self-Incompatibility Locus in the Brassicaceae Genus <i>Leavenworthia</i> . <i>PLoS Biology</i> , 2013, 11, e1001560.	2.6	54
260	De Novo ORFs in <i>Drosophila</i> Are Important to Organismal Fitness and Evolved Rapidly from Previously Non-coding Sequences. <i>PLoS Genetics</i> , 2013, 9, e1003860.	1.5	124
261	The Genome of <i>Tolypocladium inflatum</i> : Evolution, Organization, and Expression of the Cyclosporin Biosynthetic Gene Cluster. <i>PLoS Genetics</i> , 2013, 9, e1003496.	1.5	144
262	Large Linear Plasmids of <i>Borrelia</i> Species That Cause Relapsing Fever. <i>Journal of Bacteriology</i> , 2013, 195, 3629-3639.	1.0	38
263	Transmission of Hypervirulence Traits via Sexual Reproduction within and between Lineages of the Human Fungal Pathogen <i>Cryptococcus gattii</i> . <i>PLoS Genetics</i> , 2013, 9, e1003771.	1.5	45
264	Distributive Conjugal Transfer in <i>Mycobacteria</i> Generates Progeny with Meiotic-Like Genome-Wide Mosaicism, Allowing Mapping of a Mating Identity Locus. <i>PLoS Biology</i> , 2013, 11, e1001602.	2.6	96
265	Expression of a Novel P22 ORFan Gene Reveals the Phage Carrier State in <i>Salmonella</i> Typhimurium. <i>PLoS Genetics</i> , 2013, 9, e1003269.	1.5	61
266	Molecular Epidemiology of Community-Associated Methicillin-resistant <i>Staphylococcus aureus</i> in the genomic era: a Cross-Sectional Study. <i>Scientific Reports</i> , 2013, 3, 1902.	1.6	49
267	Comparative Genome Structure, Secondary Metabolite, and Effector Coding Capacity across <i>Cochliobolus</i> Pathogens. <i>PLoS Genetics</i> , 2013, 9, e1003233.	1.5	232
268	Dialects of the DNA Uptake Sequence in <i>Neisseriaceae</i> . <i>PLoS Genetics</i> , 2013, 9, e1003458.	1.5	82
269	<i>Drosophila americana</i> as a Model Species for Comparative Studies on the Molecular Basis of Phenotypic Variation. <i>Genome Biology and Evolution</i> , 2013, 5, 661-679.	1.1	24
270	The tRNA <sup>arg</sup> Gene and <i>engA</i> Are Essential Genes on the 1.7-Mb pSymB Megaplasmid of <i>Sinorhizobium meliloti</i> and Were Translocated Together from the Chromosome in an Ancestral Strain. <i>Journal of Bacteriology</i> , 2013, 195, 202-212.	1.0	40
271	Variation of the Virus-Related Elements within Syntenic Genomes of the Hyperthermophilic Archaeon <i>Aeropyrum</i> . <i>Applied and Environmental Microbiology</i> , 2013, 79, 5891-5898.	1.4	3



#	ARTICLE	IF	CITATIONS
272	Co-phylog: an assembly-free phylogenomic approach for closely related organisms. <i>Nucleic Acids Research</i> , 2013, 41, e75-e75.	6.5	101
273	Genome-wide patterns of natural variation reveal strong selective sweeps and ongoing genomic conflict in <i>Drosophila mauritiana</i> . <i>Genome Research</i> , 2013, 23, 99-110.	2.4	73
274	Comparative Genomic Analysis of Phylogenetically Closely Related <i>Hydrogenobaculum</i> sp. Isolates from Yellowstone National Park. <i>Applied and Environmental Microbiology</i> , 2013, 79, 2932-2943.	1.4	39
275	Comparison of Metabolic Capacities and Inference of Gene Content Evolution in Mosquito-Associated <i>Spiroplasma diminutum</i> and <i>S. taiwanense</i> . <i>Genome Biology and Evolution</i> , 2013, 5, 1512-1523.	1.1	35
276	Comparative Genomics of <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> Reveals a Strict Monophyletic Bifidobacterial Taxon. <i>Applied and Environmental Microbiology</i> , 2013, 79, 4304-4315.	1.4	74
277	Differential Genomic Variation between Short- and Long-Term Bacterial Evolution Revealed by Ultradeep Sequencing. <i>Genome Biology and Evolution</i> , 2013, 5, 572-577.	1.1	3
278	Complete Genomes of Two Dipteran-Associated Spiroplasmas Provided Insights into the Origin, Dynamics, and Impacts of Viral Invasion in <i>Spiroplasma</i> . <i>Genome Biology and Evolution</i> , 2013, 5, 1151-1164.	1.1	75
279	Progressive genome-wide introgression in agricultural <i>Campylobacter coli</i> . <i>Molecular Ecology</i> , 2013, 22, 1051-1064.	2.0	128
280	Comparative Sequence Analysis of a Multidrug-Resistant Plasmid from <i>Aeromonas hydrophila</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 120-129.	1.4	92
281	Compensation of the Metabolic Costs of Antibiotic Resistance by Physiological Adaptation in <i>Escherichia coli</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 3752-3762.	1.4	68
282	Comparative Genomic and Transcriptomic Analyses Reveal Habitat Differentiation and Different Transcriptional Responses during Pectin Metabolism in <i>Alishewanella</i> Species. <i>Applied and Environmental Microbiology</i> , 2013, 79, 6351-6361.	1.4	11
283	Genome Sequence of <i>Dickeya solani</i> , a New soft Rot Pathogen of Potato, Suggests its Emergence May Be Related to a Novel Combination of Non-Ribosomal Peptide/Polyketide Synthetase Clusters. <i>Diversity</i> , 2013, 5, 824-842.	0.7	54
284	Comparative genome analysis of <i>Lactobacillus casei</i> strains isolated from <i>Actinomyces</i> and <i>Streptococcus</i> products reveals marked similarities and points to a common origin. <i>Microbial Biotechnology</i> , 2013, 6, 576-587.	2.0	27
285	Complete Genome Sequence of Probiotic Strain <i>Lactobacillus acidophilus</i> La-14. <i>Genome Announcements</i> , 2013, 1, .	0.8	28
286	Complete Nucleotide Sequences of <i>bla</i> <sub>KPC-4</sub> and <i>bla</i> <sub>KPC-5</sub> -Harboring IncN and IncX Plasmids from <i>Klebsiella pneumoniae</i> Strains Isolated in New Jersey. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 269-276.	1.4	88
287	The VanE operon in <i>Enterococcus faecalis</i> N00-410 is found on a putative integrative and conjugative element, Tn6202. <i>Journal of Antimicrobial Chemotherapy</i> , 2013, 68, 294-299.	1.3	5
288	Genomics of <i>Loa loa</i> , a Wolbachia-free filarial parasite of humans. <i>Nature Genetics</i> , 2013, 45, 495-500.	9.4	173
289	To Tree or Not to Tree? Genome-Wide Quantification of Recombination and Reticulate Evolution during the Diversification of Strict Intracellular Bacteria. <i>Genome Biology and Evolution</i> , 2013, 5, 2305-2317.	1.1	21

#	ARTICLE	IF	CITATIONS
290	Genome sequence and description of the heavy metal tolerant bacterium <i>Lysinibacillus sphaericus</i> strain OT4b.31. <i>Standards in Genomic Sciences</i> , 2013, 9, 42-56.	1.5	35
291	The Genomic Blueprint of <i>Salmonella enterica</i> subspecies <i>enterica</i> serovar Typhi P-stx-12. <i>Standards in Genomic Sciences</i> , 2013, 7, 483-496.	1.5	6
292	Draft Genome Sequences of Two Pairs of Human Intestinal <i>Bifidobacterium longum</i> subsp. <i>longum</i> Strains, 44B and 1-6B and 35B and 2-2B, Consecutively Isolated from Two Children after a 5-Year Time Period. <i>Genome Announcements</i> , 2013, 1, .	0.8	12
293	Draft Genome Sequence of <i>Dietzia</i> sp. Strain UCD-THP (Phylum <i>Actinobacteria</i> ). <i>Genome Announcements</i> , 2013, 1, .	0.8	5
294	Genome Sequence of <i>Salmonella enterica</i> Serotype Tennessee Strain CDC07-0191, Implicated in the 2006-2007 Multistate Food-Borne Outbreak Linked to Peanut Butter in the United States. <i>Genome Announcements</i> , 2013, 1, .	0.8	4
295	Genome Sequences of Two Pathogenic <i>Streptococcus agalactiae</i> Isolates from the One-Humped Camel <i>Camelus dromedarius</i> . <i>Genome Announcements</i> , 2013, 1, .	0.8	9
296	Genomics and genetics of <i>Sulfolobus islandicus</i> LAL14/1, a model hyperthermophilic archaeon. <i>Open Biology</i> , 2013, 3, 130010.	1.5	55
297	Microevolution of the Chromosomal Region of Acute Disease Antigen A ( <i>adaA</i> ) in the Query (Q) Fever Agent <i>Coxiella burnetii</i> . <i>PLoS ONE</i> , 2013, 8, e53440.	1.1	17
298	Genomic Comparison between <i>Salmonella Gallinarum</i> and <i>Pullorum</i> : Differential Pseudogene Formation under Common Host Restriction. <i>PLoS ONE</i> , 2013, 8, e59427.	1.1	29
299	Within-Host Evolution of <i>Staphylococcus aureus</i> during Asymptomatic Carriage. <i>PLoS ONE</i> , 2013, 8, e61319.	1.1	194
300	No Ancient DNA Damage in Actinobacteria from the Neanderthal Bone. <i>PLoS ONE</i> , 2013, 8, e62799.	1.1	17
301	Plasmidome-Analysis of ESBL-Producing <i>Escherichia coli</i> Using Conventional Typing and High-Throughput Sequencing. <i>PLoS ONE</i> , 2013, 8, e65793.	1.1	44
302	The Plastid Genome of the Red Macroalga <i>Grateloupia taiwanensis</i> (Halymeniaceae). <i>PLoS ONE</i> , 2013, 8, e68246.	1.1	26
303	Balanced Gene Losses, Duplications and Intensive Rearrangements Led to an Unusual Regularly Sized Genome in <i>Arbutus unedo</i> Chloroplasts. <i>PLoS ONE</i> , 2013, 8, e79685.	1.1	47
304	Prediction and Characterization of Small Non-Coding RNAs Related to Secondary Metabolites in <i>Saccharopolyspora erythraea</i> . <i>PLoS ONE</i> , 2013, 8, e80676.	1.1	5
305	Isolation and Characterization of Two Novel Bacteria <i>Afipia cberi</i> and <i>Mesorhizobium hominis</i> from Blood of a Patient Afflicted with Fatal Pulmonary Illness. <i>PLoS ONE</i> , 2013, 8, e82673.	1.1	7
306	Comparative Genomic Analyses of <i>Streptococcus pseudopneumoniae</i> Provide Insight into Virulence and Commensalism Dynamics. <i>PLoS ONE</i> , 2013, 8, e65670.	1.1	21
307	Characterization and Phylogenetic Analysis of the Mitochondrial Genome of <i>Glarea lozoyensis</i> Indicates High Diversity within the Order Helotiales. <i>PLoS ONE</i> , 2013, 8, e74792.	1.1	9

#	ARTICLE	IF	CITATIONS
308	Complete Genome Analysis of Three <i>Acinetobacter baumannii</i> Clinical Isolates in China for Insight into the Diversification of Drug Resistance Elements. <i>PLoS ONE</i> , 2013, 8, e66584.	1.1	107
309	Evolutionary Genomics and Adaptive Evolution of the Hedgehog Gene Family (Shh, Ihh and Dhh) in Vertebrates. <i>PLoS ONE</i> , 2014, 9, e74132.	1.1	27
310	Ultra Deep Sequencing of <i>Listeria monocytogenes</i> sRNA Transcriptome Revealed New Antisense RNAs. <i>PLoS ONE</i> , 2014, 9, e83979.	1.1	31
311	Eight New Genomes and Synthetic Controls Increase the Accessibility of Rapid Melt-MAMA SNP Typing of <i>Coxiella burnetii</i> . <i>PLoS ONE</i> , 2014, 9, e85417.	1.1	17
312	Distribution of Gifsy-3 and of Variants of ST64B and Gifsy-1 Prophages amongst <i>Salmonella enterica</i> Serovar Typhimurium Isolates: Evidence that Combinations of Prophages Promote Clonality. <i>PLoS ONE</i> , 2014, 9, e86203.	1.1	32
313	Genome Sequencing of <i>Listeria monocytogenes</i> Quargel Listeriosis Outbreak Strains Reveals Two Different Strains with Distinct In Vitro Virulence Potential. <i>PLoS ONE</i> , 2014, 9, e89964.	1.1	55
314	MC64-ClustalWP2: A Highly-Parallel Hybrid Strategy to Align Multiple Sequences in Many-Core Architectures. <i>PLoS ONE</i> , 2014, 9, e94044.	1.1	13
315	Comparative Population Genomics of the <i>Borrelia burgdorferi</i> Species Complex Reveals High Degree of Genetic Isolation among Species and Underscores Benefits and Constraints to Studying Intra-Specific Epidemiological Processes. <i>PLoS ONE</i> , 2014, 9, e94384.	1.1	25
316	Characterization of Nontypable <i>Haemophilus influenzae</i> Isolates Recovered from Adult Patients with Underlying Chronic Lung Disease Reveals Genotypic and Phenotypic Traits Associated with Persistent Infection. <i>PLoS ONE</i> , 2014, 9, e97020.	1.1	29
317	Insights from the Genome Annotation of <i>Elizabethkingia anophelis</i> from the Malaria Vector <i>Anopheles gambiae</i> . <i>PLoS ONE</i> , 2014, 9, e97715.	1.1	56
318	The Complete Genome Sequence of <i>Escherichia coli</i> EC958: A High Quality Reference Sequence for the Globally Disseminated Multidrug Resistant <i>E. coli</i> O25b:H4-ST131 Clone. <i>PLoS ONE</i> , 2014, 9, e104400.	1.1	116
319	Choice of Reference Sequence and Assembler for Alignment of <i>Listeria monocytogenes</i> Short-Read Sequence Data Greatly Influences Rates of Error in SNP Analyses. <i>PLoS ONE</i> , 2014, 9, e104579.	1.1	88
320	Genome Analysis of <i>Bacillus amyloliquefaciens</i> Subsp. <i>plantarum</i> UCMB5113: A Rhizobacterium That Improves Plant Growth and Stress Management. <i>PLoS ONE</i> , 2014, 9, e104651.	1.1	114
321	Sequence and Annotation of the Apicoplast Genome of the Human Pathogen <i>Babesia microti</i> . <i>PLoS ONE</i> , 2014, 9, e107939.	1.1	26
322	Genome Features of the Endophytic Actinobacterium <i>Micromonospora lupini</i> Strain Lupac 08: On the Process of Adaptation to an Endophytic Life Style?. <i>PLoS ONE</i> , 2014, 9, e108522.	1.1	74
323	Phylogenomic Reconstruction Indicates Mitochondrial Ancestor Was an Energy Parasite. <i>PLoS ONE</i> , 2014, 9, e110685.	1.1	53
324	Global dissemination of a multidrug resistant <i>Escherichia coli</i> clone. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 5694-5699.	3.3	498
325	Inference of the Properties of the Recombination Process from Whole Bacterial Genomes. <i>Genetics</i> , 2014, 196, 253-265.	1.2	41

#	ARTICLE	IF	CITATIONS
326	Whole-Genome Sequencing for Rapid and Accurate Identification of Bacterial Transmission Pathways. <i>Methods in Microbiology</i> , 2014, 41, 123-152.	0.4	4
327	Genetic distance in the whole-genome perspective on <i>Listeria monocytogenes</i> strains F2-382 and NIHS-28 that show similar subtyping results. <i>BMC Microbiology</i> , 2014, 14, 309.	1.3	3
328	Chloroplast Genome of Novel Rice Germplasm Identified in Northern Australia. <i>Tropical Plant Biology</i> , 2014, 7, 111-120.	1.0	43
329	Whole genome sequence and comparative genomic analysis of multidrug-resistant <i>Staphylococcus capitis</i> subsp. <i>urealyticus</i> strain LNZR-1. <i>Gut Pathogens</i> , 2014, 6, 45.	1.6	10
330	Gene order alignment on trees with multiOrthoAlign. <i>BMC Genomics</i> , 2014, 15, S5.	1.2	2
331	Comparative genomics of planktonic Flavobacteriaceae from the Gulf of Maine using metagenomic data. <i>Microbiome</i> , 2014, 2, 34.	4.9	28
332	Analysis of genomic rearrangements, horizontal gene transfer and role of plasmids in the evolution of industrial important <i>Thermus</i> species. <i>BMC Genomics</i> , 2014, 15, 813.	1.2	19
333	The Genome of <i>Cardinium</i> cBtQ1 Provides Insights into Genome Reduction, Symbiont Motility, and Its Settlement in <i>Bemisia tabaci</i> . <i>Genome Biology and Evolution</i> , 2014, 6, 1013-1030.	1.1	68
334	Genome analysis of <i>Campylobacter jejuni</i> strains isolated from a waterborne outbreak. <i>BMC Genomics</i> , 2014, 15, 768.	1.2	40
335	The Plastid Genome of Mycoheterotrophic Monocot <i>Petrosavia stellaris</i> Exhibits Both Gene Losses and Multiple Rearrangements. <i>Genome Biology and Evolution</i> , 2014, 6, 238-246.	1.1	75
336	Strain-level genomic variation in natural populations of <i>Lebetimonas</i> from an erupting deep-sea volcano. <i>ISME Journal</i> , 2014, 8, 867-880.	4.4	38
337	Predominant and Substoichiometric Isomers of the Plastid Genome Coexist within <i>Juniperus</i> Plants and Have Shifted Multiple Times during Cupressophyte Evolution. <i>Genome Biology and Evolution</i> , 2014, 6, 580-590.	1.1	91
338	Strain Diversity of CTX-M-Producing Enterobacteriaceae in Individual Pigs: Insights into the Dynamics of Shedding during the Production Cycle. <i>Applied and Environmental Microbiology</i> , 2014, 80, 6620-6626.	1.4	15
339	Characterization of the morphology and genome of an <i>Escherichia coli</i> podovirus. <i>Archives of Virology</i> , 2014, 159, 3249-3256.	0.9	12
340	Use of whole genome sequences to develop a molecular phylogenetic framework for <i>Rhodococcus fascians</i> and the <i>Rhodococcus</i> genus. <i>Frontiers in Plant Science</i> , 2014, 5, 406.	1.7	29
341	Plastid and nuclear genomic resources of a relict and endangered plant species: <i>Chamaedaphne calyculata</i> (L.) Moench (Ericaceae). <i>Turkish Journal of Botany</i> , 2014, 38, 1229-1238.	0.5	18
342	Big data challenges for estimating genome assembler quality. , 2014, , .		1
343	Complete Genome Sequence of <i>Haemophilus influenzae</i> Strain 375 from the Middle Ear of a Pediatric Patient with Otitis Media. <i>Genome Announcements</i> , 2014, 2, .	0.8	14

#	ARTICLE	IF	CITATIONS
344	Evolution and Comparative Genomics of <i>Campylobacter jejuni</i> ST-677 Clonal Complex. <i>Genome Biology and Evolution</i> , 2014, 6, 2424-2438.	1.1	21
345	Plasmid Flux in <i>Escherichia coli</i> ST131 Sublineages, Analyzed by Plasmid Constellation Network (PLACNET), a New Method for Plasmid Reconstruction from Whole Genome Sequences. <i>PLoS Genetics</i> , 2014, 10, e1004766.	1.5	179
346	The Glanville fritillary genome retains an ancient karyotype and reveals selective chromosomal fusions in Lepidoptera. <i>Nature Communications</i> , 2014, 5, 4737.	5.8	196
347	The methylome of the gut microbiome: disparate Dam methylation patterns in intestinal <i>Bacteroides dorei</i> . <i>Frontiers in Microbiology</i> , 2014, 5, 361.	1.5	36
348	Characterization and comparative analysis of antibiotic resistance plasmids isolated from a wastewater treatment plant. <i>Frontiers in Microbiology</i> , 2014, 5, 558.	1.5	37
349	Genome Sequence of <i>Lactobacillus fabifermentans</i> Strain T30PCM01, Isolated from Fermenting Grape Marc. <i>Genome Announcements</i> , 2014, 2, .	0.8	4
350	Draft Genome Sequence of <i>Salmonella enterica</i> Serovar Typhi Strain STH2370. <i>Genome Announcements</i> , 2014, 2, .	0.8	16
351	Complete Genome Sequence for the <i>Fusarium</i> Head Blight Antagonist <i>Bacillus amyloliquefaciens</i> Strain TrigoCor 1448. <i>Genome Announcements</i> , 2014, 2, .	0.8	8
352	Draft Genome Sequences of Six Ruminant <i>Coxiella burnetii</i> Isolates of European Origin. <i>Genome Announcements</i> , 2014, 2, .	0.8	13
353	Genome Sequence of <i>Serratia plymuthica</i> V4. <i>Genome Announcements</i> , 2014, 2, .	0.8	8
354	Complete Genome Sequences of <i>Lactobacillus johnsonii</i> Strain N6.2 and <i>Lactobacillus reuteri</i> Strain TD1. <i>Genome Announcements</i> , 2014, 2, .	0.8	25
355	Draft Genome Sequence of <i>Enterococcus hirae</i> Strain INF E1 Isolated from Cultured Milk. <i>Genome Announcements</i> , 2014, 2, .	0.8	1
356	Complete Genome Sequence of the <i>Streptococcus</i> sp. Strain VT 162, Isolated from the Saliva of Pediatric Oncohematology Patients. <i>Genome Announcements</i> , 2014, 2, .	0.8	6
357	Genome Sequence of <i>Candidatus</i> <i>Arthromitus</i> sp. Strain SFB-Mouse-NL, a Commensal Bacterium with a Key Role in Postnatal Maturation of Gut Immune Functions. <i>Genome Announcements</i> , 2014, 2, .	0.8	35
358	Draft Genome Sequence of a New <i>Shigella flexneri</i> Subserotype, 4S BJ10610. <i>Genome Announcements</i> , 2014, 2, .	0.8	1
359	Draft Genome Sequence of <i>Leuconostoc mesenteroides</i> P45 Isolated from Pulque, a Traditional Mexican Alcoholic Fermented Beverage. <i>Genome Announcements</i> , 2014, 2, .	0.8	7
360	Draft Genome Sequence of <i>Coxiella burnetii</i> Strain Cb196, an Agent of Endocarditis in Saudi Arabia. <i>Genome Announcements</i> , 2014, 2, .	0.8	5
361	Complete Genome Sequence of <i>Francisella endociliophora</i> Strain FSC1006, Isolated from a Laboratory Culture of the Marine Ciliate <i>Euplotes raikovi</i> . <i>Genome Announcements</i> , 2014, 2, .	0.8	23

#	ARTICLE	IF	CITATIONS
362	Phyldynamic Analysis of Clinical and Environmental <i>Vibrio cholerae</i> Isolates from Haiti Reveals Diversification Driven by Positive Selection. <i>MBio</i> , 2014, 5, .	1.8	45
363	Highly conserved organellar genomes in the Gracilariales as inferred using new data from the Hawaiian invasive alga <i>Gracilaria salicornia</i> (Rhodophyta). <i>Phycologia</i> , 2014, 53, 109-116.	0.6	26
364	The complete genome sequences of poxviruses isolated from a penguin and a pigeon in South Africa and comparison to other sequenced avipoxviruses. <i>BMC Genomics</i> , 2014, 15, 463.	1.2	37
365	Alignathon: a competitive assessment of whole-genome alignment methods. <i>Genome Research</i> , 2014, 24, 2077-2089.	2.4	102
366	Genome Sequencing of <i>Mycobacterium abscessus</i> Isolates from Patients in the United States and Comparisons to Globally Diverse Clinical Strains. <i>Journal of Clinical Microbiology</i> , 2014, 52, 3573-3582.	1.8	64
367	Recovery of a Medieval <i>Brucella melitensis</i> Genome Using Shotgun Metagenomics. <i>MBio</i> , 2014, 5, e01337-14.	1.8	67
368	Draft Genome Sequence of <i>Burkholderia dolosa</i> PC543 Isolated from Cystic Fibrosis Airways. <i>Genome Announcements</i> , 2014, 2, .	0.8	9
369	Fast alignment-free sequence comparison using spaced-word frequencies. <i>Bioinformatics</i> , 2014, 30, 1991-1999.	1.8	117
370	Conservation of Transcription Start Sites within Genes across a Bacterial Genus. <i>MBio</i> , 2014, 5, e01398-14.	1.8	56
371	Complete Genome Sequence of a Mosaic Bacteriophage, Waukesha92. <i>Genome Announcements</i> , 2014, 2, .	0.8	5
372	Whole-Genome Sequence Analysis of the Naturally Competent <i>Acinetobacter baumannii</i> Clinical Isolate A118. <i>Genome Biology and Evolution</i> , 2014, 6, 2235-2239.	1.1	85
373	Draft Genome Sequence of an Invasive Multidrug-Resistant Strain, <i>Pseudomonas aeruginosa</i> BK1, Isolated from a Keratitis Patient. <i>Genome Announcements</i> , 2014, 2, .	0.8	2
374	Highly rearranged and size-variable chloroplast genomes in conifers <i>scp&gt;II&lt;/scp&gt;</i> clade (cupressophytes): evolution towards shorter intergenic spacers. <i>Plant Biotechnology Journal</i> , 2014, 12, 344-353.	4.1	87
375	Strategy for Genome Sequencing Analysis and Assembly for Comparative Genomics of <i>Pseudomonas</i> Genomes. <i>Methods in Molecular Biology</i> , 2014, 1149, 565-577.	0.4	3
376	Recombination Shapes Genome Architecture in an Organism from the Archaeal Domain. <i>Genome Biology and Evolution</i> , 2014, 6, 170-178.	1.1	14
377	Comparative Genome Analysis of Two Isolates of the Fish Pathogen <i>Piscirickettsia salmonis</i> from Different Hosts Reveals Major Differences in Virulence-Associated Secretion Systems. <i>Genome Announcements</i> , 2014, 2, .	0.8	45
378	Comparative genomics of closely related <i>Salmonella enterica</i> serovar Typhi strains reveals genome dynamics and the acquisition of novel pathogenic elements. <i>BMC Genomics</i> , 2014, 15, 1007.	1.2	18
379	Comparative genomic analysis of clinical and environmental strains provides insight into the pathogenicity and evolution of <i>Vibrio parahaemolyticus</i> . <i>BMC Genomics</i> , 2014, 15, 1135.	1.2	19



#	ARTICLE	IF	CITATIONS
380	A genome-guided analysis of energy conservation in the thermophilic, cytochrome-free acetogenic bacterium <i>Thermoanaerobacter</i> Rivui. <i>BMC Genomics</i> , 2014, 15, 1139.	1.2	63
381	Core and accessory genome architecture in a group of <i>Pseudomonas aeruginosa</i> Mu-like phages. <i>BMC Genomics</i> , 2014, 15, 1146.	1.2	33
382	Comparative and genetic analysis of the four sequenced <i>Paenibacillus polymyxa</i> genomes reveals a diverse metabolism and conservation of genes relevant to plant-growth promotion and competitiveness. <i>BMC Genomics</i> , 2014, 15, 851.	1.2	72
383	CRISPR-Cas systems in the marine actinomycete <i>Salinispora</i> : linkages with phage defense, microdiversity and biogeography. <i>BMC Genomics</i> , 2014, 15, 936.	1.2	10
384	Mycobacteriophage-driven diversification of <i>Mycobacterium abscessus</i> . <i>Biology Direct</i> , 2014, 9, 19.	1.9	16
385	Evolutionary origin of highly repetitive plastid genomes within the clover genus ( <i>Trifolium</i> ). <i>BMC Evolutionary Biology</i> , 2014, 14, 228.	3.2	49
386	Gene flow in environmental <i>Legionella pneumophila</i> leads to genetic and pathogenic heterogeneity within a Legionnaires' disease outbreak. <i>Genome Biology</i> , 2014, 15, 504.	3.8	36
387	The Harvest suite for rapid core-genome alignment and visualization of thousands of intraspecific microbial genomes. <i>Genome Biology</i> , 2014, 15, 524.	3.8	1,428
388	Next generation sequencing analysis of nine <i>Corynebacterium ulcerans</i> isolates reveals zoonotic transmission and a novel putative diphtheria toxin-encoding pathogenicity island. <i>Genome Medicine</i> , 2014, 6, 113.	3.6	47
389	Evaluating synteny for improved comparative studies. <i>Bioinformatics</i> , 2014, 30, i9-i18.	1.8	77
390	Massive Expansion of Ubiquitination-Related Gene Families within the Chlamydiae. <i>Molecular Biology and Evolution</i> , 2014, 31, 2890-2904.	3.5	43
391	Widespread differences in cortex DNA methylation of the <i>language gene</i> CNTNAP2 between humans and chimpanzees. <i>Epigenetics</i> , 2014, 9, 533-545.	1.3	30
392	Genomic Signatures of Distributive Conjugal Transfer among Mycobacteria. <i>Genome Biology and Evolution</i> , 2014, 6, 2489-2500.	1.1	48
393	Mining the <i>Pseudomonas</i> Genome. <i>Methods in Molecular Biology</i> , 2014, 1149, 417-432.	0.4	4
394	Insights into organohalide respiration and the versatile catabolism of <i>Sulfurospirillum multivorans</i> gained from comparative genomics and physiological studies. <i>Environmental Microbiology</i> , 2014, 16, 3562-3580.	1.8	76
395	Genome Sequence of <i>Bacillus pumilus</i> MTCC B6033. <i>Genome Announcements</i> , 2014, 2, .	0.8	11
396	Ecology Drives the Distribution of Specialized Tyrosine Metabolism Modules in Fungi. <i>Genome Biology and Evolution</i> , 2014, 6, 121-132.	1.1	37
397	Evolutionary relationships within Triops (Branchiopoda: Notostraca) using complete mitochondrial genomes. <i>Journal of Crustacean Biology</i> , 2014, 34, 795-800.	0.3	7

#	ARTICLE	IF	CITATIONS
398	Genome Diversity and Divergence in <i>Drosophila mauritiana</i> : Multiple Signatures of Faster X Evolution. <i>Genome Biology and Evolution</i> , 2014, 6, 2444-2458.	1.1	59
399	Whole Genome Sequencing and Analysis of Plant Growth Promoting Bacteria Isolated from the Rhizosphere of Plantation Crops Coconut, Cocoa and Arecanut. <i>PLoS ONE</i> , 2014, 9, e104259.	1.1	97
400	The Complete Mitochondrial Genome Sequence of Hepatozoon catesbiana (Apicomplexa: Coccidia: Tj ETQq0 0 0 rgBT /Overlock 10 Tf Parasitology, 2014, 100, 651.	0.3	20
401	MetaGenIE: Characterizing Human Clinical Samples Using Deep Metagenomic Sequencing. <i>PLoS ONE</i> , 2014, 9, e110915.	1.1	14
402	Genomic analysis of three African strains of <i>Bacillus anthracis</i> demonstrates that they are part of the clonal expansion of an exclusively pathogenic bacterium. <i>New Microbes and New Infections</i> , 2014, 2, 161-169.	0.8	16
403	The Ellis Island Effect. <i>Mobile Genetic Elements</i> , 2014, 4, e29801.	1.8	20
404	Global Phylogenomic Analysis of Nonencapsulated <i>Streptococcus pneumoniae</i> Reveals a Deep-Branching Classic Lineage That Is Distinct from Multiple Sporadic Lineages. <i>Genome Biology and Evolution</i> , 2014, 6, 3281-3294.	1.1	63
405	Draft Genome Sequence of <i>Enterococcus faecalis</i> Strain PF3, Isolated from AdÃ©lie Penguin Feces from Antarctica. <i>Genome Announcements</i> , 2014, 2, .	0.8	3
406	Comparative Genomic Analysis and Virulence Differences in Closely Related <i>Salmonella enterica</i> Serotype Heidelberg Isolates from Humans, Retail Meats, and Animals. <i>Genome Biology and Evolution</i> , 2014, 6, 1046-1068.	1.1	123
407	Ancient Nuclear Plastid DNA in the Yew Family (Taxaceae). <i>Genome Biology and Evolution</i> , 2014, 6, 2111-2121.	1.1	35
408	A suggested classification for two groups of <i>Campylobacter myoviruses</i> . <i>Archives of Virology</i> , 2014, 159, 181-190.	0.9	63
409	Group-theoretic models of the inversion process in bacterial genomes. <i>Journal of Mathematical Biology</i> , 2014, 69, 243-265.	0.8	23
410	Comparative genomics of enterohemorrhagic <i>Escherichia coli</i> O145:H28 demonstrates a common evolutionary lineage with <i>Escherichia coli</i> O157:H7. <i>BMC Genomics</i> , 2014, 15, 17.	1.2	84
411	UFV-P2 as a member of the Luz24likevirus genus: a new overview on comparative functional genome analyses of the LUZ24-like phages. <i>BMC Genomics</i> , 2014, 15, 7.	1.2	27
412	Genomic and phylogenetic traits of <i>Staphylococcus</i> phages S25-3 and S25-4 (family Myoviridae, genus) Tj ETQq0 0,0 rgBT /Oyerlock 10 Tf	1.1	20
413	Effect of growth rate and selection pressure on rates of transfer of an antibiotic resistance plasmid between <i>E. coli</i> strains. <i>Plasmid</i> , 2014, 72, 1-8.	0.4	50
414	Evolutionary and biotechnology implications of plastid genome variation in the invertedâ€repeatâ€lacking clade of legumes. <i>Plant Biotechnology Journal</i> , 2014, 12, 743-754.	4.1	146
415	Genome sequence and comparative analysis of a <i>Vibrio cholerae</i> O139 strain E306 isolated from a cholera case in China. <i>Gut Pathogens</i> , 2014, 6, 3.	1.6	8



#	ARTICLE	IF	CITATIONS
416	Comparative analysis of the complete genome of KPC-2-producing <i>Klebsiella pneumoniae</i> Kp13 reveals remarkable genome plasticity and a wide repertoire of virulence and resistance mechanisms. <i>BMC Genomics</i> , 2014, 15, 54.	1.2	109
417	Single-Cell Genomics Reveals Hundreds of Coexisting Subpopulations in Wild <i>Prochlorococcus</i> . <i>Science</i> , 2014, 344, 416-420.	6.0	506
418	The Plastid Genomes of Flowering Plants. <i>Methods in Molecular Biology</i> , 2014, 1132, 3-38.	0.4	151
419	<i>Serratia marcescens</i> harbouring SME-type class A carbapenemases in Canada and the presence of bla <sub>SME</sub> on a novel genomic island, SmarGII-1. <i>Journal of Antimicrobial Chemotherapy</i> , 2014, 69, 1825-1829.	1.3	27
420	Comparative genomics analysis of <i>Lactobacillus</i> species associated with weight gain or weight protection. <i>Nutrition and Diabetes</i> , 2014, 4, e109-e109.	1.5	95
421	Complete genome sequencing and comparative analysis of the linezolid-resistant <i>Enterococcus faecalis</i> strain DENG1. <i>Archives of Microbiology</i> , 2014, 196, 513-516.	1.0	3
422	Cloning and expression of three ladA-type alkane monooxygenase genes from an extremely thermophilic alkane-degrading bacterium <i>Geobacillus thermoleovorans</i> B23. <i>Extremophiles</i> , 2014, 18, 515-523.	0.9	27
423	Metagenomic analysis of the microbial community in fermented grape marc reveals that <i>Lactobacillus fabifermentans</i> is one of the dominant species: insights into its genome structure. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 6015-6037.	1.7	35
424	GenomeVISTA™ an integrated software package for whole-genome alignment and visualization. <i>Bioinformatics</i> , 2014, 30, 2654-2655.	1.8	27
425	A high-density linkage map enables a second-generation collared flycatcher genome assembly and reveals the patterns of avian recombination rate variation and chromosomal evolution. <i>Molecular Ecology</i> , 2014, 23, 4035-4058.	2.0	220
426	Characterization of Invasive Group B <i>Streptococcus</i> Strains from the Greater Toronto Area, Canada. <i>Journal of Clinical Microbiology</i> , 2014, 52, 1441-1447.	1.8	74
427	Predominant <i>Acidilobus</i> -Like Populations from Geothermal Environments in Yellowstone National Park Exhibit Similar Metabolic Potential in Different Hypoxic Microbial Communities. <i>Applied and Environmental Microbiology</i> , 2014, 80, 294-305.	1.4	20
428	Comparative genomic analysis shows that <i>Streptococcus suis</i> meningitis isolate SC070731 contains a unique 105K genomic island. <i>Gene</i> , 2014, 535, 156-164.	1.0	45
429	Reconstruction of the Ancestral Plastid Genome in Geraniaceae Reveals a Correlation between Genome Rearrangements, Repeats, and Nucleotide Substitution Rates. <i>Molecular Biology and Evolution</i> , 2014, 31, 645-659.	3.5	306
430	New Copper Resistance Determinants in the Extremophile <i>Acidithiobacillus ferrooxidans</i> : A Quantitative Proteomic Analysis. <i>Journal of Proteome Research</i> , 2014, 13, 946-960.	1.8	64
431	Phylogenetics and diversification of morning glories (tribe Ipomoeae, Convolvulaceae) based on whole plastome sequences. <i>American Journal of Botany</i> , 2014, 101, 92-103.	0.8	64
432	A molecular scheme for <i>Yersinia enterocolitica</i> patho-serotyping derived from genome-wide analysis. <i>International Journal of Medical Microbiology</i> , 2014, 304, 275-283.	1.5	42
433	Response to copper of <i>Acidithiobacillus ferrooxidans</i> ATCC 23270 grown in elemental sulfur. <i>Research in Microbiology</i> , 2014, 165, 761-772.	1.0	25

#	ARTICLE	IF	CITATIONS
434	An Outbreak of Respiratory Tularemia Caused by Diverse Clones of <i>Francisella tularensis</i> . <i>Clinical Infectious Diseases</i> , 2014, 59, 1546-1553.	2.9	61
435	High Variability of Mitochondrial Gene Order among Fungi. <i>Genome Biology and Evolution</i> , 2014, 6, 451-465.	1.1	223
436	Multilocus Sequence Typing (MLST) and Whole-Genome MLST of <i>Campylobacter jejuni</i> Isolates from Human Infections in Three Districts during a Seasonal Peak in Finland. <i>Journal of Clinical Microbiology</i> , 2014, 52, 4147-4154.	1.8	67
437	Complete Nucleotide Sequence of a <i>Citrobacter freundii</i> Plasmid Carrying KPC-2 in a Unique Genetic Environment. <i>Genome Announcements</i> , 2014, 2, .	0.8	12
438	Identification and Characterization of a Peculiar $\lambda$ -Converting Phage Frequently Present in Verocytotoxin-Producing <i>Escherichia coli</i> O157 Isolated from Human Infections. <i>Infection and Immunity</i> , 2014, 82, 3023-3032.	1.0	11
439	Comparative assembly hubs: Web-accessible browsers for comparative genomics. <i>Bioinformatics</i> , 2014, 30, 3293-3301.	1.8	33
440	Second-Pandemic Strain of <i>Vibrio cholerae</i> from the Philadelphia Cholera Outbreak of 1849. <i>New England Journal of Medicine</i> , 2014, 370, 334-340.	13.9	134
441	Isolation and characterization of a new <i>Staphylococcus epidermidis</i> broad-spectrum bacteriophage. <i>Journal of General Virology</i> , 2014, 95, 506-515.	1.3	59
442	Next-generation sequencing, FISH mapping and synteny-based modeling reveal mechanisms of decreasing dysploidy in <i>Cucumis</i> . <i>Plant Journal</i> , 2014, 77, 16-30.	2.8	90
443	Comparative Genomic Analysis of KPC-Encoding pKpQIL-Like Plasmids and Their Distribution in New Jersey and New York Hospitals. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 2871-2877.	1.4	105
444	Symbiont shift towards <i>Rhizobium</i> nodulation in a group of phylogenetically related <i>Phaseolus</i> species. <i>Molecular Phylogenetics and Evolution</i> , 2014, 79, 1-11.	1.2	20
445	Epidemic <i>Klebsiella pneumoniae</i> ST258 Is a Hybrid Strain. <i>MBio</i> , 2014, 5, e01355-14.	1.8	189
446	Metabolic engineering of <i>Corynebacterium glutamicum</i> for L-arginine production. <i>Nature Communications</i> , 2014, 5, 4618.	5.8	209
447	Recombination drives genome evolution in outbreak-related <i>Legionella pneumophila</i> isolates. <i>Nature Genetics</i> , 2014, 46, 1205-1211.	9.4	76
448	CanSNPer: a hierarchical genotype classifier of clonal pathogens. <i>Bioinformatics</i> , 2014, 30, 1762-1764.	1.8	63
449	Whole genome phylogeny of <i>Prochlorococcus marinus</i> group of cyanobacteria: genome alignment and overlapping gene approach. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2014, 6, 149-157.	2.2	5
450	A unifying model of genome evolution under parsimony. <i>BMC Bioinformatics</i> , 2014, 15, 206.	1.2	8
451	Comparative genomics of <i>Bradyrhizobium japonicum</i> CPAC 15 and <i>Bradyrhizobium diazoefficiens</i> CPAC 7: elite model strains for understanding symbiotic performance with soybean. <i>BMC Genomics</i> , 2014, 15, 420.	1.2	71

#	ARTICLE	IF	CITATIONS
452	Whole-genome sequencing of <i>Mesorhizobium huakuii</i> 7653R provides molecular insights into host specificity and symbiosis island dynamics. <i>BMC Genomics</i> , 2014, 15, 440.	1.2	52
453	<i>Stenotrophomonas</i> comparative genomics reveals genes and functions that differentiate beneficial and pathogenic bacteria. <i>BMC Genomics</i> , 2014, 15, 482.	1.2	90
454	Genome sequencing of two <i>Neorhizobium galegae</i> strains reveals a <i>noeT</i> gene responsible for the unusual acetylation of the nodulation factors. <i>BMC Genomics</i> , 2014, 15, 500.	1.2	30
455	Genome sequences characterizing five mutations in RNA polymerase and major capsid of phages $\phi$ A318 and $\phi$ As51 of <i>Vibrio alginolyticus</i> with different burst efficiencies. <i>BMC Genomics</i> , 2014, 15, 505.	1.2	18
456	Comparative genomics of methicillin-resistant <i>Staphylococcus aureus</i> ST239: distinct geographical variants in Beijing and Hong Kong. <i>BMC Genomics</i> , 2014, 15, 529.	1.2	40
457	Whole genome sequence comparison of <i>vtx2</i> -converting phages from Enteroaggregative Haemorrhagic <i>Escherichia coli</i> strains. <i>BMC Genomics</i> , 2014, 15, 574.	1.2	13
458	Comparative genomics of 274 <i>Vibrio cholerae</i> genomes reveals mobile functions structuring three niche dimensions. <i>BMC Genomics</i> , 2014, 15, 654.	1.2	24
459	Comparative genomics of koala, cattle and sheep strains of <i>Chlamydia pecorum</i> . <i>BMC Genomics</i> , 2014, 15, 667.	1.2	33
460	Revealing the Genetic Basis of Natural Bacterial Phenotypic Divergence. <i>Journal of Bacteriology</i> , 2014, 196, 825-839.	1.0	7
461	Analysis of novel <i>kitasatosporae</i> reveals significant evolutionary changes in conserved developmental genes between <i>Kitasatospora</i> and <i>Streptomyces</i> . <i>Antonie Van Leeuwenhoek</i> , 2014, 106, 365-380.	0.7	34
462	Sylvatic Plague in a Canadian Black-Tailed Prairie Dog ( <i>Cynomys ludovicianus</i> ). <i>Journal of Wildlife Diseases</i> , 2014, 50, 699-702.	0.3	11
463	Transmission of Methicillin-Resistant <i>Staphylococcus aureus</i> via Deceased Donor Liver Transplantation Confirmed by Whole Genome Sequencing. <i>American Journal of Transplantation</i> , 2014, 14, 2640-2644.	2.6	41
464	Draft Genome Comparison of Representatives of the Three Dominant Genotype Groups of Dairy <i>Bacillus licheniformis</i> Strains. <i>Applied and Environmental Microbiology</i> , 2014, 80, 3453-3462.	1.4	13
465	Virulence genes in clinical and environmental <i>Stenotrophomas maltophilia</i> isolates: A genome sequencing and gene expression approach. <i>Microbial Pathogenesis</i> , 2014, 67-68, 20-30.	1.3	34
466	The genomic landscape underlying phenotypic integrity in the face of gene flow in crows. <i>Science</i> , 2014, 344, 1410-1414.	6.0	490
467	Genomic differentiation among two strains of the PS1 clade isolated from geographically separated marine habitats. <i>FEMS Microbiology Ecology</i> , 2014, 89, 181-197.	1.3	22
468	The impact of genomic variability on gene expression in environmental <i>Saccharomyces cerevisiae</i> strains. <i>Environmental Microbiology</i> , 2014, 16, 1378-1397.	1.8	59
469	Population Dynamics of an <i>Acinetobacter baumannii</i> Clonal Complex during Colonization of Patients. <i>Journal of Clinical Microbiology</i> , 2014, 52, 3200-3208.	1.8	29

#	ARTICLE	IF	CITATIONS
470	Disproportional Plastome-Wide Increase of Substitution Rates and Relaxed Purifying Selection in Genes of Carnivorous Lentibulariaceae. <i>Molecular Biology and Evolution</i> , 2014, 31, 529-545.	3.5	92
471	Comparative Genomic Analysis of Malaria Mosquito Vector-Associated Novel Pathogen <i>Elizabethkingia anophelis</i> . <i>Genome Biology and Evolution</i> , 2014, 6, 1158-1165.	1.1	52
472	Insights on evolution of virulence and resistance from the whole-genome analysis of a predominant methicillin-resistant <i>Staphylococcus aureus</i> clone sequence type 239 in China. <i>Science Bulletin</i> , 2014, 59, 1104-1112.	1.7	7
473	Genome alignment with graph data structures: a comparison. <i>BMC Bioinformatics</i> , 2014, 15, 99.	1.2	32
474	Genomic characteristics and comparative genomics analysis of <i>Penicillium chrysogenum</i> KF-25. <i>BMC Genomics</i> , 2014, 15, 144.	1.2	14
475	A ddRAD-based genetic map and its integration with the genome assembly of Japanese eel ( <i>Anguilla</i> ) Tj ETQq1 1 0.784314 rgBT /Overl... <i>Genomics</i> , 2014, 15, 233.	1.2	63
476	Comparative genomics of the dairy isolate <i>Streptococcus macedonicus</i> ACA-DC 198 against related members of the <i>Streptococcus bovis</i> / <i>Streptococcus equinus</i> complex. <i>BMC Genomics</i> , 2014, 15, 272.	1.2	74
477	Plastid and mitochondrion genomic sequences from Arctic <i>Chlorella</i> sp. ArM0029B. <i>BMC Genomics</i> , 2014, 15, 286.	1.2	28
478	Comparative analysis of mitochondrial genomes between the hau cytoplasmic male sterility (CMS) line and its iso-nuclear maintainer line in <i>Brassica juncea</i> to reveal the origin of the CMS-associated gene orf288. <i>BMC Genomics</i> , 2014, 15, 322.	1.2	57
479	Genome analysis reveals three genomospecies in <i>Mycobacterium abscessus</i> . <i>BMC Genomics</i> , 2014, 15, 359.	1.2	79
480	Comparative genome analysis of pathogenic and non-pathogenic <i>Clavibacter</i> strains reveals adaptations to their lifestyle. <i>BMC Genomics</i> , 2014, 15, 392.	1.2	32
481	A high resolution map of mammalian X chromosome fragile regions assessed by large-scale comparative genomics. <i>Mammalian Genome</i> , 2014, 25, 618-635.	1.0	5
482	Abundant and Diverse Clustered Regularly Interspaced Short Palindromic Repeat Spacers in <i>Clostridium difficile</i> Strains and Prophages Target Multiple Phage Types within This Pathogen. <i>MBio</i> , 2014, 5, e01045-13.	1.8	67
483	Phylogenetic characterization of <i>Escherichia coli</i> O157:H7 based on IS629 distribution and Shiga toxin genotype. <i>Microbiology (United Kingdom)</i> , 2014, 160, 502-513.	0.7	32
484	Comparative proteomic analysis of <i>Clostridium difficile</i> isolates of varying virulence. <i>Journal of Medical Microbiology</i> , 2014, 63, 489-503.	0.7	26
485	Multidisciplinary Analysis of a Nontoxigenic <i>Clostridium difficile</i> Strain with Stable Resistance to Metronidazole. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 4957-4960.	1.4	42
486	Integrative Analysis of Salmonellosis in Israel Reveals Association of <i>Salmonella enterica</i> Serovar 9,12:l,v:~ with Extraintestinal Infections, Dissemination of Endemic <i>S. enterica</i> Serovar Typhimurium DT104 Biotypes, and Severe Underreporting of Outbreaks. <i>Journal of Clinical Microbiology</i> , 2014, 52, 2078-2088.	1.8	14
487	Serial Gene Losses and Foreign DNA Underlie Size and Sequence Variation in the Plastid Genomes of Diatoms. <i>Genome Biology and Evolution</i> , 2014, 6, 644-654.	1.1	72

#	ARTICLE	IF	CITATIONS
488	Genomic Technologies. , 2014, , 55-72.		3
489	Comparative Genomics of the Pine Pathogens and Beetle Symbionts in the Genus <i>Grosmannia</i> . <i>Molecular Biology and Evolution</i> , 2014, 31, 1454-1474.	3.5	9
490	Molecular Epidemiology of KPC-Producing <i>Escherichia coli</i> : Occurrence of ST131- <i>fimH30</i> Subclone Harboring pKpQIL-Like IncFIIk Plasmid. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 4234-4237.	1.4	36
491	Genomic and comparative genomic analyses of <i>Rickettsia heilongjiangensis</i> provide insight into its evolution and pathogenesis. <i>Infection, Genetics and Evolution</i> , 2014, 26, 274-282.	1.0	7
492	Identification of two allelic variants of <i>toxB</i> gene and investigation of their distribution among Verocytotoxin-producing <i>Escherichia coli</i> . <i>International Journal of Medical Microbiology</i> , 2014, 304, 730-734.	1.5	6
493	Four <i>Escherichia coli</i> O157:H7 Phages: A New Bacteriophage Genus and Taxonomic Classification of T1-Like Phages. <i>PLoS ONE</i> , 2014, 9, e100426.	1.1	55
494	Genomes of diverse isolates of the marine cyanobacterium <i>Prochlorococcus</i> . <i>Scientific Data</i> , 2014, 1, 140034.	2.4	114
495	Personal genome analysis: a tread towards personalised medicine. <i>International Journal of Functional Informatics and Personalised Medicine</i> , 2014, 4, 198.	0.4	0
496	Plasmid-Mediated Antibiotic Resistance and Virulence in Gram-Negatives: the <i>Klebsiella pneumoniae</i> Paradigm. <i>Microbiology Spectrum</i> , 2014, 2, 1-15.	1.2	93
497	Comparison of single-molecule sequencing and hybrid approaches for finishing the genome of <i>Clostridium autoethanogenum</i> and analysis of CRISPR systems in industrial relevant <i>Clostridia</i> . <i>Biotechnology for Biofuels</i> , 2014, 7, 40.	6.2	135
498	A comparison of the <i>Caulobacter</i> NA1000 and K31 genomes reveals extensive genome rearrangements and differences in metabolic potential. <i>Open Biology</i> , 2014, 4, 140128.	1.5	16
499	The Mitochondrial Genome of <i>Grateloupia taiwanensis</i> (Halymeniaceae, Rhodophyta) and Comparative Mitochondrial Genomics of Red Algae. <i>Biological Bulletin</i> , 2014, 227, 191-200.	0.7	11
500	Empirical Transition Probability Indexing Sparse-Coding Belief Propagation (ETPI-SCoBeP) Genome Sequence Alignment. <i>Cancer Informatics</i> , 2014, 13s1, CIN.S13887.	0.9	0
501	Draft Genome Sequence of Environmental <i>Vibrio cholerae</i> 2012EL-1759 with Similarities to the <i>V. cholerae</i> O1 Classical Biotype. <i>Genome Announcements</i> , 2014, 2, .	0.8	5
502	Draft genome sequence of <i>Gluconobacter thailandicus</i> NBRC 3257. <i>Standards in Genomic Sciences</i> , 2014, 9, 614-623.	1.5	12
503	Complete genome sequence of a plant associated bacterium <i>Bacillus amyloliquefaciens</i> subsp. <i>plantarum</i> UCMB5033. <i>Standards in Genomic Sciences</i> , 2014, 9, 718-725.	1.5	21
504	Genome Sequence of <i>Pseudomonas chlororaphis</i> Strain PA23. <i>Genome Announcements</i> , 2014, 2, .	0.8	16
505	Comparative genomics and metabolic profiling of the genus <i>Lysobacter</i> . <i>BMC Genomics</i> , 2015, 16, 991.	1.2	103

#	ARTICLE	IF	CITATIONS
506	Comparative genomics of <i>Pseudomonas syringae</i> pv. <i>syringae</i> strains B301D and <i>HS</i> 191 and insights into intrapathovar traits associated with plant pathogenesis. <i>MicrobiologyOpen</i> , 2015, 4, 553-573.	1.2	35
507	Plastid genome sequences of legumes reveal parallel inversions and multiple losses of <i>rps16</i> in papilionoids. <i>Journal of Systematics and Evolution</i> , 2015, 53, 458-468.	1.6	125
508	Multiplex Real-Time PCR Assay for the Detection and Differentiation of Poxviruses and Poxvirus Vectors. <i>Applied Biosafety</i> , 2015, 20, 192-200.	0.2	4
509	Characterization of Cichopeptins, New Phytotoxic Cyclic Lipodepsipeptides Produced by <i>Pseudomonas cichorii</i> SF1-54 and Their Role in Bacterial Midrib Rot Disease of Lettuce. <i>Molecular Plant-Microbe Interactions</i> , 2015, 28, 1009-1022.	1.4	35
510	Genomes of <i>Candidatus Liberibacter solanacearum</i> ™ Haplotype A from New Zealand and the United States Suggest Significant Genome Plasticity in the Species. <i>Phytopathology</i> , 2015, 105, 863-871.	1.1	35
511	Genomic insights into the TTSS island of enteropathogenic <i>E. coli</i> and <i>Salmonella</i> and its conjugational transfer. <i>Molecular Genetics, Microbiology and Virology</i> , 2015, 30, 225-232.	0.0	0
512	Genomic and transcriptomic insights into the efficient entomopathogenicity of <i>Bacillus thuringiensis</i> . <i>Scientific Reports</i> , 2015, 5, 14129.	1.6	33
513	Comparative genomics and genome biology of invasive <i>Campylobacter jejuni</i> . <i>Scientific Reports</i> , 2015, 5, 17300.	1.6	18
514	Donkey genome and insight into the imprinting of fast karyotype evolution. <i>Scientific Reports</i> , 2015, 5, 14106.	1.6	29
515	In Silico Scrutiny of Genes Revealing Phylogenetic Congruence with Clinical Prevalence or Tropism Properties of <i>Chlamydia trachomatis</i> Strains. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 9-19.	0.8	14
516	Pan-Tetris: an interactive visualisation for Pan-genomes. <i>BMC Bioinformatics</i> , 2015, 16, S3.	1.2	22
517	Allelic variation contributes to bacterial host specificity. <i>Nature Communications</i> , 2015, 6, 8754.	5.8	100
518	An alignment-free method to find and visualise rearrangements between pairs of DNA sequences. <i>Scientific Reports</i> , 2015, 5, 10203.	1.6	27
519	Complete Genome Sequence of <i>Corynebacterium pseudotuberculosis</i> Strain E19, Isolated from a Horse in Chile. <i>Genome Announcements</i> , 2015, 3, .	0.8	3
520	<i>Escherichia coli</i> O157:H7 strains harbor at least three distinct sequence types of Shiga toxin 2a-converting phages. <i>BMC Genomics</i> , 2015, 16, 733.	1.2	47
521	Genome expansion in bacteria: the curious case of <i>Chlamydia trachomatis</i> . <i>BMC Research Notes</i> , 2015, 8, 512.	0.6	3
522	Split-alignment of genomes finds orthologies more accurately. <i>Genome Biology</i> , 2015, 16, 106.	3.8	85
523	Genomics and transcriptomics of <i>Xanthomonas campestris</i> species challenge the concept of core type III effectome. <i>BMC Genomics</i> , 2015, 16, 975.	1.2	62



#	ARTICLE	IF	CITATIONS
524	The pan-genome of <i>Lactobacillus reuteri</i> strains originating from the pig gastrointestinal tract. <i>BMC Genomics</i> , 2015, 16, 1023.	1.2	64
525	Draft genome sequence of <i>Methylibium</i> sp. strain T29, a novel fuel oxygenate-degrading bacterial isolate from Hungary. <i>Standards in Genomic Sciences</i> , 2015, 10, 39.	1.5	9
526	High quality draft genomic sequence of <i>Arenimonas donghaensis</i> DSM 18148T. <i>Standards in Genomic Sciences</i> , 2015, 10, 59.	1.5	6
527	Working draft genome sequence of the mesophilic acetate oxidizing bacterium <i>Syntrophaceticus schinkii</i> strain Sp3. <i>Standards in Genomic Sciences</i> , 2015, 10, 99.	1.5	19
528	Complete genome sequence of <i>Staphylococcus aureus</i> , strain LLRI_Eymole1/1, isolated from a Kenyan dromedary camel. <i>Standards in Genomic Sciences</i> , 2015, 10, 109.	1.5	16
529	Inventory of the <sc>GH</sc>70 enzymes encoded by <i>Leuconostoc</i> <sc>NRRL</sc> Bâ€299 â€ identification of three novel Î±â€transglucosylases. <i>FEBS Journal</i> , 2015, 282, 2115-2130.	2.2	49
530	Draft Genome Sequence of <i>Burkholderia cordobensis</i> Type Strain LMG 27620, Isolated from Agricultural Soils in Argentina. <i>Genome Announcements</i> , 2015, 3, .	0.8	0
531	Draft Genome Sequence of <i>Pedobacter</i> sp. Strain Hv1, an Isolate from Medicinal Leech Mucosal Castings. <i>Genome Announcements</i> , 2015, 3, .	0.8	0
532	Draft genome sequence and characterization of <i>Desulfitobacterium hafniense</i> PCE-S. <i>Standards in Genomic Sciences</i> , 2015, 10, 15.	1.5	25
533	Massive horizontal gene transfer, strictly vertical inheritance and ancient duplications differentially shape the evolution of <i>Bacillus cereus</i> enterotoxin operons hbl, cytK and nhe. <i>BMC Evolutionary Biology</i> , 2015, 15, 246.	3.2	97
534	Genetic diversity in the plasticity zone and the presence of the chlamydial plasmid differentiates <i>Chlamydia pecorum</i> strains from pigs, sheep, cattle, and koalas. <i>BMC Genomics</i> , 2015, 16, 893.	1.2	40
535	Phylogenetic analysis of human <i>Chlamydia pneumoniae</i> strains reveals a distinct Australian indigenous clade that predates European exploration of the continent. <i>BMC Genomics</i> , 2015, 16, 1094.	1.2	5
536	Comparative genome analysis of <i>Weissella ceti</i> , an emerging pathogen of farm-raised rainbow trout. <i>BMC Genomics</i> , 2015, 16, 1095.	1.2	12
537	Pan-genomic analysis to redefine species and subspecies based on quantum discontinuous variation: the <i>Klebsiella</i> paradigm. <i>Biology Direct</i> , 2015, 10, 55.	1.9	33
538	Identification of putative adhesins of <i>Actinobacillus suis</i> and their homologues in other members of the family Pasteurellaceae. <i>BMC Research Notes</i> , 2015, 8, 675.	0.6	12
539	A viability-linked metagenomic analysis of cleanroom environments: eukarya, prokaryotes, and viruses. <i>Microbiome</i> , 2015, 3, 62.	4.9	56
540	Draft genome sequence of â€ <i>Treponema phagedenis</i> â€™ strain V1, isolated from bovine digital dermatitis. <i>Standards in Genomic Sciences</i> , 2015, 10, 67.	1.5	6
541	Complete genome sequences of <i>Geobacillus</i> sp. Y412MC52, a xylan-degrading strain isolated from obsidian hot spring in Yellowstone National Park. <i>Standards in Genomic Sciences</i> , 2015, 10, 81.	1.5	12

#	ARTICLE	IF	CITATIONS
542	Complete Genome Sequence of the Acetogenic Bacterium <i>Moorella thermoacetica</i> DSM 2955 <sup>T</sup>. <i>Genome Announcements</i> , 2015, 3, .	0.8	21
543	Where did all the trees come from? A novel multispecies approach reveals the impacts of biogeographical history and functional diversity on rain forest assembly. <i>Journal of Biogeography</i> , 2015, 42, 2172-2186.	1.4	30
544	Complete Genome Sequence of the Type Strain of the Acetogenic Bacterium <i>Moorella thermoacetica</i> DSM 521 <sup>T</sup>. <i>Genome Announcements</i> , 2015, 3, .	0.8	25
545	Two types of genetic carrier, the <scp>IncP</scp> genomic island and the novel <scp>IncP</scp>- $\alpha$ 1 <sup>2</sup> plasmid, for the <i>aac(2)- $\alphacidovorax avenae ssp. <i>avenae</i>. Molecular Plant Pathology, 2015, 16, 288-300.$	2.0	10
546	Genomic analysis of a nontoxigenic, invasive <i>Corynebacterium diphtheriae</i> strain from Brazil. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2015, 110, 817-819.	0.8	3
547	Molecular Variation and Horizontal Gene Transfer of the Homocysteine Methyltransferase Gene <i>mmuM</i> and its Distribution in Clinical Pathogens. <i>International Journal of Biological Sciences</i> , 2015, 11, 11-21.	2.6	7
548	Characterization of enteropathogenic and Shiga toxin-producing <i>Escherichia coli</i> in cattle and deer in a shared agroecosystem. <i>Frontiers in Cellular and Infection Microbiology</i> , 2015, 5, 29.	1.8	43
549	Whole genome sequencing of extended-spectrum $\beta$ -lactamase producing <i>Klebsiella pneumoniae</i> isolated from a patient in Lebanon. <i>Frontiers in Cellular and Infection Microbiology</i> , 2015, 5, 32.	1.8	20
550	Combining genomic sequencing methods to explore viral diversity and reveal potential virus-host interactions. <i>Frontiers in Microbiology</i> , 2015, 6, 265.	1.5	72
551	Genomes of sequence type 121 <i>Listeria monocytogenes</i> strains harbor highly conserved plasmids and prophages. <i>Frontiers in Microbiology</i> , 2015, 6, 380.	1.5	87
552	Characterization of a CTX-M-15 Producing <i>Klebsiella Pneumoniae</i> Outbreak Strain Assigned to a Novel Sequence Type (1427). <i>Frontiers in Microbiology</i> , 2015, 6, 1250.	1.5	52
553	Comparative Genomic Insights into Ecophysiology of Neutrophilic, Microaerophilic Iron Oxidizing Bacteria. <i>Frontiers in Microbiology</i> , 2015, 6, 1265.	1.5	78
554	Pan-Genome Analysis of Brazilian Lineage A Amoebal Mimiviruses. <i>Viruses</i> , 2015, 7, 3483-3499.	1.5	26
555	Complete Genome Sequence of <i>Borrelia afzelii</i> K78 and Comparative Genome Analysis. <i>PLoS ONE</i> , 2015, 10, e0120548.	1.1	16
556	Identification of New Genomespecies in the <i>Mycobacterium terrae</i> Complex. <i>PLoS ONE</i> , 2015, 10, e0120789.	1.1	10
557	Comparative Genome Analyses of <i>Serratia marcescens</i> FS14 Reveals Its High Antagonistic Potential. <i>PLoS ONE</i> , 2015, 10, e0123061.	1.1	51
558	<i>Francisella tularensis</i> Subtype A.II Genomic Plasticity in Comparison with Subtype A.I. <i>PLoS ONE</i> , 2015, 10, e0124906.	1.1	8
559	Genomic Comparison of the Closely-Related <i>Salmonella enterica</i> Serovars Enteritidis, Dublin and Gallinarum. <i>PLoS ONE</i> , 2015, 10, e0126883.	1.1	39



#	ARTICLE	IF	CITATIONS
560	Complete Chloroplast Genome of the Wollemi Pine ( <i>Wollemia nobilis</i> ): Structure and Evolution. PLoS ONE, 2015, 10, e0128126.	1.1	29
561	Genomic Comparison of Non-Typhoidal <i>Salmonella enterica</i> Serovars Typhimurium, Enteritidis, Heidelberg, Hadar and Kentucky Isolates from Broiler Chickens. PLoS ONE, 2015, 10, e0128773.	1.1	53
562	Discovery of Novel ncRNA Sequences in Multiple Genome Alignments on the Basis of Conserved and Stable Secondary Structures. PLoS ONE, 2015, 10, e0130200.	1.1	26
563	Comparative Genomic Analysis of Asian Haemorrhagic Septicaemia-Associated Strains of <i>Pasteurella multocida</i> Identifies More than 90 Haemorrhagic Septicaemia-Specific Genes. PLoS ONE, 2015, 10, e0130296.	1.1	45
564	Patterns of MHC-G-Like and MHC-B Diversification in New World Monkeys. PLoS ONE, 2015, 10, e0131343.	1.1	5
565	Bioinformatic Analysis of <i>Chlamydia trachomatis</i> Polymorphic Membrane Proteins PmpE, PmpF, PmpG and PmpH as Potential Vaccine Antigens. PLoS ONE, 2015, 10, e0131695.	1.1	13
566	The Origin and Evolution of Baeyer-Villiger Monooxygenases (BVMOs): An Ancestral Family of Flavin Monooxygenases. PLoS ONE, 2015, 10, e0132689.	1.1	42
567	Genomic and Phenomic Study of Mammary Pathogenic <i>Escherichia coli</i> . PLoS ONE, 2015, 10, e0136387.	1.1	46
568	Intraspecies Genomic Diversity and Long-Term Persistence of <i>Bifidobacterium longum</i> . PLoS ONE, 2015, 10, e0135658.	1.1	46
569	TAL effectors and activation of predicted host targets distinguish Asian from African strains of the rice pathogen <i>Xanthomonas oryzae</i> pv. <i>oryzicola</i> while strict conservation suggests universal importance of five TAL effectors. <i>Frontiers in Plant Science</i> , 2015, 6, 536.	1.7	105
570	Comparative genomic analysis of duplicated homoeologous regions involved in the resistance of <i>Brassica napus</i> to stem canker. <i>Frontiers in Plant Science</i> , 2015, 6, 772.	1.7	38
571	An Effective Big Data Supervised Imbalanced Classification Approach for Ortholog Detection in Related Yeast Species. <i>BioMed Research International</i> , 2015, 2015, 1-12.	0.9	17
572	<i>De Novo</i> Sequences of <i>Haloquadratum walsbyi</i> from Lake Tyrrell, Australia, Reveal a Variable Genomic Landscape. <i>Archaea</i> , 2015, 2015, 1-12.	2.3	26
573	Analysis of horse genomes provides insight into the diversification and adaptive evolution of karyotype. <i>Scientific Reports</i> , 2014, 4, 4958.	1.6	108
574	Metagenome sequence of <i>Elaphomyces granulatus</i> from sporocarp tissue reveals Ascomycota ectomycorrhizal fingerprints of genome expansion and a Proteobacteria-rich microbiome. <i>Environmental Microbiology</i> , 2015, 17, 2952-2968.	1.8	34
575	Draft Genome Sequence of <i>Acinetobacter oleivorans</i> PF1, a Diesel-Degrading and Plant-Growth-Promoting Endophytic Strain Isolated from Poplar Trees Growing on a Diesel-Contaminated Plume. <i>Genome Announcements</i> , 2015, 3, .	0.8	7
576	<i>Acinetobacter calcoaceticus</i> from a fatal case of pneumonia harboring blaNDM-1 on a widely distributed plasmid. <i>BMC Infectious Diseases</i> , 2015, 15, 131.	1.3	33
577	Recent Origin of the Methacrylate Redox System in <i>Geobacter sulfurreducens</i> AM-1 through Horizontal Gene Transfer. PLoS ONE, 2015, 10, e0125888.	1.1	5

#	ARTICLE	IF	CITATIONS
578	Complete Genome Sequence of a Porcine Epidemic Diarrhea S Gene Indel Strain Isolated in France in December 2014. <i>Genome Announcements</i> , 2015, 3, .	0.8	66
579	Comparative Analysis of Denitrifying Activities of <i>Hyphomicrobium nitrativorans</i> , <i>Hyphomicrobium denitrificans</i> , and <i>Hyphomicrobium zavarzinii</i> . <i>Applied and Environmental Microbiology</i> , 2015, 81, 5003-5014.	1.4	114
580	Fungal metabolic gene clusters—caravans traveling across genomes and environments. <i>Frontiers in Microbiology</i> , 2015, 6, 161.	1.5	136
581	Analysis of yeh Fimbrial Gene Cluster in <i>Escherichia coli</i> O157:H7 in Order to Find a Genetic Marker for this Serotype. <i>Current Microbiology</i> , 2015, 71, 274-282.	1.0	21
582	Complete genome sequence of endophytic nitrogen-fixing <i>Klebsiella variicola</i> strain DX120E. <i>Standards in Genomic Sciences</i> , 2015, 10, 22.	1.5	66
583	Genomic and phenotypic analyses of <i>Carnobacterium jeotgali</i> strain MS3T, a lactate-producing candidate biopreservative bacterium isolated from salt-fermented shrimp. <i>FEMS Microbiology Letters</i> , 2015, 362, .	0.7	3
584	Whole-Genome Sequencing of Kaposi's Sarcoma-Associated Herpesvirus from Zambian Kaposi's Sarcoma Biopsy Specimens Reveals Unique Viral Diversity. <i>Journal of Virology</i> , 2015, 89, 12299-12308.	1.5	41
585	Comprehensive insights in the <i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> genome using new WGS data of sheep strain JIII-386 from Germany. <i>Genome Biology and Evolution</i> , 2015, 7, evv154.	1.1	31
586	Comparative Genomics of Sibling Fungal Pathogenic Taxa Identifies Adaptive Evolution without Divergence in Pathogenicity Genes or Genomic Structure. <i>Genome Biology and Evolution</i> , 2015, 7, 3190-3206.	1.1	32
587	Breaking the computational barriers of pairwise genome comparison. <i>BMC Bioinformatics</i> , 2015, 16, 250.	1.2	16
588	Multiple Conserved Heteroplasmic Sites in tRNA Genes in the Mitochondrial Genomes of Terrestrial Isopods (Oniscidea). <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1317-1322.	0.8	13
589	Genome sequence of <i>Clostridium sporogenes</i> DSM 795T, an amino acid-degrading, nontoxic surrogate of neurotoxin-producing <i>Clostridium botulinum</i> . <i>Standards in Genomic Sciences</i> , 2015, 10, 40.	1.5	13
590	As Clear as Mud? Determining the Diversity and Prevalence of Prophages in the Draft Genomes of Estuarine Isolates of <i>Clostridium difficile</i> . <i>Genome Biology and Evolution</i> , 2015, 7, 1842-1855.	1.1	20
591	Dynamic Evolution of the Chloroplast Genome in the Green Algal Classes <i>Pedinophyceae</i> and <i>Trebouxiophyceae</i> . <i>Genome Biology and Evolution</i> , 2015, 7, 2062-2082.	1.1	72
592	Moss phylogeny reconstruction using nucleotide pangenome of complete Mitogenome sequences. <i>Biochemistry (Moscow)</i> , 2015, 80, 1522-1527.	0.7	4
593	Complete Genome Sequence of <i>Francisella guangzhouensis</i> Strain 08HL01032 <sup>T</sup> , Isolated from Air-Conditioning Systems in China. <i>Genome Announcements</i> , 2015, 3, .	0.8	6
594	Whole-Genome Sequencing of a Pandoravirus Isolated from Keratitis-Inducing <i>Acanthamoeba</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	63
595	Complete Genome Sequences of Two Strains of <i>Candidatus</i> <i>Filomicrobium marinum</i> , a Methanesulfonate-Degrading Species. <i>Genome Announcements</i> , 2015, 3, .	0.8	13

#	ARTICLE	IF	CITATIONS
596	Draft Genome Sequence of Erythromycin-Resistant <i>Streptococcus gallolyticus</i> subsp. <i>gallolyticus</i> NTS 31106099 Isolated from a Patient with Infective Endocarditis and Colorectal Cancer. <i>Genome Announcements</i> , 2015, 3, .	0.8	5
597	Draft Genome Sequence of a Highly Virulent Rabbit <i>Staphylococcus aureus</i> Strain. <i>Genome Announcements</i> , 2015, 3, .	0.8	3
598	Draft Genome Sequence of <i>Mycobacterium chelonae</i> Type Strain ATCC 35752. <i>Genome Announcements</i> , 2015, 3, .	0.8	5
599	Draft Genome Sequences of <i>Bacillus anthracis</i> Strains Stored for Several Decades in Japan. <i>Genome Announcements</i> , 2015, 3, .	0.8	6
600	Draft Genome Sequence of <i>Lactobacillus</i> sp. Strain TCF032-E4, Isolated from Fermented Radish. <i>Genome Announcements</i> , 2015, 3, .	0.8	1
601	Draft Genome Sequence of <i>Streptomyces</i> sp. Strain Wb2n-11, a Desert Isolate with Broad-Spectrum Antagonism against Soilborne Phytopathogens. <i>Genome Announcements</i> , 2015, 3, .	0.8	14
602	Draft Genome Sequences of <i>Mycobacterium setense</i> Type Strain DSM-45070 and the Nonpathogenic Strain <i>Manresensis</i> , Isolated from the Bank of the Cardener River in Manresa, Catalonia, Spain. <i>Genome Announcements</i> , 2015, 3, .	0.8	11
603	Complete Genome Sequence of the Nitrogen-Fixing and Solvent-Producing <i>Clostridium pasteurianum</i> DSM 525. <i>Genome Announcements</i> , 2015, 3, .	0.8	20
604	A Novel Member of <i>Chitinophagaceae</i> Isolated from a Human Peritoneal Tumor. <i>Genome Announcements</i> , 2015, 3, .	0.8	6
605	Comparative genome analysis of <i>Lysinibacillus</i> B1-CDA, a bacterium that accumulates arsenic. <i>Genomics</i> , 2015, 106, 384-392.	1.3	17
606	<i>Chlamydiaceae</i> Genomics Reveals Interspecies Admixture and the Recent Evolution of <i>Chlamydia abortus</i> Infecting Lower Mammalian Species and Humans. <i>Genome Biology and Evolution</i> , 2015, 7, 3070-3084.	1.1	30
607	The bacterial pangenome as a new tool for analysing pathogenic bacteria. <i>New Microbes and New Infections</i> , 2015, 7, 72-85.	0.8	241
608	Computational Synteny Block: A framework to identify evolutionary events. , 2015, , .		0
609	The complete genome, structural proteome, comparative genomics and phylogenetic analysis of a broad host lytic bacteriophage $\phi$ -D3 infecting pectinolytic <i>Dickeya</i> spp.. <i>Standards in Genomic Sciences</i> , 2015, 10, 68.	1.5	16
610	Understanding the virulence of the entero-aggregative <i>E. coli</i> O104:H4. <i>International Journal of Bioinformatics Research and Applications</i> , 2015, 11, 187.	0.1	1
611	Comparative genomic analysis of human <i>Chlamydia pneumoniae</i> isolates from respiratory, brain and cardiac tissues. <i>Genomics</i> , 2015, 106, 373-383.	1.3	23
612	Genomic Epidemiology of Hypervirulent Serogroup W, ST-11 <i>Neisseria meningitidis</i> . <i>EBioMedicine</i> , 2015, 2, 1447-1455.	2.7	51
613	Molecular Analysis of Asymptomatic Bacteriuria <i>Escherichia coli</i> Strain VR50 Reveals Adaptation to the Urinary Tract by Gene Acquisition. <i>Infection and Immunity</i> , 2015, 83, 1749-1764.	1.0	24

#	ARTICLE	IF	CITATIONS
614	A single natural nucleotide mutation alters bacterial pathogen host tropism. <i>Nature Genetics</i> , 2015, 47, 361-366.	9.4	106
615	Positive selection is the main driving force for evolution of citrus canker-causing <i>Xanthomonas</i> . <i>ISME Journal</i> , 2015, 9, 2128-2138.	4.4	35
616	ST2249-MRSA-III: a second major recombinant methicillin-resistant <i>Staphylococcus aureus</i> clone causing healthcare infection in the 1970s. <i>Clinical Microbiology and Infection</i> , 2015, 21, 444-450.	2.8	22
617	The mosaic genome structure and phylogeny of Shiga toxin-producing <i>Escherichia coli</i> O104:H4 is driven by short-term adaptation. <i>Clinical Microbiology and Infection</i> , 2015, 21, 468.e7-468.e18.	2.8	26
618	Genome-Wide Patterns of Recombination in the Opportunistic Human Pathogen <i>Pseudomonas aeruginosa</i> . <i>Genome Biology and Evolution</i> , 2015, 7, 18-34.	1.1	29
619	Molecular cloning, expression, and evolution analysis of type II CHI gene from peanut ( <i>Arachis</i> ) Tj ETQq1 1 0.784314 rgBT / Overlock 10	0.48	10
620	Recombination is a key driver of genomic and phenotypic diversity in a <i>Pseudomonas aeruginosa</i> population during cystic fibrosis infection. <i>Scientific Reports</i> , 2015, 5, 7649.	1.6	134
621	Aquifer environment selects for microbial species cohorts in sediment and groundwater. <i>ISME Journal</i> , 2015, 9, 1846-1856.	4.4	88
622	Analysis of a long-term outbreak of XDR <i>Pseudomonas aeruginosa</i> : a molecular epidemiological study. <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, 1322-1330.	1.3	46
623	Genomic Diversification in Strains of <i>Rickettsia felis</i> Isolated from Different Arthropods. <i>Genome Biology and Evolution</i> , 2015, 7, 35-56.	1.1	66
624	Genome Sequence and Phenotypic Characterization of <i>Caulobacter segnis</i> . <i>Current Microbiology</i> , 2015, 70, 355-363.	1.0	13
625	Genomic and phenotypic differentiation among <i>Methanosarcina mazei</i> populations from Columbia River sediment. <i>ISME Journal</i> , 2015, 9, 2191-2205.	4.4	42
626	Two Phages, phiPLA-RODI and phiPLA-C1C, Lyse Mono- and Dual-Species <i>Staphylococcal</i> Biofilms. <i>Applied and Environmental Microbiology</i> , 2015, 81, 3336-3348.	1.4	124
627	A proposed new bacteriophage subfamily: <i>Jerseyvirinae</i> . <i>Archives of Virology</i> , 2015, 160, 1021-1033.	0.9	22
628	A complete bacterial genome assembled de novo using only nanopore sequencing data. <i>Nature Methods</i> , 2015, 12, 733-735.	9.0	1,176
630	Identification of staphylococcal phage with reduced transcription in human blood through transcriptome sequencing. <i>Frontiers in Microbiology</i> , 2015, 6, 216.	1.5	4
631	Elucidation of the <i>Photobacterium aerophilum</i> Genome and Generation of a Transposon Mutant Library To Identify Motility Mutants Altered in Pathogenesis. <i>Journal of Bacteriology</i> , 2015, 197, 2201-2216.	1.0	10
632	Mutation Rate, Spectrum, Topology, and Context-Dependency in the DNA Mismatch Repair-Deficient <i>Pseudomonas fluorescens</i> ATCC948. <i>Genome Biology and Evolution</i> , 2015, 7, 262-271.	1.1	62

#	ARTICLE	IF	CITATIONS
633	Pyrobaculum yellowstonensis Strain WP30 Respires on Elemental Sulfur and/or Arsenate in Circumneutral Sulfidic Geothermal Sediments of Yellowstone National Park. Applied and Environmental Microbiology, 2015, 81, 5907-5916.	1.4	26
634	Tracking Nosocomial Klebsiella pneumoniae Infections and Outbreaks by Whole-Genome Analysis: Small-Scale Italian Scenario within a Single Hospital. Journal of Clinical Microbiology, 2015, 53, 2861-2868.	1.8	71
635	Accurate Whole-Genome Sequencing-Based Epidemiological Surveillance of Mycobacterium Tuberculosis. Methods in Microbiology, 2015, 42, 359-394.	0.4	6
636	Development and validation of an rDNA operon based primer walking strategy applicable to de novo bacterial genome finishing. Frontiers in Microbiology, 2014, 5, 769.	1.5	5
637	Insight into proteomic investigations of Neisseria meningitidis serogroup C strain L91543 from analysis of its genome sequence. FEMS Microbiology Letters, 2015, 362, .	0.7	6
638	In silico identification of AMPylating enzymes and study of their divergent evolution. Scientific Reports, 2015, 5, 10804.	1.6	32
639	Genome dynamics and evolution of Salmonella Typhi strains from the typhoid-endemic zones. Scientific Reports, 2015, 4, 7457.	1.6	19
640	Chaos of Rearrangements in the Mating-Type Chromosomes of the Anther-Smut Fungus <i>Microbotryum lychnidis-dioicae</i>. Genetics, 2015, 200, 1275-1284.	1.2	78
641	Worldwide Population Structure, Long-Term Demography, and Local Adaptation of <i>Helicobacter pylori</i>. Genetics, 2015, 200, 947-963.	1.2	65
642	Recombinant transfer in the basic genome of <i>Escherichia coli</i>. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 9070-9075.	3.3	77
643	Complete nucleotide sequence of phiCHU: a Luz24likevirus infecting Pseudomonas aeruginosa and displaying a unique host range. FEMS Microbiology Letters, 2015, 362, .	0.7	5
644	Using quantitative PCR with retrotransposon-based insertion polymorphisms as markers in sugarcane. Journal of Experimental Botany, 2015, 66, 4239-4250.	2.4	10
645	Coexistence of Heavy Metal and Antibiotic Resistance within a Novel Composite Staphylococcal Cassette Chromosome in a Staphylococcus haemolyticus Isolate from Bovine Mastitis Milk. Antimicrobial Agents and Chemotherapy, 2015, 59, 5788-5792.	1.4	27
646	Genomic reconnaissance of clinical isolates of emerging human pathogen Mycobacterium abscessus reveals high evolutionary potential. Scientific Reports, 2014, 4, 4061.	1.6	96
647	Complete genome sequence of BS49 and draft genome sequence of BS34A, Bacillus subtilis strains carrying Tn916. FEMS Microbiology Letters, 2015, 362, 1-4.	0.7	13
648	A novel salt-tolerant chitobiosidase discovered by genetic screening of a metagenomic library derived from chitin-amended agricultural soil. Applied Microbiology and Biotechnology, 2015, 99, 8199-8215.	1.7	20
649	Whole-Genome Sequence Analysis and Genome-Wide Virulence Gene Identification of Riemerella anatipestifer Strain Yb2. Applied and Environmental Microbiology, 2015, 81, 5093-5102.	1.4	35
650	Defining the Core Genome of Salmonella enterica Serovar Typhimurium for Genomic Surveillance and Epidemiological Typing. Journal of Clinical Microbiology, 2015, 53, 2530-2538.	1.8	29

#	ARTICLE	IF	CITATIONS
651	Evolution of tRNA Repertoires in <i>Bacillus</i> Inferred with OrthoAlign. <i>Molecular Biology and Evolution</i> , 2015, 32, 1643-1656.	3.5	16
652	Whole-Genome Sequencing Allows for Improved Identification of Persistent <i>Listeria monocytogenes</i> in Food-Associated Environments. <i>Applied and Environmental Microbiology</i> , 2015, 81, 6024-6037.	1.4	127
653	Progressive genomic convergence of two <i>Helicobacter pylori</i> strains during mixed infection of a patient with chronic gastritis. <i>Gut</i> , 2015, 64, 554-561.	6.1	47
654	Temperature Dependence of the Proteome Profile of the Psychrotolerant Pathogenic Food Spoiler <i>Bacillus weihenstephanensis</i> Type Strain WSBC 10204. <i>Journal of Proteome Research</i> , 2015, 14, 2169-2176.	1.8	12
655	Whole-Genome Sequencing of <i>Burkholderia pseudomallei</i> Isolates from an Unusual Melioidosis Case Identifies a Polyclonal Infection with the Same Multilocus Sequence Type. <i>Journal of Clinical Microbiology</i> , 2015, 53, 282-286.	1.8	32
656	Delineating Community Outbreaks of <i>Salmonella enterica</i> Serovar Typhimurium by Use of Whole-Genome Sequencing: Insights into Genomic Variability within an Outbreak. <i>Journal of Clinical Microbiology</i> , 2015, 53, 1063-1071.	1.8	76
657	Deep comparative genomics among <i>Chlamydia trachomatis</i> lymphogranuloma venereum isolates highlights genes potentially involved in pathoadaptation. <i>Infection, Genetics and Evolution</i> , 2015, 32, 74-88.	1.0	17
658	<i>Chlamydia psittaci</i> comparative genomics reveals intraspecies variations in the putative outer membrane and type III secretion system genes. <i>Microbiology (United Kingdom)</i> , 2015, 161, 1378-1391.	0.7	24
659	Complete Genome Sequence of <i>Bifidobacterium longum</i> GT15: Identification and Characterization of Unique and Global Regulatory Genes. <i>Microbial Ecology</i> , 2015, 70, 819-834.	1.4	19
660	Comparative Genome Analysis of <i>Lactobacillus casei</i> : Insights into Genomic Diversification for Niche Expansion. <i>Indian Journal of Microbiology</i> , 2015, 55, 102-107.	1.5	11
661	Comparison of mitochondrial genomes provides insights into intron dynamics and evolution in the caterpillar fungus <i>Cordyceps militaris</i> . <i>Fungal Genetics and Biology</i> , 2015, 77, 95-107.	0.9	86
662	Complete genome sequence of the <i>Clostridium difficile</i> laboratory strain 630 <sup>†</sup> erm reveals differences from strain 630, including translocation of the mobile element CTn5. <i>BMC Genomics</i> , 2015, 16, 31.	1.2	76
663	The genome sequence of <i>Pseudoplusia includens</i> single nucleopolyhedrovirus and an analysis of p26 gene evolution in the baculoviruses. <i>BMC Genomics</i> , 2015, 16, 127.	1.2	22
664	Comparative genomic analysis of a multiple antimicrobial resistant enterotoxigenic <i>E. coli</i> O157 lineage from Australian pigs. <i>BMC Genomics</i> , 2015, 16, 165.	1.2	34
665	The <i>Alternaria</i> genomes database: a comprehensive resource for a fungal genus comprised of saprophytes, plant pathogens, and allergenic species. <i>BMC Genomics</i> , 2015, 16, 239.	1.2	105
666	Whole-genome assembly of <i>Akkermansia muciniphila</i> sequenced directly from human stool. <i>Biology Direct</i> , 2015, 10, 5.	1.9	32
667	Measurably evolving pathogens in the genomic era. <i>Trends in Ecology and Evolution</i> , 2015, 30, 306-313.	4.2	241
668	Identification and Molecular Characterisation of a Novel Mu-Like Bacteriophage, SfMu, of <i>Shigella flexneri</i> . <i>PLoS ONE</i> , 2015, 10, e0124053.	1.1	19



#	ARTICLE	IF	CITATIONS
669	Complete genome sequence of <i>Bacillus pumilus</i> W3: A strain exhibiting high laccase activity. <i>Journal of Biotechnology</i> , 2015, 207, 8-9.	1.9	11
670	Draft Genome Sequence of <i>Pantoea</i> sp. Strain MBLJ3, Isolated in a Laboratory Environmental Control Study. <i>Genome Announcements</i> , 2015, 3, .	0.8	0
671	Differential Single Nucleotide Polymorphism-Based Analysis of an Outbreak Caused by <i>Salmonella enterica</i> Serovar Manhattan Reveals Epidemiological Details Missed by Standard Pulsed-Field Gel Electrophoresis. <i>Journal of Clinical Microbiology</i> , 2015, 53, 1227-1238.	1.8	19
672	Minimally destructive sampling of type specimens of <i>Pyropia</i> (Bangiales, Rhodophyta) recovers complete plastid and mitochondrial genomes. <i>Scientific Reports</i> , 2014, 4, 5113.	1.6	53
673	Complete Genome Sequences of T4-Like Bacteriophages RB3, RB5, RB6, RB7, RB9, RB10, RB27, RB33, RB55, RB59, and RB68. <i>Genome Announcements</i> , 2015, 3, .	0.8	11
674	The New Macrolide-Lincosamide-Streptogramin B Resistance Geneerm(45) Is Located within a Genomic Island in <i>Staphylococcus fleurettii</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 3578-3581.	1.4	29
675	Rapid phylogenetic analysis of large samples of recombinant bacterial whole genome sequences using Gubbins. <i>Nucleic Acids Research</i> , 2015, 43, e15-e15.	6.5	1,834
676	Recent and Massive Expansion of the Mating-Type-Specific Region in the Smut Fungus <i>Microbotryum</i> . <i>Genetics</i> , 2015, 199, 809-816.	1.2	18
677	A <i>Coxiella</i> -Like Endosymbiont Is a Potential Vitamin Source for the Lone Star Tick. <i>Genome Biology and Evolution</i> , 2015, 7, 831-838.	1.1	204
678	Comparative genomic analysis of coffee-infecting <i>Xylella fastidiosa</i> strains isolated from Brazil. <i>Microbiology (United Kingdom)</i> , 2015, 161, 1018-1033.	0.7	9
679	<i>Streptococcus gallolyticus</i> subsp. <i>gallolyticus</i> from Human and Animal Origins: Genetic Diversity, Antimicrobial Susceptibility, and Characterization of a Vancomycin-Resistant Calf Isolate Carrying a <i>vanA</i> -Tn <sub>1546</sub> -Like Element. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 2006-2015.	1.4	15
680	M <sub>e</sub> D <sub>u</sub> S <sub>a</sub> : a multi-draft based scaffolder. <i>Bioinformatics</i> , 2015, 31, 2443-2451.	1.8	359
681	Transmission and Microevolution of USA300 MRSA in U.S. Households: Evidence from Whole-Genome Sequencing. <i>MBio</i> , 2015, 6, e00054.	1.8	97
682	A Genomic Virulence Reference Map of <i>Enterococcus faecalis</i> Reveals an Important Contribution of Phage03-Like Elements in Nosocomial Genetic Lineages to Pathogenicity in a <i>Caenorhabditis elegans</i> Infection Model. <i>Infection and Immunity</i> , 2015, 83, 2156-2167.	1.0	15
683	SRD: a <i>Staphylococcus</i> regulatory RNA database. <i>Rna</i> , 2015, 21, 1005-1017.	1.6	58
684	Matrix-Assisted Laser Desorption Ionization-“Time of Flight and Comparative Genomic Analysis of M-18 Group A <i>Streptococcus</i> Strains Associated with an Acute Rheumatic Fever Outbreak in Northeast Italy in 2012 and 2013. <i>Journal of Clinical Microbiology</i> , 2015, 53, 1562-1572.	1.8	7
685	Novel Type XII Staphylococcal Cassette Chromosome <i>mec</i> Harboring a New Cassette Chromosome Recombinase, CcrC2. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 7597-7601.	1.4	101
686	Comparative Genomics of a Plant-Parasitic Nematode Endosymbiont Suggest a Role in Nutritional Symbiosis. <i>Genome Biology and Evolution</i> , 2015, 7, 2727-2746.	1.1	42



#	ARTICLE	IF	CITATIONS
687	Approach for classification and taxonomy within family Rickettsiaceae based on the Formal Order Analysis. <i>Microbes and Infection</i> , 2015, 17, 839-844.	1.0	14
688	Functionally Structured Genomes in <i>Lactobacillus kunkeei</i> Colonizing the Honey Crop and Food Products of Honeybees and Stingless Bees. <i>Genome Biology and Evolution</i> , 2015, 7, 1455-1473.	1.1	50
689	Genetic determinants of in vivo fitness and diet responsiveness in multiple human gut <i>Bacteroides</i> . <i>Science</i> , 2015, 350, aac5992.	6.0	229
690	Identification of Recombination and Positively Selected Genes in <i>Brucella</i> . <i>Indian Journal of Microbiology</i> , 2015, 55, 384-391.	1.5	8
691	Genomic analyses of pneumococci reveal a wide diversity of bacteriocins including pneumocyclin, a novel circular bacteriocin. <i>BMC Genomics</i> , 2015, 16, 554.	1.2	67
692	Construction of a virtual <i>Mycobacterium tuberculosis</i> consensus genome and its application to data from a next generation sequencer. <i>BMC Genomics</i> , 2015, 16, 218.	1.2	8
693	Comparative genome analysis of <i>Mycoplasma pneumoniae</i> . <i>BMC Genomics</i> , 2015, 16, 610.	1.2	59
694	Survey of clustered regularly interspaced short palindromic repeats and their associated Cas proteins (CRISPR/Cas) systems in multiple sequenced strains of <i>Klebsiella pneumoniae</i> . <i>BMC Research Notes</i> , 2015, 8, 332.	0.6	37
695	Molecular mapping of the hybrid necrosis gene <i>NetJingY176</i> in <i>Aegilops tauschii</i> using microsatellite markers. <i>Crop Journal</i> , 2015, 3, 298-304.	2.3	3
696	Identifying new sex-linked genes through BAC sequencing in the dioecious plant <i>Silene latifolia</i> . <i>BMC Genomics</i> , 2015, 16, 546.	1.2	22
697	Genome sequence and comparative analysis of a putative entomopathogenic <i>Serratia</i> isolated from <i>Caenorhabditis briggsae</i> . <i>BMC Genomics</i> , 2015, 16, 531.	1.2	27
698	Mapping the Evolution of Hypervirulent <i>Klebsiella pneumoniae</i> . <i>MBio</i> , 2015, 6, e00630.	1.8	270
699	Isolation and characterization of a crude oil degrading bacteria from formation water: comparative genomic analysis of environmental <i>Ochrobactrum intermedium</i> isolate versus clinical strains. <i>Journal of Zhejiang University: Science B</i> , 2015, 16, 865-874.	1.3	15
700	Genomic comparison between pathogenic <i>Streptococcus agalactiae</i> isolated from Nile tilapia in Thailand and fish-derived ST7 strains. <i>Infection, Genetics and Evolution</i> , 2015, 36, 307-314.	1.0	18
701	YOC, A new strategy for pairwise alignment of collinear genomes. <i>BMC Bioinformatics</i> , 2015, 16, 111.	1.2	8
702	Unearthing the genomes of plant-beneficial <i>Pseudomonas</i> model strains WCS358, WCS374 and WCS417. <i>BMC Genomics</i> , 2015, 16, 539.	1.2	184
703	<i>Helicobacter pullorum</i> Isolated from Fresh Chicken Meat: Antibiotic Resistance and Genomic Traits of an Emerging Foodborne Pathogen. <i>Applied and Environmental Microbiology</i> , 2015, 81, 8155-8163.	1.4	32
704	The chloroplast genomes of <i>Bryopsis plumosa</i> and <i>Tydemania expeditiones</i> (Bryopsidales, Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	1.2	63

#	ARTICLE	IF	CITATIONS
705	The genome of the truffle-parasite <i>Tolyposcladium ophioglossoides</i> and the evolution of antifungal peptaibiotics. <i>BMC Genomics</i> , 2015, 16, 553.	1.2	46
706	Fitness Trade-Offs Determine the Role of the Molecular Chaperonin GroEL in Buffering Mutations. <i>Molecular Biology and Evolution</i> , 2015, 32, 2681-2693.	3.5	43
707	Genomic Variability of Serial Human Isolates of <i>Salmonella enterica</i> Serovar Typhimurium Associated with Prolonged Carriage. <i>Journal of Clinical Microbiology</i> , 2015, 53, 3507-3514.	1.8	23
708	Genomically Informed Surveillance for Carbapenem-Resistant Enterobacteriaceae in a Health Care System. <i>MBio</i> , 2015, 6, e01030.	1.8	90
709	A novel method of consensus pan-chromosome assembly and large-scale comparative analysis reveal the highly flexible pan-genome of <i>Acinetobacter baumannii</i> . <i>Genome Biology</i> , 2015, 16, 143.	13.9	122
710	A single nucleotide change in <i>mutY</i> increases the emergence of antibiotic-resistant <i>Campylobacter jejuni</i> mutants. <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, 2739-2748.	1.3	13
711	Genomic factors related to tissue tropism in <i>Chlamydia pneumoniae</i> infection. <i>BMC Genomics</i> , 2015, 16, 268.	1.2	13
712	Complete Genome Sequences of Two Outbreak Strains of <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Thompson Associated with Cilantro. <i>Genome Announcements</i> , 2015, 3, .	0.8	1
713	Whole genome sequence analysis of <i>Mycobacterium suricattae</i> . <i>Tuberculosis</i> , 2015, 95, 682-688.	0.8	52
714	Attenuation of monkeypox virus by deletion of genomic regions. <i>Virology</i> , 2015, 475, 129-138.	1.1	28
715	Evidence for extensive gene flow and <i>Thermotoga</i> subpopulations in subsurface and marine environments. <i>ISME Journal</i> , 2015, 9, 1532-1542.	4.4	36
716	Characterization of 17 strains belonging to the <i>Mycobacterium simiae</i> complex and description of <i>Mycobacterium paraense</i> sp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 656-662.	0.8	31
717	Integration of genomic and proteomic analyses in the classification of the Siphoviridae family. <i>Virology</i> , 2015, 477, 144-154.	1.1	52
718	Genomic Epidemiology of <i>Klebsiella pneumoniae</i> in Italy and Novel Insights into the Origin and Global Evolution of Its Resistance to Carbapenem Antibiotics. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 389-396.	1.4	97
719	Comparative genome analysis of <i>Pseudomonas knackmussii</i> B-13, the first bacterium known to degrade chloroaromatic compounds. <i>Environmental Microbiology</i> , 2015, 17, 91-104.	1.8	52
720	Comparison of Genome Sequencing Technology and Assembly Methods for the Analysis of a GC-Rich Bacterial Genome. <i>Current Microbiology</i> , 2015, 70, 338-344.	1.0	24
721	Patho-genetics of <i>Clostridium chauvoei</i> . <i>Research in Microbiology</i> , 2015, 166, 384-392.	1.0	37
722	Pan-Genome of <i>Brucella</i> Species. <i>Indian Journal of Microbiology</i> , 2015, 55, 88-101.	1.5	9

#	ARTICLE	IF	CITATIONS
723	Vancomycin-intermediate livestock-associated methicillin-resistant <i>Staphylococcus aureus</i> ST398/t9538 from swine in Brazil. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2016, 111, 659-661.	0.8	15
724	Draft Genome Sequence of Highly Rifampin-Resistant <i>Propionibacterium namnetense</i> NTS 31307302 Isolated from a Patient with a Bone Infection. <i>Genome Announcements</i> , 2016, 4, .	0.8	10
725	Comparative Genomics of Two Closely Related <i>Wolbachia</i> with Different Reproductive Effects on Hosts. <i>Genome Biology and Evolution</i> , 2016, 8, 1526-1542.	1.1	35
726	Pan-genome analysis of Senegalese and Gambian strains of <i>Bacillus anthracis</i> . <i>African Journal of Biotechnology</i> , 2016, 15, 2538-2546.	0.3	1
728	Hierarchical Map of Orthologous Genomic Regions Reconstructed from Two Closely Related Genomes: Cucumber Case Study. <i>Plant Genome</i> , 2016, 9, plantgenome2015.10.0099.	1.6	1
729	<i>Bordetella pertussis</i> Strain Lacking Pertactin and Pertussis Toxin. <i>Emerging Infectious Diseases</i> , 2016, 22, 319-322.	2.0	62
730	Complete Genome Sequence of <i>Bordetella pertussis</i> Strain VA-190 Isolated from a Vaccinated 10-Year-Old Patient with Whooping Cough. <i>Genome Announcements</i> , 2016, 4, .	0.8	0
731	Serotype IV Sequence Type 468 Group B <i>Streptococcus</i> Neonatal Invasive Disease, Minnesota, USA. <i>Emerging Infectious Diseases</i> , 2016, 22, 1937-1940.	2.0	6
732	Draft Genome Sequences of Four <i>Propionibacterium acnes</i> Strains Isolated from Implant-Related Infections. <i>Genome Announcements</i> , 2016, 4, .	0.8	5
733	Comparative genomic analysis of Brazilian <i>Leptospira kirschneri</i> serogroup Pomona serovar Mozdok. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2016, 111, 539-541.	0.8	3
734	Distribution of Suicin Gene Clusters in <i>Streptococcus suis</i> Serotype 2 Belonging to Sequence Types 25 and 28. <i>BioMed Research International</i> , 2016, 2016, 1-7.	0.9	6
735	Genomic Analysis of a Serotype 5 <i>Streptococcus pneumoniae</i> Outbreak in British Columbia, Canada, 2005–2009. <i>Canadian Journal of Infectious Diseases and Medical Microbiology</i> , 2016, 2016, 1-7.	0.7	6
736	Sister Dehalobacter Genomes Reveal Specialization in Organohalide Respiration and Recent Strain Differentiation Likely Driven by Chlorinated Substrates. <i>Frontiers in Microbiology</i> , 2016, 7, 100.	1.5	18
737	Genomics of Three New Bacteriophages Useful in the Biocontrol of <i>Salmonella</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 545.	1.5	48
738	Genome Structure of the Symbiont <i>Bifidobacterium pseudocatenulatum</i> CECT 7765 and Gene Expression Profiling in Response to Lactulose-Derived Oligosaccharides. <i>Frontiers in Microbiology</i> , 2016, 7, 624.	1.5	12
739	A Terpene Synthase Is Involved in the Synthesis of the Volatile Organic Compound Sodorifen of <i>Serratia plymuthica</i> 4Rx13. <i>Frontiers in Microbiology</i> , 2016, 7, 737.	1.5	29
740	Gene Loss and Horizontal Gene Transfer Contributed to the Genome Evolution of the Extreme Acidophile <i>Ferroplasma</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 797.	1.5	42
741	<i>Klebsiella pneumoniae</i> Asparagine tDNAs Are Integration Hotspots for Different Genomic Islands Encoding Microcin E492 Production Determinants and Other Putative Virulence Factors Present in Hypervirulent Strains. <i>Frontiers in Microbiology</i> , 2016, 7, 849.	1.5	40

#	ARTICLE	IF	CITATIONS
742	The Complete Sequences and Ecological Roles of Two IncP-1 <sup>+</sup> Plasmids, pHB44 and pBS64, Isolated from the Mycosphere of <i>Laccaria proxima</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 909.	1.5	5
743	Whole Genome Sequencing for Genomics-Guided Investigations of <i>Escherichia coli</i> O157:H7 Outbreaks. <i>Frontiers in Microbiology</i> , 2016, 7, 985.	1.5	70
744	Evolution and Diversity of <i>Listeria monocytogenes</i> from Clinical and Food Samples in Shanghai, China. <i>Frontiers in Microbiology</i> , 2016, 7, 1138.	1.5	26
745	<i>Leisingera</i> sp. JC1, a Bacterial Isolate from Hawaiian Bobtail Squid Eggs, Produces Indigoidine and Differentially Inhibits <i>Vibrios</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 1342.	1.5	70
746	Genome Sequencing and Comparative Genomics Analysis Revealed Pathogenic Potential in <i>Penicillium capsulatum</i> as a Novel Fungal Pathogen Belonging to Eurotiales. <i>Frontiers in Microbiology</i> , 2016, 7, 1541.	1.5	11
747	Comparative Analysis of Two <i>Helicobacter pylori</i> Strains using Genomics and Mass Spectrometry-Based Proteomics. <i>Frontiers in Microbiology</i> , 2016, 7, 1757.	1.5	10
748	Single-Molecule Sequencing (PacBio) of the <i>Staphylococcus capitis</i> NRCS-A Clone Reveals the Basis of Multidrug Resistance and Adaptation to the Neonatal Intensive Care Unit Environment. <i>Frontiers in Microbiology</i> , 2016, 7, 1991.	1.5	18
749	Evolution of Variable Number Tandem Repeats and Its Relationship with Genomic Diversity in <i>Salmonella</i> Typhimurium. <i>Frontiers in Microbiology</i> , 2016, 7, 2002.	1.5	8
750	Bioinformatic Analyses of Unique (Orphan) Core Genes of the Genus <i>Acidithiobacillus</i> : Functional Inferences and Use As Molecular Probes for Genomic and Metagenomic/Transcriptomic Interrogation. <i>Frontiers in Microbiology</i> , 2016, 7, 2035.	1.5	16
751	Molecular Genetic Characterization of an Anthrabenzoquinone Gene Cluster in <i>Streptomyces</i> Sp. FJS31-2 for the Biosynthesis of BE-24566B and Zunyimycin A. <i>Molecules</i> , 2016, 21, 711.	1.7	10
752	Genomic Recombination Leading to Decreased Virulence of Group B <i>Streptococcus</i> in a Mouse Model of Adult Invasive Disease. <i>Pathogens</i> , 2016, 5, 54.	1.2	7
753	H-NS Facilitates Sequence Diversification of Horizontally Transferred DNAs during Their Integration in Host Chromosomes. <i>PLoS Genetics</i> , 2016, 12, e1005796.	1.5	25
754	Plasmid Characterization and Chromosome Analysis of Two netF+ <i>Clostridium perfringens</i> Isolates Associated with Foal and Canine Necrotizing Enteritis. <i>PLoS ONE</i> , 2016, 11, e0148344.	1.1	32
755	Association of a Chromosomal Rearrangement Event with Mouse Posterior Polymorphous Corneal Dystrophy and Alterations in <i>Csrp2bp</i> , <i>Dzank1</i> , and <i>Ovol2</i> Gene Expression. <i>PLoS ONE</i> , 2016, 11, e0157577.	1.1	6
756	The First Complete Plastid Genome from Joinvilleaceae ( <i>J. ascendens</i> ; Poales) Shows Unique and Unpredicted Rearrangements. <i>PLoS ONE</i> , 2016, 11, e0163218.	1.1	12
757	Low Prevalence of Conjunctival Infection with <i>Chlamydia trachomatis</i> in a Treatment-Na <sup>-</sup> ve Trachoma-Endemic Region of the Solomon Islands. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004863.	1.3	42
758	Population Structure and Antimicrobial Resistance Profiles of <i>Streptococcus suis</i> Serotype 2 Sequence Type 25 Strains. <i>PLoS ONE</i> , 2016, 11, e0150908.	1.1	32
759	Mitochondrial Genome Analysis of Wild Rice ( <i>Oryza minuta</i> ) and Its Comparison with Other Related Species. <i>PLoS ONE</i> , 2016, 11, e0152937.	1.1	31

#	ARTICLE	IF	CITATIONS
760	Shallow Whole Genome Sequencing for the Assembly of Complete Chloroplast Genome Sequence of <i>Arachis hypogaea</i> L. <i>Frontiers in Plant Science</i> , 2016, 7, 1106.	1.7	13
761	Acquired resistance to innate immune clearance promotes <i>Klebsiella pneumoniae</i> ST258 pulmonary infection. <i>JCI Insight</i> , 2016, 1, e89704.	2.3	52
762	Large-scale maps of variable infection efficiencies in aquatic <i>Bacteroidetes</i> phage-host model systems. <i>Environmental Microbiology</i> , 2016, 18, 3949-3961.	1.8	22
763	Population genomics of the symbiotic plasmids of sympatric nitrogen-fixing <i>Rhizobium</i> species associated with <i>Phaseolus vulgaris</i> . <i>Environmental Microbiology</i> , 2016, 18, 2660-2676.	1.8	72
764	<i>Yersinia enterocolitica</i> -Specific Infection by Bacteriophages TG1 and R1-RT Is Dependent on Temperature-Regulated Expression of the Phage Host Receptor OmpF. <i>Applied and Environmental Microbiology</i> , 2016, 82, 5340-5353.	1.4	44
765	Computational Synteny Block: A Framework to Identify Evolutionary Events. <i>IEEE Transactions on Nanobioscience</i> , 2016, 15, 343-353.	2.2	4
766	Genome Sequence of <i>Listeria monocytogenes</i> Strain F6540 (Sequence Type 360) Collected from Food Samples in Ontario, Canada. <i>Genome Announcements</i> , 2016, 4, .	0.8	0
767	A Prophage-Encoded Small RNA Controls Metabolism and Cell Division in <i>Escherichia coli</i> . <i>MSystems</i> , 2016, 1, .	1.7	38
768	Novel viral genomes identified from six metagenomes reveal wide distribution of archaeal viruses and high viral diversity in terrestrial hot springs. <i>Environmental Microbiology</i> , 2016, 18, 863-874.	1.8	53
769	The microbiome of the leaf surface of <i>Arabidopsis</i> protects against a fungal pathogen. <i>New Phytologist</i> , 2016, 210, 1033-1043.	3.5	295
770	Draft Genome Sequences of Four <i>Enterococcus faecium</i> Strains Isolated from Argentine Cheese. <i>Genome Announcements</i> , 2016, 4, .	0.8	4
771	Detection of homologous recombination in closely related strains. <i>Journal of Bioinformatics and Computational Biology</i> , 2016, 14, 1641001.	0.3	1
772	Complete Genome Sequence of <i>Mycobacterium abscessus</i> subsp. <i>bolletii</i> . <i>Genome Announcements</i> , 2016, 4, .	0.8	5
773	The distribution, diversity and function of predominant <i>Thermoproteales</i> in high-temperature environments of Yellowstone National Park. <i>Environmental Microbiology</i> , 2016, 18, 4755-4769.	1.8	24
774	Bacterial sensing underlies artificial sweetener-induced growth of gut <i>Lactobacillus</i> . <i>Environmental Microbiology</i> , 2016, 18, 2159-2171.	1.8	27
775	Analysis of the core genome and pangenome of <i>Pseudomonas putida</i> . <i>Environmental Microbiology</i> , 2016, 18, 3268-3283.	1.8	65
776	Genomic resources for identification of the minimal <i>N<sub>2</sub></i> -fixing symbiotic genome. <i>Environmental Microbiology</i> , 2016, 18, 2534-2547.	1.8	36
777	Complete Genomic Sequence of an Avian Pathogenic <i>Escherichia coli</i> Strain of Serotype O7:HNT. <i>Genome Announcements</i> , 2016, 4, .	0.8	8

#	ARTICLE	IF	CITATIONS
778	Use of whole-genome sequencing to trace, control and characterize the regional expansion of extended-spectrum $\beta$ -lactamase producing ST15 <i>Klebsiella pneumoniae</i> . <i>Scientific Reports</i> , 2016, 6, 20840.	1.6	117
779	Trans-Atlantic exchanges have shaped the population structure of the Lyme disease agent <i>Borrelia burgdorferi sensu stricto</i> . <i>Scientific Reports</i> , 2016, 6, 22794.	1.6	22
780	Complete Genome Sequencing and Comparative Genomic Analysis of the Thermotolerant Acetic Acid Bacterium, <i>Acetobacter pasteurianus</i> SKU1108, Provide a New Insight into Thermotolerance. <i>Microbes and Environments</i> , 2016, 31, 395-400.	0.7	13
781	Complete genome sequence of <i>Pseudomonas citronellolis</i> P3B5, a candidate for microbial phyllo-remediation of hydrocarbon-contaminated sites. <i>Standards in Genomic Sciences</i> , 2016, 11, 75.	1.5	49
782	<i>Salmonella</i> Degrades the Host Glycocalyx Leading to Altered Infection and Glycan Remodeling. <i>Scientific Reports</i> , 2016, 6, 29525.	1.6	66
783	A survey of whole genome alignment tools and frameworks based on Hadoop's MapReduce. , 2016, , .		1
784	Adhesion of the genome-sequenced <i>Lactococcus lactis</i> subsp. <i>cremoris</i> IBB477 strain is mediated by specific molecular determinants. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 9605-9617.	1.7	22
785	Genomic evidence for plant-parasitic nematodes as the earliest <i>Wolbachia</i> hosts. <i>Scientific Reports</i> , 2016, 6, 34955.	1.6	54
786	An account of Genomic Islands of zoonotic origin <i>Staphylococcus aureus</i> genomes " In silico approach. , 2016, , .		0
787	Genome analysis of the kiwifruit canker pathogen <i>Pseudomonas syringae</i> pv. <i>actinidiae</i> biovar 5. <i>Scientific Reports</i> , 2016, 6, 21399.	1.6	95
788	Complete Genome Sequence of <i>Mycobacterium chimaera</i> Strain AH16. <i>Genome Announcements</i> , 2016, 4, .	0.8	11
789	Mitogenomes from type specimens, a genotyping tool for morphologically simple species: ten genomes of agar-producing red algae. <i>Scientific Reports</i> , 2016, 6, 35337.	1.6	41
790	Complete Genome Sequence of vB_EcoM-UFV13, a New Bacteriophage Able To Disrupt <i>Trueperella pyogenes</i> Biofilm. <i>Genome Announcements</i> , 2016, 4, .	0.8	5
791	Comparative genomic and functional analysis reveal conservation of plant growth promoting traits in <i>Paenibacillus polymyxa</i> and its closely related species. <i>Scientific Reports</i> , 2016, 6, 21329.	1.6	129
792	Evolution of mitosome metabolism and invasion-related proteins in <i>Cryptosporidium</i> . <i>BMC Genomics</i> , 2016, 17, 1006.	1.2	63
793	Mitochondrial genome sequences from wild and cultivated barley ( <i>Hordeum vulgare</i> ). <i>BMC Genomics</i> , 2016, 17, 824.	1.2	41
794	The evolutionary pathway of the staphylococcal cassette chromosome element. <i>Biologia (Poland)</i> , 2016, 71, 1195-1203.	0.8	10
795	Detection of linezolid resistance due to the <i>optrA</i> gene in <i>Enterococcus faecalis</i> from poultry meat from the American continent (Colombia). <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, dkw490.	1.3	61



#	ARTICLE	IF	CITATIONS
796	Recent Outbreaks of Shigellosis in California Caused by Two Distinct Populations of <i>Shigella sonnei</i> with either Increased Virulence or Fluoroquinolone Resistance. <i>MSphere</i> , 2016, 1, .	1.3	40
797	Comparative sequence analysis of <i>Cyclospora cayetanensis</i> apicoplast genomes originating from diverse geographical regions. <i>Parasites and Vectors</i> , 2016, 9, 611.	1.0	24
798	Clonal Complex 17 Group B <i>Streptococcus</i> strains causing invasive disease in neonates and adults originate from the same genetic pool. <i>Scientific Reports</i> , 2016, 6, 20047.	1.6	40
799	AnnoTALE: bioinformatics tools for identification, annotation and nomenclature of TALEs from <i>Xanthomonas</i> genomic sequences. <i>Scientific Reports</i> , 2016, 6, 21077.	1.6	119
800	Large-Scale Comparative Analysis Reveals the Mechanisms Driving Plastomic Compaction, Reduction, and Inversions in Conifers II (Cupressophytes). <i>Genome Biology and Evolution</i> , 2016, 8, evw278.	1.1	41
801	Comprehensive analysis of draft genomes of two closely related <i>Pseudomonas syringae</i> phylogroup 2b strains infecting mono- and dicotyledon host plants. <i>BMC Genomics</i> , 2016, 17, 1010.	1.2	8
802	Genomic approaches toward understanding the actinorhizal symbiosis: an update on the status of the Frankia genomes. <i>Symbiosis</i> , 2016, 70, 5-16.	1.2	57
803	Differences down-under: alcohol-fueled methanogenesis by archaea present in Australian macropodids. <i>ISME Journal</i> , 2016, 10, 2376-2388.	4.4	41
804	Plastid genomes reveal support for deep phylogenetic relationships and extensive rate variation among palms and other commelinid monocots. <i>New Phytologist</i> , 2016, 209, 855-870.	3.5	181
805	Comparative analyses of chloroplast genome data representing nine green algae in Sphaeropleales (Chlorophyceae, Chlorophyta). <i>Data in Brief</i> , 2016, 7, 558-570.	0.5	12
806	Genomic Signatures of Speciation in Sympatric and Allopatric Hawaiian Picture-Winged <i>Drosophila</i> . <i>Genome Biology and Evolution</i> , 2016, 8, 1482-1488.	1.1	21
807	Parallel Evolution in <i>Streptococcus pneumoniae</i> Biofilms. <i>Genome Biology and Evolution</i> , 2016, 8, 1316-1326.	1.1	8
808	Lateral Gene Transfer in a Heavy Metal-Contaminated-Groundwater Microbial Community. <i>MBio</i> , 2016, 7, e02234-15.	1.8	105
809	Finished genome sequence and methylome of the cyanide-degrading <i>Pseudomonas pseudoalcaligenes</i> strain CECT5344 as resolved by single-molecule real-time sequencing. <i>Journal of Biotechnology</i> , 2016, 232, 61-68.	1.9	20
810	A genome-wide SNP-based phylogenetic analysis distinguishes different biovars of <i>Brucella suis</i> . <i>Infection, Genetics and Evolution</i> , 2016, 41, 213-217.	1.0	23
811	Population structure and drug resistance patterns of emerging non-PCV-13 <i>Streptococcus pneumoniae</i> serotypes 22F, 15A, and 8 isolated from adults in Ontario, Canada. <i>Infection, Genetics and Evolution</i> , 2016, 42, 1-8.	1.0	17
812	Characterization of a genomic island harbouring a new <i>vanD</i> allele from <i>Enterococcus faecium</i> N15-508 isolated in Canada. <i>Journal of Antimicrobial Chemotherapy</i> , 2016, 71, 2052-2054.	1.3	11
813	Conservation of the Essential Genome Among <i>Caulobacter</i> and <i>Brevundimonas</i> Species. <i>Current Microbiology</i> , 2016, 72, 503-510.	1.0	13



#	ARTICLE	IF	CITATIONS
814	The <i>Chthonomonas calidirosea</i> Genome Is Highly Conserved across Geographic Locations and Distinct Chemical and Microbial Environments in New Zealand's Taupō Volcanic Zone. <i>Applied and Environmental Microbiology</i> , 2016, 82, 3572-3581.	1.4	9
815	Bacterial Genomic Data Analysis in the Next-Generation Sequencing Era. <i>Methods in Molecular Biology</i> , 2016, 1415, 407-422.	0.4	5
816	A genomic comparison of 13 symbiotic <i>Vibrio fischeri</i> isolates from the perspective of their host source and colonization behavior. <i>ISME Journal</i> , 2016, 10, 2907-2917.	4.4	49
817	Variable presence of the inverted repeat and plastome stability in <i>Erodium</i> . <i>Annals of Botany</i> , 2016, 117, 1209-1220.	1.4	94
818	Sequential Acquisition of Virulence and Fluoroquinolone Resistance Has Shaped the Evolution of <i>Escherichia coli</i> ST131. <i>MBio</i> , 2016, 7, e00347-16.	1.8	164
819	Data characterizing the chloroplast genomes of extinct and endangered Hawaiian endemic mints (Lamiaceae) and their close relatives. <i>Data in Brief</i> , 2016, 7, 900-922.	0.5	4
820	Complete plastid genome of an ecologically important brown alga <i>Sargassum thunbergii</i> (Fucales). <i>Journal of Applied Phycology</i> , 2016, 30, 107-117.	0.4	7
821	A barrier to homologous recombination between sympatric strains of the cooperative soil bacterium <i>Myxococcus xanthus</i> . <i>ISME Journal</i> , 2016, 10, 2468-2477.	4.4	52
822	Molecular Diversity and Plasmid Analysis of KPC-Producing <i>Escherichia coli</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 4073-4081.	1.4	33
823	Draft Genome Sequence of <i>Lactococcus lactis</i> subsp. <i>lactis</i> bv. <i>diacetylactis</i> CRL264, a Citrate-Fermenting Strain. <i>Genome Announcements</i> , 2016, 4, .	0.8	5
824	Coevolution between Nuclear-Encoded DNA Replication, Recombination, and Repair Genes and Plastid Genome Complexity. <i>Genome Biology and Evolution</i> , 2016, 8, 622-634.	1.1	51
825	Genomic and Transcriptional Mapping of PaMx41, Archetype of a New Lineage of Bacteriophages Infecting <i>Pseudomonas aeruginosa</i> . <i>Applied and Environmental Microbiology</i> , 2016, 82, 6541-6547.	1.4	10
826	A Primer on Infectious Disease Bacterial Genomics. <i>Clinical Microbiology Reviews</i> , 2016, 29, 881-913.	5.7	42
827	High-Quality Genome Assembly and Annotation for <i>Plasmodium coatneyi</i> , Generated Using Single-Molecule Real-Time PacBio Technology. <i>Genome Announcements</i> , 2016, 4, .	0.8	33
828	Complete genome sequencing and comparative analyses of broad-spectrum antimicrobial-producing <i>Micromonospora</i> sp. HK10. <i>Gene</i> , 2016, 594, 97-107.	1.0	10
829	Polysaccharide utilisation loci of <i>Bacteroidetes</i> from two contrasting open ocean sites in the North Atlantic. <i>Environmental Microbiology</i> , 2016, 18, 4456-4470.	1.8	56
830	Phylogenomic re-assessment of the thermophilic genus <i>Geobacillus</i> . <i>Systematic and Applied Microbiology</i> , 2016, 39, 527-533.	1.2	116
831	Genomic Comparison of <i>Campylobacter</i> spp. and Their Potential for Zoonotic Transmission between Birds, Primates, and Livestock. <i>Applied and Environmental Microbiology</i> , 2016, 82, 7165-7175.	1.4	73

#	ARTICLE	IF	CITATIONS
832	Complete genome sequencing and comparative genomic analysis of functionally diverse <i>Lysinibacillus sphaericus</i> III(3)7. <i>Genomics Data</i> , 2016, 9, 78-86.	1.3	12
833	The genome of the insecticidal <i>Chromobacterium subtsugae</i> PRAA4-1 and its comparison with that of <i>Chromobacterium violaceum</i> ATCC 12472. <i>Genomics Data</i> , 2016, 10, 1-3.	1.3	4
834	Whole-Genome Sequencing Identifies <i>In Vivo</i> Acquisition of a <i>bla</i> CTX-M-27-Carrying IncFII Transmissible Plasmid as the Cause of Ceftriaxone Treatment Failure for an Invasive <i>Salmonella enterica</i> Serovar Typhimurium Infection. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 7224-7235.	1.4	26
835	Complete Genome Sequence of the MRSA Isolate HC1335 from ST239 Lineage Displaying a Truncated AgrC Histidine Kinase Receptor. <i>Genome Biology and Evolution</i> , 2016, 8, 3187-3192.	1.1	40
836	Characterization and genome sequencing of a <i>Citrobacter freundii</i> phage CfP1 harboring a lysin active against multidrug-resistant isolates. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 10543-10553.	1.7	40
837	Multi-omics Quantification of Species Variation of <i>Escherichia coli</i> Links Molecular Features with Strain Phenotypes. <i>Cell Systems</i> , 2016, 3, 238-251.e12.	2.9	124
838	Complete genome sequence of <i>Bacillus amyloliquefaciens</i> subsp. <i>plantarum</i> S499, a rhizobacterium that triggers plant defences and inhibits fungal phytopathogens. <i>Journal of Biotechnology</i> , 2016, 238, 56-59.	1.9	29
839	Draft Genome Sequences of the Probiotic <i>Enterococcus faecalis</i> Symbioflor 1 Clones DSM16430 and DSM16434. <i>Genome Announcements</i> , 2016, 4, .	0.8	1
840	Clonality of erythromycin resistance in <i>Francisella tularensis</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2016, 71, 2815-2823.	1.3	39
841	Complete Genome Sequences of 17 Rapidly Growing Nontuberculous Mycobacterial Strains. <i>Genome Announcements</i> , 2016, 4, .	0.8	4
842	Recurrent selection explains parallel evolution of genomic regions of high relative but low absolute differentiation in a ring species. <i>Molecular Ecology</i> , 2016, 25, 4488-4507.	2.0	98
843	Rare Spontaneous Loss of Multiresistance Gene Carrying IncI/ST12 Plasmid in <i>Escherichia coli</i> in Pig Microbiota. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 6046-6049.	1.4	8
844	Comparative genomic evidence for duplication of TLR1 subfamily and miuuy croaker TLR1 perceives LPS stimulation via MyD88 and TIRAP. <i>Fish and Shellfish Immunology</i> , 2016, 56, 336-348.	1.6	39
845	Comparative genome-wide analysis reveals that <i>Burkholderia contaminans</i> MS14 possesses multiple antimicrobial biosynthesis genes but not major genetic loci required for pathogenesis. <i>MicrobiologyOpen</i> , 2016, 5, 353-369.	1.2	44
846	Unexpected genomic relationships between <i>Bacillus anthracis</i> strains from Bangladesh and Central Europe. <i>Infection, Genetics and Evolution</i> , 2016, 45, 66-74.	1.0	5
847	<i>Vibrio natriegens</i> as a fast-growing host for molecular biology. <i>Nature Methods</i> , 2016, 13, 849-851.	9.0	203
848	Repeated replacement of an intrabacterial symbiont in the tripartite nested mealybug symbiosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E5416-24.	3.3	222
849	Indel Group in Genomes (IGG) Molecular Genetic Markers. <i>Plant Physiology</i> , 2016, 172, 38-61.	2.3	5

#	ARTICLE	IF	CITATIONS
850	Tetracycline Selective Pressure and Homologous Recombination Shape the Evolution of <i>Chlamydia suis</i> : A Recently Identified Zoonotic Pathogen. <i>Genome Biology and Evolution</i> , 2016, 8, 2613-2623.	1.1	35
851	Genetic features of livestock-associated <i>Staphylococcus aureus</i> ST9 isolates from Chinese pigs that carry the <i>Isa(E)</i> gene for quinupristin/dalfopristin resistance. <i>International Journal of Medical Microbiology</i> , 2016, 306, 722-729.	1.5	25
852	Whole genome sequencing of emerging multidrug resistant <i>Candida auris</i> isolates in India demonstrates low genetic variation. <i>New Microbes and New Infections</i> , 2016, 13, 77-82.	0.8	149
853	<i>Lysobacter</i> species: a potential source of novel antibiotics. <i>Archives of Microbiology</i> , 2016, 198, 839-845.	1.0	85
854	Islands of linkage in an ocean of pervasive recombination reveals two-speed evolution of human cytomegalovirus genomes. <i>Virus Evolution</i> , 2016, 2, vew017.	2.2	83
855	PCR Primers for Detection of <i>Pantoea ananatis</i> , <i>Burkholderia</i> spp., and <i>Enterobacter</i> sp. from Onion. <i>Plant Disease</i> , 2016, 100, 836-846.	0.7	23
856	A genomic island in <i>Vibrio cholerae</i> with VPI-1 site-specific recombination characteristics contains CRISPR-Cas and type VI secretion modules. <i>Scientific Reports</i> , 2016, 6, 36891.	1.6	40
857	Population Evolution of <i>Helicobacter pylori</i> through Diversification in DNA Methylation and Interstrain Sequence Homogenization. <i>Molecular Biology and Evolution</i> , 2016, 33, 2848-2859.	3.5	29
858	Draft Genome Sequence of <i>Lactobacillus delbrueckii</i> Strain #22 Isolated from a Patient with Short Bowel Syndrome and Previous <i>D</i> -Lactic Acidosis and Encephalopathy. <i>Genome Announcements</i> , 2016, 4, .	0.8	5
859	Molecular, genetic and evolutionary analysis of a paracentric inversion in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2016, 88, 159-178.	2.8	81
860	Complete chloroplast genome sequences of <i>Solanum commersonii</i> and its application to chloroplast genotype in somatic hybrids with <i>Solanum tuberosum</i> . <i>Plant Cell Reports</i> , 2016, 35, 2113-2123.	2.8	54
861	A Thousand Fly Genomes: An Expanded <i>Drosophila</i> Genome Nexus. <i>Molecular Biology and Evolution</i> , 2016, 33, 3308-3313.	3.5	160
862	Draft Genome Sequence and Complete Plasmid Sequence of <i>Acinetobacter lwoffii</i> F78, an Isolate with Strong Allergy-Protective Properties. <i>Genome Announcements</i> , 2016, 4, .	0.8	0
863	Complete Genome Sequences of <i>Bordetella flabilis</i> , <i>Bordetella bronchialis</i> , and <i>Bordetella pseudohinzii</i> . <i>Genome Announcements</i> , 2016, 4, .	0.8	7
864	The genomic content and context of auxiliary metabolic genes in marine cyanomyoviruses. <i>Virology</i> , 2016, 499, 219-229.	1.1	99
865	Chromosomal inversions and ecotypic differentiation in <i>Anopheles gambiae</i> : the perspective from whole-genome sequencing. <i>Molecular Ecology</i> , 2016, 25, 5889-5906.	2.0	35
866	An assemblage of Frankia Cluster II strains from California contains the canonical nod genes and also the sulfotransferase gene <i>nodH</i> . <i>BMC Genomics</i> , 2016, 17, 796.	1.2	97
867	Microbial metabolisms in a 2.5-km-deep ecosystem created by hydraulic fracturing in shales. <i>Nature Microbiology</i> , 2016, 1, 16146.	5.9	207

#	ARTICLE	IF	CITATIONS
868	Unraveling genomic and phenotypic nature of multidrug-resistant (MDR) <i>Pseudomonas aeruginosa</i> VRFPA04 isolated from keratitis patient. <i>Microbiological Research</i> , 2016, 193, 140-149.	2.5	24
869	Large Sequence Diversity within the Biosynthesis Locus and Common Biochemical Features of <i>Campylobacter coli</i> Lipooligosaccharides. <i>Journal of Bacteriology</i> , 2016, 198, 2829-2840.	1.0	13
870	Dynamics of genome change among <i>Legionella</i> species. <i>Scientific Reports</i> , 2016, 6, 33442.	1.6	18
871	Australian human and parrot <i>Chlamydia psittaci</i> strains cluster within the highly virulent 6BC clade of this important zoonotic pathogen. <i>Scientific Reports</i> , 2016, 6, 30019.	1.6	58
872	Evolution of short inverted repeat in cupressophytes, transfer of <i>accD</i> to nucleus in <i>Sciadopitys verticillata</i> and phylogenetic position of <i>Sciadopityaceae</i> . <i>Scientific Reports</i> , 2016, 6, 20934.	1.6	25
873	Serotype IV <i>Streptococcus agalactiae</i> ST-452 has arisen from large genomic recombination events between CC23 and the hypervirulent CC17 lineages. <i>Scientific Reports</i> , 2016, 6, 29799.	1.6	26
874	The Establishment and Diversification of Epidemic-Associated Serogroup W <i>Meningococcus</i> in the African Meningitis Belt, 1994 to 2012. <i>MSphere</i> , 2016, 1, .	1.3	29
875	Draft Genome Sequences of Three Strains of <i>Ehrlichia ruminantium</i> , a Tick-Borne Pathogen of Ruminants, Isolated from Zimbabwe, The Gambia, and Ghana. <i>Genome Announcements</i> , 2016, 4, .	0.8	4
876	Refining borders of genome-rearrangements including repetitions. <i>BMC Genomics</i> , 2016, 17, 804.	1.2	0
877	Complete genome sequence of new bacteriophage phiE142, which causes simultaneously lysis of multidrug-resistant <i>Escherichia coli</i> O157:H7 and <i>Salmonella enterica</i> . <i>Standards in Genomic Sciences</i> , 2016, 11, 89.	1.5	17
878	Draft Genome Sequence of an <i>Enterococcus thailandicus</i> Strain Isolated from Bovine Feces. <i>Genome Announcements</i> , 2016, 4, .	0.8	2
879	MALDI-TOF MS portrait of emetic and non-emetic <i>Bacillus cereus</i> group members. <i>Electrophoresis</i> , 2016, 37, 2235-2247.	1.3	16
880	The Presence of Phage Orthologous Genes in <i>Helicobacter pylori</i> Correlates with the Presence of the Virulence Factors <i>CagA</i> and <i>VacA</i> . <i>Helicobacter</i> , 2016, 21, 226-233.	1.6	16
881	Massive intracellular gene transfer during plastid genome reduction in nongreen <i>Orobanchaceae</i> . <i>New Phytologist</i> , 2016, 210, 680-693.	3.5	86
882	Structurally distinct <i>Arabidopsis thaliana</i> NLR immune receptors recognize tandem WY domains of an oomycete effector. <i>New Phytologist</i> , 2016, 210, 984-996.	3.5	35
883	Complete Genome Sequence of Bluetongue Virus Serotype 8, Which Reemerged in France in August 2015. <i>Genome Announcements</i> , 2016, 4, .	0.8	23
884	Complete Genome Sequence of <i>Staphylococcus aureus</i> MCRF184, a Necrotizing Fasciitis-Causing Methicillin-Sensitive Sequence Type 45 <i>Staphylococcus</i> Strain. <i>Genome Announcements</i> , 2016, 4, .	0.8	5
885	Influence of Host Ecology and Behavior on <i>Campylobacter jejuni</i> Prevalence and Environmental Contamination Risk in a Synanthropic Wild Bird Species. <i>Applied and Environmental Microbiology</i> , 2016, 82, 4811-4820.	1.4	33

#	ARTICLE	IF	CITATIONS
886	Complete genome sequence and comparative genome analysis of a new special <i>Yersinia enterocolitica</i> . <i>Archives of Microbiology</i> , 2016, 198, 673-687.	1.0	6
887	Comparative genomic analyses reveal broad diversity in botulinum-toxin-producing <i>Clostridia</i> . <i>BMC Genomics</i> , 2016, 17, 180.	1.2	71
888	Insights into Symbiont Population Structure among Three Vestimentiferan Tubeworm Host Species at Eastern Pacific Spreading Centers. <i>Applied and Environmental Microbiology</i> , 2016, 82, 5197-5205.	1.4	28
889	Whole-Genome Comparative Analysis of Two Carbapenem-Resistant ST-258 <i>Klebsiella pneumoniae</i> Strains Isolated during a North-Eastern Ohio Outbreak: Differences within the High Heterogeneity Zones. <i>Genome Biology and Evolution</i> , 2016, 8, 2036-2043.	1.1	28
890	Characterization of KPC-encoding plasmids from two endemic settings, Greece and Italy. <i>Journal of Antimicrobial Chemotherapy</i> , 2016, 71, 2824-2830.	1.3	53
891	Aligning the unalignable: bacteriophage whole genome alignments. <i>BMC Bioinformatics</i> , 2016, 17, 30.	1.2	8
892	Genomic signatures of domestication on neurogenetic genes in <i>Drosophila melanogaster</i> . <i>BMC Evolutionary Biology</i> , 2016, 16, 6.	3.2	23
893	Complete genome of <i>Staphylococcus aureus</i> Tager 104 provides evidence of its relation to modern systemic hospital-acquired strains. <i>BMC Genomics</i> , 2016, 17, 179.	1.2	6
894	Large genomic differences between <i>Moraxella bovoculi</i> isolates acquired from the eyes of cattle with infectious bovine keratoconjunctivitis versus the deep nasopharynx of asymptomatic cattle. <i>Veterinary Research</i> , 2016, 47, 31.	1.1	38
895	Draft genome of the <i>Arabidopsis thaliana</i> phyllosphere bacterium, <i>Williamsia</i> sp. ARP1. <i>Standards in Genomic Sciences</i> , 2016, 11, 8.	1.5	10
896	Draft genome sequence for virulent and avirulent strains of <i>Xanthomonas arboricola</i> isolated from <i>Prunus</i> spp. in Spain. <i>Standards in Genomic Sciences</i> , 2016, 11, 12.	1.5	16
897	Draft genome sequences of <i>Pantoea agglomerans</i> and <i>Pantoea vagans</i> isolates associated with termites. <i>Standards in Genomic Sciences</i> , 2016, 11, 23.	1.5	29
898	Complete genome sequences of <i>Francisella noatunensis</i> subsp. <i>orientalis</i> strains FNO12, FNO24 and FNO190: a fish pathogen with genomic clonal behavior. <i>Standards in Genomic Sciences</i> , 2016, 11, 30.	1.5	13
899	Characterization of tet(Y)-carrying LowGC plasmids exogenously captured from cow manure at a conventional dairy farm. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiv075.	1.3	11
900	Adaptation by Deletogenic Replication Slippage in a Nascent Symbiont. <i>Molecular Biology and Evolution</i> , 2016, 33, 1957-1966.	3.5	18
901	Pangenome Evolution in the Marine Bacterium <i>Alteromonas</i> . <i>Genome Biology and Evolution</i> , 2016, 8, 1556-1570.	1.1	73
902	Molecular Evolution of a <i>Klebsiella pneumoniae</i> ST278 Isolate Harboring bla <sub>NDM-7</sub> and Involved in Nosocomial Transmission. <i>Journal of Infectious Diseases</i> , 2016, 214, 798-806.	1.9	27
903	Draft Genome Sequence of <i>Bacillus licheniformis</i> CG-B52, a Highly Virulent Bacterium of Pacific White Shrimp ( <i>Litopenaeus vannamei</i> ), Isolated from a Colombian Caribbean Aquaculture Outbreak. <i>Genome Announcements</i> , 2016, 4, .	0.8	2

#	ARTICLE	IF	CITATIONS
904	Whole-Genome Sequence of <i>Salmonella enterica</i> Serovar Enteritidis Phage Type 4, Isolated from a Brazilian Poultry Farm. <i>Genome Announcements</i> , 2016, 4, .	0.8	4
905	Draft Whole-Genome Sequence of <i>Haemophilus ducreyi</i> Strain AUSPNG1, Isolated from a Cutaneous Ulcer of a Child from Papua New Guinea. <i>Genome Announcements</i> , 2016, 4, .	0.8	8
906	Genome Structural Diversity among 31 <i>Bordetella pertussis</i> Isolates from Two Recent U.S. Whooping Cough Statewide Epidemics. <i>MSphere</i> , 2016, 1, .	1.3	51
907	Whole genomic DNA sequencing and comparative genomic analysis of <i>Arthrospira platensis</i> : high genome plasticity and genetic diversity. <i>DNA Research</i> , 2016, 23, 325-338.	1.5	30
908	Development of chloroplast genomic resources for <i>Cynara</i> . <i>Molecular Ecology Resources</i> , 2016, 16, 562-573.	2.2	30
909	Evolutionary signals of selection on cognition from the great tit genome and methylome. <i>Nature Communications</i> , 2016, 7, 10474.	5.8	172
910	Single-Cell-Genomics-Facilitated Read Binning of Candidate Phylum EM19 Genomes from Geothermal Spring Metagenomes. <i>Applied and Environmental Microbiology</i> , 2016, 82, 992-1003.	1.4	36
911	Safety evaluation of AB-LIFE <sup>®</sup> ( <i>Lactobacillus plantarum</i> CECT 7527, 7528 and 7529): Antibiotic resistance and 90-day repeated-dose study in rats. <i>Food and Chemical Toxicology</i> , 2016, 92, 117-128.	1.8	31
912	Evolutionary History of the Global Emergence of the <i>Escherichia coli</i> Epidemic Clone ST131. <i>MBio</i> , 2016, 7, e02162.	1.8	289
913	Latin-American-Mediterranean lineage of <i>Mycobacterium tuberculosis</i> : Human traces across pathogen's phylogeography. <i>Molecular Phylogenetics and Evolution</i> , 2016, 99, 133-143.	1.2	42
914	Analysis of the complete genome sequence of the archaeon <i>Pyrococcus chitonophagus</i> DSM 10152 (formerly <i>Thermococcus chitonophagus</i> ). <i>Extremophiles</i> , 2016, 20, 351-361.	0.9	7
915	<i>Microvirga massiliensis</i> sp. nov., the human commensal with the largest genome. <i>MicrobiologyOpen</i> , 2016, 5, 307-322.	1.2	27
916	Effects of sequence diversity and recombination on the accuracy of phylogenetic trees estimated by $k$ SNP. <i>Cladistics</i> , 2016, 32, 90-99.	1.5	5
917	Genome Sequence and Analysis of <i>Escherichia coli</i> MRE600, a Colicinogenic, Nonmotile Strain that Lacks RNase I and the Type I Methyltransferase, EcoKI. <i>Genome Biology and Evolution</i> , 2016, 8, 742-752.	1.1	35
918	A Comparative Analysis of Mitochondrial Genomes in Eustigmatophyte Algae. <i>Genome Biology and Evolution</i> , 2016, 8, 705-722.	1.1	33
919	Whole-genome sequence analysis and exploration of the zoonotic potential of a rat-borne <i>Bartonella elizabethae</i> . <i>Acta Tropica</i> , 2016, 155, 25-33.	0.9	8
920	Introgression maintains the genetic integrity of the mating-type determining chromosome of the fungus <i>Neurospora tetrasperma</i> . <i>Genome Research</i> , 2016, 26, 486-498.	2.4	39
921	Major Improvements to the <i>Heliconius melpomene</i> Genome Assembly Used to Confirm 10 Chromosome Fusion Events in 6 Million Years of Butterfly Evolution. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 695-708.	0.8	149



#	ARTICLE	IF	CITATIONS
922	Genome sequencing of a virulent avian <i>Pasteurella multocida</i> strain GX-Pm reveals the candidate genes involved in the pathogenesis. <i>Research in Veterinary Science</i> , 2016, 105, 23-27.	0.9	15
923	<i>Ginkgo</i> and <i>Welwitschia</i> Mitogenomes Reveal Extreme Contrasts in Gymnosperm Mitochondrial Evolution. <i>Molecular Biology and Evolution</i> , 2016, 33, 1448-1460.	3.5	151
924	Genomic dissection of Australian <i>Bordetella pertussis</i> isolates from the 2008–2012 epidemic. <i>Journal of Infection</i> , 2016, 72, 468-477.	1.7	52
925	Combining reverse-transcription multiplex PCR and microfluidic electrophoresis to simultaneously detect seven mosquito-transmitted zoonotic encephalomyelitis viruses. <i>Veterinary Journal</i> , 2016, 212, 27-35.	0.6	6
926	Genomic Comparison of Two O111:H <sup>+</sup> Enterohemorrhagic <i>Escherichia coli</i> Isolates from a Historic Hemolytic-Uremic Syndrome Outbreak in Australia. <i>Infection and Immunity</i> , 2016, 84, 775-781.	1.0	14
927	Evidence of horizontal gene transfer between obligate leaf nodule symbionts. <i>ISME Journal</i> , 2016, 10, 2092-2105.	4.4	63
928	US Gulf-like toxigenic O1 <i>Vibrio cholerae</i> causing sporadic cholera outbreaks in China. <i>Journal of Infection</i> , 2016, 72, 564-572.	1.7	12
929	Intraspecies Transfer of the Chromosomal <i>Acinetobacter baumannii</i> bla <sub>NDM-1</sub> Carbapenemase Gene. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 3032-3040.	1.4	65
930	Human symbionts inject and neutralize antibacterial toxins to persist in the gut. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 3639-3644.	3.3	190
931	The Use of Recombined Ribosomal RNA Operon (rrn) Type-Specific Flanking Genes to Investigate rrn Differences Between <i>Vibrio parahaemolyticus</i> Environmental and Clinical Strains. <i>Gene Reports</i> , 2016, 4, 16-25.	0.4	2
932	The quest to resolve recent radiations: Plastid phylogenomics of extinct and endangered Hawaiian endemic mints (Lamiaceae). <i>Molecular Phylogenetics and Evolution</i> , 2016, 99, 16-33.	1.2	47
933	Genomic islands 1 and 2 play key roles in the evolution of extensively drug-resistant ST235 isolates of <i>Pseudomonas aeruginosa</i> . <i>Open Biology</i> , 2016, 6, 150175.	1.5	47
934	The complete chloroplast genome sequence of Indian mustard ( <i>Brassica juncea</i> L.). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 4622-4623.	0.7	10
935	Distribution and characterization of <i>Clostridium difficile</i> isolated from dogs in Japan. <i>Anaerobe</i> , 2016, 37, 58-61.	1.0	20
936	Comparative genomic study of three species within the genus <i>Ornithinibacillus</i> , reflecting the adaptation to different habitats. <i>Gene</i> , 2016, 578, 25-31.	1.0	6
937	Complete chloroplast genome of <i>Ficus racemosa</i> (Moraceae). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 4655-4656.	0.7	4
938	Phylogenomic and structural analyses of 18 complete plastomes across nearly all families of early-diverging eudicots, including an angiosperm-wide analysis of IR gene content evolution. <i>Molecular Phylogenetics and Evolution</i> , 2016, 96, 93-101.	1.2	92
939	Precision methylome characterization of <i>Mycobacterium tuberculosis</i> complex (MTBC) using PacBio single-molecule real-time (SMRT) technology. <i>Nucleic Acids Research</i> , 2016, 44, 730-743.	6.5	124



#	ARTICLE	IF	CITATIONS
940	Comparative genomic analysis of the swine pathogen <i>Bordetella bronchiseptica</i> strain KM22. <i>Veterinary Microbiology</i> , 2016, 182, 87-94.	0.8	4
941	Increase in bacteraemia cases in the East Midlands region of the UK due to MDREscherichia coliST73: high levels of genomic and plasmid diversity in causative isolates. <i>Journal of Antimicrobial Chemotherapy</i> , 2016, 71, 339-343.	1.3	24
942	The Connection between Persistent, Disinfectant-Resistant <i>Listeria monocytogenes</i> Strains from Two Geographically Separate Iberian Pork Processing Plants: Evidence from Comparative Genome Analysis. <i>Applied and Environmental Microbiology</i> , 2016, 82, 308-317.	1.4	95
943	The chloroplast genome of the marine green macroalga <i>Ulva fasciata</i> Delile (Ulvophyceae, Tj ETQq1 1 0.784314 rgBT /Overloc	0.7	9
944	Sorting Circular Permutations by Super Short Reversals. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017, 14, 620-633.	1.9	9
945	Natural coinfection by <i>Streptococcus agalactiae</i> and <i>Francisella noatunensis</i> subsp. <i>orientalis</i> in farmed Nile tilapia ( <i>Oreochromis niloticus</i> L.). <i>Journal of Fish Diseases</i> , 2017, 40, 51-63.	0.9	45
946	Comparative genomic analysis of wide and narrow host range strains of <i>Xanthomonas citri</i> subsp. <i>citri</i> , showing differences in the genetic content of their pathogenicity and virulence factors. <i>Australasian Plant Pathology</i> , 2017, 46, 49-61.	0.5	6
947	Genome sequencing and analysis of <i>Kloeckera apiculata</i> strain 34-9, a biocontrol agent against postharvest pathogens in citrus. <i>Genes and Genomics</i> , 2017, 39, 87-99.	0.5	6
948	Characterization of carbapenemase-producing Enterobacteriaceae in the West Midlands region of England: 2007-14. <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, dkw560.	1.3	21
949	Evolutionary genomics of the cold-adapted diatom <i>Fragilariopsis cylindrus</i> . <i>Nature</i> , 2017, 541, 536-540.	13.7	332
950	Draft Genome Sequences of Pandrug-Resistant <i>Serratia marcescens</i> Clinical Isolates Harboring <i>bla</i> <sub>NDM-1</sub> . <i>Genome Announcements</i> , 2017, 5, .	0.8	2
951	Importance of whole genome sequencing for the assessment of outbreaks in diagnostic laboratories: analysis of a case series of invasive <i>Streptococcus pyogenes</i> infections. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2017, 36, 1173-1180.	1.3	22
952	Population and evolutionary dynamics of Shiga toxin producing <i>Escherichia coli</i> O157 in a beef herd: A longitudinal study. <i>Environmental Microbiology</i> , 2017, 19, 1836-1844.	1.8	3
953	<i>Enterobacter cloacae</i> Complex Isolates Harboring <i>bla</i> <sub>NMC-A</sub> or <i>bla</i> <sub>IMI</sub> -Type Class A Carbapenemase Genes on Novel Chromosomal Integrative Elements and Plasmids. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	38
954	Convergent patterns in the evolution of mealybug symbioses involving different intrabacterial symbionts. <i>ISME Journal</i> , 2017, 11, 715-726.	4.4	49
955	Genome of a giant bacteriophage from a decaying <i>Trichodesmium</i> bloom. <i>Marine Genomics</i> , 2017, 33, 21-25.	0.4	7
956	Mixed transmission modes and dynamic genome evolution in an obligate animal-bacterial symbiosis. <i>ISME Journal</i> , 2017, 11, 1359-1371.	4.4	35
957	Genomic structure and insertion sites of <i>Helicobacter pylori</i> prophages from various geographical origins. <i>Scientific Reports</i> , 2017, 7, 42471.	1.6	34

#	ARTICLE	IF	CITATIONS
958	Adaptation of the pathogen, <i>Pseudomonas syringae</i> , during experimental evolution on a native vs. alternative host plant. <i>Molecular Ecology</i> , 2017, 26, 1790-1801.	2.0	14
959	Dissection of genomic features and variations of three pathotypes of <i>Puccinia striiformis</i> through whole genome sequencing. <i>Scientific Reports</i> , 2017, 7, 42419.	1.6	55
960	Neanderthal behaviour, diet, and disease inferred from ancient DNA in dental calculus. <i>Nature</i> , 2017, 544, 357-361.	13.7	398
961	Aquatic adaptation of a laterally acquired pectin degradation pathway in marine gammaproteobacteria. <i>Environmental Microbiology</i> , 2017, 19, 2320-2333.	1.8	57
962	Genome sequence of <i>Methanobacterium congolense</i> strain Buetzberg, a hydrogenotrophic, methanogenic archaeon, isolated from a mesophilic industrial-scale biogas plant utilizing bio-waste. <i>Journal of Biotechnology</i> , 2017, 247, 1-5.	1.9	48
963	Complete Genome Sequence of <i>Mycoplasma pneumoniae</i> Type 2 Reference Strain FH Using Single-Molecule Real-Time Sequencing Technology. <i>Genome Announcements</i> , 2017, 5, .	0.8	3
964	Ancient bacteria of the $\tilde{\text{A}}\text{-tzi}\tilde{\text{A}}^{\text{TM}}$ s microbiome: a genomic tale from the Copper Age. <i>Microbiome</i> , 2017, 5, 5.	4.9	45
965	An antimicrobial peptide-resistant minor subpopulation of <i>Photobacterium luminescens</i> is responsible for virulence. <i>Scientific Reports</i> , 2017, 7, 43670.	1.6	23
966	Global Molecular Epidemiology of IMP-Producing Enterobacteriaceae. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	61
967	Comparative <i>scn</i> DNA sequence analyses of <i>Pyramimonas parkeae</i> (Prasinophyceae) chloroplast genomes. <i>Journal of Phycology</i> , 2017, 53, 415-424.	1.0	9
968	The History of <i>Bordetella pertussis</i> Genome Evolution Includes Structural Rearrangement. <i>Journal of Bacteriology</i> , 2017, 199, .	1.0	59
969	Towards long-read metagenomics: complete assembly of three novel genomes from bacteria dependent on a diazotrophic cyanobacterium in a freshwater lake co-culture. <i>Standards in Genomic Sciences</i> , 2017, 12, 9.	1.5	53
970	Heterologous Complementation Reveals a Specialized Activity for BacA in the <i>Medicago</i> – <i>Sinorhizobium meliloti</i> Symbiosis. <i>Molecular Plant-Microbe Interactions</i> , 2017, 30, 312-324.	1.4	24
971	The first complete genome sequences of the <i>acl</i> lineage, the most abundant freshwater Actinobacteria, obtained by whole-genome-amplification of dilution-to-extinction cultures. <i>Scientific Reports</i> , 2017, 7, 42252.	1.6	42
972	Complete mitochondrial genomes of prasinophyte algae <i>Pyramimonas parkeae</i> and <i>Cymbomonas tetramitiformis</i> . <i>Journal of Phycology</i> , 2017, 53, 601-615.	1.0	10
973	Diversity of the Photosynthetic <i>Paulinella</i> Species, with the Description of <i>Paulinella micropora</i> sp. nov. and the Chromatophore Genome Sequence for strain KR01. <i>Protist</i> , 2017, 168, 155-170.	0.6	28
974	Experimental Evaluation of Host Adaptation of <i>Lactobacillus reuteri</i> to Different Vertebrate Species. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	87
975	Draft Genome Sequence of <i>Bacillus licheniformis</i> VSD4, a Diesel Fuel–Degrading and Plant Growth–Promoting Phyllospheric Bacterium. <i>Genome Announcements</i> , 2017, 5, .	0.8	3

#	ARTICLE	IF	CITATIONS
976	Characterization and genomic analyses of two newly isolated Morganella phages define distant members among Tevenvirinae and Autographivirinae subfamilies. <i>Scientific Reports</i> , 2017, 7, 46157.	1.6	23
977	Sequence of the R1 plasmid and comparison to F and R100. <i>Plasmid</i> , 2017, 91, 53-60.	0.4	33
978	Recombination-independent replication and gene conversion homogenize repeat sequences and diversify plastid genome structure. <i>American Journal of Botany</i> , 2017, 104, 559-572.	0.8	86
979	A potential role of transposon IS431 in the loss of <i>mecA</i> gene. <i>Scientific Reports</i> , 2017, 7, 41237.	1.6	9
980	Whole-genome sequencing of <i>Klebsiella pneumoniae</i> MDR strain isolated in a Syrian refugee. <i>Pathogens and Global Health</i> , 2017, 111, 212-215.	1.0	4
981	Genomic Diversity of Type B3 Bacteriophages of <i>Caulobacter crescentus</i> . <i>Current Microbiology</i> , 2017, 74, 779-786.	1.0	12
982	A maternal-effect selfish genetic element in <i>Caenorhabditis elegans</i> . <i>Science</i> , 2017, 356, 1051-1055.	6.0	93
983	Horizontal transfer of chromosomal markers mediated by the large conjugative plasmid pXO16 from <i>Bacillus thuringiensis</i> serovar israelensis. <i>Plasmid</i> , 2017, 91, 76-81.	0.4	12
984	A Test for Gene Flow among Sympatric and Allopatric Hawaiian Picture-Winged <i>Drosophila</i> . <i>Journal of Molecular Evolution</i> , 2017, 84, 259-266.	0.8	5
985	Genome Stability in Engineered Strains of the Extremely Thermophilic Lignocellulose-Degrading Bacterium <i>Caldicellulosiruptor bescii</i> . <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	17
986	Rapid, field-based screening for chital ( <i>Axis axis</i> ) DNA in illegal meat markets. <i>Conservation Genetics Resources</i> , 2017, 9, 523-525.	0.4	4
987	Distinct cis-acting regions control <i>six6</i> expression during eye field and optic cup stages of eye formation. <i>Developmental Biology</i> , 2017, 426, 418-428.	0.9	13
988	Disruption of <i>tetR</i> type regulator <i>adeN</i> by mobile genetic element confers elevated virulence in <i>Acinetobacter baumannii</i> . <i>Virulence</i> , 2017, 8, 1316-1334.	1.8	35
989	Emergence and Evolution of Multidrug-Resistant <i>Klebsiella pneumoniae</i> with both <i>bla</i> and <i>KPC</i> and <i>bla</i> <i>CTX-M</i> Integrated in the Chromosome. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	66
990	Reconstructing the Ancestral Relationships Between Bacterial Pathogen Genomes. <i>Methods in Molecular Biology</i> , 2017, 1535, 109-137.	0.4	5
991	Pneumococcal Capsule Synthesis Locus <i>cps</i> as Evolutionary Hotspot with Potential to Generate Novel Serotypes by Recombination. <i>Molecular Biology and Evolution</i> , 2017, 34, 2537-2554.	3.5	65
992	Insights from the complete genome sequence of <i>Clostridium tyrobutyricum</i> provide a platform for biotechnological and industrial applications. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2017, 44, 1245-1260.	1.4	16
993	Two level parallelism and I/O reduction in genome comparisons. <i>Cluster Computing</i> , 2017, 20, 1925-1936.	3.5	2

#	ARTICLE	IF	CITATIONS
994	Genomic epidemiology of global VIM-producing Enterobacteriaceae. <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 2249-2258.	1.3	47
995	Loss of the <i>ssrA</i> genome island led to partial debromination in the PBDE respiring <i>Dehalococcoides mccartyi</i> strain CY50. <i>Environmental Microbiology</i> , 2017, 19, 2906-2915.	1.8	27
996	Whole-Genome Sequence and Variant Analysis of W303, a Widely-Used Strain of <i>Saccharomyces cerevisiae</i> . <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2219-2226.	0.8	49
997	The New Red Algal Subphylum Proteorhodophytina Comprises the Largest and Most Divergent Plastid Genomes Known. <i>Current Biology</i> , 2017, 27, 1677-1684.e4.	1.8	89
998	Long-read sequencing improves assembly of <i>Trichinella</i> genomes 10-fold, revealing substantial synteny between lineages diverged over 7 million years. <i>Parasitology</i> , 2017, 144, 1302-1315.	0.7	5
999	<i>Mycobacterium massiliopolynesiensis</i> sp. nov., a rapidly-growing mycobacterium of medical interest related to <i>Mycobacterium phlei</i> . <i>Scientific Reports</i> , 2017, 7, 40443.	1.6	6
1000	TAL effector driven induction of a SWEET gene confers susceptibility to bacterial blight of cotton. <i>Nature Communications</i> , 2017, 8, 15588.	5.8	144
1001	NLR locus-mediated trade-off between abiotic and biotic stress adaptation in <i>Arabidopsis</i> . <i>Nature Plants</i> , 2017, 3, 17072.	4.7	53
1002	Draft Genome Sequence of <i>Rhodococcus erythropolis</i> VSD3, a Diesel Fuel-Degrading and Plant Growth-Promoting Bacterium Isolated from <i>Hedera helix</i> Leaves. <i>Genome Announcements</i> , 2017, 5, .	0.8	4
1003	Correlated evolutionary rates across genomic compartments in Annonaceae. <i>Molecular Phylogenetics and Evolution</i> , 2017, 114, 63-72.	1.2	13
1004	Characterization of a deletion in the <i>Hsp70</i> cluster in the bovine reference genome. <i>Animal Genetics</i> , 2017, 48, 377-385.	0.6	2
1005	chainCleaner improves genome alignment specificity and sensitivity. <i>Bioinformatics</i> , 2017, 33, 1596-1603.	1.8	33
1006	Adaptation to copper stress influences biofilm formation in <i>Alteromonas macleodii</i> . <i>Biofouling</i> , 2017, 33, 505-519.	0.8	8
1007	The gut bacterium and pathobiont <i>Bacteroides vulgatus</i> activates NF- $\kappa$ B in a human gut epithelial cell line in a strain and growth phase dependent manner. <i>Anaerobe</i> , 2017, 47, 209-217.	1.0	55
1008	Complete Genome Sequence of <i>Burkholderia cenocepacia</i> CR318, a Phosphate-Solubilizing Bacterium Isolated from Corn Root. <i>Genome Announcements</i> , 2017, 5, .	0.8	4
1009	Draft Genome Sequence of <i>Serratia proteamaculans</i> MFPA44A14-05, a Model Organism for the Study of Meat and Seafood Spoilage. <i>Genome Announcements</i> , 2017, 5, .	0.8	6
1010	Complete genome sequence analysis of a novel <i>Staphylococcus</i> phage StAP1 and proposal of a new species in the genus <i>Silviavirus</i> . <i>Archives of Virology</i> , 2017, 162, 2145-2148.	0.9	3
1011	Functional and comparative genome analysis of novel virulent actinophages belonging to <i>Streptomyces flavovirens</i> . <i>BMC Microbiology</i> , 2017, 17, 51.	1.3	6

#	ARTICLE	IF	CITATIONS
1012	Genomic structure of the horse major histocompatibility complex class II region resolved using PacBio long-read sequencing technology. <i>Scientific Reports</i> , 2017, 7, 45518.	1.6	48
1013	Genome sequencing and comparative analysis of an NDM-1-producing <i>Klebsiella pneumoniae</i> ST15 isolated from a refugee patient. <i>Pathogens and Global Health</i> , 2017, 111, 166-175.	1.0	18
1014	Emergence of a plasmid-borne multidrug resistance gene <i>cfr</i> (C) in foodborne pathogen <i>Campylobacter</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 1581-1588.	1.3	80
1015	Draft Genome Sequence of <i>Corynebacterium pseudotuberculosis</i> Strain PA05 Isolated from an Ovine Host in Pará State, Brazil. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
1016	Whole-Genome Sequences of <i>Burkholderia pseudomallei</i> Isolates Exhibiting Decreased Meropenem Susceptibility. <i>Genome Announcements</i> , 2017, 5, .	0.8	15
1018	Genomic heterogeneity of <i>Salmonella enterica</i> serovar Typhimurium bacteriuria from chronic infection. <i>Infection, Genetics and Evolution</i> , 2017, 51, 17-20.	1.0	2
1019	Identification of different cytoplasmic based on newly developed mitotype-specific markers for marker-assisted selection breeding in <i>Brassica napus</i> L.. <i>Plant Cell Reports</i> , 2017, 36, 901-909.	2.8	17
1020	Identification and genomic analysis of antifungal property of a tomato root endophyte <i>Pseudomonas</i> sp. p21. <i>Antonie Van Leeuwenhoek</i> , 2017, 110, 387-397.	0.7	16
1021	Comparative genomics provides a timeframe for <i>Wolbachia</i> evolution and exposes a recent biotin synthesis operon transfer. <i>Nature Microbiology</i> , 2017, 2, 16241.	5.9	113
1022	Insight into the Genome of <i>Brochothrix thermosphacta</i> , a Problematic Meat Spoilage Bacterium. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	61
1023	Differentiation of <i>Staphylococcus argenteus</i> (formerly: <i>Staphylococcus aureus</i> clonal complex 75) by mass spectrometry from <i>S. aureus</i> using the first strain isolated from a wild African great ape. <i>International Journal of Medical Microbiology</i> , 2017, 307, 57-63.	1.5	42
1024	Expansion of inverted repeat does not decrease substitution rates in <i>Pelargonium</i> plastid genomes. <i>New Phytologist</i> , 2017, 214, 842-851.	3.5	99
1025	Protracted Regional Dissemination of GIM-1-Producing <i>Serratia marcescens</i> in Western Germany. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	6
1026	Experimental pathogenicity and complete genome characterization of a pig origin <i>Pasteurella multocida</i> serogroup F isolate HN07. <i>Veterinary Microbiology</i> , 2017, 198, 23-33.	0.8	30
1027	Unusual Legionnaires' outbreak in cool, dry Western Canada: an investigation using genomic epidemiology. <i>Epidemiology and Infection</i> , 2017, 145, 254-265.	1.0	6
1028	Complete chloroplast genome sequences contribute to plant species delimitation: A case study of the <i>Anemopaegma</i> species complex. <i>American Journal of Botany</i> , 2017, 104, 1493-1509.	0.8	54
1029	Convergence of plasmid architectures drives emergence of multi-drug resistance in a clonally diverse <i>Escherichia coli</i> population from a veterinary clinical care setting. <i>Veterinary Microbiology</i> , 2017, 211, 6-14.	0.8	15
1030	Geographically widespread honeybee gut symbiont subgroups show locally distinct antibiotic-resistant patterns. <i>Molecular Ecology</i> , 2017, 26, 6590-6607.	2.0	26

#	ARTICLE	IF	CITATIONS
1031	Gene Acquisition by a Distinct Phyletic Group within <i>Streptococcus pneumoniae</i> Promotes Adhesion to the Ocular Epithelium. <i>MSphere</i> , 2017, 2, .	1.3	9
1032	Analysis of the CRISPR-Cas system in bacteriophages active on epidemic strains of <i>Vibrio cholerae</i> in Bangladesh. <i>Scientific Reports</i> , 2017, 7, 14880.	1.6	31
1033	Cytoplasmic Male Sterility and Mitochondrial Genome Variations in Radish. <i>Compendium of Plant Genomes</i> , 2017, , 93-108.	0.3	2
1034	Molecular Characterization of Carbapenemase-Producing <i>Pseudomonas aeruginosa</i> of Czech Origin and Evidence for Clonal Spread of Extensively Resistant Sequence Type 357 Expressing IMP-7 Metallo- $\beta$ -Lactamase. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	45
1035	Comparative genomics of <i>Lactobacillus kefirianofaciens</i> ZW3 and related members of <i>Lactobacillus</i> spp reveal adaptations to dairy and gut environments. <i>Scientific Reports</i> , 2017, 7, 12827.	1.6	33
1036	Genome analysis reveals insights of the endophytic <i>Bacillus toyonensis</i> BAC3151 as a potentially novel agent for biocontrol of plant pathogens. <i>World Journal of Microbiology and Biotechnology</i> , 2017, 33, 185.	1.7	30
1037	Gene losses and partial deletion of small single-copy regions of the chloroplast genomes of two hemiparasitic <i>Taxillus</i> species. <i>Scientific Reports</i> , 2017, 7, 12834.	1.6	67
1038	Sequencing and comparative analysis of the <i>Amblyomma sculptum</i> mitogenome. <i>Veterinary Parasitology</i> , 2017, 247, 121-128.	0.7	14
1039	Complete Genome Sequence of <i>Mycobacterium chimaera</i> Strain CDC2015-22-71. <i>Genome Announcements</i> , 2017, 5, .	0.8	6
1040	Draft Genome Sequence of an Atypical Highly Virulent Rabbit <i>Staphylococcus aureus</i> Strain. <i>Genome Announcements</i> , 2017, 5, .	0.8	0
1041	Draft Genome Sequence of a Novel Chitinophaga sp. Strain, MD30, Isolated from a Biofilm in an Air Conditioner Condensate Pipe. <i>Genome Announcements</i> , 2017, 5, .	0.8	2
1042	Physiological and ecological implications of an iron- or hydrogen-oxidizing member of the Zetaproteobacteria, <i>Ghiorsea bivora</i> , gen. nov., sp. nov.. <i>ISME Journal</i> , 2017, 11, 2624-2636.	4.4	55
1043	The Arsenic Resistance-Associated <i>Listeria</i> Genomic Island LGI2 Exhibits Sequence and Integration Site Diversity and a Propensity for Three <i>Listeria monocytogenes</i> Clones with Enhanced Virulence. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	50
1044	Complete Genome Sequence of the Yogurt Isolate <i>Lactobacillus delbrueckii</i> subsp. <i>bulgaricus</i> ACA-DC 87. <i>Genome Announcements</i> , 2017, 5, .	0.8	2
1045	The Environmental <i>Acinetobacter baumannii</i> Isolate DSM30011 Reveals Clues into the Preantibiotic Era Genome Diversity, Virulence Potential, and Niche Range of a Predominant Nosocomial Pathogen. <i>Genome Biology and Evolution</i> , 2017, 9, 2292-2307.	1.1	61
1046	CONE: Community Oriented Network Estimation Is a Versatile Framework for Inferring Population Structure in Large-Scale Sequencing Data. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3359-3377.	0.8	12
1047	Replication and refinement of a vaginal microbial signature of preterm birth in two racially distinct cohorts of US women. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 9966-9971.	3.3	297
1048	The rapid <i>in vivo</i> evolution of <i>Pseudomonas aeruginosa</i> in ventilator-associated pneumonia patients leads to attenuated virulence. <i>Open Biology</i> , 2017, 7, 170029.	1.5	50



#	ARTICLE	IF	CITATIONS
1049	Complete Nucleotide Sequence of Klebsiella pneumoniae Bacteriophage vB_KpnM_KpV477. Genome Announcements, 2017, 5, .	0.8	7
1050	Genome characterization of two bile-isolated Vibrio fluvialis strains: an insight into pathogenicity and bile salt adaption. Scientific Reports, 2017, 7, 11827.	1.6	14
1051	Complete Genome Sequence of Mycobacterium chimaera SJ42, a Nonoutbreak Strain from an Immunocompromised Patient with Pulmonary Disease. Genome Announcements, 2017, 5, .	0.8	3
1052	Colonic Spirochetes: What Has Genomics Taught Us?. Current Topics in Microbiology and Immunology, 2017, 415, 273-294.	0.7	5
1053	Transcriptomic analysis of nickel exposure in Sphingobium sp. ba1 cells using RNA-seq. Scientific Reports, 2017, 7, 8262.	1.6	11
1054	Genomic insights of <i>Pannonibacter phragmitetus</i> strain 31801 isolated from a patient with a liver abscess. MicrobiologyOpen, 2017, 6, e00515.	1.2	10
1055	Comparative genomics of Australian and international isolates of Salmonella Typhimurium: correlation of core genome evolution with CRISPR and prophage profiles. Scientific Reports, 2017, 7, 9733.	1.6	26
1056	A novel inducible prophage from the mycosphere inhabitant Paraburkholderia terrae BS437. Scientific Reports, 2017, 7, 9156.	1.6	19
1057	Multi-drug resistant Klebsiella pneumoniae strains circulating in hospital setting: whole-genome sequencing and Bayesian phylogenetic analysis for outbreak investigations. Scientific Reports, 2017, 7, 3534.	1.6	22
1058	Development of a novel multiplexed qPCR and Pyrosequencing method for the detection of human pathogenic yersiniae. International Journal of Food Microbiology, 2017, 257, 247-253.	2.1	6
1059	First report of two complete Clostridium chauvoei genome sequences and detailed in silico genome analysis. Infection, Genetics and Evolution, 2017, 54, 287-298.	1.0	16
1060	Mitochondrial genomes of the green macroalga <i>Ulva pertusa</i> (Ulvophyceae, Chlorophyta): novel insights into the evolution of mitogenomes in the Ulvophyceae. Journal of Phycology, 2017, 53, 1010-1019.	1.0	23
1061	Identification of three homologous latex-clearing protein (lcp) genes from the genome of Streptomyces sp. strain CFMR 7. Gene, 2017, 628, 146-155.	1.0	10
1062	Rates and relations of mitochondrial genome evolution across the Echinoidea, with special focus on the superfamily Odontophora. Ecology and Evolution, 2017, 7, 4543-4551.	0.8	11
1063	Genome Sequence and Composition of a Tolyporphin-Producing Cyanobacterium-Microbial Community. Applied and Environmental Microbiology, 2017, 83, .	1.4	18
1064	Locus of Adhesion and Autoaggregation (LAA), a pathogenicity island present in emerging Shiga Toxin-producing Escherichia coli strains. Scientific Reports, 2017, 7, 7011.	1.6	69
1065	Habitat type and dispersal mode underlie the capacity for plant migration across an intermittent seaway. Annals of Botany, 2017, 120, 539-549.	1.4	15
1066	Plastome Sequencing of Ten Nonmodel Crop Species Uncovers a Large Insertion of Mitochondrial DNA in Cashew. Plant Genome, 2017, 10, plantgenome2017.03.0020.	1.6	56



#	ARTICLE	IF	CITATIONS
1067	Whole genome comparative analysis of four Georgian grape cultivars. <i>Molecular Genetics and Genomics</i> , 2017, 292, 1377-1389.	1.0	9
1068	Whole-Genome Shotgun Sequences of Three Multidrug-Resistant <i>Mycobacterium tuberculosis</i> Strains Isolated from Morocco. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
1069	Plastid Genome of <i>Dictyopteris divaricata</i> (Dictyotales, Phaeophyceae): Understanding the Evolution of Plastid Genomes in Brown Algae. <i>Marine Biotechnology</i> , 2017, 19, 627-637.	1.1	22
1070	Shared ancestry of herpes simplex virus 1 strain Patton with recent clinical isolates from Asia and with strain KOS63. <i>Virology</i> , 2017, 512, 124-131.	1.1	5
1071	Safety evaluation of HOWARUÂ® Restore ( <i>Lactobacillus acidophilus</i> NCFM, <i>Lactobacillus paracasei</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 genomic risk factors, and acute toxicity. <i>Food and Chemical Toxicology</i> , 2017, 110, 316-324.	1.8	40
1072	Genome sequence and analysis of <i>Escherichia coli</i> production strain LS5218. <i>Metabolic Engineering Communications</i> , 2017, 5, 78-83.	1.9	9
1073	Characterization of the Complete Nucleotide Sequences of IncA/C <sub>2</sub> Plasmids Carrying In809-Like Integrations from Enterobacteriaceae Isolates of Wildlife Origin. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	35
1075	The complete genome of the tetrachloroethene-respiring <i>Epsilonproteobacterium Sulfurospirillum halorespirans</i> . <i>Journal of Biotechnology</i> , 2017, 255, 33-36.	1.9	20
1076	Genomic analysis of the marine fish pathogen <i>Photobacterium damsela</i> subsp. <i>piscicida</i> : Insertion sequences proliferation is associated with chromosomal reorganisations and rampant gene decay. <i>Infection, Genetics and Evolution</i> , 2017, 54, 221-229.	1.0	15
1077	Complete Genome Sequence of <i>Acinetobacter calcoaceticus</i> CA16, a Bacterium Capable of Degrading Diesel and Lignin. <i>Genome Announcements</i> , 2017, 5, .	0.8	8
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.	1.2	35
1079	Comparison of molecular serotyping approaches of <i>Streptococcus agalactiae</i> from genomic sequences. <i>BMC Genomics</i> , 2017, 18, 429.	1.2	25
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.	1.2	33
1081	Comparative genomics of <i>Enterococcus</i> spp. isolated from bovine feces. <i>BMC Microbiology</i> , 2017, 17, 52.	1.3	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
1083	Draft genome sequence of type strain HBR26T and description of <i>Rhizobium aethiopicum</i> sp. nov.. <i>Standards in Genomic Sciences</i> , 2017, 12, 14.	1.5	26
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
1085	Detection of the cryptic prophage-like molecule pBtic235 in <i>Bacillus thuringiensis</i> subsp. <i>israelensis</i> . <i>Research in Microbiology</i> , 2017, 168, 319-330.	1.0	19

#	ARTICLE	IF	CITATIONS
1086	Genome-scale analysis of the non-cultivable <i>Treponema pallidum</i> reveals extensive within-patient genetic variation. <i>Nature Microbiology</i> , 2017, 2, 16190.	5.9	81
1087	Molecular Characterization of OXA-48-Like-Producing Enterobacteriaceae in the Czech Republic and Evidence for Horizontal Transfer of pOXA-48-Like Plasmids. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	74
1088	Genomic analysis of the multi-drug-resistant clinical isolate <i>Myroides odoratimimus</i> PR63039. <i>Molecular Genetics and Genomics</i> , 2017, 292, 133-144.	1.0	14
1089	Lactate- and acetate-based cross-feeding interactions between selected strains of lactobacilli, bifidobacteria and colon bacteria in the presence of inulin-type fructans. <i>International Journal of Food Microbiology</i> , 2017, 241, 225-236.	2.1	123
1090	Analysis of the complete plastomes of three species of Membranoptera (Ceramiales, Rhodophyta) from Pacific North America. <i>Journal of Phycology</i> , 2017, 53, 32-43.	1.0	12
1091	Microdiversification of a Pelagic Polynucleobacter Species Is Mainly Driven by Acquisition of Genomic Islands from a Partially Interspecific Gene Pool. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	55
1092	The use of Oxford Nanopore native barcoding for complete genome assembly. <i>GigaScience</i> , 2017, 6, 1-6.	3.3	19
1093	Complete Genome Sequence of <i>Lactobacillus acidophilus</i> Strain ATCC 53544. <i>Genome Announcements</i> , 2017, 5, .	0.8	5
1094	Nanopore DNA Sequencing and Genome Assembly on the International Space Station. <i>Scientific Reports</i> , 2017, 7, 18022.	1.6	264
1095	Genomic Analysis of Factors Associated with Low Prevalence of Antibiotic Resistance in Extraintestinal Pathogenic <i>Escherichia coli</i> Sequence Type 95 Strains. <i>MSphere</i> , 2017, 2, .	1.3	37
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.	1.6	47
1097	Draft Genome Sequence of a <i>Pseudomonas aeruginosa</i> NA04 Bacterium Isolated from an Entomopathogenic Nematode. <i>Genome Announcements</i> , 2017, 5, .	0.8	3
1098	Insights into the Existence of Isomeric Plastomes in Cupressoideae (Cupressaceae). <i>Genome Biology and Evolution</i> , 2017, 9, 1110-1119.	1.1	53
1099	Computational Methods in Microbial Population Genomics. <i>Population Genomics</i> , 2017, , 3-29.	0.2	2
1100	Trajectories and Drivers of Genome Evolution in Surface-Associated Marine <i>Phaeobacter</i> . <i>Genome Biology and Evolution</i> , 2017, 9, 3297-3311.	1.1	13
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.	1.7	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.	0.9	7
1103	accD nuclear transfer of <i>Platycodon grandiflorum</i> and the plastid of early Campanulaceae. <i>BMC Genomics</i> , 2017, 18, 607.	1.2	20

#	ARTICLE	IF	CITATIONS
1104	Complete plastome sequencing of both living species of Circaeasteraceae (Ranunculales) reveals unusual rearrangements and the loss of the <i>ndh</i> gene family. <i>BMC Genomics</i> , 2017, 18, 592.	1.2	51
1105	How to Name and Classify Your Phage: An Informal Guide. <i>Viruses</i> , 2017, 9, 70.	1.5	323
1106	The Complete Chloroplast Genome Sequences of Six <i>Rehmannia</i> Species. <i>Genes</i> , 2017, 8, 103.	1.0	78
1107	Complete Genome Sequences of Two Acetic Acid-Producing <i>Acetobacter pasteurianus</i> Strains (Subsp.) Tj ETQq1 1 0.784314 rgBT /Over 2017, 5, 33.	2.0	9
1108	Complete Genome Sequence and Comparative Analysis of <i>Staphylococcus condimenti</i> DSM 11674, a Potential Starter Culture Isolated from Soy Sauce Mash. <i>Frontiers in Bioengineering and Biotechnology</i> , 2017, 5, 56.	2.0	1
1109	Comparative Genomics of the Zoonotic Pathogen <i>Ehrlichia chaffeensis</i> Reveals Candidate Type IV Effectors and Putative Host Cell Targets. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 6, 204.	1.8	5
1110	The Bioinformatics Analysis of Comparative Genomics of <i>Mycobacterium tuberculosis</i> Complex (MTBC) Provides Insight into Dissimilarities between Intraspecific Groups Differing in Host Association, Virulence, and Epitope Diversity. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 88.	1.8	69
1111	The Glycolytic Versatility of <i>Bacteroides uniformis</i> CECT 7771 and Its Genome Response to Oligo and Polysaccharides. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 383.	1.8	47
1112	Key Impact of an Uncommon Plasmid on <i>Bacillus amyloliquefaciens</i> subsp. <i>plantarum</i> S499 Developmental Traits and Lipopeptide Production. <i>Frontiers in Microbiology</i> , 2017, 8, 17.	1.5	15
1113	The Histidine Decarboxylase Gene Cluster of <i>Lactobacillus parabuchneri</i> Was Gained by Horizontal Gene Transfer and Is Mobile within the Species. <i>Frontiers in Microbiology</i> , 2017, 8, 218.	1.5	40
1114	Genome-Guided Insights into the Plant Growth Promotion Capabilities of the Physiologically Versatile <i>Bacillus aryabhatai</i> Strain AB211. <i>Frontiers in Microbiology</i> , 2017, 8, 411.	1.5	98
1115	Pan-Genomic Analysis Permits Differentiation of Virulent and Non-virulent Strains of <i>Xanthomonas arboricola</i> That Cohabit <i>Prunus</i> spp. and Elucidate Bacterial Virulence Factors. <i>Frontiers in Microbiology</i> , 2017, 8, 573.	1.5	38
1116	In silico Prediction, in vitro Antibacterial Spectrum, and Physicochemical Properties of a Putative Bacteriocin Produced by <i>Lactobacillus rhamnosus</i> Strain L156.4. <i>Frontiers in Microbiology</i> , 2017, 8, 876.	1.5	29
1117	Comparative Genomic Characterization of the Highly Persistent and Potentially Virulent <i>Cronobacter sakazakii</i> ST83, CC65 Strain H322 and Other ST83 Strains. <i>Frontiers in Microbiology</i> , 2017, 8, 1136.	1.5	31
1118	Insights into a Novel <i>bla</i> KPC-2-Encoding IncP-6 Plasmid Reveal Carbapenem-Resistance Circulation in Several Enterobacteriaceae Species from Wastewater and a Hospital Source in Spain. <i>Frontiers in Microbiology</i> , 2017, 8, 1143.	1.5	50
1119	Comparative Analysis of the <i>Flavobacterium columnare</i> Genomovar I and II Genomes. <i>Frontiers in Microbiology</i> , 2017, 8, 1375.	1.5	37
1120	Complete Genome Analysis of <i>Thermus parvatiensis</i> and Comparative Genomics of <i>Thermus</i> spp. Provide Insights into Genetic Variability and Evolution of Natural Competence as Strategic Survival Attributes. <i>Frontiers in Microbiology</i> , 2017, 8, 1410.	1.5	16
1121	Comparative Sequence Analysis of Multidrug-Resistant IncA/C Plasmids from <i>Salmonella enterica</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 1459.	1.5	50

#	ARTICLE	IF	CITATIONS
1122	Oyster RNA-seq Data Support the Development of Malacoherpesviridae Genomics. <i>Frontiers in Microbiology</i> , 2017, 8, 1515.	1.5	20
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.	1.5	28
1124	Phylogenomic, Pan-genomic, Pathogenomic and Evolutionary Genomic Insights into the Agronomically Relevant Enterobacteria <i>Pantoea ananatis</i> and <i>Pantoea stewartii</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 1755.	1.5	20
1125	Characterization of Four Multidrug Resistance Plasmids Captured from the Sediments of an Urban Coastal Wetland. <i>Frontiers in Microbiology</i> , 2017, 8, 1922.	1.5	33
1126	Genomic Comparison among Lethal Invasive Strains of <i>Streptococcus pyogenes</i> Serotype M1. <i>Frontiers in Microbiology</i> , 2017, 8, 1993.	1.5	2
1127	Complete Genome Sequence Analysis of <i>Enterobacter</i> sp. SA187, a Plant Multi-Stress Tolerance Promoting Endophytic Bacterium. <i>Frontiers in Microbiology</i> , 2017, 8, 2023.	1.5	83
1128	Genomic Comparisons Reveal Microevolutionary Differences in <i>Mycobacterium abscessus</i> Subspecies. <i>Frontiers in Microbiology</i> , 2017, 8, 2042.	1.5	16
1129	Toward Understanding Phage:Host Interactions in the Rumen; Complete Genome Sequences of Lytic Phages Infecting Rumen Bacteria. <i>Frontiers in Microbiology</i> , 2017, 8, 2340.	1.5	28
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.	1.5	15
1131	Synergistic Antimicrobial Interaction between Honey and Phage against <i>Escherichia coli</i> Biofilms. <i>Frontiers in Microbiology</i> , 2017, 8, 2407.	1.5	64
1132	Genome Characterization of the First Mimiviruses of Lineage C Isolated in Brazil. <i>Frontiers in Microbiology</i> , 2017, 8, 2562.	1.5	16
1133	Exception to the Rule: Genomic Characterization of Naturally Occurring Unusual <i>Vibrio cholerae</i> Strains with a Single Chromosome. <i>International Journal of Genomics</i> , 2017, 2017, 1-14.	0.8	18
1134	Genomic divergence and cohesion in a species of pelagic freshwater bacteria. <i>BMC Genomics</i> , 2017, 18, 794.	1.2	14
1135	Evolutionary Context of Non-“Sorbitol-Fermenting Shiga Toxin”-Producing <i>Escherichia coli</i> O55:H7. <i>Emerging Infectious Diseases</i> , 2017, 23, 1966-1973.	2.0	24
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
1137	Rapid evolutionary divergence of diploid and allotetraploid <i>Gossypium</i> mitochondrial genomes. <i>BMC Genomics</i> , 2017, 18, 876.	1.2	23
1138	Draft Genome Sequences of the Multiresistant <i>Escherichia coli</i> C20 Strain, Isolated from Domestic Chicken Gut Microbiota. <i>Genome Announcements</i> , 2017, 5, .	0.8	0
1139	Genetic Analysis of <i>Vibrio parahaemolyticus</i> O3:K6 Strains That Have Been Isolated in Mexico Since 1998. <i>PLoS ONE</i> , 2017, 12, e0169722.	1.1	12

#	ARTICLE	IF	CITATIONS
1140	Within-host whole genome analysis of an antibiotic resistant <i>Pseudomonas aeruginosa</i> strain sub-type in cystic fibrosis. <i>PLoS ONE</i> , 2017, 12, e0172179.	1.1	31
1141	Comprehensive bioinformatics analysis of <i>Mycoplasma pneumoniae</i> genomes to investigate underlying population structure and type-specific determinants. <i>PLoS ONE</i> , 2017, 12, e0174701.	1.1	27
1142	Analyses of the probiotic property and stress resistance-related genes of <i>Lactococcus lactis</i> subsp. <i>lactis</i> NCDO 2118 through comparative genomics and in vitro assays. <i>PLoS ONE</i> , 2017, 12, e0175116.	1.1	51
1143	Comparative genomic analysis between <i>Corynebacterium pseudotuberculosis</i> strains isolated from buffalo. <i>PLoS ONE</i> , 2017, 12, e0176347.	1.1	30
1144	Characterization of the emerging zoonotic pathogen <i>Arcobacter thereius</i> by whole genome sequencing and comparative genomics. <i>PLoS ONE</i> , 2017, 12, e0180493.	1.1	21
1145	Comparative genomics of two super-shedder isolates of <i>Escherichia coli</i> O157:H7. <i>PLoS ONE</i> , 2017, 12, e0182940.	1.1	19
1146	Plastid and mitochondrial genomes of <i>Coccoloba langsdorfii</i> (Fucales, Phaeophyceae) and the utility of molecular markers. <i>PLoS ONE</i> , 2017, 12, e0187104.	1.1	9
1147	Promiscuous signaling by a regulatory system unique to the pandemic PMEN1 pneumococcal lineage. <i>PLoS Pathogens</i> , 2017, 13, e1006339.	2.1	38
1148	Horizontal acquisition of a hypoxia-responsive molybdenum cofactor biosynthesis pathway contributed to <i>Mycobacterium tuberculosis</i> pathoadaptation. <i>PLoS Pathogens</i> , 2017, 13, e1006752.	2.1	32
1149	Patterns and Processes of <i>Mycobacterium bovis</i> Evolution Revealed by Phylogenomic Analyses. <i>Genome Biology and Evolution</i> , 2017, 9, 521-535.	1.1	31
1150	Genomics-enabled analysis of the emergent disease cotton bacterial blight. <i>PLoS Genetics</i> , 2017, 13, e1007003.	1.5	36
1151	Whole genome sequence of the <i>Treponema pallidum</i> subsp. <i>pallidum</i> strain Amoy: An Asian isolate highly similar to SS14. <i>PLoS ONE</i> , 2017, 12, e0182768.	1.1	47
1152	Identification of a mouse <i>Lactobacillus johnsonii</i> strain with deconjugase activity against the FXR antagonist T-12-MCA. <i>PLoS ONE</i> , 2017, 12, e0183564.	1.1	28
1153	A highly specific phage defense system is a conserved feature of the <i>Vibrio cholerae</i> mobilome. <i>PLoS Genetics</i> , 2017, 13, e1006838.	1.5	101
1154	Expression and evolutionary patterns of mycobacteriophage D29 and its temperate close relatives. <i>BMC Microbiology</i> , 2017, 17, 225.	1.3	24
1155	Alignment-free sequence comparison: benefits, applications, and tools. <i>Genome Biology</i> , 2017, 18, 186.	3.8	371
1156	Genome characterization of a novel binary toxin-positive strain of <i>Clostridium difficile</i> and comparison with the epidemic O27 and O78 strains. <i>Gut Pathogens</i> , 2017, 9, 42.	1.6	15
1157	Draft genome sequences of <i>Bradyrhizobium shewense</i> sp. nov. ERR11T and <i>Bradyrhizobium yuanmingense</i> CCBAU 10071T. <i>Standards in Genomic Sciences</i> , 2017, 12, 74.	1.5	29

#	ARTICLE	IF	CITATIONS
1158	The genomic study of an environmental isolate of <i>Scedosporium apiospermum</i> shows its metabolic potential to degrade hydrocarbons. <i>Standards in Genomic Sciences</i> , 2017, 12, 71.	1.5	25
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
1161	Pneumococcal 23B Molecular Subtype Identified Using Whole Genome Sequencing. <i>Genome Biology and Evolution</i> , 2017, 9, 2145-2158.	1.1	12
1162	Fatal Outbreak in Tonkean Macaques Caused by Possibly Novel Orthopoxvirus, Italy, January 20151. <i>Emerging Infectious Diseases</i> , 2017, 23, 1941-1949.	2.0	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.	1.1	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.	2.0	21
1165	Coccolithoviruses: A Review of Cross-Kingdom Genomic Thievery and Metabolic Thuggery. <i>Viruses</i> , 2017, 9, 52.	1.5	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.	1.5	18
1167	De novo assembly of genomes from long sequence reads reveals uncharted territories of <i>Propionibacterium freudenreichii</i> . <i>BMC Genomics</i> , 2017, 18, 790.	1.2	16
1168	From genomes to genotypes: molecular epidemiological analysis of <i>Chlamydia gallinacea</i> reveals a high level of genetic diversity for this newly emerging chlamydial pathogen. <i>BMC Genomics</i> , 2017, 18, 949.	1.2	15
1169	Draft Genome Sequence of <i>Lawsonia intracellularis</i> Strain E40504, Isolated from a Horse Diagnosed with Equine Proliferative Enteropathy. <i>Genome Announcements</i> , 2017, 5, .	0.8	5
1170	The complete plastid genome and nuclear genome markers provide molecular evidence for the hybrid origin of <i>Pulsatilla hackettii</i> Pohl.. <i>Turkish Journal of Botany</i> , 2017, 41, 329-337.	0.5	10
1171	Complete Genome Sequence of <i>Mycobacterium avium</i> subsp. <i>hominissuis</i> Strain H87 Isolated from an Indoor Water Sample. <i>Genome Announcements</i> , 2017, 5, .	0.8	17
1172	Transferable vancomycin resistance in clade B commensal-type <i>Enterococcus faecium</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2018, 73, 1479-1486.	1.3	20
1173	Culture-Facilitated Comparative Genomics of the Facultative Symbiont <i>Hamiltonella defensa</i> . <i>Genome Biology and Evolution</i> , 2018, 10, 786-802.	1.1	37
1174	Selection of hyperproduction of AmpC and SME-1 in a carbapenem-resistant <i>Serratia marcescens</i> isolate during antibiotic therapy. <i>Journal of Antimicrobial Chemotherapy</i> , 2018, 73, 1256-1262.	1.3	13
1175	Rates of Mutation and Recombination in Siphoviridae Phage Genome Evolution over Three Decades. <i>Molecular Biology and Evolution</i> , 2018, 35, 1147-1159.	3.5	61



#	ARTICLE	IF	CITATIONS
1176	Complete Genome Sequence of a New Zealand Isolate of the Bovine Pathogen <i>Streptococcus uberis</i> . <i>Genome Announcements</i> , 2018, 6, .	0.8	3
1177	Rhizobacteria improve sugarcane growth and photosynthesis under well-watered conditions. <i>Annals of Applied Biology</i> , 2018, 172, 309-320.	1.3	13
1178	Characterization of the Complete Nucleotide Sequences of IMP-4-Encoding Plasmids, Belonging to Diverse Inc Families, Recovered from Enterobacteriaceae Isolates of Wildlife Origin. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	1.4	22
1179	Phylogenomic analysis demonstrates a pattern of rare and long-lasting concerted evolution in prokaryotes. <i>Communications Biology</i> , 2018, 1, 12.	2.0	16
1180	First Description in Greece of <i>mpHC</i> -Positive Staphylococci Causing Subclinical Mastitis in Ewes. <i>Microbial Drug Resistance</i> , 2018, 24, 1050-1053.	0.9	1
1181	Dense infraspecific sampling reveals rapid and independent trajectories of plastome degradation in a heterotrophic orchid complex. <i>New Phytologist</i> , 2018, 218, 1192-1204.	3.5	56
1182	Prediction of Fluoroquinolone Susceptibility Directly from Whole-Genome Sequence Data by Using Liquid Chromatography-Tandem Mass Spectrometry To Identify Mutant Genotypes. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	1.4	13
1183	Draft Genome Sequences of Four Clinical <i>Legionella pneumophila</i> Isolates from Ontario, Canada. <i>Genome Announcements</i> , 2018, 6, .	0.8	0
1184	Comparative genomics of Cp8viruses with special reference to <i>Campylobacter</i> phage vB_CjeM_loS1, isolated from a slaughterhouse in Ireland. <i>Archives of Virology</i> , 2018, 163, 2139-2154.	0.9	7
1185	Genetic exchange and reassignment in <i>Porphyromonas gingivalis</i> . <i>Journal of Oral Microbiology</i> , 2018, 10, 1457373.	1.2	16
1186	Characterization of Extensively Drug-Resistant or Pandrug-Resistant Sequence Type 147 and 101 OXA-48-Producing <i>Klebsiella pneumoniae</i> Causing Bloodstream Infections in Patients in an Intensive Care Unit. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	1.4	54
1187	Plasmids carrying DHA-1 $\beta$ -lactamases. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2018, 37, 1197-1209.	1.3	21
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.	1.0	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.	0.8	16
1190	The reduced genome of <i>Candidatus</i> <i>Kinetoplastibacterium sorsogonicusi</i> , the endosymbiont of <i>Kentomonas sorsogonicus</i> (Trypanosomatidae): loss of the haem-synthesis pathway. <i>Parasitology</i> , 2018, 145, 1287-1293.	0.7	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, .	1.3	14
1192	Plastid phylogenomics resolves infrafamilial relationships of the Styracaceae and sheds light on the backbone relationships of the Ericales. <i>Molecular Phylogenetics and Evolution</i> , 2018, 121, 198-211.	1.2	42
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.	0.4	15

#	ARTICLE	IF	CITATIONS
1194	Fitness Tradeoffs of Antibiotic Resistance in Extraintestinal Pathogenic <i>Escherichia coli</i> . <i>Genome Biology and Evolution</i> , 2018, 10, 667-679.	1.1	49
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, .	1.8	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.	1.7	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, .	1.0	27
1199	Biochemical and genetic characterization of a novel metallo-β-lactamase from marine bacterium <i>Erythrobacter litoralis</i> HTCC 2594. <i>Scientific Reports</i> , 2018, 8, 803.	1.6	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.	1.0	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.	1.6	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.	1.8	14
1203	Bioinformatic Approaches for Comparative Analysis of Viruses. <i>Methods in Molecular Biology</i> , 2018, 1704, 401-417.	0.4	1
1204	Pan-Genome Storage and Analysis Techniques. <i>Methods in Molecular Biology</i> , 2018, 1704, 29-53.	0.4	24
1205	Phylogenomics. <i>Methods in Molecular Biology</i> , 2018, 1704, 103-187.	0.4	15
1206	Sequence-Based Synteny Analysis of Multiple Large Genomes. <i>Methods in Molecular Biology</i> , 2018, 1704, 317-329.	0.4	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, .	1.8	51
1208	Aureo Wiki  µ The repository of the <i>Staphylococcus aureus</i> research and annotation community. <i>International Journal of Medical Microbiology</i> , 2018, 308, 558-568.	1.5	99
1209	Characterization of KPC-Encoding Plasmids from <i>Enterobacteriaceae</i> Isolated in a Czech Hospital. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	1.4	13
1210	Transmission and persistence of IncF conjugative plasmids in the gut microbiota of full-term infants. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	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.	1.0	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.	1.9	5
1213	Genetic Competence Drives Genome Diversity in <i>Bacillus subtilis</i> . <i>Genome Biology and Evolution</i> , 2018, 10, 108-124.	1.1	67
1214	Organelle 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.	0.8	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.	1.2	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.	1.2	24
1218	A hybrid reference-guided de novo assembly approach for generating <i>Cyclospora</i> mitochondrion genomes. <i>Gut Pathogens</i> , 2018, 10, 15.	1.6	17
1219	Ancient DNA study reveals HLA susceptibility locus for leprosy in medieval Europeans. <i>Nature Communications</i> , 2018, 9, 1569.	5.8	67
1220	Male-killing toxin in a bacterial symbiont of <i>Drosophila</i> . <i>Nature</i> , 2018, 557, 252-255.	13.7	111
1221	A new strategy to infer circularity applied to four new complete frog mitogenomes. <i>Ecology and Evolution</i> , 2018, 8, 4011-4018.	0.8	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.	1.5	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.	1.0	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.	0.9	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, .	1.4	15
1226	Hitting with a BAM: Selective Killing by Lectin-Like Bacteriocins. <i>MBio</i> , 2018, 9, .	1.8	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.	1.6	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.	5.1	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.	2.0	122

#	ARTICLE	IF	CITATIONS
1230	A high-resolution genetic map of the cereal crown rot pathogen <i>Fusarium pseudograminearum</i> provides a near-complete genome assembly. <i>Molecular Plant Pathology</i> , 2018, 19, 217-226.	2.0	35
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.	1.0	40
1232	Organization of plastid genomes in the freshwater red algal order Batrachospermales (Rhodophyta). <i>Journal of Phycology</i> , 2018, 54, 25-33.	1.0	8
1233	Tropical soils are a reservoir for fluorescent <i>Pseudomonas</i> spp. biodiversity. <i>Environmental Microbiology</i> , 2018, 20, 62-74.	1.8	28
1234	The repeat structure of two paralogous genes, <i>Yersinia ruckeri</i> invasin ( <i>yrInv</i> ) and a <i>Y. ruckeri</i> invasin-like molecule ( <i>yrllm</i> ) sheds light on the evolution of adhesive capacities of a fish pathogen. <i>Journal of Structural Biology</i> , 2018, 201, 171-183.	1.3	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.	2.2	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.	1.3	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.	0.8	3
1238	Acquisition of the Phosphate Transporter <i>NptA</i> Enhances <i>Staphylococcus aureus</i> Pathogenesis by Improving Phosphate Uptake in Divergent Environments. <i>Infection and Immunity</i> , 2018, 86, .	1.0	20
1239	The gut virome of the protochordate model organism, <i>Ciona intestinalis</i> subtype A. <i>Virus Research</i> , 2018, 244, 137-146.	1.1	17
1240	Bacteriophage Taxonomy: An Evolving Discipline. <i>Methods in Molecular Biology</i> , 2018, 1693, 57-71.	0.4	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.	1.8	22
1242	Essential Steps in Characterizing Bacteriophages: Biology, Taxonomy, and Genome Analysis. <i>Methods in Molecular Biology</i> , 2018, 1681, 197-215.	0.4	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, .	0.3	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, .	0.3	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.	1.1	4
1246	New Reference Genome Sequences for 17 Bacterial Strains of the Honey Bee Gut Microbiota. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	14
1247	Complete Genome Sequence of <i>Ferriphaseelus amnicola</i> Strain OYT1, a Neutrophilic, Stalk-Forming, Iron-Oxidizing Bacterium. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	4

#	ARTICLE	IF	CITATIONS
1248	Comparative genomic analysis of <i>Parageobacillus thermoglucosidasius</i> strains with distinct hydrogenogenic capacities. <i>BMC Genomics</i> , 2018, 19, 880.	1.2	20
1249	Visualization-assisted binning of metagenome assemblies reveals potential new pathogenic profiles in idiopathic travelers' diarrhea. <i>Microbiome</i> , 2018, 6, 201.	4.9	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, .	1.0	47
1251	The Enterococcus Cassette Chromosome, a Genomic Variation Enabler in Enterococci. <i>MSphere</i> , 2018, 3, .	1.3	7
1252	Complete mitochondrial genomes of six species of the freshwater red algal order Batrachospermales (Rhodophyta). <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 607-610.	0.2	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.	1.5	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.	1.1	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.	1.6	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> IV <sub>m</sub> ) containing the <i>tetK</i> gene. <i>Infection and Drug Resistance</i> , 2018, Volume 11, 2583-2592.	1.1	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.	1.1	19
1258	Genetic Loci Associated With Fluoride Resistance in <i>Streptococcus mutans</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 3093.	1.5	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, .	0.3	7
1260	Complete Genome Sequence of <i>Klebsiella pneumoniae</i> Siphophage Sugarland. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	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, .	0.3	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.	1.5	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.	1.0	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, .	0.3	8
1265	Loss of Bacitracin Resistance Due to a Large Genomic Deletion among <i>Bacillus anthracis</i> Strains. <i>MSystems</i> , 2018, 3, .	1.7	9

#	ARTICLE	IF	CITATIONS
1266	Phenotypic and genomic analyses of bacteriophages targeting environmental and clinical CS3-expressing enterotoxigenic <i>Escherichia coli</i> (ETEC) strains. <i>PLoS ONE</i> , 2018, 13, e0209357.	1.1	8
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.	1.5	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.	1.6	12
1270	The mitochondrial genome of <i>Endoconidiophora resinifera</i> is intron rich. <i>Scientific Reports</i> , 2018, 8, 17591.	1.6	56
1271	A Strain of an Emerging Indian <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> Pathotype Defeats the Rice Bacterial Blight Resistance Gene <i>xa13</i> Without Inducing a Clade III SWEET Gene and Is Nearly Identical to a Recent Thai Isolate. <i>Frontiers in Microbiology</i> , 2018, 9, 2703.	1.5	17
1272	Genome Analysis of Haplotype D of <i>Candidatus Liberibacter Solanacearum</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 2933.	1.5	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.	1.5	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.	1.6	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.	1.2	26
1276	Genome-wide analysis of <i>Borrelia turcica</i> and <i>Candidatus Borrelia tachyglossi</i> <sup>TM</sup> 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.	1.0	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.	1.2	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, .	1.4	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.	0.8	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.	1.5	50
1282	S-plot2: Rapid Visual and Statistical Analysis of Genomic Sequences. <i>Evolutionary Bioinformatics</i> , 2018, 14, 117693431879735.	0.6	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.	1.1	9



#	ARTICLE	IF	CITATIONS
1284	A Mechanism for Genome Size Reduction Following Genomic Rearrangements. <i>Frontiers in Genetics</i> , 2018, 9, 454.	1.1	23
1285	Achieving Accurate Sequence and Annotation Data for <i>Caulobacter vibrioides</i> CB13. <i>Current Microbiology</i> , 2018, 75, 1642-1648.	1.0	6
1286	Function of BriC peptide in the pneumococcal competence and virulence portfolio. <i>PLoS Pathogens</i> , 2018, 14, e1007328.	2.1	44
1287	Comparative Genomics of the First and Complete Genome of <i>Actinobacillus porcitonisillarum</i> Supports the Novel Species Hypothesis. <i>International Journal of Genomics</i> , 2018, 2018, 1-8.	0.8	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.	0.8	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.	1.5	31
1290	Prophage-driven genomic structural changes promote <i>Bartonella</i> vertical evolution. <i>Genome Biology and Evolution</i> , 2018, 10, 3089-3103.	1.1	13
1291	Genome sequence of <i>Shigella sonnei</i> 4303. <i>Gut Pathogens</i> , 2018, 10, 47.	1.6	2
1292	Comparative study on mitogenomes of green tide algae. <i>Genetica</i> , 2018, 146, 529-540.	0.5	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.	1.6	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
1295	Conversion of Methionine to Cysteine in <i>Lactobacillus paracasei</i> Depends on the Highly Mobile <i>cysK-ctl-cysE</i> Gene Cluster. <i>Frontiers in Microbiology</i> , 2018, 9, 2415.	1.5	10
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.	1.8	9
1297	Insights into the genome sequence of ovine <i>Pasteurella multocida</i> type A strain associated with pneumonic pasteurellosis. <i>Small Ruminant Research</i> , 2018, 169, 167-175.	0.6	5
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.	1.3	24
1299	Comparative Genomics of <i>Wolbachia</i> Cardinium Dual Endosymbiosis in a Plant-Parasitic Nematode. <i>Frontiers in Microbiology</i> , 2018, 9, 2482.	1.5	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.	1.5	6
1301	<i>Cupriavidus metallidurans</i> Strains with Different Mobilomes and from Distinct Environments Have Comparable Phenomes. <i>Genes</i> , 2018, 9, 507.	1.0	21

#	ARTICLE	IF	CITATIONS
1302	Genome-scale analysis of <i>Acetobacterium bakii</i> reveals the cold adaptation of psychrotolerant acetogens by post-transcriptional regulation. <i>Rna</i> , 2018, 24, 1839-1855.	1.6	10
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.	0.8	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.	1.5	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.	1.3	2
1306	Coordinate systems for supergenomes. <i>Algorithms for Molecular Biology</i> , 2018, 13, 15.	0.3	10
1307	Homology Search and Multiple Alignment. <i>Computational Biology</i> , 2018, , 325-360.	0.1	0
1308	Evaluating the origin and virulence of a <i>Helicobacter pylori</i> <i>cagA</i> -positive strain isolated from a non-human primate. <i>Scientific Reports</i> , 2018, 8, 15981.	1.6	11
1309	Dynamic evolution of inverted repeats in Euglenophyta plastid genomes. <i>Scientific Reports</i> , 2018, 8, 16071.	1.6	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.	1.5	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, .	1.8	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, .	1.4	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.	1.5	43
1314	Spread of Carbapenem Resistance by Transposition and Conjugation Among <i>Pseudomonas aeruginosa</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 2057.	1.5	38
1315	Comparative genomics of Czech vaccine strains of <i>Bordetella pertussis</i> . <i>Pathogens and Disease</i> , 2018, 76, .	0.8	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.	0.9	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.	1.2	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.	1.2	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.	1.2	16

#	ARTICLE	IF	CITATIONS
1320	A Phylogenomic Study of <i>Acanthamoeba polyphaga</i> Draft Genome Sequences Suggests Genetic Exchanges With Giant Viruses. <i>Frontiers in Microbiology</i> , 2018, 9, 2098.	1.5	27
1321	Approximate, simultaneous comparison of microbial genome architectures via syntenic anchoring of quiver representations. <i>Bioinformatics</i> , 2018, 34, i732-i742.	1.8	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.	2.4	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, .	0.3	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.	1.6	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.	6.5	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.	3.5	60
1327	PGAweb: A Web Server for Bacterial Pan-Genome Analysis. <i>Frontiers in Microbiology</i> , 2018, 9, 1910.	1.5	24
1328	PGAP-X: extension on pan-genome analysis pipeline. <i>BMC Genomics</i> , 2018, 19, 36.	1.2	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.	1.2	28
1330	Evolution of the U.S. Biological Select Agent <i>Rathayibacter toxicus</i> . <i>MBio</i> , 2018, 9, .	1.8	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.	1.2	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.	1.1	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.	1.1	12
1334	Complete Genome Sequence of Cd(II)-Resistant <i>Arthrobacter</i> sp. PGP41, a Plant Growth-Promoting Bacterium with Potential in Microbe-Assisted Phytoremediation. <i>Current Microbiology</i> , 2018, 75, 1231-1239.	1.0	29
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
1336	<i>Raphidocelis subcapitata</i> (= <i>Pseudokirchneriella subcapitata</i> ) provides an insight into genome evolution and environmental adaptations in the Sphaeropleales. <i>Scientific Reports</i> , 2018, 8, 8058.	1.6	52
1337	Disruption of <i>mplA</i> Activates $\beta$ -Lactamase Production in <i>Stenotrophomonas maltophilia</i> and <i>Pseudomonas aeruginosa</i> Clinical Isolates. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	1.4	13

#	ARTICLE	IF	CITATIONS
1338	Genomic and Geographic Context for the Evolution of High-Risk Carbapenem-Resistant <i>Enterobacter cloacae</i> Complex Clones ST171 and ST78. <i>MBio</i> , 2018, 9, .	1.8	67
1339	Transmission of <i>Clostridium difficile</i> from asymptotically colonized or infected long-term care facility residents. <i>Infection Control and Hospital Epidemiology</i> , 2018, 39, 909-916.	1.0	38
1340	A closely-related clade of globally distributed bloom-forming cyanobacteria within the Nostocales. <i>Harmful Algae</i> , 2018, 77, 93-107.	2.2	27
1341	Genome Sequences of <i>Shewanella baltica</i> and <i>Shewanella morhuae</i> Strains Isolated from the Gastrointestinal Tract of Freshwater Fish. <i>Genome Announcements</i> , 2018, 6, .	0.8	5
1342	Screening and characterization of prophages in <i>Desulfovibrio</i> genomes. <i>Scientific Reports</i> , 2018, 8, 9273.	1.6	31
1343	MrBait: universal identification and design of targeted-enrichment capture probes. <i>Bioinformatics</i> , 2018, 34, 4293-4296.	1.8	17
1344	Center Rot of Onion ( <i>Allium cepa</i> ) Caused by <i>Pantoea ananatis</i> Requires <i>pepM</i> , a Predicted Phosphonate-Related Gene. <i>Molecular Plant-Microbe Interactions</i> , 2018, 31, 1291-1300.	1.4	37
1345	Genome of <i>Serratia nematodiphila</i> MB307 offers unique insights into its diverse traits. <i>Genome</i> , 2018, 61, 469-476.	0.9	15
1346	Characterization and Comparative Analysis of the Complete Chloroplast Genome of the Critically Endangered Species <i>Streptocarpus teitensis</i> (Gesneriaceae). <i>BioMed Research International</i> , 2018, 2018, 1-11.	0.9	6
1347	Genomics reveals abundant speciation in the coral reef building alga <i>Porolithon onkodes</i> (Corallinales, Rhodophyta). <i>Journal of Phycology</i> , 2018, 54, 429-434.	1.0	87
1348	Complete Genome Sequence of a Ciprofloxacin-Resistant <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Kentucky Sequence Type 198 Strain, PU131, Isolated from a Human Patient in Washington State. <i>Genome Announcements</i> , 2018, 6, .	0.8	9
1349	TERribly Difficult: Searching for Telomerase RNAs in <i>Saccharomycetes</i> . <i>Genes</i> , 2018, 9, 372.	1.0	12
1350	Utilization of Hybrid Assembly Approach to Determine the Genome of an Opportunistic Pathogenic Fungus, <i>Candida albicans</i> TIMM 1768. <i>Genome Biology and Evolution</i> , 2018, 10, 2017-2022.	1.1	30
1351	Diversity of DHA-1-encoding plasmids in <i>Klebsiella pneumoniae</i> isolates from 16 French hospitals. <i>Journal of Antimicrobial Chemotherapy</i> , 2018, 73, 2981-2989.	1.3	10
1352	Functional annotation and distribution overview of RNA families in 27 <i>Streptococcus agalactiae</i> genomes. <i>BMC Genomics</i> , 2018, 19, 556.	1.2	11
1353	Culture- and metagenomics-enabled analyses of the <i>Methanosphaera</i> genus reveals their monophyletic origin and differentiation according to genome size. <i>ISME Journal</i> , 2018, 12, 2942-2953.	4.4	24
1354	INSaFLU: an automated open web-based bioinformatics suite "from-reads" for influenza whole-genome-sequencing-based surveillance. <i>Genome Medicine</i> , 2018, 10, 46.	3.6	55
1355	The dorsoventral patterning of <i>Musca domestica</i> embryos: insights into BMP/Dpp evolution from the base of the lower cyclorraphan flies. <i>EvoDevo</i> , 2018, 9, 13.	1.3	5

#	ARTICLE	IF	CITATIONS
1356	Comparative Analysis of Complete Chloroplast Genomes of <i>Anemoclema</i> , <i>Anemone</i> , <i>Pulsatilla</i> , and <i>Hepatica</i> Revealing Structural Variations Among Genera in Tribe Anemoneae (Ranunculaceae). <i>Frontiers in Plant Science</i> , 2018, 9, 1097.	1.7	53
1357	Growth of <i>Carnobacterium</i> spp. isolated from chilled vacuum-packaged meat under relevant acidic conditions. <i>International Journal of Food Microbiology</i> , 2018, 286, 120-127.	2.1	20
1358	Mesophilic Sporeformers Identified in Whey Powder by Using Shotgun Metagenomic Sequencing. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	15
1359	High Quality Draft Genomes of the Type Strains <i>Geobacillus thermocatenulatus</i> DSM 730T, <i>G. uzenensis</i> DSM 23175T And <i>Parageobacillus galactosidasius</i> DSM 18751T. <i>Journal of Genomics</i> , 2018, 6, 20-23.	0.6	3
1360	Plastid Genome Evolution in the Early-Diverging Legume Subfamily Cercidoideae (Fabaceae). <i>Frontiers in Plant Science</i> , 2018, 9, 138.	1.7	97
1361	Low-Level Antimicrobials in the Medicinal Leech Select for Resistant Pathogens That Spread to Patients. <i>MBio</i> , 2018, 9, .	1.8	25
1362	Comparative genomic analyses of two novel qnrVC6 carrying multidrug-resistant <i>Pseudomonas</i> spp strains. <i>Microbial Pathogenesis</i> , 2018, 123, 269-274.	1.3	7
1363	Global Scale Dissemination of ST93: A Divergent <i>Staphylococcus aureus</i> Epidemic Lineage That Has Recently Emerged From Remote Northern Australia. <i>Frontiers in Microbiology</i> , 2018, 9, 1453.	1.5	29
1364	Genomic profiling of four cultivated <i>Candidatus Nitrotoga</i> spp. predicts broad metabolic potential and environmental distribution. <i>ISME Journal</i> , 2018, 12, 2864-2882.	4.4	42
1365	A Large Open Pangenome and a Small Core Genome for Giant Pandoraviruses. <i>Frontiers in Microbiology</i> , 2018, 9, 1486.	1.5	48
1366	Characterization of NDM-Encoding Plasmids From Enterobacteriaceae Recovered From Czech Hospitals. <i>Frontiers in Microbiology</i> , 2018, 9, 1549.	1.5	55
1367	Distribution and characterization of Shiga toxin converting temperate phages carried by <i>Shigella flexneri</i> in Hispaniola. <i>Infection, Genetics and Evolution</i> , 2018, 65, 321-328.	1.0	13
1368	Mutation of Agr Is Associated with the Adaptation of <i>Staphylococcus aureus</i> to the Host during Chronic Osteomyelitis. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 18.	1.8	64
1369	<i>Galleria mellonella</i> Reveals Niche Differences Between Highly Pathogenic and Closely Related Strains of <i>Francisella</i> spp.. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 188.	1.8	14
1370	<i>Enterococcus faecalis</i> AHG0090 is a Genetically Tractable Bacterium and Produces a Secreted Peptidic Bioactive that Suppresses Nuclear Factor Kappa B Activation in Human Gut Epithelial Cells. <i>Frontiers in Immunology</i> , 2018, 9, 790.	2.2	15
1371	New Aspects on <i>Listeria monocytogenes</i> ST5-ECVI Predominance in a Heavily Contaminated Cheese Processing Environment. <i>Frontiers in Microbiology</i> , 2018, 9, 64.	1.5	45
1372	Site-Specific Recombination at XerC/D Sites Mediates the Formation and Resolution of Plasmid Co-integrates Carrying a blaOXA-58- and TnaphA6-Resistance Module in <i>Acinetobacter baumannii</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 66.	1.5	65
1373	Analyzing AbrB-Knockout Effects through Genome and Transcriptome Sequencing of <i>Bacillus licheniformis</i> DW2. <i>Frontiers in Microbiology</i> , 2018, 9, 307.	1.5	24

#	ARTICLE	IF	CITATIONS
1374	Comparative Genomics and Biosynthetic Potential Analysis of Two Lichen-Isolated Amycolatopsis Strains. <i>Frontiers in Microbiology</i> , 2018, 9, 369.	1.5	18
1375	Comparative Genomic Analysis of <i>Holospira</i> spp., Intranuclear Symbionts of <i>Paramecia</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 738.	1.5	29
1376	The Genomic Basis of Intrinsic and Acquired Antibiotic Resistance in the Genus <i>Serratia</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 828.	1.5	53
1377	Convergent Loss of ABC Transporter Genes From <i>Clostridioides difficile</i> Genomes Is Associated With Impaired Tyrosine Uptake and p-Cresol Production. <i>Frontiers in Microbiology</i> , 2018, 9, 901.	1.5	30
1378	The Use of a Combined Bioinformatics Approach to Locate Antibiotic Resistance Genes on Plasmids From Whole Genome Sequences of <i>Salmonella enterica</i> Serovars From Humans in Ghana. <i>Frontiers in Microbiology</i> , 2018, 9, 1010.	1.5	38
1379	Arginine Catabolic Mobile Elements in Livestock-Associated Methicillin-Resistant Staphylococcal Isolates From Bovine Mastitic Milk in China. <i>Frontiers in Microbiology</i> , 2018, 9, 1031.	1.5	7
1380	Comparative Genomics of <i>Lactobacillus acidipiscis</i> ACA-DC 1533 Isolated From Traditional Greek Kopanisti Cheese Against Species Within the <i>Lactobacillus salivarius</i> Clade. <i>Frontiers in Microbiology</i> , 2018, 9, 1244.	1.5	22
1381	Comparative Genomics Provides Insights Into the Marine Adaptation in Sponge-Derived <i>Kocuriaflava</i> S43. <i>Frontiers in Microbiology</i> , 2018, 9, 1257.	1.5	22
1382	Integrative and Conjugative Elements (ICEs) in Pasteurellaceae Species and Their Detection by Multiplex PCR. <i>Frontiers in Microbiology</i> , 2018, 9, 1329.	1.5	26
1383	Investigating the Molecular Genetic Basis of Cytoplasmic Sex Determination Caused by <i>Wolbachia</i> Endosymbionts in Terrestrial Isopods. <i>Genes</i> , 2018, 9, 290.	1.0	17
1384	Plastome organization, genome-based phylogeny and evolution of plastid genes in Podophylloideae (Berberidaceae). <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 978-987.	1.2	44
1385	A Colicin M-Type Bacteriocin from <i>Pseudomonas aeruginosa</i> Targeting the HxuC Heme Receptor Requires a Novel Immunity Partner. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	16
1386	Complete Genome Sequence of <i>Escherichia coli</i> J53, an Azide-Resistant Laboratory Strain Used for Conjugation Experiments. <i>Genome Announcements</i> , 2018, 6, .	0.8	18
1387	Complete Chloroplast Genome of <i>Cercis chuniana</i> (Fabaceae) with Structural and Genetic Comparison to Six Species in Caesalpinioideae. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1286.	1.8	28
1388	Characterization of a New <i>Staphylococcus aureus</i> Kayvirus Harboring a Lysin Active against Biofilms. <i>Viruses</i> , 2018, 10, 182.	1.5	47
1389	Complete Nucleotide Sequence Analysis of a Novel <i>Bacillus subtilis</i> -Infecting Bacteriophage BSP10 and Its Effect on Poly-Gamma-Glutamic Acid Degradation. <i>Viruses</i> , 2018, 10, 240.	1.5	21
1390	Analysis of 19 Highly Conserved <i>Vibrio cholerae</i> Bacteriophages Isolated from Environmental and Patient Sources Over a Twelve-Year Period. <i>Viruses</i> , 2018, 10, 299.	1.5	29
1391	The <i>Nothoaspis amazoniensis</i> Complete Mitogenome: A Comparative and Phylogenetic Analysis. <i>Veterinary Sciences</i> , 2018, 5, 37.	0.6	4



#	ARTICLE	IF	CITATIONS
1392	Recombination Signal in Mycobacterium tuberculosis Stems from Reference-guided Assemblies and Alignment Artefacts. <i>Genome Biology and Evolution</i> , 2018, 10, 1920-1926.	1.1	27
1393	Organellar genomics: a useful tool to study evolutionary relationships and molecular evolution in Gracilariaceae (Rhodophyta). <i>Journal of Phycology</i> , 2018, 54, 775-787.	1.0	17
1394	Two different Xylella fastidiosa strains circulating in Italy: phylogenetic and evolutionary analyses. <i>Journal of Plant Interactions</i> , 2018, 13, 428-432.	1.0	6
1395	Molecular characterization of invasive meningococcal isolates in Burkina Faso as the relative importance of serogroups X and W increases, 2008–2012. <i>BMC Infectious Diseases</i> , 2018, 18, 337.	1.3	8
1396	Complete Genome Sequence of Clostridium kluveri JZZ Applied in Chinese Strong-Flavor Liquor Production. <i>Current Microbiology</i> , 2018, 75, 1429-1433.	1.0	11
1397	seq-seq-pan: building a computational pan-genome data structure on whole genome alignment. <i>BMC Genomics</i> , 2018, 19, 47.	1.2	25
1398	Genomic comparison of Clostridium species with the potential of utilizing red algal biomass for biobutanol production. <i>Biotechnology for Biofuels</i> , 2018, 11, 42.	6.2	41
1399	Comparative genomics of <i>Pseudomonas syringae</i> reveals convergent gene gain and loss associated with specialization onto cherry ( <i>Prunus avium</i> ). <i>New Phytologist</i> , 2018, 219, 672-696.	3.5	52
1400	The Siderophore Piscibactin Is a Relevant Virulence Factor for Vibrio anguillarum Favored at Low Temperatures. <i>Frontiers in Microbiology</i> , 2018, 9, 1766.	1.5	40
1401	Draft Genome Sequences of Nine Strains of Brochothrix thermosphacta, Carnobacterium divergens, Lactobacillus algidus, Lactobacillus fuchuensis, Lactococcus piscium, Leuconostoc gelidum subsp. gasicomitatum, Pseudomonas lundensis, and Weissella viridescens, a Collection of Psychrotrophic Species Involved in Meat and Seafood Spoilage. <i>Genome Announcements</i> , 2018, 6, .	0.8	7
1402	Developing a <i>Bacteroides</i> System for Function-Based Screening of DNA from the Human Gut Microbiome. <i>MSystems</i> , 2018, 3, .	1.7	9
1403	Characterization and induction of prophages in human gut-associated Bifidobacterium hosts. <i>Scientific Reports</i> , 2018, 8, 12772.	1.6	26
1404	Genomic analysis of the original Elberg <i>Brucella melitensis</i> Rev.1 vaccine strain reveals insights into virulence attenuation. <i>Virulence</i> , 2018, 9, 1436-1448.	1.8	10
1405	Genome Variation in the Model Halophilic Bacterium Salinibacter ruber. <i>Frontiers in Microbiology</i> , 2018, 9, 1499.	1.5	12
1406	Pathogenic adaptations of Colletotrichum fungi revealed by genome wide gene family evolutionary analyses. <i>PLoS ONE</i> , 2018, 13, e0196303.	1.1	46
1407	Genomic characterization of NDM-1 and 5, and OXA-181 carbapenemases in uropathogenic Escherichia coli isolates from Riyadh, Saudi Arabia. <i>PLoS ONE</i> , 2018, 13, e0201613.	1.1	34
1408	Evolution of Sequence Type 4821 Clonal Complex Meningococcal Strains in China from Prequinolone to Quinolone Era, 1972–2013. <i>Emerging Infectious Diseases</i> , 2018, 24, 683-690.	2.0	11
1409	Comparative Genomics and Phylogenetic Analysis Revealed the Chloroplast Genome Variation and Interspecific Relationships of Corylus (Betulaceae) Species. <i>Frontiers in Plant Science</i> , 2018, 9, 927.	1.7	48

#	ARTICLE	IF	CITATIONS
1410	Plastid Genome Degradation in the Endangered, Mycoheterotrophic, North American Orchid <i>Hexalectris warnockii</i> . <i>Genome Biology and Evolution</i> , 2018, 10, 1657-1662.	1.1	24
1411	Azithromycin Resistance through Interspecific Acquisition of an Epistasis-Dependent Efflux Pump Component and Transcriptional Regulator in <i>Neisseria gonorrhoeae</i> . <i>MBio</i> , 2018, 9, .	1.8	133
1412	Tracing mother-infant transmission of bacteriophages by means of a novel analytical tool for shotgun metagenomic datasets: METAnnotatorX. <i>Microbiome</i> , 2018, 6, 145.	4.9	54
1413	Functional and Genome Sequence-Driven Characterization of tal Effector Gene Repertoires Reveals Novel Variants With Altered Specificities in Closely Related Malian <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> Strains. <i>Frontiers in Microbiology</i> , 2018, 9, 1657.	1.5	40
1414	Comparative Transcriptomic Analysis of <i>Streptococcus thermophilus</i> TH1436 and TH1477 Showing Different Capability in the Use of Galactose. <i>Frontiers in Microbiology</i> , 2018, 9, 1765.	1.5	40
1415	Acquisition of resistance to carbapenem and macrolide-mediated quorum sensing inhibition by <i>Pseudomonas aeruginosa</i> via ICE <sub>Tn43716385</sub> . <i>Communications Biology</i> , 2018, 1, 57.	2.0	29
1416	Reassessing the Role of Type II Toxin-Antitoxin Systems in Formation of <i>Escherichia coli</i> Type II Persister Cells. <i>MBio</i> , 2018, 9, .	1.8	174
1417	Non-antibiotic antimicrobial triclosan induces multiple antibiotic resistance through genetic mutation. <i>Environment International</i> , 2018, 118, 257-265.	4.8	131
1418	Draft Genome Sequence of the Intimin-Positive Enteropathogenic <i>Escherichia albertii</i> Strain MBT-EA1, Isolated from Lettuce. <i>Genome Announcements</i> , 2018, 6, .	0.8	3
1419	Comprehensive analysis of single molecule sequencing-derived complete genome and whole transcriptome of <i>Hyposidra talaca</i> nuclear polyhedrosis virus. <i>Scientific Reports</i> , 2018, 8, 8924.	1.6	8
1420	Phylogenomic Analysis of <i>Lactobacillus curvatus</i> Reveals Two Lineages Distinguished by Genes for Fermenting Plant-Derived Carbohydrates. <i>Genome Biology and Evolution</i> , 2018, 10, 1516-1525.	1.1	21
1421	Genome Rearrangement Shapes <i>Prochlorococcus</i> Ecological Adaptation. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	17
1422	Resistome of carbapenem- and colistin-resistant <i>Klebsiella pneumoniae</i> clinical isolates. <i>PLoS ONE</i> , 2018, 13, e0198526.	1.1	53
1423	Comparative genomic analysis of <i>Myroides odoratimimus</i> isolates. <i>MicrobiologyOpen</i> , 2019, 8, e00634.	1.2	19
1424	Genome Alignment. , 2019, , 268-283.		0
1425	Accurate multiple alignment of distantly related genome sequences using filtered spaced word matches as anchor points. <i>Bioinformatics</i> , 2019, 35, 211-218.	1.8	11
1426	Complete Sequence of Succinamopine Ti-Plasmid pTiEU6 Reveals Its Evolutionary Relatedness with Nopaline-Type Ti-Plasmids. <i>Genome Biology and Evolution</i> , 2019, 11, 2480-2491.	1.1	14
1427	Genomic and physiological analyses reveal that extremely thermophilic <i>Caldicellulosiruptor changbaiensis</i> deploys uncommon cellulose attachment mechanisms. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2019, 46, 1251-1263.	1.4	4

#	ARTICLE	IF	CITATIONS
1428	Rates of Molecular Evolution in a Marine Synechococcus Phage Lineage. <i>Viruses</i> , 2019, 11, 720.	1.5	12
1429	Comparative analysis of <i>Chlorosarcinopsis eremi</i> mitochondrial genome with some <i>Chlamydomonadales</i> algae. <i>Physiology and Molecular Biology of Plants</i> , 2019, 25, 1301-1310.	1.4	3
1430	Genomic Polymorphism Associated with the Emergence of Virulent Isolates of <i>Mycobacterium bovis</i> in the Nile Delta. <i>Scientific Reports</i> , 2019, 9, 11657.	1.6	17
1431	Evolutionary mechanism leading to the multi-cagA genotype in <i>Helicobacter pylori</i> . <i>Scientific Reports</i> , 2019, 9, 11203.	1.6	12
1432	Complete genome and plasmid sequence of a novel <i>Bacillus</i> sp. BD59S, a parasporal protein synthesizing bacterium. <i>3 Biotech</i> , 2019, 9, 318.	1.1	1
1433	The impact of antimicrobials on gonococcal evolution. <i>Nature Microbiology</i> , 2019, 4, 1941-1950.	5.9	91
1434	Incompatibility of <i>Vibrio fischeri</i> Strains during Symbiosis Establishment Depends on Two Functionally Redundant <i>hcp</i> Genes. <i>Journal of Bacteriology</i> , 2019, 201, .	1.0	13
1435	Genome-wide nucleotide variation distinguishes <i>Aspergillus flavus</i> from <i>Aspergillus oryzae</i> and helps to reveal origins of atoxigenic <i>A. flavus</i> biocontrol strains. <i>Journal of Applied Microbiology</i> , 2019, 127, 1511-1520.	1.4	15
1436	Whole-Genome Alignment. <i>Methods in Molecular Biology</i> , 2019, 1910, 121-147.	0.4	5
1437	Expansion and loss events characterized the occurrence of MIF-like genes in bivalves. <i>Fish and Shellfish Immunology</i> , 2019, 93, 39-49.	1.6	4
1438	Comparative analysis of apicoplast genomes of <i>Babesia</i> infective to small ruminants in China. <i>Parasites and Vectors</i> , 2019, 12, 312.	1.0	7
1439	A likelihood ratio-based approach for improved source attribution in microbiological forensic investigations. <i>Forensic Science International</i> , 2019, 302, 109869.	1.3	3
1440	Complete Genome Sequence of <i>Agrobacterium tumefaciens</i> Myophage Milano. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	6
1441	Complete Genome Sequence of <i>Serratia marcescens</i> Myophage Moabite. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	3
1442	Complete Genome Sequence of the Novel <i>Klebsiella pneumoniae</i> Phage Marfa. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	3
1443	Complete Genome Sequence of <i>Staphylococcus aureus</i> Siphophage Sebago. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	2
1444	Efficient merging of genome profile alignments. <i>Bioinformatics</i> , 2019, 35, i71-i80.	1.8	1
1445	Complete Genome Sequences of <i>Staphylococcus epidermidis</i> Myophages Quidividi, Terranova, and Twillingate. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	5

#	ARTICLE	IF	CITATIONS
1446	Chloroplast and mitochondrial genetic variation of larches at the Siberian tundra-taiga ecotone revealed by de novo assembly. <i>PLoS ONE</i> , 2019, 14, e0216966.	1.1	13
1447	Extended-spectrum $\beta$ -lactamase-producing Enterobacteriaceae among geckos ( <i>Hemidactylus brookii</i> ) in a Ghanaian hospital. <i>Clinical Microbiology and Infection</i> , 2019, 25, 1048-1050.	2.8	4
1448	The first clawed lobster virus <i>Homarus gammarus nudivirus</i> (HgNV n. sp.) expands the diversity of the Nudiviridae. <i>Scientific Reports</i> , 2019, 9, 10086.	1.6	15
1449	Genomic Comparison of <i>Lactobacillus helveticus</i> Strains Highlights Probiotic Potential. <i>Frontiers in Microbiology</i> , 2019, 10, 1380.	1.5	50
1450	Type III Secretion System of Beneficial Rhizobacteria <i>Pseudomonas simiae</i> WCS417 and <i>Pseudomonas defensor</i> WCS374. <i>Frontiers in Microbiology</i> , 2019, 10, 1631.	1.5	36
1451	<i>Vibrio chemaguriensis</i> sp. nov., from Sundarbans, Bay of Bengal. <i>Current Microbiology</i> , 2019, 76, 1118-1127.	1.0	6
1452	Molecular Genetic and Functional Analysis of the Genome of Bacteria <i>Bacillus velezensis</i> BIM B-439D. <i>Applied Biochemistry and Microbiology</i> , 2019, 55, 386-396.	0.3	8
1453	Re-addressing the biosafety issues of plant growth promoting rhizobacteria. <i>Science of the Total Environment</i> , 2019, 690, 841-852.	3.9	94
1454	Dictyochophyceae Plastid Genomes Reveal Unusual Variability in Their Organization. <i>Journal of Phycology</i> , 2019, 55, 1166-1180.	1.0	37
1455	Development of a marker for detection of <i>Xanthomonas campestris</i> pv. <i>campestris</i> races 1 and 2 in <i>Brassica oleracea</i> . <i>Horticulture Environment and Biotechnology</i> , 2019, 60, 511-517.	0.7	6
1456	Pan-Genomic and Polymorphic Driven Prediction of Antibiotic Resistance in <i>Elizabethkingia</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 1446.	1.5	14
1457	Comparative Analysis of <i>Listeria monocytogenes</i> Plasmids and Expression Levels of Plasmid-Encoded Genes during Growth under Salt and Acid Stress Conditions. <i>Toxins</i> , 2019, 11, 426.	1.5	54
1458	Genomic analysis of a novel <i>Rhodococcus</i> ( <i>Prescottella</i> ) <i>equi</i> isolate from a bovine host. <i>Archives of Microbiology</i> , 2019, 201, 1317-1321.	1.0	4
1459	Mycoheterotrophic <i>Epirixanthes</i> ( <i>Polygalaceae</i> ) has a typical angiosperm mitogenome but unorthodox plastid genomes. <i>Annals of Botany</i> , 2019, 124, 791-807.	1.4	14
1460	Synergetic effect of non-complementary 5' AT-rich sequences on the development of a multiplex TaqMan real-time PCR for specific and robust detection of <i>Clavibacter michiganensis</i> and <i>C. michiganensis</i> subsp. <i>nebraskensis</i> . <i>PLoS ONE</i> , 2019, 14, e0218530.	1.1	12
1461	Draft Genome Sequence of <i>Enterococcus durans</i> OSY-EGY, a Multiple-Antimicrobial-Peptide Producer Isolated from Egyptian Hard Cheese. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	3
1462	Complete Genome Sequence of <i>Salmonella enterica</i> Serovar Typhimurium Siphophage Skate. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	5
1463	Complete Genome Sequence of <i>Serratia marcescens</i> Podophage Parlo. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	16

#	ARTICLE	IF	CITATIONS
1464	Retrospective Analysis of Archived Pyrazinamide Resistant Mycobacterium tuberculosis Complex Isolates from Uganda—Evidence of Interspecies Transmission. <i>Microorganisms</i> , 2019, 7, 221.	1.6	6
1465	Analysis of isolates from Bangladesh highlights multiple ways to carry resistance genes in Salmonella Typhi. <i>BMC Genomics</i> , 2019, 20, 530.	1.2	14
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.	1.5	3
1467	Plastome phylogenomics of <i>Saussurea</i> (Asteraceae: Cardueae). <i>BMC Plant Biology</i> , 2019, 19, 290.	1.6	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.	1.5	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.	1.9	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.	1.6	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.	2.9	39
1472	Molecular epidemiology of <i>Mycoplasma hyorhinis</i> porcine field isolates in the United States. <i>PLoS ONE</i> , 2019, 14, e0223653.	1.1	12
1473	The PATRIC Bioinformatics Resource Center: expanding data and analysis capabilities. <i>Nucleic Acids Research</i> , 2020, 48, D606-D612.	6.5	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.	1.6	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.	1.6	10
1476	Organelle genome composition and candidate gene identification for <i>Nsa</i> cytoplasmic male sterility in <i>Brassica napus</i> . <i>BMC Genomics</i> , 2019, 20, 813.	1.2	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.	1.1	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.	1.6	10
1479	Multiplex PCR for genotyping <i>Flavobacterium columnare</i> . <i>Journal of Fish Diseases</i> , 2019, 42, 1531-1542.	0.9	17
1480	GenGraph: a python module for the simple generation and manipulation of genome graphs. <i>BMC Bioinformatics</i> , 2019, 20, 519.	1.2	4
1481	Isolation of <i>Legionella pneumophila</i> by Co-culture with Local Ameba, Canada. <i>Emerging Infectious Diseases</i> , 2019, 25, 2104-2107.	2.0	7

#	ARTICLE	IF	CITATIONS
1482	Sulfobacillus thermotolerans: new insights into resistance and metabolic capacities of acidophilic chemolithotrophs. Scientific Reports, 2019, 9, 15069.	1.6	25
1483	The complete chloroplast genomes of two species in threatened monocot genus Caldesia in China. Genetica, 2019, 147, 381-390.	0.5	4
1484	Origin and Evolution of Hybrid Shiga Toxin-Producing and Uropathogenic Escherichia coli Strains of Sequence Type 141. Journal of Clinical Microbiology, 2019, 58, .	1.8	31
1485	Origin and diversification of Xanthomonas citri subsp. citri pathotypes revealed by inclusive phylogenomic, dating, and biogeographic analyses. BMC Genomics, 2019, 20, 700.	1.2	33
1486	Staphylococcus aureus Small Colony Variants (SCVs): News From a Chronic Prosthetic Joint Infection. Frontiers in Cellular and Infection Microbiology, 2019, 9, 363.	1.8	63
1487	Complete genome analysis of a novel temperate bacteriophage induced from Corynebacterium striatum. Archives of Virology, 2019, 164, 2877-2880.	0.9	7
1488	Characterization of new chloroplast markers to determine biogeographical origin and crop type of Cannabis sativa. International Journal of Legal Medicine, 2019, 133, 1721-1732.	1.2	15
1489	Plastome Reduction in the Only Parasitic Gymnosperm Parasitaxus Is Due to Losses of Photosynthesis but Not Housekeeping Genes and Apparently Involves the Secondary Gain of a Large Inverted Repeat. Genome Biology and Evolution, 2019, 11, 2789-2796.	1.1	31
1490	Pasteurella multocida: Genotypes and Genomics. Microbiology and Molecular Biology Reviews, 2019, 83, .	2.9	100
1491	CRISPR-Cas System of a Prevalent Human Gut Bacterium Reveals Hyper-targeting against Phages in a Human Virome Catalog. Cell Host and Microbe, 2019, 26, 325-335.e5.	5.1	53
1492	Z/II Hybrid Virulence Plasmids Carrying Antimicrobial Resistance genes in S. Typhimurium from Australian Food Animal Production. Microorganisms, 2019, 7, 299.	1.6	7
1493	Using the wax moth larva <i>Galleria mellonella</i> infection model to detect emerging bacterial pathogens. PeerJ, 2019, 6, e6150.	0.9	24
1494	Chlamydia pan-genomic analysis reveals balance between host adaptation and selective pressure to genome reduction. BMC Genomics, 2019, 20, 710.	1.2	20
1495	Horizontal Gene Transfer and Acquired Antibiotic Resistance in Salmonella enterica Serovar Heidelberg following <i>In Vitro</i> Incubation in Broiler Ceca. Applied and Environmental Microbiology, 2019, 85, .	1.4	39
1496	Genomic epidemiology of Iranian <i>Bordetella pertussis</i> : 50 years after the implementation of whole cell vaccine. Emerging Microbes and Infections, 2019, 8, 1416-1427.	3.0	23
1497	Bacteriophage Application for Difficult-to-treat Musculoskeletal Infections: Development of a Standardized Multidisciplinary Treatment Protocol. Viruses, 2019, 11, 891.	1.5	98
1498	Characterization and Whole Genome Sequencing of AR23, a Highly Toxic Bacillus thuringiensis Strain Isolated from Lebanese Soil. Current Microbiology, 2019, 76, 1503-1511.	1.0	9
1499	Comparative Genomics and Phylogenomic Analysis of the Genus Salinivibrio. Frontiers in Microbiology, 2019, 10, 2104.	1.5	23



#	ARTICLE	IF	CITATIONS
1500	Shiga toxin sub-type 2a increases the efficiency of Escherichia coli O157 transmission between animals and restricts epithelial regeneration in bovine enteroids. PLoS Pathogens, 2019, 15, e1008003.	2.1	42
1501	Population Genomics Insights into Adaptive Evolution and Ecological Differentiation in Streptomyces. Applied and Environmental Microbiology, 2019, 85, .	1.4	16
1502	A comparative analysis of complete plastid genomes from <i>Prangos fedtschenkoi</i> and <i>Prangos lipskyi</i> (Apiaceae). Ecology and Evolution, 2019, 9, 364-377.	0.8	13
1503	Impact of Homologous Recombination on the Evolution of Prokaryotic Core Genomes. MBio, 2019, 10, .	1.8	60
1504	Children With Cystic Fibrosis Are Infected With Multiple Subpopulations of Mycobacterium abscessus With Different Antimicrobial Resistance Profiles. Clinical Infectious Diseases, 2019, 69, 1678-1686.	2.9	33
1505	Lactococcus lactis subsp. lactis as a natural anti-listerial agent in the mushroom industry. Food Microbiology, 2019, 82, 30-35.	2.1	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. Antimicrobial Agents and Chemotherapy, 2019, 63, .	1.4	17
1507	Comparative analysis reveals the Genomic Islands in Pasteurella multocida population genetics: on Symbiosis and adaptability. BMC Genomics, 2019, 20, 63.	1.2	9
1508	Analysis of genetic diversity of Xanthomonas oryzae pv. oryzae populations in Taiwan. Scientific Reports, 2019, 9, 316.	1.6	11
1509	Whole-genome sequence of the bovine blood fluke Schistosoma bovis supports interspecific hybridization with S. haematobium. PLoS Pathogens, 2019, 15, e1007513.	2.1	49
1510	Metabolic diversity within the globally abundant Marine Group II Euryarchaea offers insight into ecological patterns. Nature Communications, 2019, 10, 271.	5.8	66
1511	Development of a PCR test for detection of Xanthomonas campestris pv. raphani. Australasian Plant Pathology, 2019, 48, 179-182.	0.5	4
1512	Compositional assessment of bacterial communities in probiotic supplements by means of metagenomic techniques. International Journal of Food Microbiology, 2019, 294, 1-9.	2.1	26
1513	<i>In Silico</i> Serotyping Based on Whole-Genome Sequencing Improves the Accuracy of <i>Shigella</i> Identification. Applied and Environmental Microbiology, 2019, 85, .	1.4	37
1514	Dissecting the Evolutionary Development of the Species <i>Bifidobacterium animalis</i> through Comparative Genomics Analyses. Applied and Environmental Microbiology, 2019, 85, .	1.4	11
1515	Evolution and Diversification of FRUITFULL Genes in Solanaceae. Frontiers in Plant Science, 2019, 10, 43.	1.7	13
1516	Complete Genome Sequence of Klebsiella pneumoniae Myophage May. Microbiology Resource Announcements, 2019, 8, .	0.3	2
1517	Complete Genome Sequence of Serratia marcescens Siphophage Serbin. Microbiology Resource Announcements, 2019, 8, .	0.3	4

#	ARTICLE	IF	CITATIONS
1518	Comparative analysis reveals conservation in genome organization among intestinal <i>Cryptosporidium</i> species and sequence divergence in potential secreted pathogenesis determinants among major human-infecting species. <i>BMC Genomics</i> , 2019, 20, 406.	1.2	37
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.	1.6	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.	0.8	14
1521	Highly accelerated rates of genomic rearrangements and nucleotide substitutions in plastid genomes of <i>Passiflora</i> subgenus <i>Decaloba</i> . <i>Molecular Phylogenetics and Evolution</i> , 2019, 138, 53-64.	1.2	53
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.	4.4	20
1523	Complete Genome Sequence of <i>Serratia marcescens</i> Phage MTx. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	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> ( <i>Bignoniaceae</i> , <i>Bignoniaceae</i> ). <i>Frontiers in Plant Science</i> , 2019, 10, 796.	1.7	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.	1.8	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.	0.4	25
1528	Two <i>Pseudomonas aeruginosa</i> clonal groups belonging to the PA14 clade are indigenous to the Churince system in Cuatro Ciénegas Coahuila, México. <i>Environmental Microbiology</i> , 2019, 21, 2964-2976.	1.8	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, .	0.3	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.	1.5	30
1531	Unprecedented Parallel Photosynthetic Losses in a Heterotrophic Orchid Genus. <i>Molecular Biology and Evolution</i> , 2019, 36, 1884-1901.	3.5	38
1532	Novel Genes and Metabolite Trends in <i>Bifidobacterium longum</i> subsp. <i>infantis</i> Bi-26 Metabolism of Human Milk Oligosaccharide 2-fucosyllactose. <i>Scientific Reports</i> , 2019, 9, 7983.	1.6	45
1533	Caught in action: fine-scale plastome evolution in the parasitic plants of <i>Cuscuta</i> section <i>Ceratophorae</i> ( <i>Convolvulaceae</i> ). <i>Plant Molecular Biology</i> , 2019, 100, 621-634.	2.0	17
1534	Complete Genome Sequence of <i>Klebsiella pneumoniae</i> Podophage Patroon. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	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.	1.8	6

#	ARTICLE	IF	CITATIONS
1536	Comparative genome sequencing and analyses of <i>Mycobacterium cosmeticum</i> reveal potential for biodesulfization of gasoline. <i>PLoS ONE</i> , 2019, 14, e0214663.	1.1	0
1537	<i>Rahnella</i> spp. are commonly isolated from onion ( <i>Allium cepa</i> ) bulbs and are weakly pathogenic. <i>Journal of Applied Microbiology</i> , 2019, 127, 812-824.	1.4	9
1538	Genomic determinants of speciation and spread of the <i>Mycobacterium tuberculosis</i> complex. <i>Science Advances</i> , 2019, 5, eaaw3307.	4.7	61
1539	Genomic erosion and extensive horizontal gene transfer in gut-associated <i>Acetobacteraceae</i> . <i>BMC Genomics</i> , 2019, 20, 472.	1.2	32
1540	Complete Genome Sequence of <i>Escherichia coli</i> Myophage Minorna. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	0
1541	Patterns of inter- and intrasubspecific homologous recombination inform eco-evolutionary dynamics of <i>Xylella fastidiosa</i> . <i>ISME Journal</i> , 2019, 13, 2319-2333.	4.4	55
1542	PGA: a software package for rapid, accurate, and flexible batch annotation of plastomes. <i>Plant Methods</i> , 2019, 15, 50.	1.9	660
1543	Long-read sequencing reveals intra-species tolerance of substantial structural variations and new subtelomere formation in <i>C. elegans</i> . <i>Genome Research</i> , 2019, 29, 1023-1035.	2.4	67
1544	Horizontal acquisition of hydrogen conversion ability and other habitat adaptations in the <i>Hydrogenovibrio</i> strains SP-41 and XCL-2. <i>BMC Genomics</i> , 2019, 20, 339.	1.2	9
1545	Genomic Comparison Reveals Natural Occurrence of Clinically Relevant Multidrug-Resistant Extended-Spectrum-β-Lactamase-Producing <i>Escherichia coli</i> Strains. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	29
1546	Genomic Characterization Provides New Insights for Detailed Phage-Resistant Mechanism for <i>Brucella abortus</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 917.	1.5	4
1547	An Integrated Systems Approach Unveils New Aspects of Microoxia-Mediated Regulation in <i>Bradyrhizobium diazoefficiens</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 924.	1.5	31
1548	Genomic characterization of four novel <i>Staphylococcus myoviruses</i> . <i>Archives of Virology</i> , 2019, 164, 2171-2173.	0.9	9
1549	Complete Genome Sequence of <i>Salmonella enterica</i> Serovar Typhimurium Myophage Mutine. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	2
1550	A Human Intestinal Infection Caused by a Novel Non-O1/O139 <i>Vibrio cholerae</i> Genotype and Its Dissemination Along the River. <i>Frontiers in Public Health</i> , 2019, 7, 100.	1.3	9
1551	Complete mitogenome of the entomopathogenic fungus <i>Sporothrix insectorum</i> RCEF 264 and comparative mitogenomics in Ophiostomatales. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 5797-5809.	1.7	10
1552	Comparative analyses of the complete chloroplast genomes of nymphoides and menyanthes species ( <i>menyanthaceae</i> ). <i>Aquatic Botany</i> , 2019, 156, 73-81.	0.8	16
1553	Challenge of drug resistance in <i>Pseudomonas aeruginosa</i> : clonal spread of NDM-1-positive ST-308 within a tertiary hospital. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 2220-2224.	1.3	21

#	ARTICLE	IF	CITATIONS
1554	Complete Genome Sequence of <i>Salmonella enterica</i> Serovar Typhimurium Siphophage Siskin. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	2
1555	Complete Genome Sequence of <i>Klebsiella pneumoniae</i> Myophage Mineola. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	1
1556	Draft Genome Sequence of <i>Lactobacillus paraplantarum</i> OSY-TC318, a Producer of the Novel Lantibiotic Paraplantaracin TC318. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	4
1557	Complete Genome Sequence of <i>Serratia marcescens</i> Siphophage Scapp. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	2
1558	Comparative Genomic Analysis of <i>Lactobacillus plantarum</i> : An Overview. <i>International Journal of Genomics</i> , 2019, 2019, 1-11.	0.8	45
1559	The Unique Evolutionary Trajectory and Dynamic Conformations of DR and IR/DR-Coexisting Plastomes of the Early Vascular Plant Selaginellaceae (Lycophyte). <i>Genome Biology and Evolution</i> , 2019, 11, 1258-1274.	1.1	26
1560	Large Enriched Fragment Targeted Sequencing (LEFT-SEQ) Applied to Capture of <i>Wolbachia</i> Genomes. <i>Scientific Reports</i> , 2019, 9, 5939.	1.6	22
1561	Antimicrobial Agent Susceptibility and Typing of Staphylococcal Isolates from Subclinical Mastitis in Ewes. <i>Microbial Drug Resistance</i> , 2019, 25, 1099-1110.	0.9	13
1562	SME-4-producing <i>Serratia marcescens</i> from Argentina belonging to clade 2 of the <i>S. marcescens</i> phylogeny. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 1836-1841.	1.3	9
1563	Lost and Found: Return of the Inverted Repeat in the Legume Clade Defined by Its Absence. <i>Genome Biology and Evolution</i> , 2019, 11, 1321-1333.	1.1	67
1564	Genomic Diversity and Recombination among <i>Xylella fastidiosa</i> Subspecies. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	63
1565	Complete Genome Sequence of <i>Klebsiella pneumoniae</i> Myophage Menlow. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	2
1566	Tracing the Evolution of the Plastome and Mitogenome in the Chloropicophyceae Uncovered Convergent tRNA Gene Losses and a Variant Plastid Genetic Code. <i>Genome Biology and Evolution</i> , 2019, 11, 1275-1292.	1.1	20
1567	Prevalence and Diversity Analysis of Candidate Prophages to Provide An Understanding on Their Roles in <i>Bacillus Thuringiensis</i> . <i>Viruses</i> , 2019, 11, 388.	1.5	17
1568	Novel staphylococcal cassette chromosome composite island (SCC-CI) with a new subtype of SCCmecVI cassette found in ST5 methicillin-resistant <i>Staphylococcus aureus</i> in France. <i>International Journal of Antimicrobial Agents</i> , 2019, 53, 694-697.	1.1	0
1569	Accessory genome of the multi-drug resistant ocular isolate of <i>Pseudomonas aeruginosa</i> PA34. <i>PLoS ONE</i> , 2019, 14, e0215038.	1.1	20
1570	Isolation and Bacteriocin-Related Typing of <i>Streptococcus dentisani</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 110.	1.8	28
1571	Comparative genomics reveal pathogenicity-related loci in <i>Pseudomonas syringae</i> pv. <i>actinidiae</i> biovar 3. <i>Molecular Plant Pathology</i> , 2019, 20, 923-942.	2.0	28

#	ARTICLE	IF	CITATIONS
1572	Genome-wide sexually antagonistic variants reveal long-standing constraints on sexual dimorphism in fruit flies. <i>PLoS Biology</i> , 2019, 17, e3000244.	2.6	82
1573	Genome Sequence of a California Isolate of <i>Fusarium oxysporum</i> f. sp. <i>lycopersici</i> Race 3, a Fungus Causing Wilt Disease on Tomato. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	6
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.	1.1	11
1575	Domestication of previously uncultivated <i>Candidatus</i> <i>Desulforudis audaxviator</i> from a deep aquifer in Siberia sheds light on its physiology and evolution. <i>ISME Journal</i> , 2019, 13, 1947-1959.	4.4	48
1576	Local Diversification of Methicillin- Resistant <i>Staphylococcus aureus</i> ST239 in South America After Its Rapid Worldwide Dissemination. <i>Frontiers in Microbiology</i> , 2019, 10, 82.	1.5	20
1577	Diazaquinomycin Biosynthetic Gene Clusters from Marine and Freshwater Actinomycetes. <i>Journal of Natural Products</i> , 2019, 82, 937-946.	1.5	18
1578	Evolution and Diversification of Kiwifruit Mitogenomes through Extensive Whole-Genome Rearrangement and Mosaic Loss of Intergenic Sequences in a Highly Variable Region. <i>Genome Biology and Evolution</i> , 2019, 11, 1192-1206.	1.1	43
1579	Genome annotation and antimicrobial properties of <i>Bacillus toyonensis</i> VUDES13, isolated from the <i>Folsomia candida</i> . <i>Entomologia Experimentalis Et Applicata</i> , 2019, 167, 269-285.	0.7	8
1580	Sensitivity to the two peptide bacteriocin plantaricin EF is dependent on CorC, a membrane-bound, magnesium/cobalt efflux protein. <i>MicrobiologyOpen</i> , 2019, 8, e827.	1.2	17
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.	0.7	22
1582	Draft Genome Sequence of <i>Sinorhizobium meliloti</i> Strain CXM1-105. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	2
1583	Draft Genome of <i>Burkholderia cenocepacia</i> TAtl-371, a Strain from the <i>Burkholderia cepacia</i> Complex Retains Antagonism in Different Carbon and Nitrogen Sources. <i>Current Microbiology</i> , 2019, 76, 566-574.	1.0	3
1584	Complete Genome Sequence of <i>Vibrio campbellii</i> DS40M4. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	8
1585	The antibiotic resistance and pathogenicity of a multidrug-resistant <i>Elizabethkingia anophelis</i> isolate. <i>MicrobiologyOpen</i> , 2019, 8, e804.	1.2	23
1586	Comparative genomics reveals the unique evolutionary status of <i>Plasmodiophora brassicae</i> and the essential role of GPCR signaling pathways. <i>Phytopathology Research</i> , 2019, 1, .	0.9	17
1587	Comparative genomics reveals structural and functional features specific to the genome of a foodborne <i>Escherichia coli</i> O157:H7. <i>BMC Genomics</i> , 2019, 20, 196.	1.2	22
1588	Aneuploidy and Ethanol Tolerance in <i>Saccharomyces cerevisiae</i> . <i>Frontiers in Genetics</i> , 2019, 10, 82.	1.1	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.	1.5	24

#	ARTICLE	IF	CITATIONS
1590	Dynamics of clonal and plasmid backgrounds of Enterobacteriaceae producing acquired AmpC in Portuguese clinical settings over time. <i>International Journal of Antimicrobial Agents</i> , 2019, 53, 650-656.	1.1	27
1591	Chloroplast and mitochondrial genomes of <i>Balbiana investiens</i> (Balbianiales, Nemaliophycidae). <i>Phycologia</i> , 2019, 58, 310-318.	0.6	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.	0.5	2
1593	Bioinformatics applied to biotechnology: A review towards bioenergy research. <i>Biomass and Bioenergy</i> , 2019, 123, 195-224.	2.9	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.	1.6	35
1595	Draft Genome Sequence of <i>Porphyromonas gingivalis</i> Strain 381 Okayama (381OKJP) Stock Culture. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	0
1596	May the Phage be With You? Prophage-Like Elements in the Genomes of Soft Rot Pectobacteriaceae: <i>Pectobacterium</i> spp. and <i>Dickeya</i> spp.. <i>Frontiers in Microbiology</i> , 2019, 10, 138.	1.5	28
1597	Host adaptation and convergent evolution increases antibiotic resistance without loss of virulence in a major human pathogen. <i>PLoS Pathogens</i> , 2019, 15, e1007218.	2.1	56
1598	A single loss of photosynthesis in the diatom order Bacillariales (Bacillariophyta). <i>American Journal of Botany</i> , 2019, 106, 560-572.	0.8	23
1599	TORMES: an automated pipeline for whole bacterial genome analysis. <i>Bioinformatics</i> , 2019, 35, 4207-4212.	1.8	82
1600	<i>gyrA</i> and <i>parC</i> mutations in fluoroquinolone-resistant <i>Neisseria gonorrhoeae</i> isolates from Kenya. <i>BMC Microbiology</i> , 2019, 19, 76.	1.3	17
1601	Evolution of the human cold/menthol receptor, TRPM8. <i>Molecular Phylogenetics and Evolution</i> , 2019, 136, 104-118.	1.2	13
1602	Sequencing of <i>Tuta absoluta</i> genome to develop SNP genotyping assays for species identification. <i>Journal of Pest Science</i> , 2019, 92, 1397-1407.	1.9	24
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.	3.0	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.	0.2	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.	1.8	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.	1.1	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 <i>vanA</i> -containing plasmid and acquisition of a heterogeneous accessory genome. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 1776-1785.	1.3	43



#	ARTICLE	IF	CITATIONS
1608	Just the Two of Us? A Family of <i>Pseudomonas</i> Megaplasms Offers a Rare Glimpse Into the Evolution of Large Mobile Elements. <i>Genome Biology and Evolution</i> , 2019, 11, 1192-1206.	1.1	11
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.	2.1	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.	0.6	3
1611	Genomic characterization and comparative analysis of <i>Leptospira kirschneri</i> serogroup Grippotyphosa UC5/2011, a strain isolated after mare abortion: Implications for genital animal leptospirosis. <i>Comparative Immunology, Microbiology and Infectious Diseases</i> , 2019, 64, 7-9.	0.7	4
1612	Genomic analyses of two <i>Alteromonas stellipolaris</i> strains reveal traits with potential biotechnological applications. <i>Scientific Reports</i> , 2019, 9, 1215.	1.6	16
1613	Multidrug Resistant Uropathogenic <i>Escherichia coli</i> ST405 With a Novel, Composite IS26 Transposon in a Unique Chromosomal Location. <i>Frontiers in Microbiology</i> , 2018, 9, 3212.	1.5	41
1614	The Complete Genome and Physiological Analysis of the Eurythermal Firmicute <i>Exiguobacterium chiriqhucha</i> Strain RW2 Isolated From a Freshwater Microbialite, Widely Adaptable to Broad Thermal, pH, and Salinity Ranges. <i>Frontiers in Microbiology</i> , 2018, 9, 3189.	1.5	32
1615	Resource Concentration Modulates the Fate of Dissimilated Nitrogen in a Dual-Pathway Actinobacterium. <i>Frontiers in Microbiology</i> , 2019, 10, 3.	1.5	20
1616	Role of Two-Component System Response Regulator <i>bceR</i> in the Antimicrobial Resistance, Virulence, Biofilm Formation, and Stress Response of Group B <i>Streptococcus</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 10.	1.5	72
1617	Extensive Losses of Photosynthesis Genes in the Plastome of a Mycoheterotrophic Orchid, <i>Cyrtosia septentrionalis</i> (Vanilloideae: Orchidaceae). <i>Genome Biology and Evolution</i> , 2019, 11, 565-571.	1.1	30
1618	NGS-based phylogeny of diphtheria-related pathogenicity factors in different <i>Corynebacterium</i> spp. implies species-specific virulence transmission. <i>BMC Microbiology</i> , 2019, 19, 28.	1.3	79
1619	Potential of the <i>Burkholderia cepacia</i> Complex to Produce 4-Hydroxy-3-Methyl-2-Alkyquinolines. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 33.	1.8	23
1620	ICESsuHN105, a Novel Multiple Antibiotic Resistant ICE in <i>Streptococcus suis</i> Serotype 5 Strain HN105. <i>Frontiers in Microbiology</i> , 2019, 10, 274.	1.5	16
1621	Hybridization is a recurrent evolutionary stimulus in wild yeast speciation. <i>Nature Communications</i> , 2019, 10, 923.	5.8	62
1622	Draft Genome Sequence of <i>Sinorhizobium meliloti</i> Strain AK170. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	2
1623	Chloroplast genomic data provide new and robust insights into the phylogeny and evolution of the Ranunculaceae. <i>Molecular Phylogenetics and Evolution</i> , 2019, 135, 12-21.	1.2	123
1624	Prevalence of isomeric plastomes and effectiveness of plastome super-barcodes in yews ( <i>Taxus</i> ) worldwide. <i>Scientific Reports</i> , 2019, 9, 2773.	1.6	54
1625	Integrated mobile genetic elements in Thaumarchaeota. <i>Environmental Microbiology</i> , 2019, 21, 2056-2078.	1.8	38

#	ARTICLE	IF	CITATIONS
1626	The plastid and mitochondrial genomes of <i>Eucalyptus grandis</i> . <i>BMC Genomics</i> , 2019, 20, 132.	1.2	35
1627	Analysis of mitochondrial and chloroplast genomes in two volvocine algae: <i>Eudorina elegans</i> and <i>Eudorina cylindrica</i> (Volvocaceae, Chlorophyta). <i>European Journal of Phycology</i> , 2019, 54, 193-205.	0.9	12
1628	Combining Strengths for Multi-genome Visual Analytics Comparison. <i>Bioinformatics and Biology Insights</i> , 2019, 13, 117793221882512.	1.0	1
1629	Identification of a novel metallo-β-lactamase, CAM-1, in clinical <i>Pseudomonas aeruginosa</i> isolates from Canada. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 1563-1567.	1.3	16
1630	Complete Genome Sequence of <i>Xanthomonas</i> Phage Pagan. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	2
1631	Conserved Patterns of Symmetric Inversion in the Genome Evolution of <i>Bordetella</i> Respiratory Pathogens. <i>MSystems</i> , 2019, 4, .	1.7	30
1632	Maintenance of Sympatric and Allopatric Populations in Free-Living Terrestrial Bacteria. <i>MBio</i> , 2019, 10, .	1.8	19
1633	Alignment-free Sequence Comparison with Multiple $k$ Values. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 18, 1-1.	1.9	0
1634	Complete Genome Sequence of <i>Vibrio natriegens</i> Phage Phriendly. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	3
1635	A Metabolic Dependency for Host Isoprenoids in the Obligate Intracellular Pathogen <i>Rickettsia parkeri</i> Underlies a Sensitivity to the Statin Class of Host-Targeted Therapeutics. <i>MSphere</i> , 2019, 4, .	1.3	8
1636	The complete chloroplast genome sequence of <i>Pinus cembra</i> L. (Pinaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 4202-4203.	0.2	3
1637	Comparative Genomics Reveals a Well-Conserved Intrinsic Resistome in the Emerging Multidrug-Resistant Pathogen <i>Cupriavidus gilardii</i> . <i>MSphere</i> , 2019, 4, .	1.3	9
1638	Reanalysis of <i>Lactobacillus paracasei</i> Lbs2 Strain and Large-Scale Comparative Genomics Places Many Strains into Their Correct Taxonomic Position. <i>Microorganisms</i> , 2019, 7, 487.	1.6	14
1639	Self-identity barcodes encoded by six expansive polymorphic toxin families discriminate kin in myxobacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 24808-24818.	3.3	21
1640	Emerging Variants of the Integrative and Conjugant Element ICEMh1 in Livestock Pathogens: Structural Insights, Potential Host Range, and Implications for Bacterial Fitness and Antimicrobial Therapy. <i>Frontiers in Microbiology</i> , 2019, 10, 2608.	1.5	7
1641	Multiple <i>Klebsiella pneumoniae</i> KPC Clones Contribute to an Extended Hospital Outbreak. <i>Frontiers in Microbiology</i> , 2019, 10, 2767.	1.5	27
1642	A Novel Benthic Phage Infecting <i>Shewanella</i> with Strong Replication Ability. <i>Viruses</i> , 2019, 11, 1081.	1.5	15
1643	Coexistence of bla <sub>TEM</sub> -1 and bla <sub>TEM</sub> -1 on a Transferrable Plasmid of a Novel ST192 <i>Klebsiella aerogenes</i> Clinical Isolate. <i>Infection and Drug Resistance</i> , 2019, Volume 12, 3883-3891.	1.1	9

#	ARTICLE	IF	CITATIONS
1644	Comparison of different technologies for the decipherment of the whole genome sequence of <i>Campylobacter jejuni</i> BfR-CA-14430. <i>Gut Pathogens</i> , 2019, 11, 59.	1.6	7
1645	First report of <i>Klebsiella quasipneumoniae</i> harboring blaKPC-2 in Saudi Arabia. <i>Antimicrobial Resistance and Infection Control</i> , 2019, 8, 203.	1.5	15
1646	The Draft Genome of a Hydrogen-producing Cyanobacterium, <i>Arthrospira platensis</i> NIES-46. <i>Journal of Genomics</i> , 2019, 7, 56-59.	0.6	6
1647	Complete Sequences of Multiple-Drug Resistant IncHI2 ST3 Plasmids in <i>Escherichia coli</i> of Porcine Origin in Australia. <i>Frontiers in Sustainable Food Systems</i> , 2019, 3, .	1.8	31
1648	Assembly, annotation, and comparison of <i>Macrophomina phaseolina</i> isolates from strawberry and other hosts. <i>BMC Genomics</i> , 2019, 20, 802.	1.2	16
1649	Re-sequencing and optical mapping reveals misassemblies and real inversions on <i>Corynebacterium pseudotuberculosis</i> genomes. <i>Scientific Reports</i> , 2019, 9, 16387.	1.6	6
1650	Genome analysis of <i>Ranavirus</i> frog virus 3 isolated from American Bullfrog ( <i>Lithobates catesbeianus</i> ) in South America. <i>Scientific Reports</i> , 2019, 9, 17135.	1.6	11
1651	Complete Genome Sequence of Shelby, a Siphophage Infecting Carbapenemase-Producing <i>Klebsiella pneumoniae</i> . <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	2
1652	Metabolomic Alterations Do Not Induce Metabolic Burden in the Industrial Yeast M2n[pBKD2-Pccbgl1]-C1 Engineered by Multiple $\lambda$ -Integration of a Fungal $\beta$ -Glucosidase Gene. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019, 7, 376.	2.0	9
1653	Genetic determinants of genus-level glycan diversity in a bacterial protein glycosylation system. <i>PLoS Genetics</i> , 2019, 15, e1008532.	1.5	16
1654	Unidirectional animal-to-human transmission of methicillin-resistant <i>Staphylococcus aureus</i> ST398 in pig farming; evidence from a surveillance study in southern Italy. <i>Antimicrobial Resistance and Infection Control</i> , 2019, 8, 187.	1.5	41
1655	Manually curated genome-scale reconstruction of the metabolic network of <i>Bacillus megaterium</i> DSM319. <i>Scientific Reports</i> , 2019, 9, 18762.	1.6	21
1656	Bacteriophage Therapy Testing Against <i>Shigella flexneri</i> in a Novel Human Intestinal Organoid-Derived Infection Model. <i>Journal of Pediatric Gastroenterology and Nutrition</i> , 2019, 68, 509-516.	0.9	34
1657	Whole-genome sequencing and gene annotation of Georgian grape cultivars. <i>Acta Horticulturae</i> , 2019, , 287-294.	0.1	0
1658	Comparative Genomics of <i>Streptococcus thermophilus</i> Support Important Traits Concerning the Evolution, Biology and Technological Properties of the Species. <i>Frontiers in Microbiology</i> , 2019, 10, 2916.	1.5	39
1659	RNAetect: efficient computational detection of novel non-coding RNAs. <i>Bioinformatics</i> , 2019, 35, 1133-1141.	1.8	7
1660	Variations on a protective theme: <i>Hamiltonella defensa</i> infections in aphids variably impact parasitoid success. <i>Current Opinion in Insect Science</i> , 2019, 32, 1-7.	2.2	65
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.	1.3	13

#	ARTICLE	IF	CITATIONS
1662	Mitochondrial genome of the entomophthoroid fungus <i>Conidiobolus heterosporus</i> provides insights into evolution of basal fungi. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 1379-1391.	1.7	31
1663	Phoenix phylogeny, and analysis of genetic variation in a diverse collection of date palm ( <i>Phoenix</i> ) Tj ETQq1 1 0.784314 rgBT /Overlo	1.8	27
1664	Expansion and Diversification of MFS Transporters in <i>Kluyveromyces marxianus</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 3330.	1.5	17
1665	Understanding the Evolution of Mitochondrial Genomes in Phaeophyceae Inferred from Mitogenomes of <i>Ishige okamurae</i> (Ishigeales) and <i>Dictyopterus divaricata</i> (Dictyotales). <i>Journal of Molecular Evolution</i> , 2019, 87, 16-26.	0.8	10
1666	Draft Genome Sequence of the Cyanotroph <i>Pseudomonas monteilii</i> BCN3. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	0
1667	MLSB-Resistant <i>Staphylococcus aureus</i> in Central Greece: Rate of Resistance and Molecular Characterization. <i>Microbial Drug Resistance</i> , 2019, 25, 543-550.	0.9	17
1668	Genomic analysis of the mesophilic Thermotogae genus <i>Mesotoga</i> reveals phylogeographic structure and genomic determinants of its distinct metabolism. <i>Environmental Microbiology</i> , 2019, 21, 456-470.	1.8	28
1669	The complete genome sequence of a second alphabaculovirus from the true armyworm, <i>Mythimna unipuncta</i> : implications for baculovirus phylogeny and host specificity. <i>Virus Genes</i> , 2019, 55, 104-116.	0.7	3
1670	Deep genomic analysis of <i>Coelastrella saipanensis</i> (Scenedesmaceae, Chlorophyta): comparative chloroplast genomics of Scenedesmaceae. <i>European Journal of Phycology</i> , 2019, 54, 52-65.	0.9	12
1671	The complete mitochondrial genome of the ChanáChua fungus <i>Isaria cicadae</i> : a tale of intron evolution in Cordycipitaceae. <i>Environmental Microbiology</i> , 2019, 21, 864-879.	1.8	28
1672	Complete Genome Sequence of Hypervirulent <i>Streptococcus pyogenes</i> emm 3 Strain 1838. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	1
1673	Characterization and Genome Analysis of <i>Staphylococcus aureus</i> Podovirus CSA13 and Its Anti-Biofilm Capacity. <i>Viruses</i> , 2019, 11, 54.	1.5	28
1674	High-Quality Draft Genome Sequence of <i>Pseudomonas aeruginosa</i> 268 Isolated from a Patient with a Left Ventricular Assist Device. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	0
1675	Construction of a Genomic Bacterial Artificial Chromosome (BAC) Library for the Prawn <i>Macrobrachium rosenbergii</i> and Initial Analysis of ZW Chromosome-Derived BAC Inserts. <i>Marine Biotechnology</i> , 2019, 21, 206-216.	1.1	11
1676	Phenotypic, molecular and genomic characterization of <i>Actinobaculum suis</i> isolated from swine in Brazil. <i>Anaerobe</i> , 2019, 56, 27-33.	1.0	0
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.	1.5	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.	1.3	7
1679	Whole-Genome Alignment and Comparative Annotation. <i>Annual Review of Animal Biosciences</i> , 2019, 7, 41-64.	3.6	62

#	ARTICLE	IF	CITATIONS
1680	A novel approach for the identification and phylogenetic delineation of human <i>Mycoplasma</i> species and strains using genomic segment sequence analysis. <i>Infection, Genetics and Evolution</i> , 2019, 68, 68-76.	1.0	2
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.	1.0	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.	1.2	8
1683	Alignment-free inference of hierarchical and reticulate phylogenomic relationships. <i>Briefings in Bioinformatics</i> , 2019, 20, 426-435.	3.2	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.	1.3	47
1685	Investigation of putative invasion determinants of <i>Actinobacillus</i> species using comparative genomics. <i>Genomics</i> , 2019, 111, 59-66.	1.3	4
1686	Complete Genome of <i>Bacillus velezensis</i> CMT-6 and Comparative Genome Analysis Reveals Lipopeptide Diversity. <i>Biochemical Genetics</i> , 2020, 58, 1-15.	0.8	14
1687	Comparative genomics analysis of <i>Mycoplasma capricolum</i> subsp. <i>capripneumoniae</i> 87001. <i>Genomics</i> , 2020, 112, 615-620.	1.3	11
1688	Phylogenetic determinants of toxin gene distribution in genomes of <i>Brevibacillus laterosporus</i> . <i>Genomics</i> , 2020, 112, 1042-1053.	1.3	19
1689	Characterization of cefotaxime-resistant urinary <i>Escherichia coli</i> from primary care in South-West England 2017-18. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 65-71.	1.3	49
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.	1.0	11
1691	Plastid phylogenomic insights into the evolution of the <i>Caprifoliaceae</i> s.l. (Dipsacales). <i>Molecular Phylogenetics and Evolution</i> , 2020, 142, 106641.	1.2	52
1692	Construction and comparative analysis of mitochondrial genome in the brown tide forming alga <i>Aureococcus anophagefferens</i> (Pelagophyceae, Ochrophyta). <i>Journal of Applied Phycology</i> , 2020, 32, 441-450.	1.5	13
1693	Fine-Scale Haplotype Structure Reveals Strong Signatures of Positive Selection in a Recombining Bacterial Pathogen. <i>Molecular Biology and Evolution</i> , 2020, 37, 417-428.	3.5	27
1694	Exploring the evolutionary dynamics of <i>Rhizobium</i> plasmids through bipartite network analysis. <i>Environmental Microbiology</i> , 2020, 22, 934-951.	1.8	7
1695	Ancient Mitochondrial Gene Transfer between Fungi and the Orchids. <i>Molecular Biology and Evolution</i> , 2020, 37, 44-57.	3.5	15
1696	Characterization of antimicrobial resistance in lactobacilli and bifidobacteria used as probiotics or starter cultures based on integration of phenotypic and in silico data. <i>International Journal of Food Microbiology</i> , 2020, 314, 108388.	2.1	62
1697	<i>Escherichia coli</i> strains producing a novel Shiga toxin 2 subtype circulate in China. <i>International Journal of Medical Microbiology</i> , 2020, 310, 151377.	1.5	82

#	ARTICLE	IF	CITATIONS
1698	The chloroplast genome of the lichen symbiont microalga <i>Trebouxia</i> sp. Tr9 (Trebouxiophyceae) is encoded by the nucleus. <i>Journal of Phycology</i> , 2020, 56, 170-184.	1.0	10
1699	Complete Genome Sequence of <i>Sphingobacterium psychroaquaticum</i> Strain SJ-25, an Aerobic Bacterium Capable of Suppressing Fungal Pathogens. <i>Current Microbiology</i> , 2020, 77, 115-122.	1.0	23
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.	3.5	11
1701	Living Trees: High-Quality Reproducible and Reusable Construction of Bacterial Phylogenetic Trees. <i>Molecular Biology and Evolution</i> , 2020, 37, 563-575.	3.5	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.	1.0	0
1703	Revealing mitogenome-wide DNA methylation and RNA editing of three Ascomycotina fungi using SMRT sequencing. <i>Mitochondrion</i> , 2020, 51, 88-96.	1.6	2
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.	5.1	119
1705	<i>Serratia marcescens</i> in the neonatal intensive care unit: A cluster investigation using molecular methods. <i>Journal of Infection and Public Health</i> , 2020, 13, 1006-1011.	1.9	17
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.	1.2	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.	2.2	24
1708	Genomic analyses reveal moderate levels of ploidy, high heterozygosity and structural variations in a Colombian isolate of <i>Leishmania (Leishmania) amazonensis</i> . <i>Acta Tropica</i> , 2020, 203, 105296.	0.9	13
1709	Organellomic data sets confirm a cryptic consensus on (unrooted) land plant relationships and provide new insights into bryophyte molecular evolution. <i>American Journal of Botany</i> , 2020, 107, 91-115.	0.8	38
1710	Conservation and innovation: Plastome evolution during rapid radiation of <i>Rhodiola</i> on the Qinghai-Tibetan Plateau. <i>Molecular Phylogenetics and Evolution</i> , 2020, 144, 106713.	1.2	30
1711	Characterization of an $17\beta$ -estradiol-degrading bacterium <i>Stenotrophomonas maltophilia</i> SJTL3 tolerant to adverse environmental factors. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 1291-1305.	1.7	15
1712	Early Stage Adaptation of a Mesophilic Green Alga to Antarctica: Systematic Increases in Abundance of Enzymes and LEA Proteins. <i>Molecular Biology and Evolution</i> , 2020, 37, 849-863.	3.5	12
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.	5.9	75
1714	Biochemical and molecular characterization of arsenic response from <i>Azospirillum brasilense</i> Cd, a bacterial strain used as plant inoculant. <i>Environmental Science and Pollution Research</i> , 2020, 27, 2287-2300.	2.7	19
1715	Evolutionary changes of an intestinal <i>Lactobacillus reuteri</i> during probiotic manufacture. <i>MicrobiologyOpen</i> , 2020, 9, e972.	1.2	3



#	ARTICLE	IF	CITATIONS
1716	The Mitogenome of Norway Spruce and a Reappraisal of Mitochondrial Recombination in Plants. <i>Genome Biology and Evolution</i> , 2020, 12, 3586-3598.	1.1	35
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.	1.5	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.	0.9	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, .	1.4	17
1720	Genomic Characteristics of Invasive <i>Streptococcus pneumoniae</i> Serotype 1 in New Caledonia Prior to the Introduction of PCV13. <i>Bioinformatics and Biology Insights</i> , 2020, 14, 117793222096210.	1.0	2
1721	Translocation of Viable Gut Microbiota to Mesenteric Adipose Drives Formation of Creeping Fat in Humans. <i>Cell</i> , 2020, 183, 666-683.e17.	13.5	211
1722	Genetic and Virulence Characteristics of a Hybrid Atypical Enteropathogenic and Uropathogenic <i>Escherichia coli</i> (aEPEC/UPEC) Strain. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 492.	1.8	25
1723	Comparative genomics of ocular <i>Pseudomonas aeruginosa</i> strains from keratitis patients with different clinical outcomes. <i>Genomics</i> , 2020, 112, 4769-4776.	1.3	12
1724	<i>Escherichia coli</i> Sequence Type 457 Is an Emerging Extended-Spectrum- $\beta$ -Lactam-Resistant Lineage with Reservoirs in Wildlife and Food-Producing Animals. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 65, .	1.4	30
1725	Sequencing and Analysis of the Complete Organellar Genomes of <i>Prototheca wickerhamii</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 1296.	1.7	5
1726	First description of antimicrobial resistance in carbapenem-susceptible <i>Klebsiella pneumoniae</i> after imipenem treatment, driven by outer membrane remodeling. <i>BMC Microbiology</i> , 2020, 20, 218.	1.3	14
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.	2.1	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.	1.5	8
1729	Phylogenomic Analysis of <i>Campylobacter fetus</i> Reveals a Clonal Structure of Insertion Element ISCfe1 Positive Genomes. <i>Frontiers in Microbiology</i> , 2020, 11, 585374.	1.5	4
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.	1.5	12
1731	Whole genome sequence of <i>Serratia marcescens</i> 39_H1, a potential hydrolytic and acidogenic strain. <i>Biotechnology Reports (Amsterdam, Netherlands)</i> , 2020, 28, e00542.	2.1	1
1732	Emergence of Multidrug Resistant Hypervirulent ST23 <i>Klebsiella pneumoniae</i> : Multidrug Resistant Plasmid Acquisition Drives Evolution. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 575289.	1.8	25
1733	Mitochondrial Genome Sequences of the Emerging Fungal Pathogen <i>Candida auris</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 560332.	1.5	6

#	ARTICLE	IF	CITATIONS
1734	A map of cis-regulatory elements and 3D genome structures in zebrafish. <i>Nature</i> , 2020, 588, 337-343.	13.7	80
1735	Genome skimming and exploration of DNA barcodes for Taiwan endemic cypresses. <i>Scientific Reports</i> , 2020, 10, 20650.	1.6	2
1736	Unlocking Survival Mechanisms for Metal and Oxidative Stress in the Extremely Acidophilic, Halotolerant Acidihalobacter Genus. <i>Genes</i> , 2020, 11, 1392.	1.0	8
1737	Multiple origins of obligate nematode and insect symbionts by a clade of bacteria closely related to plant pathogens. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 31979-31986.	3.3	40
1738	Comparative genomics in <i>Candidatus Kuenenia stuttgartiensis</i> reveal high genomic plasticity in the overall genome structure, CRISPR loci and surface proteins. <i>BMC Genomics</i> , 2020, 21, 851.	1.2	10
1739	Virulence characterization and comparative genomics of <i>Listeria monocytogenes</i> sequence type 155 strains. <i>BMC Genomics</i> , 2020, 21, 847.	1.2	26
1740	Genomic analysis of <i>Helicobacter himalayensis</i> sp. nov. isolated from <i>Marmota himalayana</i> . <i>BMC Genomics</i> , 2020, 21, 826.	1.2	4
1741	Progressive Cactus is a multiple-genome aligner for the thousand-genome era. <i>Nature</i> , 2020, 587, 246-251.	13.7	256
1742	VIRIDICâ€”A Novel Tool to Calculate the Intergenomic Similarities of Prokaryote-Infecting Viruses. <i>Viruses</i> , 2020, 12, 1268.	1.5	274
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.	1.6	1
1744	Mitochondrial and plastid genome variability of <i>Corallina officinalis</i> (Corallinales). <i>Trends in Microbiology</i> , 2020, 10, 342-344.	0.6	1
1745	Characterization and genomic analysis of a diesel-degrading bacterium, <i>Acinetobacter calcoaceticus</i> CA16, isolated from Canadian soil. <i>BMC Biotechnology</i> , 2020, 20, 39.	1.7	20
1746	A Hopeful Sea-Monster: A Very Large Homologous Recombination Event Impacting the Core Genome of the Marine Pathogen <i>Vibrio anguillarum</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 1430.	1.5	7
1747	Production of Highly Active Extracellular Amylase and Cellulase From <i>Bacillus subtilis</i> ZIM3 and a Recombinant Strain With a Potential Application in Tobacco Fermentation. <i>Frontiers in Microbiology</i> , 2020, 11, 1539.	1.5	41
1748	Smash++: an alignment-free and memory-efficient tool to find genomic rearrangements. <i>GigaScience</i> , 2020, 9, .	3.3	13
1749	Evolution of <i>Listeria monocytogenes</i> During a Persistent Human Prosthetic Hip Joint Infection. <i>Frontiers in Microbiology</i> , 2020, 11, 1726.	1.5	10
1750	Potential evolutionary impact of integrative and conjugative elements (ICEs) and genomic islands in the <i>Ralstonia solanacearum</i> species complex. <i>Scientific Reports</i> , 2020, 10, 12498.	1.6	13
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.	1.1	49

#	ARTICLE	IF	CITATIONS
1752	Plastome Phylogenomic and Biogeographical Study on <i>Thuja</i> (Cupressaceae). <i>BioMed Research International</i> , 2020, 2020, 1-13.	0.9	5
1753	Reconstructing plastome evolution across the phylogenetic backbone of the parasitic plant genus <i>Cuscuta</i> (Convolvulaceae). <i>Botanical Journal of the Linnean Society</i> , 2020, 194, 423-438.	0.8	9
1754	Insights into the phylogenetic relationships and drug targets of <i>Babesia</i> isolates infective to small ruminants from the mitochondrial genomes. <i>Parasites and Vectors</i> , 2020, 13, 378.	1.0	9
1755	A novel community-acquired MRSA clone, USA300-LV/J, uniquely evolved in Japan. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 3131-3134.	1.3	12
1756	Scalable Pairwise Whole-Genome Homology Mapping of Long Genomes with BubbZ. <i>IScience</i> , 2020, 23, 101224.	1.9	11
1757	Comparative Genome Analysis Reveals <i>Cyanidiococcus</i> gen. nov., A New Extremophilic Red Algal Genus Sister to <i>Cyanidioschyzon</i> (Cyanidioschyzonaceae, Rhodophyta). <i>Journal of Phycology</i> , 2020, 56, 1428-1442.	1.0	22
1758	Draft Genome Assembly of <i>Rhodobacter sphaeroides</i> 2.4.1 Substrain H2 from Nanopore Data. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	2
1759	First characterization of the complete mitochondrial genome of fungal plant-pathogen <i>Monilinia laxa</i> which represents the mobile intron rich structure. <i>Scientific Reports</i> , 2020, 10, 13644.	1.6	12
1760	Differences in Blood-Derived <i>Francisella tularensis</i> Type B Strains from Clinical Cases of Tularemia. <i>Microorganisms</i> , 2020, 8, 1515.	1.6	3
1761	Taxonomy and Phylogenetic Research on <i>Ralstonia solanacearum</i> Species Complex: A Complex Pathogen with Extraordinary Economic Consequences. <i>Pathogens</i> , 2020, 9, 886.	1.2	44
1762	Pangenomics in Crop Plants. <i>Population Genomics</i> , 2020, , 1.	0.2	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. <i>Nutrients</i> , 2020, 12, 3247.	1.7	46
1764	Mucoidy, a general mechanism for maintaining lytic phage in populations of bacteria. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	21
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. <i>BMC Genomics</i> , 2020, 21, 564.	1.2	3
1766	Comparative chloroplast genome analyses of <i>Avena</i> : insights into evolutionary dynamics and phylogeny. <i>BMC Plant Biology</i> , 2020, 20, 406.	1.6	53
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. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	6
1768	A persistently replicating SARS-CoV-2 variant derived from an asymptomatic individual. <i>Journal of Translational Medicine</i> , 2020, 18, 362.	1.8	46
1769	Novel <i>Caulobacter</i> bacteriophages illustrate the diversity of the podovirus genus <i>Rauchvirus</i> . <i>Archives of Virology</i> , 2020, 165, 2549-2554.	0.9	0

#	ARTICLE	IF	CITATIONS
1770	The role of epiphytic populations in pathogenesis of the genus <i>Xanthomonas</i> bacteria. <i>BIO Web of Conferences</i> , 2020, 23, 03010.	0.1	1
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). <i>Journal of Fish Diseases</i> , 2020, 43, 1287-1298.	0.9	7
1772	Horizontal transmission and recombination maintain forever young bacterial symbiont genomes. <i>PLoS Genetics</i> , 2020, 16, e1008935.	1.5	87
1773	The Genome of <i>Staphylococcus epidermidis</i> O47. <i>Frontiers in Microbiology</i> , 2020, 11, 2061.	1.5	13
1774	Analytical Performance Validation of Next-Generation Sequencing Based Clinical Microbiology Assays Using a K-mer Analysis Workflow. <i>Frontiers in Microbiology</i> , 2020, 11, 1883.	1.5	12
1775	Characterization of methicillin-resistant <i>Staphylococcus aureus</i> through genomics approach. <i>3 Biotech</i> , 2020, 10, 401.	1.1	14
1776	Potential causes and consequences of rapid mitochondrial genome evolution in thermoacidophilic <i>Galdieria</i> (Rhodophyta). <i>BMC Evolutionary Biology</i> , 2020, 20, 112.	3.2	13
1777	In vitro propagation and genome sequencing of three "atypical" <i>Ehrlichia ruminantium</i> isolates. <i>Onderstepoort Journal of Veterinary Research</i> , 2020, 87, e1-e14.	0.6	2
1778	New insights into the biodiversity of coliphages in the intestine of poultry. <i>Scientific Reports</i> , 2020, 10, 15220.	1.6	13
1779	Genomic Signatures of Honey Bee Association in an Acetic Acid Symbiont. <i>Genome Biology and Evolution</i> , 2020, 12, 1882-1894.	1.1	18
1780	Draft Genome Sequence of <i>Lactobacillus rhamnosus</i> OSU-PECh-69, a Cheese Isolate with Antibacterial Activity. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
1781	A drift-barrier model drives the genomic landscape of a structured bacterial population. <i>Molecular Ecology</i> , 2020, 29, 4143-4156.	2.0	3
1782	Cryptic speciation of a pelagic <i>Roseobacter</i> population varying at a few thousand nucleotide sites. <i>ISME Journal</i> , 2020, 14, 3106-3119.	4.4	11
1783	Tracking of Antibiotic Resistance Transfer and Rapid Plasmid Evolution in a Hospital Setting by Nanopore Sequencing. <i>MSphere</i> , 2020, 5, .	1.3	51
1784	Scalable multiple whole-genome alignment and locally collinear block construction with SibeliaZ. <i>Nature Communications</i> , 2020, 11, 6327.	5.8	39
1785	Pandemic <i>Vibrio cholerae</i> shuts down site-specific recombination to retain an interbacterial defence mechanism. <i>Nature Communications</i> , 2020, 11, 6246.	5.8	17
1786	Dissection for Floral Micromorphology and Plastid Genome of Valuable Medicinal Borages <i>Arnebia</i> and <i>Lithospermum</i> (Boraginaceae). <i>Frontiers in Plant Science</i> , 2020, 11, 606463.	1.7	16
1787	Biological and Genomic Characterization of a Novel Jumbo Bacteriophage, vB_VhaM_pir03 with Broad Host Lytic Activity against <i>Vibrio harveyi</i> . <i>Pathogens</i> , 2020, 9, 1051.	1.2	20

#	ARTICLE	IF	CITATIONS
1788	An integrated model system to gain mechanistic insights into biofilm-associated antimicrobial resistance in <i>Pseudomonas aeruginosa</i> MPAO1. <i>Npj Biofilms and Microbiomes</i> , 2020, 6, 46.	2.9	31
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.	1.2	12
1790	Diverse Horizontally-Acquired Gene Clusters Confer Sucrose Utilization to Different Lineages of the Marine Pathogen <i>Photobacterium damsela</i> subsp. <i>damsela</i> . <i>Genes</i> , 2020, 11, 1244.	1.0	4
1791	MALDI-TOF MS and genomic analysis can make the difference in the clarification of canine brucellosis outbreaks. <i>Scientific Reports</i> , 2020, 10, 19246.	1.6	9
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.	1.5	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.	1.2	11
1794	Characterisation of mobile genetic elements in <i>Mycoplasma hominis</i> with the description of ICEHo-II, a variant mycoplasma integrative and conjugative element. <i>Mobile DNA</i> , 2020, 11, 30.	1.3	4
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.	1.6	14
1796	Novel Mechanisms of Efflux-Mediated Levofloxacin Resistance and Reduced Amikacin Susceptibility in <i>Stenotrophomonas maltophilia</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 65, .	1.4	7
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.	1.3	21
1798	Complete Genome Sequence of <i>Serratia marcescens</i> Podophage Pila. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	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.	1.3	11
1800	A Tailspike with Exopolysaccharide Depolymerase Activity from a New <i>Providencia stuartii</i> Phage Makes Multidrug-Resistant Bacteria Susceptible to Serum-Mediated Killing. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	22
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, .	0.3	2
1802	Complete Genome Sequence of <i>Salmonella enterica</i> Siphophage Shemara. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	0
1803	Intrinsically disordered regions are abundant in simplexvirus proteomes and display signatures of positive selection. <i>Virus Evolution</i> , 2020, 6, veaa028.	2.2	10
1804	Complete Genome Sequence of <i>Stenotrophomonas</i> Phage Mendera. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	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, .	1.0	16

#	ARTICLE	IF	CITATIONS
1806	Genome Comparison Identifies Different <i>Bacillus</i> Species in a Bast Fibre-Retting Bacterial Consortium and Provides Insights into Pectin Degrading Genes. <i>Scientific Reports</i> , 2020, 10, 8169.	1.6	22
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.	1.5	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.	1.8	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.	1.1	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.	1.6	16
1811	Past and ongoing adaptation of human cytomegalovirus to its host. <i>PLoS Pathogens</i> , 2020, 16, e1008476.	2.1	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 <i>in silico</i> Analyses. <i>Frontiers in Microbiology</i> , 2020, 11, 751.	1.5	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.	1.6	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, .	1.8	22
1815	Two new bacilladnaviruses associated with the diatom <i>Haslea ostrearia</i> . <i>European Journal of Phycology</i> , 2020, 55, 444-453.	0.9	1
1816	Unprecedented Intraindividual Structural Heteroplasmy in <i>Eleocharis</i> (Cyperaceae, Poales) Plastomes. <i>Genome Biology and Evolution</i> , 2020, 12, 641-655.	1.1	22
1817	Complete Genome Sequence of an Alphabaculovirus from <i>Choristoneura diversana</i> . <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	0
1818	Discovery of thermophilic Bacillales using reduced-representation genotyping for identification. <i>BMC Microbiology</i> , 2020, 20, 114.	1.3	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.	1.6	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.	0.5	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.	0.7	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, .	1.5	5
1823	Pan-GWAS of <i>Streptococcus agalactiae</i> Highlights Lineage-Specific Genes Associated with Virulence and Niche Adaptation. <i>MBio</i> , 2020, 11, .	1.8	47



#	ARTICLE	IF	CITATIONS
1824	The Complete Plastomes of Five Hemiparasitic Plants ( <i>Osyris wightiana</i> , <i>Pyralaria edulis</i> , <i>Santalum</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 Santalales. <i>Frontiers in Genetics</i> , 2020, 11, 597.	1.1	10
1825	Unexpected conservation and global transmission of agrobacterial virulence plasmids. <i>Science</i> , 2020, 368, .	6.0	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.	1.5	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.	1.6	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.	3.8	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.	1.8	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.	1.5	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.	1.1	5
1832	Characterization of Extremely Drug-Resistant and Hypervirulent <i>Acinetobacter baumannii</i> ABO30. <i>Antibiotics</i> , 2020, 9, 328.	1.5	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.	4.4	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.	1.5	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.	2.0	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.	1.2	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.	1.3	22
1838	Plastome Evolution and Phylogeny of Orchidaceae, With 24 New Sequences. <i>Frontiers in Plant Science</i> , 2020, 11, 22.	1.7	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.	1.0	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.	1.5	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.	2.4	9

#	ARTICLE	IF	CITATIONS
1842	Identification of a Locus Conferring Dominant Susceptibility to <i>Pyrenophora tritici-repentis</i> in Barley. <i>Frontiers in Plant Science</i> , 2020, 11, 158.	1.7	5
1843	Population structure and adaptation of a bacterial pathogen in California grapevines. <i>Environmental Microbiology</i> , 2020, 22, 2625-2638.	1.8	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.	1.1	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.	1.1	8
1846	Taxonomic scheme of the order Chaetophorales (Chlorophyceae, Chlorophyta) based on chloroplast genomes. <i>BMC Genomics</i> , 2020, 21, 442.	1.2	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 /Over 2020, 5, .	1.3	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.	0.6	7
1849	Introducing Lu-1, a Novel <i>Lactobacillus jensenii</i> Phage Abundant in the Urogenital Tract. <i>PLoS ONE</i> , 2020, 15, e0234159.	1.1	10
1850	The Loss of the Inverted Repeat in the Putranjivoid Clade of Malpighiales. <i>Frontiers in Plant Science</i> , 2020, 11, 942.	1.7	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, .	1.3	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.	0.8	3
1853	Plastome Structural Conservation and Evolution in the Clusioid Clade of Malpighiales. <i>Scientific Reports</i> , 2020, 10, 9091.	1.6	22
1854	The Origin and Evolution of Plastid Genome Downsizing in Southern Hemispheric Cypresses ( <i>Cupressaceae</i> ). <i>Frontiers in Plant Science</i> , 2020, 11, 901.	1.7	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.	0.5	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.	1.5	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.	1.2	6
1858	High-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.	2.2	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.	1.7	10

#	ARTICLE	IF	CITATIONS
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.	1.7	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.	1.0	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.	1.0	4
1863	CRISPR-Cas9-Mediated Carbapenemase Gene and Plasmid Curing in Carbapenem-Resistant <i>Enterobacteriaceae</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	1.4	50
1864	Phylogeographical Analyses and Antibiotic Resistance Genes of <i>Acinetobacter johnsonii</i> Highlight Its Clinical Relevance. <i>MSphere</i> , 2020, 5, .	1.3	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.	1.6	33
1866	Comparative genomics of multidrug-resistant <i>Enterococcus</i> spp. isolated from wastewater treatment plants. <i>BMC Microbiology</i> , 2020, 20, 20.	1.3	31
1867	<p></p>Consequences Of Long-Term Bacteria's Exposure To Silver Nanoformulations With Different PhysicoChemical Properties</p>. <i>International Journal of Nanomedicine</i> , 2020, Volume 15, 199-213.	3.3	14
1868	Comparative Analysis of <i>Actaea</i> Chloroplast Genomes and Molecular Marker Development for the Identification of Authentic <i>Cimicifugae</i> Rhizoma. <i>Plants</i> , 2020, 9, 157.	1.6	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.	1.6	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.	1.5	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.	1.8	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.	1.5	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.	0.5	4
1874	Organelle inheritance and genome architecture variation in isogamous brown algae. <i>Scientific Reports</i> , 2020, 10, 2048.	1.6	12
1875	Characterization and Genome Analysis of a Novel <i>Salmonella</i> Phage vB_SenS_SE1. <i>Current Microbiology</i> , 2020, 77, 1308-1315.	1.0	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.	1.0	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.	1.0	6

#	ARTICLE	IF	CITATIONS
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.	2.1	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.	0.8	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.	1.2	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.	2.5	0
1882	Complete organelle genomes of <i>Sinapis arvensis</i> and their evolutionary implications. <i>Crop Journal</i> , 2020, 8, 505-514.	2.3	12
1883	Comparative genome characterization of the periodontal pathogen <i>Tannerella forsythia</i> . <i>BMC Genomics</i> , 2020, 21, 150.	1.2	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.	1.1	4
1885	Phylogenetic Analysis and Substitution Rate Estimation of Colonial Volvocine Algae Based on Mitochondrial Genomes. <i>Genes</i> , 2020, 11, 115.	1.0	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.	1.4	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.	1.0	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.	1.8	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.	0.8	7
1890	Complete Chloroplast Genome Sequence of Chinese Lacquer Tree ( <i>Toxicodendron vernicifluum</i> ), Tj ETQq0 0.0rgBT/Overlock 10	0.9	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.	1.5	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.	1.5	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.	1.5	11
1894	Evolution and Genetic Diversity of Primate Cytomegaloviruses. <i>Microorganisms</i> , 2020, 8, 624.	1.6	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.	0.9	14

#	ARTICLE	IF	CITATIONS
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.	1.6	14
1898	Parallel Evolution in the Integration of a Co-obligate Aphid Symbiosis. <i>Current Biology</i> , 2020, 30, 1949-1957.e6.	1.8	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.	1.0	22
1900	Complete Genome Sequence of <i>Stenotrophomonas maltophilia</i> Myophage Moby. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	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.	1.5	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.	1.6	4
1903	Complete Genome Sequence of <i>Serratia</i> Phage Muldoon. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	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, .	1.0	17
1905	Mutation of <i>kvrA</i> Causes <i>OmpK35</i> and <i>OmpK36</i> Porin Downregulation and Reduced Meropenem-Vaborbactam Susceptibility in KPC-Producing <i>Klebsiella pneumoniae</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	1.4	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.	0.5	4
1907	Complete Genome Sequence of <i>Escherichia coli</i> BL21-AI. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	8
1908	Complete Genome Sequence of <i>Serratia marcescens</i> Siphophage Slocum. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	3
1909	Complete Genome Sequence of Myophage <i>Ec_Makalu_002</i> , Which Infects Uropathogenic <i>Escherichia coli</i> . <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	2
1910	Wide crossing diversify mitogenomes of rice. <i>BMC Plant Biology</i> , 2020, 20, 159.	1.6	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.	1.6	23
1912	Evolution of Predicted Acid Resistance Mechanisms in the Extremely Acidophilic <i>Leptospirillum</i> Genus. <i>Genes</i> , 2020, 11, 389.	1.0	23
1913	The First Glimpse of <i>Streptocarpus ionanthus</i> ( <i>Gesneriaceae</i> ) Phylogenomics: Analysis of Five Subspecies' Chloroplast Genomes. <i>Plants</i> , 2020, 9, 456.	1.6	13

#	ARTICLE	IF	CITATIONS
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.	1.1	26
1915	Pan-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.	1.3	19
1916	Plastid phylogenomic insights into the evolution of subfamily Dialioideae (Leguminosae). <i>Plant Diversity</i> , 2021, 43, 27-34.	1.8	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.	1.0	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.	0.4	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.	1.0	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, .	1.1	6
1921	Plastome phylogenomics of <i>Cephalotaxus</i> (Cephalotaxaceae) and allied genera. <i>Annals of Botany</i> , 2021, 127, 697-708.	1.4	14
1922	ICEHpsaHPS7, a Novel Multiple Drug Resistance Integrative Conjugative Element in <i>Glaesserella parasuis</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, .	1.4	7
1923	Diversification of methanogens into hyperalkaline serpentinizing environments through adaptations to minimize oxidant limitation. <i>ISME Journal</i> , 2021, 15, 1121-1135.	4.4	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.	2.0	10
1925	De novo assembly and comparative analysis of the complete mitochondrial genome sequence of the pistachio psyllid, <i>Agonoscena pistaciae</i> (Hemiptera: Aphalaridae). <i>International Journal of Tropical Insect Science</i> , 2021, 41, 1387-1396.	0.4	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.	1.0	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.	0.7	12
1928	Repeats in mitochondrial and chloroplast genomes characterize the ecotypes of the <i>Oryza</i> . <i>Molecular Breeding</i> , 2021, 41, 1.	1.0	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, .	0.3	0
1930	Evolutionary Rescue of an Environmental <i>Pseudomonas otitidis</i> in Response to Anthropogenic Perturbation. <i>Frontiers in Microbiology</i> , 2020, 11, 563885.	1.5	5
1931	Comparative Virulence and Genomic Analysis of <i>Streptococcus suis</i> Isolates. <i>Frontiers in Microbiology</i> , 2020, 11, 620843.	1.5	11



#	ARTICLE	IF	CITATIONS
1932	Complete Genome Sequence of <i>Rhizobium japonicum</i> Podophage Pasto. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	2
1933	Complete Genome Sequence of <i>Streptomyces</i> Siphophage Sycamore. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	0
1934	Increasing New Delhi metallo- $\beta$ -lactamase-positive <i>Escherichia coli</i> among carbapenem non-susceptible Enterobacteriaceae in Taiwan during 2016 to 2018. <i>Scientific Reports</i> , 2021, 11, 2609.	1.6	16
1935	Genome-wide comparison of four MRSA clinical isolates from Germany and Hungary. <i>PeerJ</i> , 2021, 9, e10185.	0.9	6
1936	Genetic diversification of persistent <i>Mycobacterium abscessus</i> within cystic fibrosis patients. <i>Virulence</i> , 2021, 12, 2415-2429.	1.8	14
1937	Plastid Genomes of Flowering Plants: Essential Principles. <i>Methods in Molecular Biology</i> , 2021, 2317, 3-47.	0.4	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. <i>Ecology and Evolution</i> , 2021, 11, 2173-2193.	0.8	9
1939	Complete Genome Sequence of <i>Rhizobium phaseoli</i> Podophage Palo. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	1
1940	Complete Genome Sequence of <i>Streptomyces</i> Siphophage Sitrop. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	0
1941	Comparative Genomics, from the Annotated Genome to Valuable Biological Information: A Case Study. <i>Methods in Molecular Biology</i> , 2021, 2242, 91-112.	0.4	0
1942	Genome Analysis of a Historical <i>Shigella dysenteriae</i> Serotype 1 Strain Carrying a Conserved Stx Prophage Region. <i>Frontiers in Microbiology</i> , 2020, 11, 614793.	1.5	1
1943	Type <i>IV</i> pili are widespread among non-pathogenic Gram-positive gut bacteria with diverse carbohydrate utilization patterns. <i>Environmental Microbiology</i> , 2021, 23, 1527-1540.	1.8	3
1944	Identification and Characterization of Mycobacterial Species Using Whole-Genome Sequences. <i>Methods in Molecular Biology</i> , 2021, 2314, 399-457.	0.4	0
1945	One is not enough: On the effects of reference genome for the mapping and subsequent analyses of short-reads. <i>PLoS Computational Biology</i> , 2021, 17, e1008678.	1.5	46
1946	Genomic Analysis of a Newly Isolated <i>Acidithiobacillus ferridurans</i> JAGS Strain Reveals Its Adaptation to Acid Mine Drainage. <i>Minerals (Basel, Switzerland)</i> , 2021, 11, 74.	0.8	15
1947	Complete Genome Sequence of <i>Streptomyces</i> Phage Shady. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	0
1948	Complete Genome Sequence of <i>Klebsiella aerogenes</i> Siphophage Solomon. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	0
1949	Complete Genome Sequence of <i>Klebsiella pneumoniae</i> Myophage Muenster. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	3

#	ARTICLE	IF	CITATIONS
1950	Complete Genome Sequence of <i>Klebsiella pneumoniae</i> Jumbo Phage Miami. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	4
1951	Reorganized Genomic Taxonomy of Francisellaceae Enables Design of Robust Environmental PCR Assays for Detection of <i>Francisella tularensis</i> . <i>Microorganisms</i> , 2021, 9, 146.	1.6	19
1952	Mitochondrial genome of the harmful algal bloom species <i>Odontella regia</i> (Mediophyceae, Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 662 To	1.5	9
1953	Phylogenetic Methods for Genome-Wide Association Studies in Bacteria. <i>Methods in Molecular Biology</i> , 2021, 2242, 205-220.	0.4	5
1954	Complete Genome Sequence of <i>Streptomyces</i> Phage Sentinel. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	0
1955	Complete Genome Sequence of <i>Streptomyces</i> Phage Salutena. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	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. <i>BMC Genomics</i> , 2021, 22, 39.	1.2	2
1958	Mitochondrial Genome Evolution in Pelagophyte Algae. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	10
1959	Examination of <i>Staphylococcus aureus</i> Prophages Circulating in Egypt. <i>Viruses</i> , 2021, 13, 337.	1.5	5
1960	Comparative plastome genomics and phylogenetic analyses of Liliaceae. <i>Botanical Journal of the Linnean Society</i> , 2021, 196, 279-293.	0.8	19
1961	Essential Amino Acid Enrichment and Positive Selection Highlight Endosymbiont's Role in a Global Virus-Vectoring Pest. <i>MSystems</i> , 2021, 6, .	1.7	3
1962	Assessing <i>Trypanosoma cruzi</i> Parasite Diversity through Comparative Genomics: Implications for Disease Epidemiology and Diagnostics. <i>Pathogens</i> , 2021, 10, 212.	1.2	24
1963	Complete Genome Sequence of <i>Klebsiella aerogenes</i> Myophage Metamorpho. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	0
1965	Comparative genomics of MRSA strains from human and canine origins reveals similar virulence gene repertoire. <i>Scientific Reports</i> , 2021, 11, 4724.	1.6	13
1966	Temporal Stability and Genetic Diversity of 48-Year-Old T-Series Phages. <i>MSystems</i> , 2021, 6, .	1.7	9
1967	Genomic analysis of a functional haloacid-degrading gene of <i>Bacillus megaterium</i> strain BHS1 isolated from Blue Lake (Mavi GI¼, Turkey). <i>Annals of Microbiology</i> , 2021, 71, .	1.1	5
1968	Complete Genome Sequence of <i>Burkholderia cenocepacia</i> Phage Mica. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	1
1969	Point mutation in the stop codon of MAV_RS14660 increases the growth rate of <i>Mycobacterium avium</i> subspecies <i>hominissuis</i> . <i>Microbiology (United Kingdom)</i> , 2021, 167, .	0.7	0

#	ARTICLE	IF	CITATIONS
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.	0.9	15
1971	Complete Genome Sequence of <i>Bradyrhizobium japonicum</i> Podophage Paso. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	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.	1.6	20
1973	Comparative analysis of <i>Phytophthora</i> genomes reveals oomycete pathogenesis in crops. <i>Heliyon</i> , 2021, 7, e06317.	1.4	3
1974	Evolution of genome structure in the <i>Drosophila simulans</i> species complex. <i>Genome Research</i> , 2021, 31, 380-396.	2.4	55
1975	Continental-Scale Gene Flow Prevents Allopatric Divergence of Pelagic Freshwater Bacteria. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	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.	1.6	5
1978	Complete Genome Sequence of <i>Burkholderia cenocepacia</i> Phage Magia. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	0
1980	Chloroplast genomes and phylogenetic analysis of two species of <i>Oedocladium</i> (Oedogoniales.) <i>Tj ETQq0 0 0 rgBT /Overlock_10 Tf 50 4</i>	0.9	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.	1.3	23
1982	A <i>Sarcina</i> bacterium linked to lethal disease in sanctuary chimpanzees in Sierra Leone. <i>Nature Communications</i> , 2021, 12, 763.	5.8	17
1983	Whole-genome comparative analysis of Malaysian <i>Burkholderia pseudomallei</i> clinical isolates. <i>Microbial Genomics</i> , 2021, 7, .	1.0	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.	1.6	7
1985	An Efficient, Counter-Selection-Based Method for Prophage Curing in <i>Pseudomonas aeruginosa</i> Strains. <i>Viruses</i> , 2021, 13, 336.	1.5	2
1987	A Novel Group of Promiscuous Podophages Infecting Diverse Gammaproteobacteria from River Communities Exhibits Dynamic Intergenous Host Adaptation. <i>MSystems</i> , 2021, 6, .	1.7	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.	1.4	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.	1.5	25
1990	The genomic content and context of auxiliary metabolic genes in roseophages. <i>Environmental Microbiology</i> , 2021, 23, 3743-3757.	1.8	18

#	ARTICLE	IF	CITATIONS
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.	2.1	28
1992	Lineage-specific plastid degradation in subtribe Gentianinae (Gentianaceae). <i>Ecology and Evolution</i> , 2021, 11, 3286-3299.	0.8	21
1993	Complete Genome Sequence of <i>Burkholderia gladioli</i> Phage Maja. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	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.	1.7	30
1995	Characterization and complete genome sequence of Privateer, a highly prolate <i>Proteus mirabilis</i> podophage. <i>PeerJ</i> , 2021, 9, e10645.	0.9	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.	1.3	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, .	1.4	3
1998	Triclosan Tolerance Is Driven by a Conserved Mechanism in Diverse <i>Pseudomonas</i> Species. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	8
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.	1.3	6
2001	Genomic insights into the host specific adaptation of the <i>Pneumocystis</i> genus. <i>Communications Biology</i> , 2021, 4, 305.	2.0	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.	2.0	16
2005	Genomic Insights Into the Pathogenicity of a Novel Biofilm-Forming <i>Enterococcus</i> sp. Bacteria ( <i>Enterococcus lacertideformus</i> ) Identified in Reptiles. <i>Frontiers in Microbiology</i> , 2021, 12, 635208.	1.5	6
2006	Apparent nosocomial adaptation of <i>Enterococcus faecalis</i> predates the modern hospital era. <i>Nature Communications</i> , 2021, 12, 1523.	5.8	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.	2.1	7
2008	Epidemic HI2 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.	1.6	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.	1.5	7
2011	Comparison of MiSeq, MinION, and hybrid genome sequencing for analysis of <i>Campylobacter jejuni</i> . <i>Scientific Reports</i> , 2021, 11, 5676.	1.6	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.	1.6	16

#	ARTICLE	IF	CITATIONS
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.	1.8	3
2014	Gene disruption by structural mutations drives selection in US rice breeding over the last century. <i>PLoS Genetics</i> , 2021, 17, e1009389.	1.5	6
2015	Engineered yeast genomes accurately assembled from pure and mixed samples. <i>Nature Communications</i> , 2021, 12, 1485.	5.8	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, .	0.3	1
2018	Complete Genome Sequence of <i>Stenotrophomonas maltophilia</i> Siphophage Salva. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	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.	1.6	5
2021	Genome Sequence and Characterization of <i>Acinetobacter</i> Phage DMU1. <i>Phage</i> , 2021, 2, 50-56.	0.8	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.	1.5	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.	1.5	5
2026	Complete Genome Sequence of <i>Bifidobacterium longum</i> subsp. <i>longum</i> JCM7052. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	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.	1.8	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.	0.8	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.	0.6	1
2030	Phage Resistance Is Associated with Decreased Virulence in KPC-Producing <i>Klebsiella pneumoniae</i> of the Clonal Group 258 Clade II Lineage. <i>Microorganisms</i> , 2021, 9, 762.	1.6	10
2031	A Novel Jumbo Phage PhiMa05 Inhibits Harmful <i>Microcystis</i> sp.. <i>Frontiers in Microbiology</i> , 2021, 12, 660351.	1.5	13
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, .	1.4	13
2034	Genomic Characterization of <i>Salmonella typhimurium</i> DT104 Strains Associated with Cattle and Beef Products. <i>Pathogens</i> , 2021, 10, 529.	1.2	7
2035	Comparative genomics of the ADA clade within the Nostocales. <i>Harmful Algae</i> , 2021, 104, 102037.	2.2	11

#	ARTICLE	IF	CITATIONS
2036	Genome sequencing and comparative genome analysis of 6 hypervirulent <i>Klebsiella pneumoniae</i> strains isolated in China. <i>Archives of Microbiology</i> , 2021, 203, 3125-3133.	1.0	3
2037	JD419, a <i>Staphylococcus aureus</i> Phage With a Unique Morphology and Broad Host Range. <i>Frontiers in Microbiology</i> , 2021, 12, 602902.	1.5	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.	2.9	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.	1.6	9
2040	Long-read-sequenced reference genomes of the seven major lineages of enterotoxigenic <i>Escherichia coli</i> (EPEC) circulating in modern time. <i>Scientific Reports</i> , 2021, 11, 9256.	1.6	12
2041	Multi-Drug Resistant Plasmids with ESBL/AmpC and <i>mcr-5.1</i> in Paraguayan Poultry Farms: The Linkage of Antibiotic Resistance and Hatcheries. <i>Microorganisms</i> , 2021, 9, 866.	1.6	6
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.	1.2	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.	5.9	43
2046	Horsing Around: <i>Escherichia coli</i> ST1250 of Equine Origin Harboring Epidemic IncHI1/ST9 Plasmid with <i>bla</i> <sub>CTX-M-1</sub> and an Operon for Short-Chain Fructooligosaccharide Metabolism. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, .	1.4	5
2047	Genome sequence, transcriptome, and annotation of rodent malaria parasite <i>Plasmodium yoelii nigeriensis</i> N67. <i>BMC Genomics</i> , 2021, 22, 303.	1.2	7
2049	<i>Haslea silbo</i> , A Novel Cosmopolitan Species of Blue Diatoms. <i>Biology</i> , 2021, 10, 328.	1.3	12
2050	Silent spread of mobile colistin resistance gene <i>mcr-9.1</i> on IncHI2 superplasmids in clinical carbapenem-resistant Enterobacterales. <i>Clinical Microbiology and Infection</i> , 2021, 27, 1856.e7-1856.e13.	2.8	37
2051	Fundamental evolution of all <i>Orthocoronavirinae</i> including three deadly lineages descendent from Chiroptera-hosted coronaviruses: SARS-CoV, MERS-CoV and SARS-CoV-2. <i>Cladistics</i> , 2021, 37, 461-488.	1.5	16
2052	Sequence analysis of tyrosine recombinases allows annotation of mobile genetic elements in prokaryotic genomes. <i>Molecular Systems Biology</i> , 2021, 17, e9880.	3.2	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.	1.0	25
2054	Complete Genome Sequence of <i>Burkholderia gladioli</i> Myophage Mana. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	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.	1.8	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.	1.6	12



#	ARTICLE	IF	CITATIONS
2058	The chloroplast genome evolution of Venus slipper ( <i>Paphiopedilum</i> ): IR expansion, SSC contraction, and highly rearranged SSC regions. <i>BMC Plant Biology</i> , 2021, 21, 248.	1.6	49
2059	Genomic GC content drifts downward in most bacterial genomes. <i>PLoS ONE</i> , 2021, 16, e0244163.	1.1	7
2060	Starch Synthesis-Related Genes (SSRG) Evolution in the Genus <i>Oryza</i> . <i>Plants</i> , 2021, 10, 1057.	1.6	0
2061	Pan-Mitogenomics Approach Discovers Diversity and Dynamism in the Prominent Brown Rot Fungal Pathogens. <i>Frontiers in Microbiology</i> , 2021, 12, 647989.	1.5	9
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.	1.5	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, .	0.3	2
2064	Characterization of bla <sub>NDM-5</sub> -harbouring <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, .	0.7	4
2065	Genomics-Enabled Novel Insight Into the Pathovar-Specific Population Structure of the Bacterial Leaf Streak Pathogen <i>Xanthomonas translucens</i> in Small Grain Cereals. <i>Frontiers in Microbiology</i> , 2021, 12, 674952.	1.5	31
2066	Phenotype profiles and adaptive preference of <i>Acinetobacter johnsonii</i> isolated from Ba River with different environmental backgrounds. <i>Environmental Research</i> , 2021, 196, 110913.	3.7	13
2067	Widespread distribution of prophages signaling the potential for adaptability and pathogenicity evolution of <i>Ralstonia solanacearum</i> species complex. <i>Genomics</i> , 2021, 113, 992-1000.	1.3	11
2068	Genomic appraisal of <i>Klebsiella</i> PGPB isolated from soil to enhance the growth of barley. <i>Genes and Genomics</i> , 2021, 43, 869-883.	0.5	1
2069	Complete Genome Sequence of <i>Klebsiella pneumoniae</i> Podophage Pune. <i>Microbiology Resource Announcements</i> , 2021, 10, e0140520.	0.3	0
2070	Evolution of virulence in a novel family of transmissible megaplasmids. <i>Environmental Microbiology</i> , 2021, 23, 5289-5304.	1.8	5
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.	1.2	3
2072	Enhanced Mutation Rate, Relaxed Selection, and the "Domino Effect" are associated with Gene Loss in <i>Blattabacterium</i> , A Cockroach Endosymbiont. <i>Molecular Biology and Evolution</i> , 2021, 38, 3820-3831.	3.5	13
2073	Comparative genome analysis of multidrug-resistant <i>Pseudomonas aeruginosa</i> JNQH-PA57, a clinically isolated mucoid strain with comprehensive carbapenem resistance mechanisms. <i>BMC Microbiology</i> , 2021, 21, 133.	1.3	10
2075	Genomic analysis of the lectotype specimens of European <i>Ulva rigida</i> and <i>Ulva lacinulata</i> ( <i>Ulvaceae</i> , <i>Chlorophyta</i> ) reveals the ongoing misapplication of names. <i>European Journal of Phycology</i> , 2022, 57, 143-153.	0.9	35
2077	Comparison among the chloroplast genomes of five species of <i>Chamaerhodos</i> ( <i>Rosaceae</i> ): Tj ETQq1 1 0.784314 rgBT 3 Overl	0.2	3

#	ARTICLE	IF	CITATIONS
2078	Ecophysiology of the Cosmopolitan OM252 Bacterioplankton ( <i>Gammaproteobacteria</i> ). <i>MSystems</i> , 2021, 6, e0027621.	1.7	5
2079	Endosymbiont Capture, a Repeated Process of Endosymbiont Transfer with Replacement in Trypanosomatids <i>Angomonas</i> spp.. <i>Pathogens</i> , 2021, 10, 702.	1.2	2
2080	How Bacteria Change after Exposure to Silver Nanoformulations: Analysis of the Genome and Outer Membrane Proteome. <i>Pathogens</i> , 2021, 10, 817.	1.2	1
2081	Precision Methylome and In Vivo Methylation Kinetics Characterization of <i>Klebsiella pneumoniae</i> . <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 418-434.	3.0	13
2082	A Single Nucleotide Polymorphism in <i>lptG</i> Increases Tolerance to Bile Salts, Acid, and Staining of Calcofluor-Binding Polysaccharides in <i>Salmonella enterica</i> Serovar Typhimurium E40. <i>Frontiers in Microbiology</i> , 2021, 12, 671453.	1.5	1
2083	Comparative genomics of <i>Bordetella pertussis</i> and prediction of new vaccines and drug targets. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 10136-10152.	2.0	4
2084	Comparative Genomics of Closely Related <i>Tetragenococcus halophilus</i> Strains Elucidate the Diversity and Microevolution of CRISPR Elements. <i>Frontiers in Microbiology</i> , 2021, 12, 687985.	1.5	5
2085	Role of AmpG in the resistance to $\beta$ -lactam agents, including cephalosporins and carbapenems: candidate for a novel antimicrobial target. <i>Annals of Clinical Microbiology and Antimicrobials</i> , 2021, 20, 45.	1.7	4
2087	Evolution of Interbacterial Antagonism in Bee Gut Microbiota Reflects Host and Symbiont Diversification. <i>MSystems</i> , 2021, 6, .	1.7	13
2088	Whole-Genome Sequencing Investigation of a Large Nosocomial Outbreak Caused by ST131 H30Rx KPC-Producing <i>Escherichia coli</i> in Italy. <i>Antibiotics</i> , 2021, 10, 718.	1.5	7
2089	Serotype-Switch Variant of Multidrug-Resistant <i>Streptococcus pneumoniae</i> Sequence Type 271. <i>Emerging Infectious Diseases</i> , 2021, 27, 1689-1692.	2.0	9
2090	Differential Bacteriophage Efficacy in Controlling <i>Salmonella</i> in Cattle Hide and Soil Models. <i>Frontiers in Microbiology</i> , 2021, 12, 657524.	1.5	4
2091	The chicken or the egg? Plastome evolution and an independent loss of the inverted repeat in papilionoid legumes. <i>Plant Journal</i> , 2021, 107, 861-875.	2.8	29
2092	New Insight into Taxonomy of European Mountain Pines, <i>Pinus mugo</i> Complex, Based on Complete Chloroplast Genomes Sequencing. <i>Plants</i> , 2021, 10, 1331.	1.6	10
2093	Molecular Evolution and Adaptation of Livestock-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> (LA-MRSA) Sequence Type 9. <i>MSystems</i> , 2021, 6, e0049221.	1.7	36
2094	Characterization and Analysis of Clustered Regularly Interspaced Short Palindromic Repeats (CRISPRs) in Pandemic and Non-Pandemic <i>Vibrio parahaemolyticus</i> Isolates from Seafood Sources. <i>Microorganisms</i> , 2021, 9, 1220.	1.6	10
2096	Whole genome sequence insight of two plant growth-promoting bacteria ( <i>B. subtilis</i> BS87 and <i>B. Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50</i> ) potentiality. <i>Microbiological Research</i> , 2021, 247, 126733.	2.5	28
2097	Simultaneous Detection and Differentiation of Clinically Relevant Relapsing Fever <i>Borrelia</i> with Semimultiplex Real-Time PCR. <i>Journal of Clinical Microbiology</i> , 2021, 59, e0298120.	1.8	6

#	ARTICLE	IF	CITATIONS
2098	Plastid genome data provide new insights into the phylogeny and evolution of the genus <i>Epimedium</i> . <i>Journal of Advanced Research</i> , 2022, 36, 175-185.	4.4	22
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.	1.1	7
2100	The complete mitogenome assemblies of 10 diploid potato clones reveal recombination and overlapping variants. <i>DNA Research</i> , 2021, 28, .	1.5	4
2101	Molecular characterization of a <i>Bacillus thuringiensis</i> strain from Argentina, toxic against Lepidoptera and Coleoptera, based on its whole-genome and Cry protein analysis. <i>Journal of Invertebrate Pathology</i> , 2021, 183, 107563.	1.5	8
2102	Plastome evolution and organisation in the <i>Hoya</i> group (Apocynaceae). <i>Scientific Reports</i> , 2021, 11, 14520.	1.6	5
2103	<i>Pseudomonas aeruginosa</i> PAO 1 In Vitro Time-kill Kinetics Using Single Phages and Phage Formulations Modulating Death, Adaptation, and Resistance. <i>Antibiotics</i> , 2021, 10, 877.	1.5	5
2104	Genome Annotation of Poly(lactic acid) Degrading <i>Pseudomonas aeruginosa</i> , <i>Sphingobacterium</i> sp. and <i>Geobacillus</i> sp.. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7385.	1.8	5
2105	Complete Genome Sequence of <i>Campylobacter jejuni</i> Strain G1, Isolated from a Patient with Guillain-Barré Syndrome. <i>Microbiology Resource Announcements</i> , 2021, 10, e0050521.	0.3	1
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.	1.8	8
2107	Pangenome analysis and virulence profiling of <i>Streptococcus intermedius</i> . <i>BMC Genomics</i> , 2021, 22, 522.	1.2	7
2108	Analysis of CRISPR systems of types II-A, I-E and I-C in strains of <i>Lactocaseibacillus</i> . <i>International Dairy Journal</i> , 2021, 118, 105027.	1.5	1
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.	1.5	10
2111	Characterization of a novel transitional group <i>Rickettsia</i> species ( <i>Rickettsia tillamookensis</i> sp. nov.) from the western black-legged tick, <i>Ixodes pacificus</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	9
2112	Whole-Genome Comparative Analysis Reveals Association Between <i>Salmonella</i> Genomic Variation and Egg Production Systems. <i>Frontiers in Veterinary Science</i> , 2021, 8, 666767.	0.9	2
2113	Sequence of the Mitochondrial Genome of <i>Lactuca virosa</i> Suggests an Unexpected Role in <i>Lactuca sativa</i> 's Evolution. <i>Frontiers in Plant Science</i> , 2021, 12, 697136.	1.7	4
2114	The Conservation of Chloroplast Genome Structure and Improved Resolution of Intrafamilial Relationships of <i>Crassulaceae</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 631884.	1.7	16
2115	Complete genome sequence and phylogenomic analysis of the first N4-like lytic bacteriophage vB_Ppp_A38 (ÎA38) infecting <i>Pectobacterium parmentieri</i> . <i>European Journal of Plant Pathology</i> , 2021, 161, 483-489.	0.8	2
2116	Natural Selection Shapes Maintenance of Orthologous sRNAs in Divergent Host-Restricted Bacterial Genomes. <i>Molecular Biology and Evolution</i> , 2021, 38, 4778-4791.	3.5	2

#	ARTICLE	IF	CITATIONS
2117	Selection of target genes for pcr diagnostics of <i>Xanthomonas arboricola</i> virulent for cereals and brassicas. , 2021, 104, 87-96.	0.4	0
2118	Field-Deployable Recombinase Polymerase Amplification Assay for Specific, Sensitive and Rapid Detection of the US Select Agent and Toxigenic Bacterium, <i>Rathayibacter toxicus</i> . <i>Biology</i> , 2021, 10, 620.	1.3	7
2119	Global biogeography of chemosynthetic symbionts reveals both localized and globally distributed symbiont groups. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	15
2120	Large Differences in the Haptophyte <i>Phaeocystis globosa</i> Mitochondrial Genomes Driven by Repeat Amplifications. <i>Frontiers in Microbiology</i> , 2021, 12, 676447.	1.5	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.	1.4	5
2122	Evolutionarily recent dual obligatory symbiosis among adelgids indicates a transition between fungus- and insect-associated lifestyles. <i>ISME Journal</i> , 2022, 16, 247-256.	4.4	16
2123	Comparative Mitogenomic Analysis Reveals Gene and Intron Dynamics in Rubiaceae and Intra-Specific Diversification in <i>Damnacanthus indicus</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 7237.	1.8	7
2124	New insights into the diversity and evolution of the archaeal mobilome from three complete genomes of <i>Saccharolobus shibatae</i> . <i>Environmental Microbiology</i> , 2021, 23, 4612-4630.	1.8	5
2125	Fha Deficient <i>Bordetella pertussis</i> Isolates in Iran with 50 Years Whole Cell Pertussis Vaccination. <i>Iranian Journal of Public Health</i> , 2021, 50, 1454-1462.	0.3	2
2126	Harmonization of whole-genome sequencing for outbreak surveillance of Enterobacteriaceae and Enterococci. <i>Microbial Genomics</i> , 2021, 7, .	1.0	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.	4.1	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.	0.9	1
2130	Genome Characterization, Comparison and Phylogenetic Analysis of Complete Mitochondrial Genome of <i>Evolvulus alsinoides</i> Reveals Highly Rearranged Gene Order in Solanales. <i>Life</i> , 2021, 11, 769.	1.1	10
2132	Horizontal Gene Transfer Is the Main Driver of Antimicrobial Resistance in Broiler Chicks Infected with <i>Salmonella enterica</i> Serovar Heidelberg. <i>MSystems</i> , 2021, 6, e0072921.	1.7	8
2133	Horizontal Transfer of Microbial Toxin Genes to Gall Midge Genomes. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	7
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.	1.7	15
2135	Complete chloroplast genome of the green alga <i>Chaetophora lobata</i> (Chlorophyceae, Chlorophyta): morphological features and phylogenetic and comparative analysis. <i>European Journal of Phycology</i> , 0, 1-12.	0.9	0
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.	2.3	3

#	ARTICLE	IF	CITATIONS
2138	The apicoplast of <i>Haemoproteus columbae</i> : A comparative study of this organelle genome in Haemosporida. <i>Molecular Phylogenetics and Evolution</i> , 2021, 161, 107185.	1.2	8
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.	0.9	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.	1.4	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.	1.6	2
2142	Tailed Lytic Bacteriophages of Soft Rot Pectobacteriaceae. <i>Microorganisms</i> , 2021, 9, 1819.	1.6	7
2144	Plastome Evolution in the Hyperdiverse Genus <i>Euphorbia</i> (Euphorbiaceae) Using Phylogenomic and Comparative Analyses: Large-Scale Expansion and Contraction of the Inverted Repeat Region. <i>Frontiers in Plant Science</i> , 2021, 12, 712064.	1.7	16
2145	Diversity in the composition of the accessory genome of Mexican <i>Pseudomonas aeruginosa</i> strains. <i>Genes and Genomics</i> , 2021, , 1.	0.5	0
2146	Genomic Analysis and Secondary Metabolites Production of the Endophytic <i>Bacillus velezensis</i> Bvel1: A Biocontrol Agent against <i>Botrytis cinerea</i> Causing Bunch Rot in Post-Harvest Table Grapes. <i>Plants</i> , 2021, 10, 1716.	1.6	34
2148	Complete Genome Resources for <i>Xylella fastidiosa</i> Strains AlmaEM3 and BB08-1 Reveal Prophage-Associated Structural Variation Among Blueberry-Infecting Strains. <i>Phytopathology</i> , 2022, 112, 732-736.	1.1	4
2149	Gene Annotation and Transcriptome Delineation on a De Novo Genome Assembly for the Reference <i>Leishmania major</i> Friedlin Strain. <i>Genes</i> , 2021, 12, 1359.	1.0	7
2150	Uncovering Diagnostic Value of Mitogenome for Identification of Cryptic Species <i>Fusarium graminearum</i> Sensu Stricto. <i>Frontiers in Microbiology</i> , 2021, 12, 714651.	1.5	2
2151	A Type I Restriction Modification System Influences Genomic Evolution Driven by Horizontal Gene Transfer in <i>Paenibacillus polymyxa</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 709571.	1.5	7
2152	Antimicrobial susceptibilities and comparative whole genome analysis of two isolates of the probiotic bacterium <i>Lactiplantibacillus plantarum</i> , strain ATCC 202195. <i>Scientific Reports</i> , 2021, 11, 15893.	1.6	6
2153	Equine Intestinal O-Seroconverting Temperate Coliphage Hf4s: Genomic and Biological Characterization. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0112421.	1.4	4
2154	Newly identified proviruses in <i>Thermotogota</i> suggest that viruses are the vehicles on the highways of interphylum gene sharing. <i>Environmental Microbiology</i> , 2021, 23, 7105-7120.	1.8	4
2155	Comparative Pan-Genome Analysis of Oral <i>Veillonella</i> Species. <i>Microorganisms</i> , 2021, 9, 1775.	1.6	7
2156	Numerical Characterization of DNA Sequences for Alignment-free Sequence Comparison – A Review. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2021, 24, .	0.6	0
2157	Efficient assembly consensus algorithms for divergent contig sets. <i>Computational Biology and Chemistry</i> , 2021, 93, 107516.	1.1	1

#	ARTICLE	IF	CITATIONS
2158	Acquisition and loss of CTX-M plasmids in <i>Shigella</i> species associated with MSM transmission in the UK. <i>Microbial Genomics</i> , 2021, 7, .	1.0	11
2159	Evolution of <i>Acinetobacter baumannii</i> in Clinical Bacteremia Patients. <i>Infection and Drug Resistance</i> , 2021, Volume 14, 3553-3562.	1.1	3
2160	Whole genome sequencing reveals possible host species adaptation of <i>Streptococcus dysgalactiae</i> . <i>Scientific Reports</i> , 2021, 11, 17350.	1.6	14
2161	Development, Phenotypic Characterization and Genomic Analysis of a <i>Francisella tularensis</i> Panel for Tularemia Vaccine Testing. <i>Frontiers in Microbiology</i> , 2021, 12, 725776.	1.5	3
2162	Comparative genomics reveals environmental adaptation differences between <i>Cronobacter</i> species. <i>Food Research International</i> , 2021, 147, 110541.	2.9	3
2163	Comparative Genomics of Three Novel Jumbo Bacteriophages Infecting <i>Staphylococcus aureus</i> . <i>Journal of Virology</i> , 2021, 95, e0239120.	1.5	13
2164	Genomic Analysis of Heterogeneous Vancomycin-Intermediate <i>Staphylococcus aureus</i> Strains from Different Clonal Lineages in South Korea. <i>Microbial Drug Resistance</i> , 2021, 27, 1271-1281.	0.9	3
2165	Chloroplast genomes of five <i>Oedogonium</i> species: genome structure, phylogenetic analysis and adaptive evolution. <i>BMC Genomics</i> , 2021, 22, 707.	1.2	11
2166	Genomic analysis revealed conserved acid tolerance mechanisms from native microorganisms in fermented feed. <i>Journal of Applied Microbiology</i> , 2022, 132, 1152-1165.	1.4	2
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.	1.6	25
2168	Genomic Stability and Genetic Defense Systems in <i>Dolosigranulum pigrum</i> , a Candidate Beneficial Bacterium from the Human Microbiome. <i>MSystems</i> , 2021, 6, e0042521.	1.7	11
2169	Whole genome analysis of <i>Gluconacetobacter azotocaptans</i> DS1 and its beneficial effects on plant growth. <i>3 Biotech</i> , 2021, 11, 450.	1.1	1
2170	Genome analysis of the salt-resistant <i>Paludifilum halophilum</i> DSM 102817T reveals genes involved in flux-tuning of ectoines and unexplored bioactive secondary metabolites. <i>World Journal of Microbiology and Biotechnology</i> , 2021, 37, 178.	1.7	5
2171	Comparative Genome Analysis and Spore Heat Resistance Assay Reveal a New Component to Population Structure and Genome Epidemiology Within <i>Clostridium perfringens</i> Enterotoxin-Carrying Isolates. <i>Frontiers in Microbiology</i> , 2021, 12, 717176.	1.5	5
2172	Organelle Genome Variation in the Red Algal Genus <i>Ahnfeltia</i> (Florideophyceae). <i>Frontiers in Genetics</i> , 2021, 12, 724734.	1.1	0
2173	Genome Evolution of Filamentous Cyanobacterium <i>Nostoc</i> Species: From Facultative Symbiosis to Free Living. <i>Microorganisms</i> , 2021, 9, 2015.	1.6	4
2174	Isolation and characterization of a lytic bacteriophage against <i>Pseudomonas aeruginosa</i> . <i>Scientific Reports</i> , 2021, 11, 19393.	1.6	27
2175	Zoonotic infection and clonal dissemination of <i>Streptococcus equi</i> subspecies <i>zooepidemicus</i> sequence type 194 isolated from humans in Thailand. <i>Transboundary and Emerging Diseases</i> , 2022, 69, .	1.3	10



#	ARTICLE	IF	CITATIONS
2176	Pan-Genome of the Genus <i>Streptomyces</i> and Prioritization of Biosynthetic Gene Clusters With Potential to Produce Antibiotic Compounds. <i>Frontiers in Microbiology</i> , 2021, 12, 677558.	1.5	21
2177	<i>Eikenella glucosivorans</i> sp. nov., isolated from a human throat swab, and emendation of the genus <i>Eikenella</i> to include saccharolytic species. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	8
2178	Phenogenomic Characterization of a Newly Domesticated and Novel Species from the Genus <i>Verrucosipora</i> . <i>Applied and Environmental Microbiology</i> , 2021, 87, e0132721.	1.4	2
2179	Resident TP712 Prophage of <i>Lactococcus lactis</i> Strain MG1363 Provides Extra Holin Functions to the P335 Phage CAP for Effective Host Lysis. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0109221.	1.4	1
2181	Confirmation of <i>Oryctes rhinoceros nudivirus</i> infections in G-haplotype coconut rhinoceros beetles ( <i>Oryctes rhinoceros</i> ) from Palauan PCR-positive populations. <i>Scientific Reports</i> , 2021, 11, 18820.	1.6	14
2182	Genomic Analysis of <i>Limosilactobacillus fermentum</i> ATCC 23271, a Potential Probiotic Strain with Anti-Candida Activity. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 794.	1.5	14
2183	Mitochondrial genome of <i>Theileria uilenbergi</i> endemic in sheep and goats in China. <i>Parasitology Research</i> , 2021, 120, 3429-3436.	0.6	1
2184	Plastome Structural Evolution and Homoplastic Inversions in <i>Neo-Astragalus</i> (Fabaceae). <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	13
2185	Genomic and biochemical characterization of antifungal compounds produced by <i>Bacillus subtilis</i> PMB102 against <i>Alternaria brassicicola</i> . <i>Microbiological Research</i> , 2021, 251, 126815.	2.5	18
2186	New Delhi Metallo- $\beta$ -Lactamase-Producing <i>Enterobacterales</i> Bacteria, Switzerland, 2019–2020. <i>Emerging Infectious Diseases</i> , 2021, 27, 2628-2637.	2.0	14
2187	Characterization of antibiotic resistance and virulence genes of ocular methicillin-resistant <i>Staphylococcus aureus</i> strains through complete genome analysis. <i>Experimental Eye Research</i> , 2021, 212, 108764.	1.2	4
2188	Complete genome sequence and virulence characterization of a neonatal meningitis <i>Escherichia coli</i> isolate. <i>Microbial Pathogenesis</i> , 2021, 160, 105199.	1.3	0
2189	Chloroplast genome analysis of <i>Chrysotila dentata</i> . <i>Gene</i> , 2021, 804, 145871.	1.0	5
2190	Distribution and characterization of prophages in <i>Lactobacillus plantarum</i> derived from kimchi. <i>Food Microbiology</i> , 2022, 102, 103913.	2.1	8
2192	Comparative analysis and implications of the chloroplast genomes of three thistles ( <i>Carduus</i> ) Tj ETQqO 0 0 rgBT /Overlock 10 TF 5	0.9	5
2194	Core and Accessory Genome Analysis of <i>Vibrio mimicus</i> . <i>Microorganisms</i> , 2021, 9, 191.	1.6	6
2195	Telomere length de novo assembly of all 7 chromosomes and mitogenome sequencing of the model entomopathogenic fungus, <i>Metarhizium brunneum</i> , by means of a novel assembly pipeline. <i>BMC Genomics</i> , 2021, 22, 87.	1.2	10
2196	Complete Genome Sequence of <i>Streptomyces</i> Phage Sperrnie. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	0

#	ARTICLE	IF	CITATIONS
2197	Draft Genome Sequence of <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Livingstone 1236H, a Desiccation-Resistant Strain That Poses a Salmonellosis Hazard in Low-Moisture Foods. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	2
2198	Population Genomics of Fungal Plant Pathogens and the Analyses of Rapidly Evolving Genome Compartments. <i>Methods in Molecular Biology</i> , 2020, 2090, 337-355.	0.4	16
2199	Processing and Analyzing Multiple Genomes Alignments with MafFilter. <i>Methods in Molecular Biology</i> , 2020, 2090, 21-48.	0.4	3
2200	Sequence Comparison Without Alignment: The SpaM Approaches. <i>Methods in Molecular Biology</i> , 2021, 2231, 121-134.	0.4	10
2201	The Potential of Family-Free Genome Comparison. <i>Computational Biology</i> , 2013, , 287-307.	0.1	12
2202	Large-Scale Multiple Sequence Alignment and Phylogeny Estimation. <i>Computational Biology</i> , 2013, , 85-146.	0.1	14
2203	Genome Sequencing of <i>Listeria monocytogenes</i> . <i>Methods in Molecular Biology</i> , 2014, 1157, 223-232.	0.4	2
2204	A Review of Pangenome Tools and Recent Studies. , 2020, , 89-112.		21
2205	Two-Level Parallelism to Accelerate Multiple Genome Comparisons. <i>Lecture Notes in Computer Science</i> , 2017, , 445-456.	1.0	1
2206	Indexing Finite Language Representation of Population Genotypes. <i>Lecture Notes in Computer Science</i> , 2011, , 270-281.	1.0	14
2208	The Family Francisellaceae. , 2014, , 287-314.		6
2210	Detection of <i>mcr-1</i> -Carrying <i>Escherichia coli</i> Causing Bloodstream Infection in a New York City Hospital: Avian Origins, Human Concerns?. <i>Open Forum Infectious Diseases</i> , 2017, 4, ofx115.	0.4	20
2211	Characterization of the microaerophilic, bacteriochlorophyll <i>a</i> -containing bacterium <i>Gemmatimonas phototrophica</i> sp. nov., and emended descriptions of the genus <i>Gemmatimonas</i> and <i>Gemmatimonas aurantiaca</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 2410-2419.	0.8	98
2212	<i>Lactobacillus herbarum</i> sp. nov., a species related to <i>Lactobacillus plantarum</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 4682-4688.	0.8	24
2213	Reclassification of <i>Wolbachia persica</i> as <i>Francisella persica</i> comb. nov. and emended description of the family Francisellaceae. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 1200-1205.	0.8	41
2214	<i>Francisella opportunistica</i> sp. nov., isolated from human blood and cerebrospinal fluid. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 1145-1151.	0.8	16
2215	<i>Bradyrhizobium ivorense</i> sp. nov. as a potential local bioinoculant for <i>Cajanus cajan</i> cultures in CÔte d'Ivoire. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 1421-1430.	0.8	17
2216	Description of <i>Citrobacter cronae</i> sp. nov., isolated from human rectal swabs and stool samples. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 2998-3003.	0.8	18

#	ARTICLE	IF	CITATIONS
2217	Closed genome sequences of <i>Staphylococcus lloydii</i> sp. nov. and <i>Staphylococcus durrellii</i> sp. nov. isolated from captive fruit bats ( <i>Pteropus livingstonii</i> ). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 71, .	0.8	18
2218	Analyses of four new <i>Caulobacter</i> Phicbkviruses indicate independent lineages. <i>Journal of General Virology</i> , 2019, 100, 321-331.	1.3	10
2219	Manual curation and reannotation of the genomes of <i>Clostridium difficile</i> 630 <sup>†</sup> erm and <i>C. difficile</i> 630. <i>Journal of Medical Microbiology</i> , 2017, 66, 286-293.	0.7	117
2220	Comparative analysis of the genomes of clinical isolates of <i>Mycobacterium avium</i> subsp. <i>hominissuis</i> regarding virulence-related genes. <i>Journal of Medical Microbiology</i> , 2017, 66, 1063-1075.	0.7	11
2221	Genetic evidence for a novel variant of the pilus island 1 backbone protein in group B <i>Streptococcus</i> . <i>Journal of Medical Microbiology</i> , 2017, 66, 1409-1415.	0.7	5
2222	Phylogenetic comparison of enteroinvasive <i>Escherichia coli</i> isolated from cases of diarrhoeal disease in England, 2005â€“2016. <i>Journal of Medical Microbiology</i> , 2018, 67, 884-888.	0.7	20
2223	Characterization of a colistin-resistant Avian Pathogenic <i>Escherichia coli</i> ST69 isolate recovered from a broiler chicken in Germany. <i>Journal of Medical Microbiology</i> , 2019, 68, 111-114.	0.7	9
2224	Recombination-mediated remodelling of hostâ€“pathogen interactions during <i>Staphylococcus aureus</i> niche adaptation. <i>Microbial Genomics</i> , 2015, 1, e000036.	1.0	39
2225	Evolutionary dynamics of <i>Enterococcus faecium</i> reveals complex genomic relationships between isolates with independent emergence of vancomycin resistance. <i>Microbial Genomics</i> , 2016, 2, .	1.0	50
2226	DNA uptake sequences in <i>Neisseria gonorrhoeae</i> as intrinsic transcriptional terminators and markers of horizontal gene transfer. <i>Microbial Genomics</i> , 2016, 2, e000069.	1.0	16
2227	Bayesian identification of bacterial strains from sequencing data. <i>Microbial Genomics</i> , 2016, 2, e000075.	1.0	19
2228	Short-term evolution of Shiga toxin-producing <i>Escherichia coli</i> O157:H7 between two food-borne outbreaks. <i>Microbial Genomics</i> , 2016, 2, e000084.	1.0	45
2229	Novel large-scale chromosomal transfer in <i>Bacteroides fragilis</i> contributes to its pan-genome and rapid environmental adaptation. <i>Microbial Genomics</i> , 2017, 3, .	1.0	23
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, .	1.0	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, .	1.0	19
2232	Extended-spectrum $\beta$ -lactamase-encoding genes are spreading on a wide range of <i>Escherichia coli</i> plasmids existing prior to the use of third-generation cephalosporins. <i>Microbial Genomics</i> , 2018, 4, .	1.0	33
2233	Resolving the complex <i>Bordetella pertussis</i> genome using barcoded nanopore sequencing. <i>Microbial Genomics</i> , 2018, 4, .	1.0	22
2234	Shared genome analyses of notable listeriosis outbreaks, highlighting the critical importance of epidemiological evidence, input datasets and interpretation criteria. <i>Microbial Genomics</i> , 2019, 5, .	1.0	11

#	ARTICLE	IF	CITATIONS
2235	An in silico survey of <i>Clostridioides difficile</i> extrachromosomal elements. <i>Microbial Genomics</i> , 2019, 5, .	1.0	6
2236	Comparative genomic analysis identifies X-factor (haemin)-independent <i>Haemophilus haemolyticus</i> : a formal re-classification of ' <i>Haemophilus intermedius</i> '. <i>Microbial Genomics</i> , 2020, 6, .	1.0	6
2237	Quantitative real-time PCR assay for the rapid identification of the intrinsically multidrug-resistant bacterial pathogen <i>Stenotrophomonas maltophilia</i> . <i>Microbial Genomics</i> , 2019, 5, .	1.0	8
2238	Enhancing genomics-based outbreak detection of endemic <i>Salmonella enterica</i> serovar Typhimurium using dynamic thresholds. <i>Microbial Genomics</i> , 2021, 7, .	1.0	16
2239	Complete hybrid genome assembly of clinical multidrug-resistant <i>Bacteroides fragilis</i> isolates enables comprehensive identification of antimicrobial-resistance genes and plasmids. <i>Microbial Genomics</i> , 2019, 5, .	1.0	16
2240	<i>Chlamydia trachomatis</i> : when the virulence-associated genome backbone imports a prevalence-associated major antigen signature. <i>Microbial Genomics</i> , 2019, 5, .	1.0	18
2241	Comparison of core-genome MLST, coreSNP and PFGE methods for <i>Klebsiella pneumoniae</i> cluster analysis. <i>Microbial Genomics</i> , 2020, 6, .	1.0	34
2242	Genomic surveillance of <i>Escherichia coli</i> ST131 identifies local expansion and serial replacement of subclones. <i>Microbial Genomics</i> , 2020, 6, .	1.0	33
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> CC1040/CC15P strains to the clinical setting. <i>Microbial Genomics</i> , 2020, 6, .	1.0	6
2244	Comparative genomic analysis of three intestinal species reveals reductions in secreted pathogenesis determinants in bovine-specific and non-pathogenic <i>Cryptosporidium</i> species. <i>Microbial Genomics</i> , 2020, 6, .	1.0	13
2245	Whole-genome sequence analysis of environmental <i>Escherichia coli</i> from the faeces of straw-necked ibis ( <i>Threskiornis spinicollis</i> ) nesting on inland wetlands. <i>Microbial Genomics</i> , 2020, 6, .	1.0	5
2246	Duplication and diversification of a unique chromosomal virulence island hosting the subtilase cytotoxin in <i>Escherichia coli</i> ST58. <i>Microbial Genomics</i> , 2020, 6, .	1.0	6
2247	socru: typing of genome-level order and orientation around ribosomal operons in bacteria. <i>Microbial Genomics</i> , 2020, 6, .	1.0	18
2248	Virulence genes and previously unexplored gene clusters in four commensal <i>Neisseria</i> spp. isolated from the human throat expand the neisserial gene repertoire. <i>Microbial Genomics</i> , 2020, 6, .	1.0	11
2249	Forensic genomics of a novel <i>Klebsiella quasipneumoniae</i> type from a neonatal intensive care unit in China reveals patterns of colonization, evolution and epidemiology. <i>Microbial Genomics</i> , 2020, 6, .	1.0	12
2250	Complete microbial genomes for public health in Australia and the Southwest Pacific. <i>Microbial Genomics</i> , 2020, 6, .	1.0	10
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.	0.7	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.	0.7	26

#	ARTICLE	IF	CITATIONS
2253	Variable virulence phenotype of <i>Xenorhabdus bovienii</i> ( $\beta$ -Proteobacteria: Enterobacteriaceae) in the absence of their vector hosts. <i>Microbiology (United Kingdom)</i> , 2017, 163, 510-522.	0.7	19
2254	Broad-spectrum antimicrobial activity by <i>Burkholderia cenocepacia</i> TAtI-371, a strain isolated from the tomato rhizosphere. <i>Microbiology (United Kingdom)</i> , 2018, 164, 1072-1086.	0.7	24
2255	Genome sequence, metabolic properties and cyanobacterial attachment of <i>Porphyrobacter</i> sp. HT-58-2 isolated from a filamentous cyanobacterium-microbial consortium. <i>Microbiology (United Kingdom)</i> , 2018, 164, 1229-1239.	0.7	15
2256	Combinatorial quorum sensing in <i>Pseudomonas aeruginosa</i> allows for novel cheating strategies. <i>Microbiology (United Kingdom)</i> , 2020, 166, 777-784.	0.7	10
2315	Phylogeny and Comparative Genomics: the Shifting Landscape in the Genomics Era. , 0, , 84-141.		23
2316	Proteomic Investigation of the Signal Transduction Pathways Controlling Colistin Resistance in <i>Klebsiella pneumoniae</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	1.4	5
2317	Genome Sequence of <i>Pseudomonas brassicacearum</i> DF41. <i>Genome Announcements</i> , 2014, 2, .	0.8	9
2318	Complete Genome Sequence of <i>Stenotrophomonas maltophilia</i> Podophage Ponderosa. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	8
2319	Complete Genome Sequence of <i>Escherichia coli</i> Myophage Mangalitsa. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	4
2320	Complete Genome Sequence of <i>Serratia marcescens</i> Myophage MyoSmar. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	2
2321	Complete Genome Sequence of <i>Klebsiella pneumoniae</i> Phage Sweeny. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	5
2322	Complete Genome Sequence of <i>Staphylococcus aureus</i> Myophage Maine. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	2
2323	Complete Genome Sequence of <i>Escherichia coli</i> Siphophage Snoke. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	1
2324	Complete Genome Sequence of <i>Escherichia coli</i> Phage Pisces. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	2
2325	Complete Genome Sequence of <i>Escherichia coli</i> Phage Paul. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	4
2326	Complete Genome Sequence of <i>Stenotrophomonas</i> Phage Pokken. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	7
2327	Detection of Five <i>mcr-9</i> -Carrying <i>Enterobacterales</i> Isolates in Four Czech Hospitals. <i>MSphere</i> , 2020, 5, .	1.3	26
2328	Sequence of <i>Trypanosoma cruzi</i> reference strain SC43 nuclear genome and kinetoplast maxicircle confirms a strong genetic structure among closely related parasite discrete typing units. <i>Genome</i> , 2021, 64, 1-7.	0.9	6

#	ARTICLE	IF	CITATIONS
2329	BioSEAL. , 2020, , .		27
2330	Gene flow in environmental <i>Legionella pneumophila</i> leads to genetic and pathogenic heterogeneity within a Legionnaires' disease outbreak. <i>Genome Biology</i> , 2014, 15, 504.	13.9	37
2332	Choice of assembly software has a critical impact on virome characterisation. <i>Microbiome</i> , 2019, 7, 12.	4.9	106
2333	NovoGraph: Human genome graph construction from multiple long-read de novo assemblies. <i>F1000Research</i> , 2018, 7, 1391.	0.8	5
2334	C-Sibelia: an easy-to-use and highly accurate tool for bacterial genome comparison. <i>F1000Research</i> , 2013, 2, 258.	0.8	29
2335	Host-Pathogen Coevolution: The Selective Advantage of <i>Bacillus thuringiensis</i> Virulence and Its Cry Toxin Genes. <i>PLoS Biology</i> , 2015, 13, e1002169.	2.6	69
2336	rasbhari: Optimizing Spaced Seeds for Database Searching, Read Mapping and Alignment-Free Sequence Comparison. <i>PLoS Computational Biology</i> , 2016, 12, e1005107.	1.5	36
2337	Galaxy and Apollo as a biologist-friendly interface for high-quality cooperative phage genome annotation. <i>PLoS Computational Biology</i> , 2020, 16, e1008214.	1.5	96
2338	A new subclass of intrinsic aminoglycoside nucleotidyltransferases, ANT(3)-II, is horizontally transferred among <i>Acinetobacter</i> spp. by homologous recombination. <i>PLoS Genetics</i> , 2017, 13, e1006602.	1.5	27
2339	<i>Haemophilus ducreyi</i> Cutaneous Ulcer Strains Are Nearly Identical to Class I Genital Ulcer Strains. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003918.	1.3	26
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.	1.3	49
2341	<i>Haemophilus ducreyi</i> Cutaneous Ulcer Strains Diverged from Both Class I and Class II Genital Ulcer Strains: Implications for Epidemiological Studies. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0005259.	1.3	10
2342	Evaluating the Fidelity of De Novo Short Read Metagenomic Assembly Using Simulated Data. <i>PLoS ONE</i> , 2011, 6, e19984.	1.1	65
2343	Use of Low-Coverage, Large-Insert, Short-Read Data for Rapid and Accurate Generation of Enhanced-Quality Draft <i>Pseudomonas</i> Genome Sequences. <i>PLoS ONE</i> , 2011, 6, e27199.	1.1	5
2344	Uncovering the Prevalence and Diversity of Integrating Conjugative Elements in Actinobacteria. <i>PLoS ONE</i> , 2011, 6, e27846.	1.1	56
2345	Genome Sequencing and Analysis of a Type A <i>Clostridium perfringens</i> Isolate from a Case of Bovine Clostridial Abomasitis. <i>PLoS ONE</i> , 2012, 7, e32271.	1.1	27
2346	Comparative Genomics Reveals Adaptation by <i>Alteromonas</i> sp. SN2 to Marine Tidal-Flat Conditions: Cold Tolerance and Aromatic Hydrocarbon Metabolism. <i>PLoS ONE</i> , 2012, 7, e35784.	1.1	132
2347	Pyrosequencing-Based Comparative Genome Analysis of <i>Vibrio vulnificus</i> Environmental Isolates. <i>PLoS ONE</i> , 2012, 7, e37553.	1.1	64



#	ARTICLE	IF	CITATIONS
2348	Sequencing of Seven Haloarchaeal Genomes Reveals Patterns of Genomic Flux. PLoS ONE, 2012, 7, e41389.	1.1	42
2349	DNA Sequence Analysis of Plasmids from Multidrug Resistant Salmonella enterica Serotype Heidelberg Isolates. PLoS ONE, 2012, 7, e51160.	1.1	88
2350	Capturing the Biofuel Wellhead and Powerhouse: The Chloroplast and Mitochondrial Genomes of the Leguminous Feedstock Tree Pongamia pinnata. PLoS ONE, 2012, 7, e51687.	1.1	73
2351	The Complete Genome and Phenome of a Community-Acquired Acinetobacter baumannii. PLoS ONE, 2013, 8, e58628.	1.1	93
2352	The Plastid Genome of Najas flexilis: Adaptation to Submersed Environments Is Accompanied by the Complete Loss of the NDH Complex in an Aquatic Angiosperm. PLoS ONE, 2013, 8, e68591.	1.1	98
2353	The Opportunistic Pathogen Propionibacterium acnes: Insights into Typing, Human Disease, Clonal Diversification and CAMP Factor Evolution. PLoS ONE, 2013, 8, e70897.	1.1	138
2354	Detection of Homologous Recombination Events in Bacterial Genomes. PLoS ONE, 2013, 8, e75230.	1.1	3
2355	Isolation of Novel Afipia septicemium and Identification of Previously Unknown Bacteria Bradyrhizobium sp. OHSU_III from Blood of Patients with Poorly Defined Illnesses. PLoS ONE, 2013, 8, e76142.	1.1	10
2356	GenomeFingerprinter: The Genome Fingerprint and the Universal Genome Fingerprint Analysis for Systematic Comparative Genomics. PLoS ONE, 2013, 8, e77912.	1.1	1
2357	Genomic Survey of Pathogenicity Determinants and VNTR Markers in the Cassava Bacterial Pathogen Xanthomonas axonopodis pv. Manihotis Strain CIO151. PLoS ONE, 2013, 8, e79704.	1.1	42
2358	When Whole-Genome Alignments Just Won't Work: kSNP v2 Software for Alignment-Free SNP Discovery and Phylogenetics of Hundreds of Microbial Genomes. PLoS ONE, 2013, 8, e81760.	1.1	228
2359	Presence and Analysis of Plasmids in Human and Animal Associated Arcobacter Species. PLoS ONE, 2014, 9, e85487.	1.1	33
2360	The Discovery of phiAGATE, A Novel Phage Infecting Bacillus pumilus, Leads to New Insights into the Phylogeny of the Subfamily Spounavirinae. PLoS ONE, 2014, 9, e86632.	1.1	29
2361	Correction of the Caulobacter crescentus NA1000 Genome Annotation. PLoS ONE, 2014, 9, e91668.	1.1	7
2362	A Multicentre Hospital Outbreak in Sweden Caused by Introduction of a vanB2 Transposon into a Stably Maintained pRUM-Plasmid in an Enterococcus faecium ST192 Clone. PLoS ONE, 2014, 9, e103274.	1.1	33
2363	Virulence and Draft Genome Sequence Overview of Multiple Strains of the Swine Pathogen Haemophilus parasuis. PLoS ONE, 2014, 9, e103787.	1.1	37
2364	Systematic Production of Inactivating and Non-Inactivating Suppressor Mutations at the relA Locus That Compensate the Detrimental Effects of Complete spoT Loss and Affect Glycogen Content in Escherichia coli. PLoS ONE, 2014, 9, e106938.	1.1	21
2365	Genome Analysis of Environmental and Clinical P. aeruginosa Isolates from Sequence Type-1146. PLoS ONE, 2014, 9, e107754.	1.1	9

#	ARTICLE	IF	CITATIONS
2366	Plasmidome Interchange between <i>Clostridium botulinum</i> , <i>Clostridium novyi</i> and <i>Clostridium haemolyticum</i> Converts Strains of Independent Lineages into Distinctly Different Pathogens. PLoS ONE, 2014, 9, e107777.	1.1	44
2367	Strain-Level Diversity of Secondary Metabolism in <i>Streptomyces albus</i> . PLoS ONE, 2015, 10, e0116457.	1.1	90
2368	Comparative Analysis of Super-Shedder Strains of <i>Escherichia coli</i> O157:H7 Reveals Distinctive Genomic Features and a Strongly Aggregative Adherent Phenotype on Bovine Rectoanal Junction Squamous Epithelial Cells. PLoS ONE, 2015, 10, e0116743.	1.1	36
2369	Genomic, Proteomic and Morphological Characterization of Two Novel Broad Host Lytic Bacteriophages $\phi$ PD10.3 and $\phi$ PD23.1 Infecting Pectinolytic <i>Pectobacterium</i> spp. and <i>Dickeya</i> spp.. PLoS ONE, 2015, 10, e0119812.	1.1	90
2370	The Complete Chloroplast and Mitochondrial Genomes of the Green Macroalga <i>Ulva</i> sp. UNA00071828 ( <i>Ulvophyceae</i> , <i>Chlorophyta</i> ). PLoS ONE, 2015, 10, e0121020.	1.1	66
2371	Genomic Analysis of a <i>Mycobacterium Bovis</i> Bacillus Calmette-Guérin Strain Isolated from an Adult Patient with Pulmonary Tuberculosis. PLoS ONE, 2015, 10, e0122403.	1.1	7
2372	Analyses of the Complete Genome and Gene Expression of Chloroplast of Sweet Potato [ <i>Ipomoea batata</i> ]. PLoS ONE, 2015, 10, e0124083.	1.1	42
2373	Complex Population Structure and Virulence Differences among Serotype 2 <i>Streptococcus suis</i> Strains Belonging to Sequence Type 28. PLoS ONE, 2015, 10, e0137760.	1.1	42
2374	In Vivo Evolution of Bacterial Resistance in Two Cases of <i>Enterobacter aerogenes</i> Infections during Treatment with Imipenem. PLoS ONE, 2015, 10, e0138828.	1.1	42
2375	Comparative Analysis of the Orphan CRISPR2 Locus in 242 <i>Enterococcus faecalis</i> Strains. PLoS ONE, 2015, 10, e0138890.	1.1	30
2376	Genome and Phenotype Microarray Analyses of <i>Rhodococcus</i> sp. BCP1 and <i>Rhodococcus opacus</i> R7: Genetic Determinants and Metabolic Abilities with Environmental Relevance. PLoS ONE, 2015, 10, e0139467.	1.1	53
2377	Whole-Genome Sequencing of Three Clonal Clinical Isolates of <i>B. cenocepacia</i> from a Patient with Cystic Fibrosis. PLoS ONE, 2015, 10, e0143472.	1.1	9
2378	Distinctive Architecture of the Chloroplast Genome in the Chlorodendrophycean Green Algae <i>Scherffelia dubia</i> and <i>Tetraselmis</i> sp. CCMP 881. PLoS ONE, 2016, 11, e0148934.	1.1	33
2379	Comparative Genomic Analysis of <i>Mannheimia haemolytica</i> from Bovine Sources. PLoS ONE, 2016, 11, e0149520.	1.1	41
2380	Identifying Likely Transmission Pathways within a 10-Year Community Outbreak of Tuberculosis by High-Depth Whole Genome Sequencing. PLoS ONE, 2016, 11, e0150550.	1.1	24
2381	Deciphering the Draft Genome of <i>Toxoplasma gondii</i> RH Strain. PLoS ONE, 2016, 11, e0157901.	1.1	28
2382	Genomic Diversity of Enterotoxigenic Strains of <i>Bacteroides fragilis</i> . PLoS ONE, 2016, 11, e0158171.	1.1	47
2383	Genomic Analysis Reveals Novel Diversity among the 1976 Philadelphia Legionnaires' Disease Outbreak Isolates and Additional ST36 Strains. PLoS ONE, 2016, 11, e0164074.	1.1	23

#	ARTICLE	IF	CITATIONS
2384	Genome Analysis of <i>Streptococcus pyogenes</i> Associated with Pharyngitis and Skin Infections. PLoS ONE, 2016, 11, e0168177.	1.1	20
2385	Whole Genome Sequence and Comparative Genomics of the Novel Lyme Borreliosis Causing Pathogen, <i>Borrelia mayonii</i> . PLoS ONE, 2016, 11, e0168994.	1.1	49
2386	Whole Genome Sequencing of 39 Invasive <i>Streptococcus pneumoniae</i> Sequence Type 199 Isolates Revealed Switches from Serotype 19A to 15B. PLoS ONE, 2017, 12, e0169370.	1.1	19
2387	The distinct plastid genome structure of <i>Maackia fauriei</i> (Fabaceae: Papilionoideae) and its systematic implications for genistoids and tribe Sophoreae. PLoS ONE, 2017, 12, e0173766.	1.1	35
2388	Comparative genomics of <i>Burkholderia multivorans</i> , a ubiquitous pathogen with a highly conserved genomic structure. PLoS ONE, 2017, 12, e0176191.	1.1	17
2389	Comparative genomics of human and non-human <i>Listeria monocytogenes</i> sequence type 121 strains. PLoS ONE, 2017, 12, e0176857.	1.1	42
2390	EcoBLMcrX, a classical modification-dependent restriction enzyme in <i>Escherichia coli</i> B: Characterization in vivo and in vitro with a new approach to cleavage site determination. PLoS ONE, 2017, 12, e0179853.	1.1	8
2391	$\beta$ 2-microglobulin gene duplication in cetartiodactyla remains intact only in pigs and possibly confers selective advantage to the species. PLoS ONE, 2017, 12, e0182322.	1.1	8
2392	Whole genome sequence of two <i>Rathayibacter toxicus</i> strains reveals a tunicamycin biosynthetic cluster similar to <i>Streptomyces chartreusis</i> . PLoS ONE, 2017, 12, e0183005.	1.1	13
2393	Shared features of cryptic plasmids from environmental and pathogenic <i>Francisella</i> species. PLoS ONE, 2017, 12, e0183554.	1.1	16
2394	Complete chloroplast genome of green tide algae <i>Ulva flexuosa</i> (Ulvophyceae, Chlorophyta) with comparative analysis. PLoS ONE, 2017, 12, e0184196.	1.1	28
2395	Recombination and gene loss occur simultaneously during bacterial horizontal gene transfer. PLoS ONE, 2020, 15, e0227987.	1.1	15
2396	The TIR Homologue Lies near Resistance Genes in <i>Staphylococcus aureus</i> , Coupling Modulation of Virulence and Antimicrobial Susceptibility. PLoS Pathogens, 2017, 13, e1006092.	2.1	30
2397	What matters in chronic <i>Burkholderia cenocepacia</i> infection in cystic fibrosis: Insights from comparative genomics. PLoS Pathogens, 2017, 13, e1006762.	2.1	28
2398	Genome sequence of plant associated rhizobacterium <i>Bacillus amyloliquefaciens</i> strain UCMB5033. EMBnet Journal, 2013, 19, 66.	0.2	1
2399	Full Mitochondrial Genome and Nuclear 18S rDNA Sequences Refine the Taxonomic Placement of <i>Chloeoeimeria taggarti</i> n. comb. from the Prostate of <i>Antechinus flavipes</i> (Yellow-Footed) Tj ETQq1 1 0.784314 rgBT.3 Overlook 10 Tf 50		
2400	Application of the Numerical Characteristic of Formal Order Analysis of the Prokaryotic Genomes for Reclassification within the Genus <i>Rickettsia</i> . Mathematical Biology and Bioinformatics, 2016, 11, 336-350.	0.1	3
2401	Genome Sequence Analysis and Identification of Genes Associated to Pesticide Degradation from <i>Enterobacter cloacae</i> Strain MR2. International Journal of Current Microbiology and Applied Sciences, 2019, 8, 2289-2304.	0.0	6

#	ARTICLE	IF	CITATIONS
2403	Identification of Horizontally-transferred Genomic Islands and Genome Segmentation Points by Using the GC Profile Method. <i>Current Genomics</i> , 2014, 15, 113-121.	0.7	26
2404	Genome Sequence of a Highly Virulent pvl-positive Vancomycin intermediate- resistant <i>Staphylococcus aureus</i> Sequence Type 30. <i>Current Genomics</i> , 2020, 21, 128-137.	0.7	2
2405	The utility of multiple molecular methods including whole genome sequencing as tools to differentiate <i>Escherichia coli</i> O157:H7 outbreaks. <i>Eurosurveillance</i> , 2015, 20, .	3.9	17
2406	Epidemiological information is key when interpreting whole genome sequence data – lessons learned from a large <i>Legionella pneumophila</i> outbreak in Warstein, Germany, 2013. <i>Eurosurveillance</i> , 2017, 22, .	3.9	31
2407	Phylogeographical pattern of <i>Francisella tularensis</i> in a nationwide outbreak of tularaemia in Norway, 2011. <i>Eurosurveillance</i> , 2015, 20, .	3.9	22
2408	Genomic analyses of <i>Francisella tularensis</i> strains confirm disease transmission from drinking water sources, Turkey, 2008, 2009 and 2012. <i>Eurosurveillance</i> , 2015, 20, .	3.9	26
2409	Cycloheximide-Producing <i>Streptomyces</i> Associated With <i>Xyleborinus saxesenii</i> and <i>Xyleborus affinis</i> Fungus-Farming Ambrosia Beetles. <i>Frontiers in Microbiology</i> , 2020, 11, 562140.	1.5	22
2410	Complete Genome Sequence Analysis and Characterization of Selected Iron Regulation Genes of <i>Pasteurella Multocida</i> Serotype A Strain PMTB2.1. <i>Genes</i> , 2019, 10, 81.	1.0	7
2411	Pan-Genome-Based Analysis as a Framework for Demarcating Two Closely Related Methanotroph Genera <i>Methylocystis</i> and <i>Methylosinus</i> . <i>Microorganisms</i> , 2020, 8, 768.	1.6	15
2412	Whole Genome Analysis Reveals New Insights into Macrolide Resistance in <i>Mycoplasma pneumoniae</i> . <i>Biomedical and Environmental Sciences</i> , 2017, 30, 343-350.	0.2	20
2413	Water Stress Responsive Differential Methylation of Organellar Genomes of <i>Zea mays</i> Z59. <i>American Journal of Plant Sciences</i> , 2020, 11, 1077-1100.	0.3	3
2414	Amino Acid Biosynthesis and Proteolysis in <i>Lactobacillus Bulgaricus</i>; Revisited: A Genomic Comparison. <i>Computational Molecular Bioscience</i> , 2012, 02, 61-77.	0.6	7
2415	Oxford Nanopore MinION Sequencing Enables Rapid Whole Genome Assembly of <i>Rickettsia typhi</i> in a Resource-Limited Setting. <i>American Journal of Tropical Medicine and Hygiene</i> , 2020, 102, 408-414.	0.6	22
2416	Race- and Isolate-specific Molecular Marker Development through Genome-Realignment Enables Detection of Korean <i>Plasmodiophora brassicae</i> Isolates, Causal agents of Clubroot Disease. <i>Plant Pathology Journal</i> , 2018, 34, 506-513.	0.7	6
2417	Gut bacteria are rarely shared by co-hospitalized premature infants, regardless of necrotizing enterocolitis development. <i>ELife</i> , 2015, 4, .	2.8	111
2418	Emergence of trait variability through the lens of nitrogen assimilation in <i>Prochlorococcus</i> . <i>ELife</i> , 2019, 8, .	2.8	57
2419	Phage integration alters the respiratory strategy of its host. <i>ELife</i> , 2019, 8, .	2.8	24
2420	Comparative genomics of non-pseudomonal bacterial species colonising paediatric cystic fibrosis patients. <i>PeerJ</i> , 2015, 3, e1223.	0.9	35

#	ARTICLE	IF	CITATIONS
2421	Comparative genomics of <i>Synechococcus</i> and proposal of the new genus <i>Parasynechococcus</i> . PeerJ, 2016, 4, e1522.	0.9	46
2422	The single-species metagenome: subtyping <i>Staphylococcus aureus</i> core genome sequences from shotgun metagenomic data. PeerJ, 2016, 4, e2571.	0.9	8
2423	Short reads from honey bee ( <i>Apis</i> sp.) sequencing projects reflect microbial associate diversity. PeerJ, 2017, 5, e3529.	0.9	13
2424	Strain- and plasmid-level deconvolution of a synthetic metagenome by sequencing proximity ligation products. PeerJ, 2014, 2, e415.	0.9	111
2425	Recent genome reduction of <i>Wolbachia</i> in <i>Drosophila recens</i> targets phage WO and narrows candidates for reproductive parasitism. PeerJ, 2014, 2, e529.	0.9	51
2426	A comparative analysis of the complete chloroplast genome sequences of four peanut botanical varieties. PeerJ, 2018, 6, e5349.	0.9	28
2427	Evidence that ebolaviruses and cuevaviruses have been diverging from marburgviruses since the Miocene. PeerJ, 2014, 2, e556.	0.9	26
2428	An evaluation of alternative methods for constructing phylogenies from whole genome sequence data: a case study with <i>Salmonella</i> . PeerJ, 2014, 2, e620.	0.9	45
2429	Detection and variability analyses of CRISPR-like loci in the <i>H. pylori</i> genome. PeerJ, 2019, 7, e6221.	0.9	4
2430	The complete chloroplast genomes of three Betulaceae species: implications for molecular phylogeny and historical biogeography. PeerJ, 2019, 7, e6320.	0.9	26
2431	Concordance and discordance of sequence survey methods for molecular epidemiology. PeerJ, 2015, 3, e761.	0.9	5
2432	Comparative analysis of chloroplast genomes for five <i>Dicliptera</i> species (Acanthaceae): molecular structure, phylogenetic relationships, and adaptive evolution. PeerJ, 2020, 8, e8450.	0.9	29
2433	<i>Impatiens glandulifera</i> (Himalayan balsam) chloroplast genome sequence as a promising target for populations studies. PeerJ, 2020, 8, e8739.	0.9	9
2434	Genome evolution in an ancient bacteria-ant symbiosis: parallel gene loss among <i>Blochmannia</i> spanning the origin of the ant tribe Camponotini. PeerJ, 2015, 3, e881.	0.9	46
2435	Long-reads reveal that <i>Rhododendron delavayi</i> plastid genome contains extensive repeat sequences, and recombination exists among plastid genomes of photosynthetic Ericaceae. PeerJ, 2020, 8, e9048.	0.9	16
2436	Plastid genomes of the North American <i>Rhus integrifolia-ovata</i> complex and phylogenomic implications of inverted repeat structural evolution in <i>Rhus</i> L.. PeerJ, 2020, 8, e9315.	0.9	4
2437	A vanA vancomycin-resistant <i>Enterococcus faecium</i> ST80 outbreak resulting from a single importation event. Journal of Antimicrobial Chemotherapy, 2021, , .	1.3	5
2438	The genome sequence of the Australian filarial nematode, <i>Cercopithifilaria johnstoni</i> . Wellcome Open Research, 2021, 6, 259.	0.9	2

#	ARTICLE	IF	CITATIONS
2440	Acinetobacter geminorum sp. nov., isolated from human throat swabs. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	10
2441	On the Species Delimitation of the Maddenia Group of Prunus (Rosaceae): Evidence From Plastome and Nuclear Sequences and Morphology. Frontiers in Plant Science, 2021, 12, 743643.	1.7	13
2443	Reference-agnostic representation and visualization of pan-genomes. BMC Bioinformatics, 2021, 22, 502.	1.2	5
2444	Genomic Comparison of Conjugative Plasmids from Salmonella enterica and Escherichia coli Encoding Beta-Lactamases and Capable of Mobilizing Kanamycin Resistance Col-like Plasmids. Microorganisms, 2021, 9, 2205.	1.6	4
2445	Genome Streamlining, Plasticity, and Metabolic Versatility Distinguish Co-occurring Toxic and Nontoxic Cyanobacterial Strains of <i>Microcoleus</i>. MBio, 2021, 12, e0223521.	1.8	11
2446	Alterations in the Transcriptional Landscape Allow Differential Desiccation Tolerance in Clinical Cronobacter sakazakii. Applied and Environmental Microbiology, 2021, 87, e0083021.	1.4	8
2447	Characterization of IncHI1B Plasmids Encoding Efflux Pump TmexCD2-ToprJ2 in Carbapenem-Resistant Klebsiella variicola, Klebsiella quasipneumoniae, and Klebsiella michiganensis Strains. Frontiers in Microbiology, 2021, 12, 759208.	1.5	13
2448	<i>Nitzschia anatoliensis</i> sp. nov., a cryptic diatom species from the highly alkaline Van Lake (Turkey). PeerJ, 2021, 9, e12220.	0.9	4
2451	Mitochondrial and Plastid Genomes of the Monoraphid Diatom Schizostauron trachyderma. International Journal of Molecular Sciences, 2021, 22, 11139.	1.8	5
2453	Genome Comparisons of the Fission Yeasts Reveal Ancient Collinear Loci Maintained by Natural Selection. Journal of Fungi (Basel, Switzerland), 2021, 7, 864.	1.5	1
2454	Comparative analysis of full-length mitochondrial genomes of five Skeletonema species reveals conserved genome organization and recent speciation. BMC Genomics, 2021, 22, 746.	1.2	4
2455	Saccharopolyspora karakumensis sp. nov., Saccharopolyspora elongata sp. nov., Saccharopolyspora aridisoli sp. nov., Saccharopolyspora terrae sp. nov. and their biotechnological potential revealed by genome analysis. Systematic and Applied Microbiology, 2021, 44, 126270.	1.2	20
2456	Hidden Breakpoints in Genome Alignments. Lecture Notes in Computer Science, 2012, , 391-403.	1.0	0
2457	Sequence Homology Handling. Computational Biology, 2013, , 301-334.	0.1	1
2458	Rough Sets in Ortholog Gene Detection. Lecture Notes in Computer Science, 2014, , 161-168.	1.0	0
2459	Aggregation of Similarity Measures for Ortholog Detection: Validation with Measures Based on Rough Set Theory. Computacion Y Sistemas, 2014, 18, .	0.2	1
2462	Plasmid-Mediated Antibiotic Resistance and Virulence in Gram-Negatives: The <i>Klebsiella pneumoniae</i> Paradigm. , 0, , 459-474.		0
2470	Alignment and Mapping. , 2017, , 105-125.		0



#	ARTICLE	IF	CITATIONS
2471	In Silico Signature Prediction Modeling in Cytolethal Distending Toxin-Producing <i>Escherichia coli</i> Strains. <i>Genomics and Informatics</i> , 2017, 15, 69.	0.4	1
2472	Genome Sequencing Analysis of Atypical <i>Shigella flexneri</i> Isolated in Korea. <i>Osong Public Health and Research Perspectives</i> , 2017, 8, 78-85.	0.7	1
2501	NET-ASAR: A Tool for DNA Sequence Search Based on Data Compression. <i>Advances in Intelligent Systems and Computing</i> , 2019, , 114-122.	0.5	0
2504	NovoGraph: Genome graph construction from multiple long-read de novo assemblies. <i>F1000Research</i> , 2018, 7, 1391.	0.8	8
2505	Comparative genome and evolution analysis of the locus of enterocyte effacement from enteropathogenic <i>Escherichia coli</i> Deng and its transcriptional response to ciprofloxacin. <i>Journal of Medical Microbiology</i> , 2018, 67, 1368-1382.	0.7	0
2512	CRISPR-Cas Immune System of a Prevalent Human Gut Bacterium Reveals Hypertargeting Against Gut Virome Phages. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
2513	Application of Genomics to Understand the Pathogenic Microbial Diversity. , 2019, , 49-82.		0
2520	A gene based bacterial whole genome comparison toolkit. <i>Revista De Informatica Teorica E Aplicada</i> , 2019, 26, 36.	0.2	0
2525	Complete Genome Sequence of <i>Klebsiella pneumoniae</i> Myophage Magnus. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	3
2526	Complete Genome Sequence of Sin4, a Siphophage Infecting Carbapenemase-Producing <i>Klebsiella pneumoniae</i> . <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	1
2527	Complete Genome Sequence of <i>Salmonella enterica</i> Siphophage Shelanagig. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	1
2528	Complete Genome Sequence of <i>Escherichia coli</i> Podophage Penshu1. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	0
2529	Complete Genome Sequence of <i>Escherichia coli</i> Myophage Mansfield. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	0
2530	Complete Genome Sequence of <i>Escherichia coli</i> Siphophage Schulenberg. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	0
2531	Complete Genome Sequence of <i>Escherichia coli</i> Podophage Peacock. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	0
2532	Complete Genome Sequence of <i>Escherichia coli</i> Siphophage Sciku. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	0
2533	Complete Genome Sequence of <i>Salmonella enterica</i> Myophage Matapan. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	1
2534	Complete Genome Sequence of <i>Xanthomonas</i> Siphophage Samson. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	2

#	ARTICLE	IF	CITATIONS
2535	Complete Genome Sequence of Escherichia coli Siphophage Shashou. Microbiology Resource Announcements, 2019, 8, .	0.3	0
2536	Complete Genome Sequence of Proteus mirabilis Siphophage Saba. Microbiology Resource Announcements, 2019, 8, .	0.3	1
2543	Comparison of the Pathogenicity of Five Clostridium perfringens Isolates Using an Eimeria maxima Coinfection Necrotic Enteritis Disease Model in Commercial Broiler Chickens. Avian Diseases, 2020, 64, 386-392.	0.4	3
2548	Complete Chloroplast Genome of Triaenophora shennongjiaensis (Orobanchaceae), an Endangered Medical Herb from China. Annales Botanici Fennici, 2020, 57, 23.	0.0	1
2552	Plastome of the mycoheterotrophic eudicot <i>Exacum paucisquama</i> (Gentianaceae) exhibits extensive gene loss and a highly expanded inverted repeat region. PeerJ, 2020, 8, e9157.	0.9	4
2557	Characterization of Genetically Modified Microorganisms Using Short- and Long-Read Whole-Genome Sequencing Reveals Contaminations of Related Origin in Multiple Commercial Food Enzyme Products. Foods, 2021, 10, 2637.	1.9	4
2558	pLS20 is the archetype of a new family of conjugative plasmids harboured by Bacillus species. NAR Genomics and Bioinformatics, 2021, 3, lqab096.	1.5	4
2559	Complete genomic sequence and phylogenomics analysis of Agrobacterium strain AB2/73: a new Rhizobium species with a unique mega-Ti plasmid. BMC Microbiology, 2021, 21, 295.	1.3	8
2560	Evaluation of Bacteriophage Cocktails Alone and in Combination with Daptomycin against Daptomycin-Nonsusceptible Enterococcus faecium. Antimicrobial Agents and Chemotherapy, 2022, 66, AAC0162321.	1.4	8
2562	The Location of Substitutions and Bacterial Genome Arrangements. Genome Biology and Evolution, 2021, 13, .	1.1	2
2564	The large genome of Synechococcus moorigangaii CMS01 isolated from a mangrove ecosystem-evidences of motility and adaptive features. IOP SciNotes, 2020, 1, 034001.	0.4	1
2567	Complete Genome Sequence of Proteus mirabilis Siphophage Stubb. Microbiology Resource Announcements, 2019, 8, .	0.3	0
2568	Bacterial Microevolution and the Pangenome. , 2020, , 129-149.		1
2572	Comparative Genome Analysis of Psychrobacillus Strain PB01, Isolated from an Iceberg. Journal of Microbiology and Biotechnology, 2020, 30, 237-243.	0.9	6
2578	Genome diversity and evolutionary characteristics of clinical isolates of Bordetella pertussis circulating in Iran. Iranian Journal of Microbiology, 0, , .	0.8	1
2580	Type VI secretion system mutations reduced competitive fitness of classical Vibrio cholerae biotype. Nature Communications, 2021, 12, 6457.	5.8	15
2581	Comparative Analysis of Chloroplast Genomes of Seven Chaetoceros Species Revealed Variation Hotspots and Speciation Time. Frontiers in Microbiology, 2021, 12, 742554.	1.5	5
2582	A Comprehensive Study of the Genus Sanguisorba (Rosaceae) Based on the Floral Micromorphology, Palynology, and Plastome Analysis. Genes, 2021, 12, 1764.	1.0	9

#	ARTICLE	IF	CITATIONS
2583	Density-based binning of gene clusters to infer function or evolutionary history using GeneGrouper. <i>Bioinformatics</i> , 2022, 38, 612-620.	1.8	4
2585	Genotypic characterization and genome comparison reveal insights into potential vaccine coverage and genealogy of <i>Neisseria meningitidis</i> in military camps in Vietnam. <i>PeerJ</i> , 2020, 8, e9502.	0.9	2
2593	Massive rhizobial genomic variation associated with partner quality in <i>Lotus</i> – <i>Mesorhizobium</i> symbiosis. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	2
2598	Genome diversity and evolutionary characteristics of clinical isolates of circulating in Iran. <i>Iranian Journal of Microbiology</i> , 2020, 12, 1-10.	0.8	4
2599	Genomic and biological characteristics of an alphabaculovirus isolated from <i>Trabala vishnou gigantina</i> . <i>Virus Research</i> , 2022, 308, 198630.	1.1	0
2600	Metagenomics approach for <i>Polymyxa betae</i> genome assembly enables comparative analysis towards deciphering the intracellular parasitic lifestyle of the plasmodiophorids. <i>Genomics</i> , 2022, 114, 9-22.	1.3	4
2602	Bilateral symmetry of linear streptomycete chromosomes. <i>Microbial Genomics</i> , 2021, 7, .	1.0	8
2603	A Potential Application of Endophytic Bacteria in Strawberry Production. <i>Horticulturae</i> , 2021, 7, 504.	1.2	9
2604	The complete chloroplast genome sequence of <i>Athrotaxis cupressoides</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 3468-3470.	0.2	0
2605	Testing assembly strategies of <i>Francisella tularensis</i> genomes to infer an evolutionary conservation analysis of genomic structures. <i>BMC Genomics</i> , 2021, 22, 822.	1.2	2
2606	Phylogenetic Relatedness and Genome Structure of <i>Yersinia ruckeri</i> Revealed by Whole Genome Sequencing and a Comparative Analysis. <i>Frontiers in Microbiology</i> , 2021, 12, 782415.	1.5	1
2607	Shotgun whole genome sequencing of drug-resistance <i>Streptococcus anginosus</i> strain 47S1 isolated from a patient with pharyngitis in Saudi Arabia. <i>Journal of Infection and Public Health</i> , 2021, 14, 1740-1749.	1.9	0
2608	Carbapenem-Resistant <i>Citrobacter</i> spp. as an Emerging Concern in the Hospital-Setting: Results From a Genome-Based Regional Surveillance Study. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 744431.	1.8	23
2609	Hybrid de novo genome-reassembly reveals new insights on pathways and pathogenicity determinants in rice blast pathogen <i>Magnaporthe oryzae</i> RMg_Dl. <i>Scientific Reports</i> , 2021, 11, 22922.	1.6	8
2610	Completing the Genome Sequence of <i>Chlamydia pecorum</i> Strains MC/MarsBar and DBDeUG: New Insights into This Enigmatic Koala ( <i>Phascolarctos cinereus</i> ) Pathogen. <i>Pathogens</i> , 2021, 10, 1543.	1.2	6
2611	Diversification of plasmids in a genus of pathogenic and nitrogen-fixing bacteria. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2022, 377, 20200466.	1.8	12
2612	Genome-wide association study of gastric cancer- and duodenal ulcer-derived <i>Helicobacter pylori</i> strains reveals discriminatory genetic variations and novel oncoprotein candidates. <i>Microbial Genomics</i> , 2021, 7, .	1.0	10
2613	Understanding the Mechanism of Action of NAI-112, a Lanthipeptide with Potent Antinociceptive Activity. <i>Molecules</i> , 2021, 26, 6764.	1.7	7

#	ARTICLE	IF	CITATIONS
2614	Active and Covert Infections of Cricket Iridovirus and Acheta domesticus Densovirus in Reared Gryllosid sigillatus Crickets. <i>Frontiers in Microbiology</i> , 2021, 12, 780796.	1.5	8
2615	Genomic Characteristics of Stx2e-Producing Escherichia coli Strains Derived from Humans, Animals, and Meats. <i>Pathogens</i> , 2021, 10, 1551.	1.2	9
2616	BOPAL 2.0 and a study of tRNA and rRNA gene evolution in Clostridium. <i>Journal of Bioinformatics and Computational Biology</i> , 2021, 19, 2140007.	0.3	2
2617	Genomic Analysis of Global Staphylococcus argenteus Strains Reveals Distinct Lineages With Differing Virulence and Antibiotic Resistance Gene Content. <i>Frontiers in Microbiology</i> , 2021, 12, 795173.	1.5	10
2618	The genome sequence of the Australian filarial nematode, Cercopithifilaria johnstoni. <i>Wellcome Open Research</i> , 0, 6, 259.	0.9	2
2619	Complete Chloroplast Genome Sequence of Sonchus brachyotus Helps to Elucidate Evolutionary Relationships with Related Species of Asteraceae. <i>BioMed Research International</i> , 2021, 2021, 1-13.	0.9	13
2620	In silico comparisons of lipid-related genes between Mycobacterium tuberculosis and BCG vaccine strains. <i>Genetics and Molecular Biology</i> , 2021, 44, e20210024.	0.6	1
2621	APTC-EC-2A: A Lytic Phage Targeting Multidrug Resistant E. coli Planktonic Cells and Biofilms. <i>Microorganisms</i> , 2022, 10, 102.	1.6	6
2623	Whole genome analysis and functional characterization of a novel Bacillus thuringiensis (Bt 62) isolate against sugarcane white grub Holotrichia serrata (F). <i>Genomics</i> , 2022, 114, 185-195.	1.3	2
2624	Genomic Analyses of Pediococcus pentosaceus ST65ACC, a Bacteriocinogenic Strain Isolated from Artisanal Raw-Milk Cheese. <i>Probiotics and Antimicrobial Proteins</i> , 2023, 15, 630-645.	1.9	7
2625	Bacillimidazoles A <sup>+</sup> F, Imidazolium-Containing Compounds Isolated from a Marine Bacillus. <i>Marine Drugs</i> , 2022, 20, 43.	2.2	8
2627	First Comparative Analysis of Clostridium septicum Genomes Provides Insights Into the Taxonomy, Species Genetic Diversity, and Virulence Related to Gas Gangrene. <i>Frontiers in Microbiology</i> , 2021, 12, 771945.	1.5	5
2628	Unstable Relationship Between Braarudosphaera bigelowii (= Chrysochromulina parkeae) and Its Nitrogen-Fixing Endosymbiont. <i>Frontiers in Plant Science</i> , 2021, 12, 749895.	1.7	6
2629	Comparative Mitogenomics of Fungal Species in Stachybotryaceae Provides Evolutionary Insights into Hypocreales. <i>International Journal of Molecular Sciences</i> , 2021, 22, 13341.	1.8	8
2630	Novel insights into the role of the mobilome in ecological diversification and success of Staphylococcus haemolyticus as an opportunistic pathogen. <i>Microbial Genomics</i> , 2022, 8, .	1.0	1
2631	Isolation, characterization and application of bacteriophage PSDA-2 against Salmonella Typhimurium in chilled mutton. <i>PLoS ONE</i> , 2022, 17, e0262946.	1.1	8
2632	Plastome Phylogenomics of Aucuba (Garryaceae). <i>Frontiers in Genetics</i> , 2022, 13, 753719.	1.1	3
2634	Benchmarking the empirical accuracy of short-read sequencing across the M. tuberculosis genome. <i>Bioinformatics</i> , 2022, 38, 1781-1787.	1.8	13

#	ARTICLE	IF	CITATIONS
2635	Natural Chromosome-Chromid Fusion across rRNA Operons in a <i>Burkholderiaceae</i> Bacterium. <i>Microbiology Spectrum</i> , 2022, 10, e0222521.	1.2	8
2636	Development of a multiplex TaqMan qPCR targeting unique genomic regions for the specific and sensitive detection of <i>Pectobacterium</i> species and <i>P. parmentieri</i> . <i>Journal of Applied Microbiology</i> , 2022, 132, 3089-3110.	1.4	7
2637	Resolving the structure of phage-bacteria interactions in the context of natural diversity. <i>Nature Communications</i> , 2022, 13, 372.	5.8	48
2638	A multiplex real-time PCR assay for differential identification of avian Chlamydia. <i>Avian Pathology</i> , 2022, , 1-29.	0.8	1
2639	Comparative genomic analysis of plasmids encoding metallo- $\beta$ -lactamase NDM-5 in Enterobacterales Korean isolates from companion dogs. <i>Scientific Reports</i> , 2022, 12, 1569.	1.6	6
2640	Comparative genomics of the black rot pathogen <i>Xanthomonas campestris</i> pv. <i>campestris</i> and non-pathogenic co-inhabitant <i>Xanthomonas melonis</i> from Trinidad reveal unique pathogenicity determinants and secretion system profiles. <i>PeerJ</i> , 2022, 9, e12632.	0.9	6
2641	Natural <i>Saccharomyces cerevisiae</i> Strain Reveals Peculiar Genomic Traits for Starch-to-Bioethanol Production: the Design of an Amyolytic Consolidated Bioprocessing Yeast. <i>Frontiers in Microbiology</i> , 2021, 12, 768562.	1.5	9
2642	Comparative genomics of <i>Bordetella pertussis</i> isolates from New Zealand, a country with an uncommonly high incidence of whooping cough. <i>Microbial Genomics</i> , 2022, 8, .	1.0	2
2643	Genome analysis of <i>Pseudomonas</i> sp. 14A reveals metabolic capabilities to support epiphytic behavior. <i>World Journal of Microbiology and Biotechnology</i> , 2022, 38, 49.	1.7	1
2644	Selective Isolation of <i>Eggerthella lenta</i> from Human Faeces and Characterisation of the Species Prophage Diversity. <i>Microorganisms</i> , 2022, 10, 195.	1.6	9
2645	Pathway Driven Target Selection in <i>Klebsiella pneumoniae</i> : Insights Into Carbapenem Exposure. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 773405.	1.8	4
2646	Evidence for Horizontal and Vertical Transmission of Mtr-Mediated Extracellular Electron Transfer among the <i>Bacteria</i> . <i>MBio</i> , 2022, 13, e0290421.	1.8	23
2647	Genomic and Functional Dissections of <i>Dickeya zeae</i> Shed Light on the Role of Type III Secretion System and Cell Wall-Degrading Enzymes to Host Range and Virulence. <i>Microbiology Spectrum</i> , 2022, 10, e0159021.	1.2	8
2648	Phenotypic and Molecular-Phylogenetic Analyses Reveal Distinct Features of Crown Gall-Associated <i>Xanthomonas</i> Strains. <i>Microbiology Spectrum</i> , 2022, 10, e0057721.	1.2	11
2649	<i>Pseudomonas aeruginosa</i> modulates alginate biosynthesis and type VI secretion system in two critically ill COVID-19 patients. <i>Cell and Bioscience</i> , 2022, 12, 14.	2.1	8
2650	Diversity in the Characteristics of <i>Klebsiella pneumoniae</i> ST101 of Human, Environmental, and Animal Origin. <i>Frontiers in Microbiology</i> , 2022, 13, 838207.	1.5	5
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.	1.5	9
2652	Bacterial ring rot of potato caused by <i>Clavibacter sepedonicus</i> : A successful example of defeating the enemy under international regulations. <i>Molecular Plant Pathology</i> , 2022, 23, 911-932.	2.0	15

#	ARTICLE	IF	CITATIONS
2653	Analysis of the Complete Plastomes of 31 Species of Hoya Group: Insights Into Their Comparative Genomics and Phylogenetic Relationships. <i>Frontiers in Plant Science</i> , 2021, 12, 814833.	1.7	12
2654	Complete Genome Sequence of a Jumbo Bacteriophage, Escherichia Phage vB_EcoM_EC001. <i>Microbiology Resource Announcements</i> , 2022, 11, e0001722.	0.3	1
2655	Single-cell genomics for resolution of conserved bacterial genes and mobile genetic elements of the human intestinal microbiota using flow cytometry. <i>Gut Microbes</i> , 2022, 14, 2029673.	4.3	5
2656	Plant-growth-promoting <i>Caulobacter</i> strains isolated from distinct plant hosts share conserved genetic factors involved in beneficial plant-bacteria interactions. <i>Archives of Microbiology</i> , 2022, 204, 43.	1.0	6
2657	Introduction and adaptation of an emerging pathogen to olive trees in Italy. <i>Microbial Genomics</i> , 2021, 7, .	1.0	14
2658	New Delhi Metallo-Beta-Lactamase Facilitates the Emergence of Cefiderocol Resistance in <i>Enterobacter cloacae</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2022, 66, AAC0201121.	1.4	42
2660	A soil bacterial catabolic pathway on the move: Transfer of nicotine catabolic genes between genus megaplasmids and invasion by mobile elements. <i>Journal of Biosciences</i> , 2020, 45, .	0.5	0
2661	SaAlign: Multiple DNA/RNA sequence alignment and phylogenetic tree construction tool for ultra-large datasets and ultra-long sequences based on suffix array. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 1487-1493.	1.9	1
2662	Population structure of bla <sub>KPC</sub> -harbouring 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.	1.3	7
2663	Persistence of a multidrug-resistant worldwide-disseminated methicillin-resistant <i>Staphylococcus epidermidis</i> clone harbouring the cfr linezolid resistance gene in a French hospital with evidence of interspecies transfer to several <i>Staphylococcus aureus</i> lineages. <i>Journal of Antimicrobial Chemotherapy</i> , 2022, 77, 1838-1846.	1.3	13
2665	Antimicrobial Susceptibility, Virulence, and Genomic Features of a Hypervirulent Serotype K2, ST65 <i>Klebsiella pneumoniae</i> Causing Meningitis in Italy. <i>Antibiotics</i> , 2022, 11, 261.	1.5	8
2667	Draft Genome Sequence of a Bacterium Isolated from Hypersaline Soil in Sonora, Mexico: <i>Halomonas</i> sp. Strain BLLS135. <i>Microbiology Resource Announcements</i> , 2022, 11, e0140920.	0.3	0
2668	Host ecology regulates interspecies recombination in bacteria of the genus <i>Campylobacter</i> . <i>ELife</i> , 2022, 11, .	2.8	17
2669	Whole-genome analyses reveal a novel prophage and cgSNPs-derived sublineages of <i>Brachyspira hyodysenteriae</i> ST196. <i>BMC Genomics</i> , 2022, 23, 131.	1.2	0
2670	Highly Resolved Papilionoid Legume Phylogeny Based on Plastid Phylogenomics. <i>Frontiers in Plant Science</i> , 2022, 13, 823190.	1.7	25
2671	Unamplified, Long-Read Metagenomic Sequencing Approach to Close Endosymbiont Genomes of Low-Biomass Insect Populations. <i>Microorganisms</i> , 2022, 10, 513.	1.6	6
2672	Genome assembly of the JD17 soybean provides a new reference genome for comparative genomics. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	7
2673	Comparison of <i>Auxenochlorella protothecoides</i> and <i>Chlorella</i> spp. Chloroplast Genomes: Evidence for Endosymbiosis and Horizontal Virus-like Gene Transfer. <i>Life</i> , 2022, 12, 458.	1.1	0



#	ARTICLE	IF	CITATIONS
2674	Healthcare-associated infections caused by chlorhexidine-tolerant <i>Serratia marcescens</i> carrying a promiscuous IncHI2 multi-drug resistance plasmid in a veterinary hospital. <i>PLoS ONE</i> , 2022, 17, e0264848.	1.1	6
2675	Complete Genome Sequence of <i>Stenotrophomonas maltophilia</i> Siphophage Suzuki. <i>Microbiology Resource Announcements</i> , 2022, , e0013622.	0.3	0
2676	Complete Genome Sequence of <i>Stenotrophomonas maltophilia</i> Myophage Marzo. <i>Microbiology Resource Announcements</i> , 2022, 11, e0120221.	0.3	0
2677	Genomic Characterisation of UFJF_PfDIW6: A Novel Lytic <i>Pseudomonas fluorescens</i> -Phage with Potential for Biocontrol in the Dairy Industry. <i>Viruses</i> , 2022, 14, 629.	1.5	3
2678	Recombination resolves the cost of horizontal gene transfer in experimental populations of <i>Helicobacter pylori</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2119010119.	3.3	12
2679	The plastome of Arctic <i>Oxytropis arctobia</i> (Fabaceae) is significantly different from that of <i>O. splendens</i> and other related species. <i>Genome</i> , 2022, , 1-13.	0.9	3
2680	Complete Genome Sequence of <i>Stenotrophomonas maltophilia</i> Siphophage Silvanus. <i>Microbiology Resource Announcements</i> , 2022, 11, e0121021.	0.3	0
2681	Complete Genome Sequence of <i>Enterococcus faecalis</i> Siphophage Sigurd. <i>Microbiology Resource Announcements</i> , 2022, , e0012322.	0.3	0
2682	Complete Genome Sequence of <i>Stenotrophomonas maltophilia</i> Podophage Ptah. <i>Microbiology Resource Announcements</i> , 2022, , e0013722.	0.3	1
2683	Complete Genome Sequence of <i>Burkholderia cenocepacia</i> Phage Paku. <i>Microbiology Resource Announcements</i> , 2022, , e0122021.	0.3	1
2685	A Novel Phage Infecting the Marine Photoheterotrophic Bacterium <i>Citromicrobium bathyomarinum</i> . <i>Viruses</i> , 2022, 14, 512.	1.5	2
2686	Whole-Genome Sequences of Two <i>Listeria monocytogenes</i> Biofilm Formers. <i>Microbiology Resource Announcements</i> , 2022, , e0106221.	0.3	0
2687	Characterization of the mitogenome of <i>Gongronella</i> sp. w5 reveals substantial variation in Mucoromycota. <i>Applied Microbiology and Biotechnology</i> , 2022, 106, 2587-2601.	1.7	1
2688	Complete Genome Sequence of <i>Stenotrophomonas maltophilia</i> Siphophage Suso. <i>Microbiology Resource Announcements</i> , 2022, 11, e0011722.	0.3	1
2689	Comparative plastome analysis of Musaceae and new insights into phylogenetic relationships. <i>BMC Genomics</i> , 2022, 23, 223.	1.2	11
2690	Deciphering Active Prophages from Metagenomes. <i>MSystems</i> , 2022, 7, e0008422.	1.7	23
2692	Diatom Biodiversity and Speciation Revealed by Comparative Analysis of Mitochondrial Genomes. <i>Frontiers in Plant Science</i> , 2022, 13, 749982.	1.7	6
2693	Complete Genome Sequence of <i>Stenotrophomonas maltophilia</i> Siphophage Summit. <i>Microbiology Resource Announcements</i> , 2022, , e0008922.	0.3	0

#	ARTICLE	IF	CITATIONS
2695	Age and episode-associated occurrence of <i>Cryptosporidium</i> species and subtypes in a birth-cohort of dairy calves. <i>Transboundary and Emerging Diseases</i> , 2022, 69, .	1.3	3
2696	Prophages Present in <i>Acinetobacter pittii</i> Influence Bacterial Virulence, Antibiotic Resistance, and Genomic Rearrangements. <i>Phage</i> , 2022, 3, 38-49.	0.8	0
2697	Complete Genome Sequence of <i>Stenotrophomonas maltophilia</i> Podophage Piffle. <i>Microbiology Resource Announcements</i> , 2022, , e0015922.	0.3	0
2698	Complete Genome Sequence of <i>Alcaligenes faecalis</i> Phage Piluca. <i>Microbiology Resource Announcements</i> , 2022, , e0012422.	0.3	0
2699	Divergent paths in the evolutionary history of maternally transmitted clam symbionts. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2022, 289, 20212137.	1.2	9
2700	Dataset for Genome Sequencing and De Novo Assembly of the Candidate Phyla Radiation in Supragingival Plaque. <i>Canadian Journal of Infectious Diseases and Medical Microbiology</i> , 2022, 2022, 1-10.	0.7	0
2701	Complete genome sequence analysis and phylogenetic classification of the novel <i>Aeromonas</i> phage AHP-1, a potential member of the genus <i>Tequatrovirus</i> . <i>Archives of Virology</i> , 2022, 167, 1225-1230.	0.9	3
2702	Isolation and Identification of a Large Green Alga Virus ( <i>Chlorella</i> Virus XW01) of <i>Mimiviridae</i> and Its Virophage ( <i>Chlorella</i> Virus Virophage SW01) by Using Unicellular Green Algal Cultures. <i>Journal of Virology</i> , 2022, 96, e0211421.	1.5	15
2704	Diverse Subclade Differentiation Attributed to the Ubiquity of <i>Prochlorococcus</i> High-Light-Adapted Clade II. <i>MBio</i> , 2022, 13, e0302721.	1.8	3
2705	Mitochondrial genome structure, phylogenetic analyses and substitution rate estimation of the <i>Oedogoniales</i> . <i>European Journal of Phycology</i> , 0, , 1-12.	0.9	2
2706	Complete Genome Sequence of <i>Stenotrophomonas maltophilia</i> Podophage Paxi. <i>Microbiology Resource Announcements</i> , 2022, , e0017922.	0.3	0
2707	The complete genome sequence of an alphabaculovirus from the brown tussock moth, <i>Olene mendosa</i> HÅ/4bner, expands our knowledge of lymantriine baculovirus diversity and evolution. <i>Virus Genes</i> , 2022, 58, 227-237.	0.7	2
2708	Phage anti-CBASS and anti-Pycsar nucleases subvert bacterial immunity. <i>Nature</i> , 2022, 605, 522-526.	18.7	70
2709	Genomic characterization of two bacteriophages (vB_EcoS-phiEc3 and vB_EcoS-phiEc4) belonging to the genus <i>Kagunavirus</i> with lytic activity against uropathogenic <i>Escherichia coli</i> . <i>Microbial Pathogenesis</i> , 2022, 165, 105494.	1.3	2
2710	Reference-Grade Genome and Large Linear Plasmid of <i>Streptomyces rimosus</i> : Pushing the Limits of Nanopore Sequencing. <i>Microbiology Spectrum</i> , 2022, 10, e0243421.	1.2	5
2712	Phage Infection Restores PQS Signaling and Enhances Growth of a <i>Pseudomonas aeruginosa</i> Quorum-Sensing Mutant. <i>Journal of Bacteriology</i> , 2022, 204, e0055721.	1.0	5
2713	Putting small and big pieces together: a genome assembly approach reveals the largest Lamiid plastome in a woody vine. <i>PeerJ</i> , 2022, 10, e13207.	0.9	3
2714	SASpector: analysis of missing genomic regions in draft genomes of prokaryotes. <i>Bioinformatics</i> , 2022, , .	1.8	0

#	ARTICLE	IF	CITATIONS
2715	Plastid Genomes of the Hemiparasitic Genus <i>Krameria</i> (Zygophyllales) Are Intact and Exhibit Little Relaxation in Selection. <i>International Journal of Plant Sciences</i> , 2022, 183, 393-403.	0.6	3
2716	Isolation and Characterisation of Bacteriophage Selective for Key <i>Acinetobacter baumannii</i> Capsule Chemotypes. <i>Pharmaceuticals</i> , 2022, 15, 443.	1.7	6
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.	1.4	5
2718	A new and effective genes-based method for phylogenetic analysis of <i>Klebsiella pneumoniae</i> . <i>Infection, Genetics and Evolution</i> , 2022, 100, 105275.	1.0	2
2719	Six Newly Sequenced Chloroplast Genomes From Trentepohliales: The Inflated Genomes, Alternative Genetic Code and Dynamic Evolution. <i>Frontiers in Plant Science</i> , 2021, 12, 780054.	1.7	2
2720	The Effects of Sub-inhibitory Antibiotic Concentrations on <i>Pseudomonas aeruginosa</i> : Reduced Susceptibility Due to Mutations. <i>Frontiers in Microbiology</i> , 2021, 12, 789550.	1.5	8
2721	Transposable element variants and their potential adaptive impact in urban populations of the malaria vector <i>Anopheles coluzzii</i> . <i>Genome Research</i> , 2022, 32, 189-202.	2.4	5
2723	Genomic Characterization of <i>Streptococcus suis</i> Serotype 24 Clonal Complex 221/234 From Human Patients. <i>Frontiers in Microbiology</i> , 2021, 12, 812436.	1.5	7
2724	Phage Annotation Guide: Guidelines for Assembly and High-Quality Annotation. <i>Phage</i> , 2021, 2, 170-182.	0.8	24
2725	<i>Bacillus cytotoxicus</i> Genomics: Chromosomal Diversity and Plasmidome Versatility. <i>Frontiers in Microbiology</i> , 2021, 12, 789929.	1.5	5
2726	Immunomodulatory potential of four candidate probiotic <i>Lactobacillus</i> strains from plant and animal origin using comparative genomic analysis. <i>Access Microbiology</i> , 2021, 3, 000299.	0.2	5
2727	Advances in Biosynthesis of Natural Products from Marine Microorganisms. <i>Microorganisms</i> , 2021, 9, 2551.	1.6	11
2728	Chloroplast Genomes for Five <i>Skeletonema</i> Species: Comparative and Phylogenetic Analysis. <i>Frontiers in Plant Science</i> , 2021, 12, 774617.	1.7	8
2729	<i>Cryptosporidium felis</i> differs from other <i>Cryptosporidium</i> spp. in codon usage. <i>Microbial Genomics</i> , 2021, 7, .	1.0	3
2730	Comparative Analysis of Chloroplast Genomes of <i>Thalassiosira</i> Species. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	6
2732	<i>Prochlorococcus</i> have low global mutation rate and small effective population size. <i>Nature Ecology and Evolution</i> , 2022, 6, 183-194.	3.4	16
2733	The Genome of the "Sea Vomit" <i>Didemnum vexillum</i> . <i>Life</i> , 2021, 11, 1377.	1.1	0
2737	Pangenome Evolution Reconciles Robustness and Instability of Rhizobial Symbiosis. <i>MBio</i> , 2022, 13, e0007422.	1.8	13

#	ARTICLE	IF	CITATIONS
2738	Cellulose-mediated floc formation by the activated sludge bacterium <i>Shinella zoogloeoides</i> ATCC 19623. <i>BMC Microbiology</i> , 2022, 22, 104.	1.3	3
2739	Complete Genome Sequence of <i>Stenotrophomonas maltophilia</i> Siphophage Sonora. <i>Microbiology Resource Announcements</i> , 2022, 11, e0016722.	0.3	0
2740	High plasmidome diversity of extended-spectrum beta-lactam-resistant <i>Escherichia coli</i> isolates collected during one year in one community hospital. <i>Genomics</i> , 2022, 114, 110368.	1.3	5
2741	Microevolution of the <i>mexT</i> and <i>lasR</i> Reinforces the Bias of Quorum Sensing System in Laboratory Strains of <i>Pseudomonas aeruginosa</i> PAO1. <i>Frontiers in Microbiology</i> , 2022, 13, 821895.	1.5	7
2742	Nationwide surveillance in Thailand revealed genotype-dependent dissemination of carbapenem-resistant Enterobacterales. <i>Microbial Genomics</i> , 2022, 8, .	1.0	13
2743	Secreted NF- $\kappa$ B suppressive microbial metabolites modulate gut inflammation. <i>Cell Reports</i> , 2022, 39, 110646.	2.9	22
2744	Prediction and Inferred Evolution of Acid Tolerance Genes in the Biotechnologically Important <i>Acidihalobacter</i> Genus. <i>Frontiers in Microbiology</i> , 2022, 13, 848410.	1.5	6
3218	Integrative Genomics Sheds Light on Evolutionary Forces Shaping the Acidithiobacillia Class Acidophilic Lifestyle. <i>Frontiers in Microbiology</i> , 2021, 12, 822229.	1.5	10
3219	Metagenomic methylation patterns resolve bacterial genomes of unusual size and structural complexity. <i>ISME Journal</i> , 2022, 16, 1921-1931.	4.4	11
3220	Characterisation of the symbionts in the Mediterranean fruit fly gut. <i>Microbial Genomics</i> , 2022, 8, .	1.0	3
3221	Complete Genome Sequence of <i>Stenotrophomonas maltophilia</i> Podophage Pepon. <i>Microbiology Resource Announcements</i> , 2022, , e0015822.	0.3	1
3222	Urban Wildlife Crisis: Australian Silver Gull Is a Bystander Host to Widespread Clinical Antibiotic Resistance. <i>MSystems</i> , 2022, 7, e0015822.	1.7	21
3223	Transposable Element Insertions into the <i>Escherichia coli</i> Polysialic Acid Gene Cluster Result in Resistance to the K1F Bacteriophage. <i>Microbiology Spectrum</i> , 2022, 10, e0211221.	1.2	3
3224	Phylogenomic approaches untangle early divergences and complex diversifications of the olive plant family. <i>BMC Biology</i> , 2022, 20, 92.	1.7	30
3225	Comparative analysis of <i>Thalassionema</i> chloroplast genomes revealed hidden biodiversity. <i>BMC Genomics</i> , 2022, 23, 327.	1.2	3
3226	A Highly Unstable and Elusive Plasmid That Encodes the Type III Secretion System Is Necessary for Full Virulence in the Marine Fish Pathogen <i>Photobacterium damsela</i> subsp. <i>piscicida</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 4729.	1.8	2
3227	Tracking the Origins of <i>Pseudomonas aeruginosa</i> Phylogroups by Diversity and Evolutionary Analysis of Important Pathogenic Marker Genes. <i>Diversity</i> , 2022, 14, 345.	0.7	3
3228	Epistatic selection on a selfish Segregation Distorter supergene “drive, recombination, and genetic load. <i>ELife</i> , 2022, 11, .	2.8	13

#	ARTICLE	IF	CITATIONS
3229	Discovery of Early-Branching Wolbachia Reveals Functional Enrichment on Horizontally Transferred Genes. <i>Frontiers in Microbiology</i> , 2022, 13, 867392.	1.5	6
3230	Comparative plastid genome analyses of Rosa: Insights into the phylogeny and gene divergence. <i>Tree Genetics and Genomes</i> , 2022, 18, 1.	0.6	11
3231	The Isolation and Characterization of a Broad Host Range Bcep22-like Podovirus JC1. <i>Viruses</i> , 2022, 14, 938.	1.5	4
3232	The antimicrobial systems of <i>Streptococcus suis</i> promote niche competition in pig tonsils. <i>Virulence</i> , 2022, 13, 781-793.	1.8	12
3233	A chromosomal inversion may facilitate adaptation despite periodic gene flow in a freshwater fish. <i>Ecology and Evolution</i> , 2022, 12, e8898.	0.8	6
3234	Viral Proteins Involved in the Adsorption Process of Deep-Purple, a Siphovirus Infecting Members of the Bacillus cereus Group. <i>Applied and Environmental Microbiology</i> , 2022, , e0247821.	1.4	1
3236	Genomic dissection of the microevolution of Australian epidemic <i>Bordetella pertussis</i> . <i>Emerging Microbes and Infections</i> , 2022, 11, 1460-1473.	3.0	4
3237	vRhyme enables binning of viral genomes from metagenomes. <i>Nucleic Acids Research</i> , 2022, 50, e83-e83.	6.5	30
3238	Comparative genomics reveals the organic acid biosynthesis metabolic pathways among five lactic acid bacterial species isolated from fermented vegetables. <i>New Biotechnology</i> , 2022, 70, 73-83.	2.4	36
3239	Complete Genome Sequence of <i>Stenotrophomonas maltophilia</i> Siphophage Siara. <i>Microbiology Resource Announcements</i> , 2022, 11, e0017722.	0.3	0
3240	Complete Genome Sequence of <i>Stenotrophomonas maltophilia</i> Phage Philippe. <i>Microbiology Resource Announcements</i> , 2022, 11, e0012522.	0.3	1
3241	De novo Nanopore Genome Sequencing of the Clinical <i>Diutina catenulata</i> Type-strain CBS565. <i>Mycopathologia</i> , 2022, , 1.	1.3	1
3243	Comparative Genomic Analysis of Two <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> Strains Isolated From Low Land and High Mountain Paddies in Guangxi, China. <i>Frontiers in Microbiology</i> , 2022, 13, 867633.	1.5	2
3244	Genomic, morphological, and biochemical analyses of a multi-metal resistant but multi-drug susceptible strain of <i>Bordetella petrii</i> from hospital soil. <i>Scientific Reports</i> , 2022, 12, 8439.	1.6	11
3245	Enabling genomic island prediction and comparison in multiple genomes to investigate bacterial evolution and outbreaks. <i>Microbial Genomics</i> , 2022, 8, .	1.0	10
3249	Comparative Analysis of Pseudo-nitzschia Chloroplast Genomes Revealed Extensive Inverted Region Variation and Pseudo-nitzschia Speciation. <i>Frontiers in Marine Science</i> , 2022, 9, .	1.2	6
3251	Comparative genomics of the Western Hemisphere soft tick-borne relapsing fever borreliae highlights extensive plasmid diversity. <i>BMC Genomics</i> , 2022, 23, .	1.2	13
3252	Whole-Genome Analysis Reveals That Bacteriophages Promote Environmental Adaptation of <i>Staphylococcus aureus</i> via Gene Exchange, Acquisition, and Loss. <i>Viruses</i> , 2022, 14, 1199.	1.5	8

#	ARTICLE	IF	CITATIONS
3253	Repetitive Elements, Sequence Turnover and Cyto-Nuclear Gene Transfer in Gymnosperm Mitogenomes. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	2
3254	Genomic structural plasticity of rodent-associated <i>Bartonella</i> in nature. <i>Molecular Ecology</i> , 0, , .	2.0	1
3256	Genomic and Biological Profile of a Novel Bacteriophage, Vibrio phage Virtus, Which Improves Survival of Sparus aurata Larvae Challenged with Vibrio harveyi. <i>Pathogens</i> , 2022, 11, 630.	1.2	16
3258	Recent genetic exchanges and admixture shape the genome and population structure of the zoonotic pathogen <i>Cryptosporidium parvum</i> . <i>Molecular Ecology</i> , 2023, 32, 2633-2645.	2.0	9
3259	Molecular basis for avirulence of spontaneous variants of <i>Porphyromonas gingivalis</i> : Genomic analysis of strains W50, BE1 and BR1. <i>Molecular Oral Microbiology</i> , 2022, 37, 122-132.	1.3	6
3260	The evolution of extremely diverged plastomes in Selaginellaceae (lycophyte) is driven by repeat patterns and the underlying <i>DNA</i> maintenance machinery. <i>Plant Journal</i> , 2022, 111, 768-784.	2.8	8
3261	Phenotypic characterization and analysis of complete genomes of two distinct strains of the proposed species <i>L. swaminathanii</i> . <i>Scientific Reports</i> , 2022, 12, .	1.6	6
3262	<i>qPCR</i> screening for <i>Yersinia ruckeri</i> clonal complex 1 against a background of putatively avirulent strains in Norwegian aquaculture. <i>Journal of Fish Diseases</i> , 0, , .	0.9	4
3263	Chromosomal integration of blaCTX-M genes in diverse Escherichia coli isolates recovered from river water in Japan. <i>Current Research in Microbial Sciences</i> , 2022, 3, 100144.	1.4	4
3264	Deep Insights Into the Plastome Evolution and Phylogenetic Relationships of the Tribe Urticeae (Family) Tj ETQq1 1.0,784314 rgBT /Oe 1.7 115	1.7	115
3266	Optimizing Molecular Detection for the Hop Downy Mildew Pathogen <i>Pseudoperonospora humuli</i> in Plant Tissue. <i>Phytopathology</i> , 2022, 112, 2426-2439.	1.1	1
3267	Taxonomy, comparative genomics and evolutionary insights of <i>Penicillium ucsense</i> : a novel species in series Oxalica. <i>Antonie Van Leeuwenhoek</i> , 2022, 115, 1009-1029.	0.7	5
3268	Complete genome sequences and genomic characterization of five plasmids harbored by environmentally persistent Cronobacter sakazakii strains ST83 H322 and ST64 GK1025B obtained from powdered infant formula manufacturing facilities. <i>Gut Pathogens</i> , 2022, 14, .	1.6	4
3269	The compact mitogenome of <i>Ceratocystopsis pallidobrunnea</i> . <i>Canadian Journal of Microbiology</i> , 2022, 68, 569-575.	0.8	1
3270	Genomic characterization of Streptococcus parasuis, a close relative of Streptococcus suis and also a potential opportunistic zoonotic pathogen. <i>BMC Genomics</i> , 2022, 23, .	1.2	6
3271	Genomic Insight Into Lactibacillus paracasei SP5, Reveals Genes and Gene Clusters of Probiotic Interest and Biotechnological Potential. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	14
3272	Simplexviruses Successfully Adapt to Their Host by Fine-Tuning Immune Responses. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	3
3273	Genomic Analysis of Carbapenem-Resistant <i>Comamonas</i> in Water Matrices: Implications for Public Health and Wastewater Treatments. <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	10



#	ARTICLE	IF	CITATIONS
3274	Annotation-free delineation of prokaryotic homology groups. <i>PLoS Computational Biology</i> , 2022, 18, e1010216.	1.5	0
3275	Introduction to the principles and methods underlying the recovery of metagenome-assembled genomes from metagenomic data. <i>MicrobiologyOpen</i> , 2022, 11, .	1.2	8
3276	<i>Fragaria</i> mitogenomes evolve rapidly in structure but slowly in sequence and incur frequent multinucleotide mutations mediated by microinversions. <i>New Phytologist</i> , 2022, 236, 745-759.	3.5	16
3277	The complete and closed genome of the facultative generalist <i>Candidatus</i> <i>Endoriftia persephone</i> from deep-sea hydrothermal vents. <i>Molecular Ecology Resources</i> , 2022, 22, 3106-3123.	2.2	7
3279	Phylogenomic and functional characterization of an evolutionary conserved cytochrome P450-based insecticide detoxification mechanism in bees. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	31
3280	Genomic Characterization of <i>Escherichia coli</i> O8 Strains Producing Shiga Toxin 2l Subtype. <i>Microorganisms</i> , 2022, 10, 1245.	1.6	7
3281	Highly Specialized Carbohydrate Metabolism Capability in <i>Bifidobacterium</i> Strains Associated with Intestinal Barrier Maturation in Early Preterm Infants. <i>MBio</i> , 2022, 13, .	1.8	10
3283	Plasmidome analysis of a hospital effluent biofilm: Status of antibiotic resistance. <i>Plasmid</i> , 2022, 122, 102638.	0.4	1
3284	Plastid and mitochondrial phylogenomics reveal correlated substitution rate variation in <i>Koenigia</i> (Polygonoideae, Polygonaceae) and a reduced plastome for <i>Koenigia delicatula</i> including loss of all <i>ndh</i> genes. <i>Molecular Phylogenetics and Evolution</i> , 2022, 174, 107544.	1.2	5
3286	Comparative genomics of <i>Acinetobacter baumannii</i> and therapeutic bacteriophages from a patient undergoing phage therapy. <i>Nature Communications</i> , 2022, 13, .	5.8	20
3287	A critical evaluation of <i>Mycobacterium bovis</i> pangenomics, with reference to its utility in outbreak investigation. <i>Microbial Genomics</i> , 2022, 8, .	1.0	7
3288	Diversity of SIRV-like Viruses from a North American Population. <i>Viruses</i> , 2022, 14, 1439.	1.5	1
3289	Impact of host demography and evolutionary history on endosymbiont molecular evolution: A test in carpenter ants (genus <i>Camponotus</i> ) and their <i>Blochmannia</i> endosymbionts. <i>Ecology and Evolution</i> , 2022, 12, .	0.8	7
3290	Comparative analysis of multiplexed PCR and short- and long-read whole genome sequencing to investigate a large <i>Klebsiella pneumoniae</i> outbreak in New York State. <i>Diagnostic Microbiology and Infectious Disease</i> , 2022, , 115765.	0.8	0
3291	Comparative Genomics and In Silico Evaluation of Genes Related to the Probiotic Potential of <i>Bifidobacterium breve</i> 1101A. , 2022, 1, 161-182.		5
3292	Complete Genomes of <i>Theileria orientalis</i> Chitose and Buffeli Genotypes Reveal within Species Translocations and Differences in ABC Transporter Content. <i>Pathogens</i> , 2022, 11, 801.	1.2	3
3293	Meta-omics approaches reveal unique small RNAs exhibited by the uncultured microorganisms dwelling deep-sea hydrothermal sediment in Guaymas Basin. <i>Archives of Microbiology</i> , 2022, 204, .	1.0	2
3294	Development of a high-resolution molecular marker for tracking <i>Rhizosolenia setigera</i> genetic diversity. <i>Journal of Applied Phycology</i> , 0, , .	1.5	0

#	ARTICLE	IF	CITATIONS
3295	Analysis of the Taxonomy, Synteny, and Virulence Factors for Soft Rot Pathogen <i>Pectobacterium atrosepticum</i> in <i>Amorpha phalloides</i> Using Comparative Genomics. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
3296	Genomic Insights Into the Interspecific Diversity and Evolution of <i>Mobiluncus</i> , a Pathogen Associated With Bacterial Vaginosis. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
3297	The Type III Secretion Effector CteG Mediates Host Cell Lytic Exit of <i>Chlamydia trachomatis</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	7
3298	Two Newly Isolated <i>Enterobacter</i> -Specific Bacteriophages: Biological Properties and Stability Studies. <i>Viruses</i> , 2022, 14, 1518.	1.5	8
3299	Identification of sex-specific markers and ZW-chromosome DNA clones from the genomic BAC library of the Chinese mitten crab <i>Eriocheir sinensis</i> . <i>Aquaculture</i> , 2022, 560, 738576.	1.7	2
3300	Prevalence, Genomic Characterization, and Risk Assessment of Human Pathogenic <i>Vibrio</i> Species in Seafood. <i>Journal of Food Protection</i> , 2022, 85, 1553-1565.	0.8	6
3301	Insights from cyanobacterial genomic and transcriptomic analyses into adaptation strategies in terrestrial environments. <i>Genomics</i> , 2022, , 110438.	1.3	1
3302	Pathogenic and genomic characterisation of a rabbit sourced <i>Pasteurella multocida</i> serogroup F isolate s4. <i>BMC Veterinary Research</i> , 2022, 18, .	0.7	2
3303	Comparative Genome Analyses of Plant Rust Pathogen Genomes Reveal a Confluence of Pathogenicity Factors to Quell Host Plant Defense Responses. <i>Plants</i> , 2022, 11, 1962.	1.6	3
3304	Phylogenomic analysis and metabolic role reconstruction of mutualistic <i>Rhizobiales</i> hindgut symbionts of <i>Acromyrmex</i> leaf-cutting ants. <i>FEMS Microbiology Ecology</i> , 2022, 98, .	1.3	1
3305	Within-farm dynamics of ESBL-producing <i>Escherichia coli</i> in dairy cattle: Resistance profiles and molecular characterization by long-read whole-genome sequencing. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5
3306	Plastid Phylogenomics and Plastomic Diversity of the Extant Lycophytes. <i>Genes</i> , 2022, 13, 1280.	1.0	4
3307	Genome sequence and comparative analysis of fungal antagonistic strain <i>Bacillus velezensis</i> LJBV19. <i>Folia Microbiologica</i> , 2023, 68, 73-86.	1.1	4
3308	Rearrangement and domestication as drivers of Rosaceae mitogenome plasticity. <i>BMC Biology</i> , 2022, 20, .	1.7	14
3309	The evolution and diversification of oakleaf butterflies. <i>Cell</i> , 2022, 185, 3138-3152.e20.	13.5	22
3310	High Prevalence and Persistence of <i>Escherichia coli</i> Strains Producing Shiga Toxin Subtype 2k in Goat Herds. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	10
3311	A large chromosomal inversion affects antimicrobial sensitivity of <i>Escherichia coli</i> to sodium deoxycholate. <i>Microbiology (United Kingdom)</i> , 2022, 168, .	0.7	2
3312	Application of a novel lytic phage vB_EcoM_SQ17 for the biocontrol of Enterohemorrhagic <i>Escherichia coli</i> O157:H7 and Enterotoxigenic <i>E. coli</i> in food matrices. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1

#	ARTICLE	IF	CITATIONS
3313	The Sixth Element: a 102-kb RepABC Plasmid of Xenologous Origin Modulates Chromosomal Gene Expression in <i>Dinoroseobacter shibae</i> . <i>MSystems</i> , 0, , .	1.7	0
3314	Mechanism of gastrointestinal adaptability and antioxidant function of infant-derived <i>Lactobacillus plantarum</i> BF_15 through genomics. <i>Food Science and Biotechnology</i> , 0, , .	1.2	2
3315	Nanopore sequencing of chloroplast genome of <i>Scapania undulata</i> (L.) Dumort., 1835 ( <i>Scapaniaceae</i> , <i>Jungermanniales</i> ). <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1424-1426.	0.2	3
3316	<i>Lightella neohaematopini</i> : A new lineage of highly reduced endosymbionts coevolving with chipmunk lice of the genus <i>Neohaematopinus</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
3317	Characterization of <i>Codonopsis pilosula</i> subsp. <i>tangshen</i> plastome and comparative analysis of <i>Codonopsis</i> species. <i>PLoS ONE</i> , 2022, 17, e0271813.	1.1	0
3318	Characterization of the virulence of three novel clade 2 <i>Clostridioides</i> ( <i>Clostridium</i> ) <i>difficile</i> strains and a two-year screening in animals and humans in Brazil. <i>PLoS ONE</i> , 2022, 17, e0273013.	1.1	4
3319	The microbiome of a bacterivorous marine choanoflagellate contains a resource-demanding obligate bacterial associate. <i>Nature Microbiology</i> , 2022, 7, 1466-1479.	5.9	5
3321	Comparative Analysis of Bacillariophyceae Chloroplast Genomes Uncovers Extensive Genome Rearrangements Associated with Speciation. <i>International Journal of Environmental Research and Public Health</i> , 2022, 19, 10024.	1.2	2
3322	Genomic Insights of First <i>ermB</i> -Positive ST338-SCCmecVT/CC59 Taiwan Clone of Community-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> in Poland. <i>International Journal of Molecular Sciences</i> , 2022, 23, 8755.	1.8	1
3323	Genome-informed multiplex conventional PCR for identification and differentiation of <i>Xanthomonas citri</i> pv. <i>citri</i> sub-pathotypes, the causal agents of Asiatic citrus canker. <i>PhytoFrontiers</i> , 0, , .	0.8	1
3324	Comparative genomics of <i>Leuconostoc lactis</i> strains isolated from human gastrointestinal system and fermented foods microbiomes. <i>BMC Genomic Data</i> , 2022, 23, .	0.7	2
3326	A butterfly pan-genome reveals that a large amount of structural variation underlies the evolution of chromatin accessibility. <i>Genome Research</i> , 2022, 32, 1862-1875.	2.4	10
3327	Genome-scale prediction of bacterial promoters. <i>BioSystems</i> , 2022, 221, 104771.	0.9	3
3328	Comparative genome analysis of four <i>Leuconostoc</i> strains with a focus on carbohydrate-active enzymes and oligosaccharide utilization pathways. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 4771-4785.	1.9	4
3329	Phage PH826 Effectively Inhibits the Formation of Multidrug-Resistant <i>Pseudomonas Aeruginosa</i> Biofilm. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
3330	Multiple genome alignment in the telomere-to-telomere assembly era. <i>Genome Biology</i> , 2022, 23, .	3.8	17
3331	Acesulfame Anoxic Biodegradation Coupled to Nitrate Reduction by Enriched Consortia and Isolated <i>Shinella</i> spp.. <i>Environmental Science &amp; Technology</i> , 2022, 56, 13096-13106.	4.6	10
3332	Molecular analysis of OXA-48-producing <i>Escherichia coli</i> in Switzerland from 2019 to 2020. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2022, 41, 1355-1360.	1.3	11

#	ARTICLE	IF	CITATIONS
3333	Reduced and Nonreduced Genomes in <i>Paraburkholderia</i> Symbionts of Social Amoebas. <i>MSystems</i> , 0, , .	1.7	5
3334	Nonadaptive molecular evolution of plastome during the speciation of <i>Actaea purpurea</i> and its relatives. <i>Ecology and Evolution</i> , 2022, 12, .	0.8	1
3335	Convergent structure with divergent adaptations in combinatorial microbiome communities. <i>FEMS Microbiology Ecology</i> , 2022, 98, .	1.3	0
3336	<i>Enterobacteria</i> Phage Ac3's Genome Annotation and Host Range Analysis Against the ECOR Reference Library. <i>Phage</i> , 2022, 3, 165-170.	0.8	1
3337	Resistance to Fluoroquinolones in <i>Pseudomonas aeruginosa</i> from Human, Animal, Food and Environmental Origin: The Role of CrpP and Mobilizable ICEs. <i>Antibiotics</i> , 2022, 11, 1271.	1.5	4
3338	Comparative analysis of <i>Listeria monocytogenes</i> plasmid transcriptomes reveals common and plasmid-specific gene expression patterns and high expression of noncoding RNAs. <i>MicrobiologyOpen</i> , 2022, 11, .	1.2	0
3341	The blue diatom <i>Haslea ostrearia</i> from the Indian Ocean coast of South Africa, with comparative analysis of <i>Haslea</i> organellar genomes. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	0
3342	Lactic acid bacteria and bifidobacteria deliberately introduced into the agro-food chain do not significantly increase the antimicrobial resistance gene pool. <i>Gut Microbes</i> , 2022, 14, .	4.3	6
3344	In silico prediction of the enzymes involved in the degradation of the herbicide molinate by <i>Gulosibacter molinivorax</i> ON4T. <i>Scientific Reports</i> , 2022, 12, .	1.6	0
3345	Antibiotic concentrations in raw hospital wastewater surpass minimal selective and minimum inhibitory concentrations of resistant <i>Acinetobacter baylyi</i> strains. <i>Environmental Microbiology</i> , 2022, 24, 5721-5733.	1.8	6
3346	Does IR-loss promote plastome structural variation and sequence evolution?. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
3347	Genome Sequence of <i>Eubacterium limosum</i> B2 and Evolution for Growth on a Mineral Medium with Methanol and CO <sub>2</sub> as Sole Carbon Sources. <i>Microorganisms</i> , 2022, 10, 1790.	1.6	5
3348	Genome sequencing of <i>Colletotrichum gloeosporioides</i> ESO026 reveals plausible pathway of HupA. <i>Molecular Biology Reports</i> , 0, , .	1.0	0
3350	Genomic analysis of two <i>Bacillus safensis</i> isolated from Merzouga desert reveals desert adaptive and potential plant growth-promoting traits. <i>Functional and Integrative Genomics</i> , 2022, 22, 1173-1187.	1.4	1
3353	De novo genome assembly of rice bean ( <i>Vigna umbellata</i> ) – A nominated nutritionally rich future crop reveals novel insights into flowering potential, habit, and palatability centric traits for efficient domestication. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	7
3354	Comprehensive Genomic Characterization of Marine Bacteria <i>Thalassospira</i> spp. Provides Insights into Their Ecological Roles in Aromatic Hydrocarbon-Exposed Environments. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	3
3356	Frequent dissemination and carriage of an SCCmec-mecC hybrid in methicillin-resistant <i>Mammaliococcus sciuri</i> in farm animals from Tunisia. <i>Journal of Global Antimicrobial Resistance</i> , 2022, 31, 228-235.	0.9	2
3357	Monkeypox virus: The changing facets of a zoonotic pathogen. <i>Infection, Genetics and Evolution</i> , 2022, 105, 105372.	1.0	16

#	ARTICLE	IF	CITATIONS
3358	Comparative chloroplast genomes of <i>Ulva prolifera</i> and <i>U. linza</i> (Ulvophyceae) provide genetic resources for the development of interspecific markers. <i>Journal of Oceanology and Limnology</i> , 0, , .	0.6	2
3359	Borgs are giant genetic elements with potential to expand metabolic capacity. <i>Nature</i> , 2022, 610, 731-736.	13.7	29
3360	The pangenome of the wheat pathogen <i>Pyrenophora tritici-repentis</i> reveals novel transposons associated with necrotrophic effectors ToxA and ToxB. <i>BMC Biology</i> , 2022, 20, .	1.7	15
3361	The RNA repair proteins RtcAB regulate transcription activator RtcR via its CRISPR-associated Rossmann fold domain. <i>IScience</i> , 2022, 25, 105425.	1.9	3
3362	The Combination of Salmonella Phage ST-3 and Antibiotics to Prevent Salmonella Typhimurium In Vitro. <i>Current Microbiology</i> , 2022, 79, .	1.0	1
3364	Genome analysis of <i>Erwinia persicina</i> reveals implications for soft rot pathogenicity in plants. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
3366	Draft Genome Sequence of Endophytic <i>Sphingomonas faeni</i> Strain ALB2, Isolated from the Leaf of a Cold-Desert Medicinal Plant. <i>Microbiology Resource Announcements</i> , 0, , .	0.3	0
3367	Genomic Analysis of a Hybrid Enteroaggregative Hemorrhagic <i>Escherichia coli</i> O181:H4 Strain Causing Colitis with Hemolytic-Uremic Syndrome. <i>Antibiotics</i> , 2022, 11, 1416.	1.5	4
3368	Isolation, Characterization, and Genome Analysis of a Novel Bacteriophage, <i>Escherichia</i> Phage vB_EcoM-4HA13, Representing a New Phage Genus in the Novel Phage Family Chaseviridae. <i>Viruses</i> , 2022, 14, 2356.	1.5	2
3369	Characterization of the complete mitochondrial genome of <i>Miamiensis avidus</i> causing flatfish scuticociliatosis. <i>Genetica</i> , 2022, 150, 407-420.	0.5	3
3370	Comparative Genomic Analysis Uncovers the Chloroplast Genome Variation and Phylogenetic Relationships of <i>Camellia</i> Species. <i>Biomolecules</i> , 2022, 12, 1474.	1.8	1
3371	<sc>IncP</sc>-type plasmids carrying genes for antibiotic resistance or for aromatic compound degradation are prevalent in sequenced <sc><i>Aromatoleum</i></sc> and <sc><i>Thauera</i></sc> strains. <i>Environmental Microbiology</i> , 2022, 24, 6411-6425.	1.8	5
3372	Evaluation of hydrogen fermentation by a newly isolated alkaline tolerant <i>Clostridium felsineum</i> strain CUEA03. <i>International Journal of Hydrogen Energy</i> , 2023, 48, 2130-2144.	3.8	1
3373	Comparative analysis of chloroplast genomes of <i>Sanguisorba</i> species and insights into phylogenetic implications and molecular dating. <i>Nordic Journal of Botany</i> , 2022, 2022, .	0.2	1
3374	Evolution of the orthopoxvirus core genome. <i>Virus Research</i> , 2023, 323, 198975.	1.1	3
3375	Mitochondrial effects on fertility and longevity in <i>Tigriopus californicus</i> contradict predictions of the mother's curse hypothesis. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2022, 289, .	1.2	4
3376	Comparative genomics of Lactobacillaceae from the gut of honey bees, <i>Apis mellifera</i>, from the Eastern United States. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	3
3377	Whole-Genome Sequences of Human Monkeypox Virus Strains from Two 2022 Global Outbreak Cases in Western New York State. <i>Microbiology Resource Announcements</i> , 2022, 11, .	0.3	4

#	ARTICLE	IF	CITATIONS
3378	The Mitogenome of <i>Sedum plumbizincicola</i> (Crassulaceae): Insights into RNA Editing, Lateral Gene Transfer, and Phylogenetic Implications. <i>Biology</i> , 2022, 11, 1661.	1.3	1
3379	Plastome sequencing of South American <i>Podocarpus</i> species reveals low rearrangement rates despite ancient gondwanan disjunctions. <i>Molecular Biology Reports</i> , 2023, 50, 309-318.	1.0	2
3380	Insights into Genomic Evolution and the Potential Genetic Basis of <i>Klebsiella variicola</i> subsp. <i>variicola</i> ZH07 Reveal Its Potential for Plant Growth Promotion and Autotoxin Degradation. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	5
3382	Deciphering the mitochondrial genome of <i>Hemerocallis citrina</i> (Asphodelaceae) using a combined assembly and comparative genomic strategy. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4
3383	Twisting development, the birth of a potential new gene. <i>IScience</i> , 2022, 25, 105627.	1.9	4
3384	Impact of <i>Salmonella</i> genome rearrangement on gene expression. <i>Evolution Letters</i> , 2022, 6, 426-437.	1.6	3
3385	Antimony oxidation and whole genome sequencing of <i>Phytobacter</i> sp. X4 isolated from contaminated soil near a flotation site. <i>Journal of Hazardous Materials</i> , 2023, 445, 130462.	6.5	5
3386	IN SILICO DEVELOPMENT OF HIGH-RESOLUTION MLVA TYPING SCHEME FOR <i>ENTEROCOCCUS FAECIUM</i> . , 2020, 48, 5-14.		0
3387	Role of DNA modifications in <i>Mycoplasma gallisepticum</i> . <i>PLoS ONE</i> , 2022, 17, e0277819.	1.1	3
3388	Phylogenomics, plastome structure and species identification in <i>Mahonia</i> (Berberidaceae). <i>BMC Genomics</i> , 2022, 23, .	1.2	3
3389	Characterization and Genomic Analysis of <i>Escherichia coli</i> O157:H7 Phage UAE_MI-01 Isolated from Birds. <i>International Journal of Molecular Sciences</i> , 2022, 23, 14846.	1.8	2
3390	Insights into the diversity of transcription activator-like effectors (TALEs) in Indian pathotype strains of <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> . <i>Phytopathology</i> , 0, , .	1.1	0
3391	Metagenomic Characterization of Multiple Genetically Modified <i>Bacillus</i> Contaminations in Commercial Microbial Fermentation Products. <i>Life</i> , 2022, 12, 1971.	1.1	3
3392	Genomic analysis of the progenitor strains of <i>Staphylococcus aureus</i> RN6390. <i>Access Microbiology</i> , 2022, 4, .	0.2	3
3393	Biocomputational Identification of sRNAs in <i>Leptospira interrogans</i> Serovar Lai. <i>Indian Journal of Microbiology</i> , 0, , .	1.5	0
3394	A regulatory hydrogenase gene cluster observed in the thioautotrophic symbiont of <i>Bathymodiolus</i> mussel in the East Pacific Rise. <i>Scientific Reports</i> , 2022, 12, .	1.6	0
3395	Complete genome sequence analysis of a plant growth-promoting phylloplane <i>Bacillus altitudinis</i> FD48 offers mechanistic insights into priming drought stress tolerance in rice. <i>Genomics</i> , 2023, 115, 110550.	1.3	8
3396	Linezolid resistance: detection of the <i>cfz</i> (B) gene in French clinical MRSA strains. <i>Journal of Antimicrobial Chemotherapy</i> , 2023, 78, 445-449.	1.3	7



#	ARTICLE	IF	CITATIONS
3397	Phylogenomic diversity of <i>Vibrio</i> species and other Gammaproteobacteria isolated from Pacific oysters ( <i>Crassostrea gigas</i> ) during a summer mortality outbreak. <i>Microbial Genomics</i> , 2022, 8, .	1.0	3
3398	Genetic Features of <i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> Strains Circulating in the West of France Deciphered by Whole-Genome Sequencing. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	6
3399	Graph-based pangenomics maximizes genotyping density and reveals structural impacts on fungal resistance in melon. <i>Nature Communications</i> , 2022, 13, .	5.8	7
3401	Comparative and phylogenetic analysis based on chloroplast genome of <i>Heteroplexis</i> (Compositae), a protected rare genus. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	1
3402	Complete organellar genomes of six <i>Sargassum</i> species and development of species-specific markers. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
3403	A highly quality genome sequence of <i>Penicillium oxalicum</i> species isolated from the root of <i>Ixora chinensis</i> in Vietnam. <i>G3: Genes, Genomes, Genetics</i> , 2023, 13, .	0.8	1
3404	Whole Genome Sequencing-Based Tracing of a 2022 Introduction and Outbreak of <i>Xanthomonas hortorum</i> pv. <i>pelargonii</i> . <i>Phytopathology</i> , 2023, 113, 975-984.	1.1	4
3405	Jack of all trades: Genome assembly of Wild Jack and comparative genomics of <i>Artocarpus</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
3406	New <i>Wolbachia pipientis</i> Genotype Increasing Heat Stress Resistance of <i>Drosophila melanogaster</i> Host Is Characterized by a Large Chromosomal Inversion. <i>International Journal of Molecular Sciences</i> , 2022, 23, 16212.	1.8	2
3407	Plastid phylogenomics uncovers multiple species in <i>Medicago truncatula</i> (Fabaceae) germplasm accessions. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
3408	Nanopore/Illumina Hybrid Whole-genome Sequence Resource of <i>Plenodomus lindquistii</i> Strain US01 Infecting Sunflower. <i>Plant Disease</i> , 0, , .	0.7	0
3409	Global Phylogeny and F Virulence Plasmid Carriage in Pandemic <i>Escherichia coli</i> ST1193. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	11
3410	Recombination Drives Evolution of Carbapenem-Resistant <i>Klebsiella pneumoniae</i> Sequence Type 11 KL47 to KL64 in China. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	3
3411	Whole genome sequencing and functional analysis of porcine-borne <i>Bacillus coagulans</i> LYBC06. <i>Biotechnology and Biotechnological Equipment</i> , 2023, 37, 79-91.	0.5	0
3412	Novel integrative elements and genomic plasticity in ocean ecosystems. <i>Cell</i> , 2023, 186, 47-62.e16.	13.5	25
3413	Systematic identification of gene-altering programmed inversions across the bacterial domain. <i>Nucleic Acids Research</i> , 2023, 51, 553-573.	6.5	5
3414	Insights into chloroplast genome structure, intraspecific variation, and phylogeny of <i>Cyclamen</i> species (Myrsinoideae). <i>Scientific Reports</i> , 2023, 13, .	1.6	2
3415	Biological and Genomic Characteristics of MaMV-DH01, a Novel Freshwater <i>Myoviridae</i> Cyanophage Strain. <i>Microbiology Spectrum</i> , 0, , .	1.2	0

#	ARTICLE	IF	CITATIONS
3416	Natural Recombination among Type I Restriction-Modification Systems Creates Diverse Genomic Methylation Patterns among <i>Xylella fastidiosa</i> Strains. <i>Applied and Environmental Microbiology</i> , 2023, 89, .	1.4	1
3418	Postglacial adaptations enabled colonization and quasi-clonal dispersal of ammonia-oxidizing archaea in modern European large lakes. <i>Science Advances</i> , 2023, 9, .	4.7	12
3419	Strain-specific alterations in gut microbiome and host immune responses elicited by tolerogenic <i>Bifidobacterium pseudolongum</i> . <i>Scientific Reports</i> , 2023, 13, .	1.6	8
3420	Genomic Analysis and In Vitro Investigation of the Hop Resistance Phenotype of Two Novel <i>Loigolactobacillus backii</i> Strains, Isolated from Spoiled Beer. <i>Microorganisms</i> , 2023, 11, 280.	1.6	2
3421	Genomic Diversity among <i>Actinomyces naeslundii</i> Strains and Closely Related Species. <i>Microorganisms</i> , 2023, 11, 254.	1.6	1
3422	Characterization and comprehensive genome analysis of novel bacteriophage, vB_Kpn_ZCKp20p, with lytic and anti-biofilm potential against clinical multidrug-resistant <i>Klebsiella pneumoniae</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 13, .	1.8	7
3423	PlantTribes2: Tools for comparative gene family analysis in plant genomics. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	5
3424	Comparative genomic and functional annotation of <i>Pseudomonas</i> spp. genomes responsible for blue discoloration of Brazilian fresh soft cheese. <i>International Dairy Journal</i> , 2023, 140, 105605.	1.5	1
3426	Evolutionary Patterns of the Chloroplast Genome in Vanilloid Orchids (Vanilloideae, Orchidaceae). <i>International Journal of Molecular Sciences</i> , 2023, 24, 3808.	1.8	2
3427	Emergence and clonal expansion of <i>Vibrio aestuarianus</i> lineages pathogenic for oysters in Europe. <i>Molecular Ecology</i> , 2023, 32, 2869-2883.	2.0	2
3428	Adaptive Radioresistance of Enterohemorrhagic <i>Escherichia coli</i> O157:H7 Results in Genomic Loss of Shiga Toxin-Encoding Prophages. <i>Applied and Environmental Microbiology</i> , 0, , .	1.4	0
3430	Genomic Analysis of Vancomycin-Resistant <i>Staphylococcus aureus</i> Isolates from the 3rd Case Identified in the United States Reveals Chromosomal Integration of the <i>vanA</i> Locus. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	2
3431	Whole-genome sequencing of a biocontrol <i>Myxococcus xanthus</i> R31 isolate and comparative genomic analysis. <i>Gene</i> , 2023, 863, 147286.	1.0	5
3432	Seven newly sequenced chloroplast genomes from the order Watanabeales (Trebouxiophyceae,) Tj ETQq1 1 0.784314 rgBT /Qverlock 11	1.0	4
3433	Woronichinia naegeliana: A common nontoxigenic component of temperate freshwater cyanobacterial blooms with 30% of its genome in transposons. <i>Harmful Algae</i> , 2023, 125, 102433.	2.2	2
3434	Exploration of urease-mediated biomineralization for defluoridation by <i>Proteus columbae</i> MLN9 with an emphasis on its genomic characterization. <i>Journal of Environmental Chemical Engineering</i> , 2023, 11, 109791.	3.3	2
3435	WGS analysis of two <i>Staphylococcus aureus</i> bacteriophages from sewage in China provides insights into the genetic feature of highly efficient lytic phages. <i>Microbiological Research</i> , 2023, 271, 127369.	2.5	4
3436	Comparative Genome-Wide Analysis of Two <i>Caryopteris x Clandonensis</i> Cultivars: Insights on the Biosynthesis of Volatile Terpenoids. <i>Plants</i> , 2023, 12, 632.	1.6	4

#	ARTICLE	IF	CITATIONS
3437	Boundaries That Prevent or May Lead Animals to be Reservoirs of Escherichia coli O104:H4. <i>Journal of Food Protection</i> , 2023, 86, 100053.	0.8	0
3438	Partial validation of a TaqMan quantitative polymerase chain reaction for the detection of the three genotypes of Infectious spleen and kidney necrosis virus. <i>PLoS ONE</i> , 2023, 18, e0281292.	1.1	0
3439	Supergroup F Wolbachia with extremely reduced genome: transition to obligate insect symbionts. <i>Microbiome</i> , 2023, 11, .	4.9	5
3440	Nisin E Is a Novel Nisin Variant Produced by Multiple <i>Streptococcus equinus</i> Strains. <i>Microorganisms</i> , 2023, 11, 427.	1.6	4
3442	High-Molecular-Weight Plasmids Carrying Carbapenemase Genes blaNDM-1, blaKPC-2, and blaOXA-48 Coexisting in Clinical <i>Klebsiella pneumoniae</i> Strains of ST39. <i>Microorganisms</i> , 2023, 11, 459.	1.6	3
3443	A Highly Effective Bacteriophage-1252 to Control Multiple Serovars of <i>Salmonella enterica</i> . <i>Foods</i> , 2023, 12, 797.	1.9	0
3444	Genomic insights into antibiotic resistance and mobilome of lactic acid bacteria and bifidobacteria. <i>Life Science Alliance</i> , 2023, 6, e202201637.	1.3	2
3445	Morphological and genomic characteristics of two novel actinomycetes, <i>Ornithinimicrobium sufpigmenti</i> sp. nov. and <i>Ornithinimicrobium faecis</i> sp. nov. isolated from bat faeces ( <i>Rousettus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock		
3446	Possible biased virulence attenuation in the Senegal strain of <i>Ehrlichia ruminantium</i> by ntrX gene conversion from an inverted segmental duplication. <i>PLoS ONE</i> , 2023, 18, e0266234.	1.1	1
3447	Evidence of structural rearrangements in ESBL-positive pESI(like) megaplasmids of <i>S. Infantis</i> . <i>FEMS Microbiology Letters</i> , 2023, 370, .	0.7	4
3448	Plastomes of <i>Garcinia mangostana</i> L. and Comparative Analysis with Other <i>Garcinia</i> Species. <i>Plants</i> , 2023, 12, 930.	1.6	4
3449	Characterization and Genomic Analysis of a Novel Lytic Phage DCp1 against <i>Clostridium perfringens</i> Biofilms. <i>International Journal of Molecular Sciences</i> , 2023, 24, 4191.	1.8	3
3450	Genomic Epidemiological Analysis of Antimicrobial-Resistant Bacteria with Nanopore Sequencing. <i>Methods in Molecular Biology</i> , 2023, , 227-246.	0.4	0
3451	The First Complete Chloroplast Genome Sequence of <i>Mortião</i> ( <i>Vaccinium floribundum</i> ) and Comparative Analyses with Other <i>Vaccinium</i> Species. <i>Horticulturae</i> , 2023, 9, 302.	1.2	3
3452	Genomic Comparative Analysis of Two Multi-Drug Resistance (MDR) <i>Acinetobacter baumannii</i> Clinical Strains Assigned to International Clonal Lineage II Recovered Pre- and Post-COVID-19 Pandemic. <i>Biology</i> , 2023, 12, 358.	1.3	2
3453	Draft genomes of three closely related low light-adapted <i>Prochlorococcus</i> . <i>BMC Genomic Data</i> , 2023, 24, .	0.7	1
3454	A comparative study across the parasitic plants of <i>Cuscuta</i> subgenus <i>Grammica</i> ( <i>Convolvulaceae</i> ) reveals a possible loss of the plastid genome in its section <i>Subulatae</i> . <i>Planta</i> , 2023, 257, .	1.6	1
3456	Genomic Analysis of Two Novel Bacteriophages Infecting <i>Acinetobacter beijerinckii</i> and <i>halotolerans</i> Species. <i>Viruses</i> , 2023, 15, 643.	1.5	0

#	ARTICLE	IF	CITATIONS
3457	Bioinformatic survey of CRISPR loci across 15 <i>Serratia</i> species. <i>MicrobiologyOpen</i> , 2023, 12, .	1.2	0
3458	Isolation and characterization of a novel <i>Tenacibaculum</i> species and a corresponding bacteriophage from a Mediterranean fish hatchery: Description of <i>Tenacibaculum larymnensis</i> sp. nov. and <i>Tenacibaculum</i> phage Larrie. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
3459	Spontaneous Genomic Variation as a Survival Strategy of Nosocomial <i>Staphylococcus haemolyticus</i> . <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	1
3460	Genomics Insight into cfr-Mediated Linezolid-Resistant LA-MRSA in Italian Pig Holdings. <i>Antibiotics</i> , 2023, 12, 530.	1.5	1
3461	Plastome variations reveal the distinct evolutionary scenarios of plastomes in the subfamily Cereoideae (Cactaceae). <i>BMC Plant Biology</i> , 2023, 23, .	1.6	6
3462	Multiple domestication events explain the origin of <i>Gossypium hirsutum</i> landraces in Mexico. <i>Ecology and Evolution</i> , 2023, 13, .	0.8	2
3467	Parallel evolution of fish bi-modal breathing and expansion of olfactory receptor (OR) genes: toward a universal ORs nomenclature. <i>Journal of Genetics and Genomics</i> , 2023, 50, 600-610.	1.7	2
3468	Complete chloroplast genome sequences of Myristicaceae species with the comparative chloroplast genomics and phylogenetic relationships among them. <i>PLoS ONE</i> , 2023, 18, e0281042.	1.1	2
3469	Elucidating the genomic history of commercially used <i>Bacillus thuringiensis</i> subsp. <i>tenebrionis</i> strain NB176. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 13, .	1.8	1
3471	Isolation and characterization of bioactive metabolites of <i>Bacillus enclensis</i> CARE-V7 strain from southeast coast of India. <i>Biomass Conversion and Biorefinery</i> , 0, , .	2.9	0
3473	Whole-genome sequencing analysis of two heat-evolved <i>Escherichia coli</i> strains. <i>BMC Genomics</i> , 2023, 24, .	1.2	1
3475	Whole-mitochondrial genomes of <i>Nannizziopsis</i> provide insights in evolution and detection. <i>Ecology and Evolution</i> , 2023, 13, .	0.8	1
3476	Analysis of the Genomics and Mouse Virulence of an Emergent Clone of <i>Streptococcus dysgalactiae</i> Subspecies <i>equisimilis</i> . <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	3
3477	Assembling highly repetitive <i>Xanthomonas</i> TALomes using Oxford Nanopore sequencing. <i>BMC Genomics</i> , 2023, 24, .	1.2	3
3478	High level of novelty under the hood of convergent evolution. <i>Science</i> , 2023, 379, 1043-1049.	6.0	17
3479	Temperate bacteriophages infecting the mucin-degrading bacterium <i>Ruminococcus gnavus</i> from the human gut. <i>Gut Microbes</i> , 2023, 15, .	4.3	2
3480	Comparative Genomic Analysis and Rapid Molecular Detection of <i>Xanthomonas euvesicatoria</i> Using Unique ATP-Dependent DNA Helicase <i>recQ</i> , <i>hrpB1</i> , and <i>hrpB2</i> Genes Isolated from <i>Physalis pubescens</i> in China. <i>Plant Pathology Journal</i> , 2023, 39, 191-206.	0.7	0
3481	Effective Treatment of <i>Staphylococcus aureus</i> Intramammary Infection in a Murine Model Using the Bacteriophage Cocktail StaphLyse. <i>Viruses</i> , 2023, 15, 887.	1.5	6

#	ARTICLE	IF	CITATIONS
3482	Genomic Relationships of <i>Glycine remota</i> , a Recently Discovered Perennial Relative of Soybean, within <i>Glycine</i> . <i>Systematic Botany</i> , 2023, 48, 78-87.	0.2	4
3484	Isolation, screening and characterization of phage. <i>Progress in Molecular Biology and Translational Science</i> , 2023, , 13-60.	0.9	0
3485	High incidence of carbapenemase-producing <i>Pseudomonas aeruginosa</i> clinical isolates from Lagos, Nigeria. <i>JAC-Antimicrobial Resistance</i> , 2023, 5, .	0.9	3
3486	A conserved hymenopteran-specific family of cytochrome P450s protects bee pollinators from toxic nectar alkaloids. <i>Science Advances</i> , 2023, 9, .	4.7	4
3487	Genome Organization of Four Brazilian <i>Xanthomonas albilineans</i> Strains Does Not Correlate with Aggressiveness. <i>Microbiology Spectrum</i> , 0, , .	1.2	1
3488	Comparative Chloroplast Genome Analysis of Chinese Lacquer Tree ( <i>Toxicodendron vernicifluum</i> ,) Tj ETQq1 1 0.784314 rgBT <sub>1</sub> /Overlock 10 Tf	0.9	1
3489	Novel insights into chloroplast genome evolution in the green macroalgal genus <i>Ulva</i> (Ulvophyceae,) Tj ETQq0 0 0 rgBT <sub>1</sub> /Overlock 10 Tf	1.7	3
3490	Comparative genomic insights into habitat adaptation of coral-associated <i>Prosthecochloris</i> . <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
3503	Phylogenetic Analysis of Bacterial Pathogen Genomes. <i>Methods in Molecular Biology</i> , 2023, , 87-99.	0.4	0
3605	Bacteriophage Taxonomy: A Continually Evolving Discipline. <i>Methods in Molecular Biology</i> , 2024, , 27-45.	0.4	0