

Mauve: Multiple Alignment of Conserved Genomic Sequences

Genome Research

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Citation Report

#	ARTICLE	IF	CITATIONS
1	A novel method for multiple alignment of sequences with repeated and shuffled elements. <i>Genome Research</i> , 2004, 14, 2336-2346.	5.5	106
2	Multiple alignment of rearranged genomes. , 0, , .		4
3	Identifying Evolutionarily Conserved Segments Among Multiple Divergent and Rearranged Genomes. <i>Lecture Notes in Computer Science</i> , 2005, , 72-84.	1.3	1
4	Genomics of enterobacteriaceae. , 2005, , .		0
5	Systematic determination of the mosaic structure of bacterial genomes: species backbone versus strain-specific loops. <i>BMC Bioinformatics</i> , 2005, 6, 171.	2.6	46
6	GATA: a graphic alignment tool for comparative sequence analysis. <i>BMC Bioinformatics</i> , 2005, 6, 9.	2.6	70
7	Current Awareness on Comparative and Functional Genomics. <i>Comparative and Functional Genomics</i> , 2005, 6, 97-112.	2.0	0
8	DNA Sequence and Comparative Genomics of pAPEC-O2-R, an Avian Pathogenic <i>Escherichia coli</i> Transmissible R Plasmid. <i>Antimicrobial Agents and Chemotherapy</i> , 2005, 49, 4681-4688.	3.2	94
9	Swine and Poultry Pathogens: the Complete Genome Sequences of Two Strains of <i>Mycoplasma hyopneumoniae</i> and a Strain of <i>Mycoplasma synoviae</i> . <i>Journal of Bacteriology</i> , 2005, 187, 5568-5577.	2.2	289
10	A Fast Algorithm Aligning Multiple Microbial Genomic Sequences. , 2005, 2006, 240-3.		0
11	ROBIN: a tool for genome rearrangement of block-interchanges. <i>Bioinformatics</i> , 2005, 21, 2780-2782.	4.1	12
12	Databases and software for the comparison of prokaryotic genomes. <i>Microbiology (United Kingdom)</i> , 2005, 151, 2125-2132.	1.8	29
13	Genome-wide detection and analysis of homologous recombination among sequenced strains of <i>Escherichia coli</i> . <i>Genome Biology</i> , 2006, 7, R44.	9.6	63
14	Multiple sequence alignment for phylogenetic purposes. <i>Australian Systematic Botany</i> , 2006, 19, 479.	0.9	131
15	Understanding Microbial Metabolism. <i>Annual Review of Microbiology</i> , 2006, 60, 533-559.	7.3	48
16	GenomeDiagram: a python package for the visualization of large-scale genomic data. <i>Bioinformatics</i> , 2006, 22, 616-617.	4.1	83
17	Complete sequence of the large virulence plasmid pSFO157 of the sorbitol-fermenting enterohemorrhagic <i>Escherichia coli</i> O157:H α strain 3072/96. <i>International Journal of Medical Microbiology</i> , 2006, 296, 467-474.	3.6	56
18	Selection for Chromosome Architecture in Bacteria. <i>Journal of Molecular Evolution</i> , 2006, 62, 615-629.	1.8	80

#	ARTICLE	IF	CITATIONS
19	M-GCAT: interactively and efficiently constructing large-scale multiple genome comparison frameworks in closely related species. BMC Bioinformatics, 2006, 7, 433.	2.6	78
20	inGeno “an integrated genome and ortholog viewer for improved genome to genome comparisons. BMC Bioinformatics, 2006, 7, 461.	2.6	8
21	ASAP: a resource for annotating, curating, comparing, and disseminating genomic data. Nucleic Acids Research, 2006, 34, D41-D45.	14.5	56
22	SPRING: a tool for the analysis of genome rearrangement using reversals and block-interchanges. Nucleic Acids Research, 2006, 34, W696-W699.	14.5	22
23	The Evolutionary Origin of Xanthomonadales Genomes and the Nature of the Horizontal Gene Transfer Process. Molecular Biology and Evolution, 2006, 23, 2049-2057.	8.9	44
24	Evolution at the nucleotide level: the problem of multiple whole-genome alignment. Human Molecular Genetics, 2006, 15, R51-R56.	2.9	51
25	An Integrative Method for Accurate Comparative Genome Mapping. PLoS Computational Biology, 2006, 2, e75.	3.2	25
26	COMPAM :visualization of combining pairwise alignments for multiple genomes. Bioinformatics, 2006, 22, 242-244.	4.1	7
27	A bimodal pattern of relatedness between the Salmonella Paratyphi A and Typhi genomes: Convergence or divergence by homologous recombination?. Genome Research, 2006, 17, 61-68.	5.5	112
28	A novel strategy for the identification of genomic islands by comparative analysis of the contents and contexts of tRNA sites in closely related bacteria. Nucleic Acids Research, 2006, 34, e3-e3.	14.5	67
29	Exposing Phylogenetic Relationships by Genome Rearrangement. Advances in Computers, 2006, , 1-57.	1.6	2
30	Computation and Analysis of Genomic Multi-Sequence Alignments. Annual Review of Genomics and Human Genetics, 2007, 8, 193-213.	6.2	30
31	Inference of Bacterial Microevolution Using Multilocus Sequence Data. Genetics, 2007, 175, 1251-1266.	2.9	616
32	MobilomeFINDER: web-based tools for in silico and experimental discovery of bacterial genomic islands. Nucleic Acids Research, 2007, 35, W97-W104.	14.5	74
33	Enteropathogen Resource Integration Center (ERIC): bioinformatics support for research on biodefense-relevant enterobacteria. Nucleic Acids Research, 2007, 36, D519-D523.	14.5	14
34	Genome Analyses of Three Strains of Rhodobacter sphaeroides : Evidence of Rapid Evolution of Chromosome II. Journal of Bacteriology, 2007, 189, 1914-1921.	2.2	81
35	Los Alamos Hepatitis C Virus Sequence and Human Immunology Databases: An Expanding Resource for Antiviral Research. Antiviral Chemistry and Chemotherapy, 2007, 18, 113-123.	0.6	10
36	National Institute of Allergy and Infectious Diseases Bioinformatics Resource Centers: New Assets for Pathogen Informatics. Infection and Immunity, 2007, 75, 3212-3219.	2.2	50

#	ARTICLE	IF	CITATIONS
37	Analyzing Patterns of Microbial Evolution Using the Mauve Genome Alignment System. <i>Methods in Molecular Biology</i> , 2007, 396, 135-152.	0.9	51
38	Living in a changing environment: Insights into host adaptation in <i>Neisseria meningitidis</i> from comparative genomics. <i>International Journal of Medical Microbiology</i> , 2007, 297, 601-613.	3.6	21
39	Analysis of invariant sequences in 266 complete genomes. <i>Gene</i> , 2007, 401, 172-180.	2.2	10
40	Genetic flux over time in the <i>Salmonella</i> lineage. <i>Genome Biology</i> , 2007, 8, R100.	9.6	71
41	Phylogenetic exploration of bacterial genomic rearrangements. <i>Bioinformatics</i> , 2007, 23, 1172-1174.	4.1	7
42	Evaluating Two Visualization Techniques for Genome Comparison. <i>Proceedings / International Conference on Information Visualisation</i> , 2007, , .	0.0	5
43	<i>Yersinia pestis</i> Evolution on a Small Timescale: Comparison of Whole Genome Sequences from North America. <i>PLoS ONE</i> , 2007, 2, e770.	2.5	34
44	Canonical Insertion-Deletion Markers for Rapid DNA Typing of <i>Francisella tularensis</i> . <i>Emerging Infectious Diseases</i> , 2007, 13, 1725-1732.	4.3	45
45	Mining the genomes of plant pathogenic bacteria: how not to drown in gigabases of sequence. <i>Molecular Plant Pathology</i> , 2007, 9, 071031023555001-???	4.2	2
46	Multiple non-collinear TF-map alignments of promoter regions. <i>BMC Bioinformatics</i> , 2007, 8, 138.	2.6	10
47	Genomorama: genome visualization and analysis. <i>BMC Bioinformatics</i> , 2007, 8, 204.	2.6	9
48	Rapid evolutionary change of common bean (<i>Phaseolus vulgaris</i> L) plastome, and the genomic diversification of legume chloroplasts. <i>BMC Genomics</i> , 2007, 8, 228.	2.8	95
49	Subtle genetic changes enhance virulence of methicillin resistant and sensitive <i>Staphylococcus aureus</i> . <i>BMC Microbiology</i> , 2007, 7, 99.	3.3	227
50	The genome of ϕ 15, a serotype-converting, Group E1 <i>Salmonella enterica</i> -specific bacteriophage. <i>Virology</i> , 2007, 369, 234-244.	2.4	60
51	Molecular Epidemiology, Evolution, and Ecology of <i>Francisella</i> . <i>Annals of the New York Academy of Sciences</i> , 2007, 1105, 30-66.	3.8	331
52	Chloroplast genomes of the diatoms <i>Phaeodactylum tricornutum</i> and <i>Thalassiosira pseudonana</i> : comparison with other plastid genomes of the red lineage. <i>Molecular Genetics and Genomics</i> , 2007, 277, 427-439.	2.1	184
53	Addressing chromosome evolution in the whole-genome sequence era. <i>Chromosome Research</i> , 2008, 16, 5-16.	2.2	13
54	Extensive Reorganization of the Plastid Genome of <i>Trifolium subterraneum</i> (Fabaceae) Is Associated with Numerous Repeated Sequences and Novel DNA Insertions. <i>Journal of Molecular Evolution</i> , 2008, 67, 696-704.	1.8	217

#	ARTICLE	IF	CITATIONS
55	Comparison of complete sequences of potato rough dwarf virus and potato virus P and their relationships to other carlaviruses. Archives of Virology, 2008, 153, 1787-1789.	2.1	6
56	The genome of Streptomyces rimosus subsp. rimosus shows a novel structure compared to other Streptomyces using DNA/DNA microarray analysis. Antonie Van Leeuwenhoek, 2008, 94, 173-186.	1.7	7
57	A small trip in the untranquil world of genomes. Theoretical Computer Science, 2008, 395, 171-192.	0.9	4
58	Hindsight in the relative abundance, metabolic potential and genome dynamics of uncultivated marine archaea from comparative metagenomic analyses of bathypelagic plankton of different oceanic regions. ISME Journal, 2008, 2, 865-886.	9.8	113
59	The CACTA transposon <i>Bot1</i> played a major role in <i>Brassica</i> genome divergence and gene proliferation. Plant Journal, 2008, 56, 1030-1044.	5.7	75
60	SeqAn An efficient, generic C++ library for sequence analysis. BMC Bioinformatics, 2008, 9, 11.	2.6	287
61	Efficient computation of absent words in genomic sequences. BMC Bioinformatics, 2008, 9, 167.	2.6	62
62	PSAT: A web tool to compare genomic neighborhoods of multiple prokaryotic genomes. BMC Bioinformatics, 2008, 9, 170.	2.6	30
63	Precise detection of rearrangement breakpoints in mammalian chromosomes. BMC Bioinformatics, 2008, 9, 286.	2.6	36
64	Evaluation of genomic island predictors using a comparative genomics approach. BMC Bioinformatics, 2008, 9, 329.	2.6	255
65	MOSAIC: an online database dedicated to the comparative genomics of bacterial strains at the intra-species level. BMC Bioinformatics, 2008, 9, 498.	2.6	19
66	Genome classification by gene distribution: An overlapping subspace clustering approach. BMC Evolutionary Biology, 2008, 8, 116.	3.2	10
67	Comparative genomics-based investigation of resequencing targets in Vibrio fischeri: Focus on point miscalls and artefactual expansions. BMC Genomics, 2008, 9, 138.	2.8	72
68	Genome sequence and rapid evolution of the rice pathogen Xanthomonas oryzae pv. oryzae PXO99A. BMC Genomics, 2008, 9, 204.	2.8	327
69	Multiple genome alignment for identifying the core structure among moderately related microbial genomes. BMC Genomics, 2008, 9, 515.	2.8	25
70	Analysis of the genetic variation in Mycobacterium tuberculosis strains by multiple genome alignments. BMC Research Notes, 2008, 1, 110.	1.4	34
71	Extending the Bacillus cereus group genomics to putative food-borne pathogens of different toxicity. Chemico-Biological Interactions, 2008, 171, 236-249.	4.0	140
72	The genome and proteome of the Kluysvera bacteriophage Kvp1 â€” another member of the T7-like Autographivirinae. Virology Journal, 2008, 5, 122.	3.4	12

#	ARTICLE	IF	CITATIONS
73	Tools for simulating evolution of aligned genomic regions with integrated parameter estimation. <i>Genome Biology</i> , 2008, 9, R147.	9.6	20
74	Role of Recombination in the Evolution of the Model Plant Pathogen <i>Pseudomonas syringae</i> pv. tomato DC3000, a Very Atypical Tomato Strain. <i>Applied and Environmental Microbiology</i> , 2008, 74, 3171-3181.	3.1	89
75	Similar ectopic gene conversion frequencies in the backbone genome of pathogenic and nonpathogenic <i>Escherichia coli</i> strains. <i>Genomics</i> , 2008, 92, 168-172.	2.9	3
76	Genomic Comparison of Virulent <i>Rickettsia rickettsii</i> Sheila Smith and Avirulent <i>Rickettsia rickettsii</i> Iowa. <i>Infection and Immunity</i> , 2008, 76, 542-550.	2.2	108
77	Whole-genome comparison of disease and carriage strains provides insights into virulence evolution in <i>Neisseria meningitidis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 3473-3478.	7.1	159
78	Evolution of the <i>iss</i> Gene in <i>Escherichia coli</i> . <i>Applied and Environmental Microbiology</i> , 2008, 74, 2360-2369.	3.1	131
79	Space Efficient Computation of Rare Maximal Exact Matches between Multiple Sequences. <i>Journal of Computational Biology</i> , 2008, 15, 357-377.	1.6	12
80	Whole-Genome Pyrosequencing of an Epidemic Multidrug-Resistant <i>Acinetobacter baumannii</i> Strain Belonging to the European Clone II Group. <i>Antimicrobial Agents and Chemotherapy</i> , 2008, 52, 2616-2625.	3.2	240
81	Dynamics of Genome Rearrangement in Bacterial Populations. <i>PLoS Genetics</i> , 2008, 4, e1000128.	3.5	216
82	Recent developments in the MAFFT multiple sequence alignment program. <i>Briefings in Bioinformatics</i> , 2008, 9, 286-298.	6.5	3,115
83	Inferring genomic flux in bacteria. <i>Genome Research</i> , 2009, 19, 306-317.	5.5	35
84	Newly introduced genomic prophage islands are critical determinants of in vivo competitiveness in the Liverpool Epidemic Strain of <i>Pseudomonas aeruginosa</i> . <i>Genome Research</i> , 2009, 19, 12-23.	5.5	317
85	Genome-wide nucleotide-level mammalian ancestor reconstruction. <i>Genome Research</i> , 2008, 18, 1829-1843.	5.5	164
86	The Complete Genome Sequence of <i>Escherichia coli</i> DH10B: Insights into the Biology of a Laboratory Workhorse. <i>Journal of Bacteriology</i> , 2008, 190, 2597-2606.	2.2	331
87	VisCHAINER: Visualizing Genome Comparison. , 2008, , .		0
88	Niche-Specificity and the Variable Fraction of the <i>Pectobacterium</i> Pan-Genome. <i>Molecular Plant-Microbe Interactions</i> , 2008, 21, 1549-1560.	2.6	93
89	CoCoNUT: an efficient system for the comparison and analysis of genomes. <i>BMC Bioinformatics</i> , 2008, 9, 476.	2.6	23
90	<i>Rickettsia</i> Phylogenomics: Unwinding the Intricacies of Obligate Intracellular Life. <i>PLoS ONE</i> , 2008, 3, e2018.	2.5	175

#	ARTICLE	IF	CITATIONS
91	Assessing the Quality of Whole Genome Alignments in Bacteria. <i>Advances in Bioinformatics</i> , 2009, 2009, 1-8.	5.7	4
92	Tracing the Evolution of Competence in <i>Haemophilus influenzae</i> . <i>PLoS ONE</i> , 2009, 4, e5854.	2.5	25
93	The NlpD Lipoprotein Is a Novel <i>Yersinia pestis</i> Virulence Factor Essential for the Development of Plague. <i>PLoS ONE</i> , 2009, 4, e7023.	2.5	79
94	Genome Sequence of the Endosymbiont <i>Rickettsia peacockii</i> and Comparison with Virulent <i>Rickettsia rickettsii</i> : Identification of Virulence Factors. <i>PLoS ONE</i> , 2009, 4, e8361.	2.5	113
95	Genome Sequence of <i>Aggregatibacter actinomycetemcomitans</i> Serotype c Strain D11S-1. <i>Journal of Bacteriology</i> , 2009, 191, 7378-7379.	2.2	34
96	A Genomic Distance Based on MUM Indicates Discontinuity between Most Bacterial Species and Genera. <i>Journal of Bacteriology</i> , 2009, 191, 91-99.	2.2	145
97	Comparative Genomics Reveal Extensive Transposon-Mediated Genomic Plasticity and Diversity among Potential Effector Proteins within the Genus <i>Coxiella</i> . <i>Infection and Immunity</i> , 2009, 77, 642-656.	2.2	197
98	<i>Pseudomonas</i> Genome Database: facilitating user-friendly, comprehensive comparisons of microbial genomes. <i>Nucleic Acids Research</i> , 2009, 37, D483-D488.	14.5	220
99	Reordering contigs of draft genomes using the Mauve Aligner. <i>Bioinformatics</i> , 2009, 25, 2071-2073.	4.1	532
100	In Silico Prediction of Horizontal Gene Transfer Events in <i>Lactobacillus bulgaricus</i> and <i>Streptococcus thermophilus</i> Reveals Protocooperation in Yogurt Manufacturing. <i>Applied and Environmental Microbiology</i> , 2009, 75, 4120-4129.	3.1	88
101	Directed Evolution of Ionizing Radiation Resistance in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2009, 191, 5240-5252.	2.2	131
102	Molecular Evolutionary Consequences of Niche Restriction in <i>Francisella tularensis</i> , a Facultative Intracellular Pathogen. <i>PLoS Pathogens</i> , 2009, 5, e1000472.	4.7	127
103	Organised Genome Dynamics in the <i>Escherichia coli</i> Species Results in Highly Diverse Adaptive Paths. <i>PLoS Genetics</i> , 2009, 5, e1000344.	3.5	1,005
104	Comparative Genomic Characterization of <i>Francisella tularensis</i> Strains Belonging to Low and High Virulence Subspecies. <i>PLoS Pathogens</i> , 2009, 5, e1000459.	4.7	112
105	Comparative ICE Genomics: Insights into the Evolution of the SXT/R391 Family of ICEs. <i>PLoS Genetics</i> , 2009, 5, e1000786.	3.5	247
106	Draft Genome Sequences of <i>Yersinia pestis</i> Isolates from Natural Foci of Endemic Plague in China. <i>Journal of Bacteriology</i> , 2009, 191, 7628-7629.	2.2	16
107	GR-Aligner: an algorithm for aligning pairwise genomic sequences containing rearrangement events. <i>Bioinformatics</i> , 2009, 25, 2188-2193.	4.1	4
108	Seevolution: visualizing chromosome evolution. <i>Bioinformatics</i> , 2009, 25, 960-961.	4.1	5

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109	ABWGAT: anchor-based whole genome analysis tool. <i>Bioinformatics</i> , 2009, 25, 3319-3320.	4.1	2
110	Complete Genome of the Broad-Host-Range <i>Erwinia amylovora</i> Phage ϕ Ea21-4 and Its Relationship to <i>Salmonella</i> Phage Felix O1. <i>Applied and Environmental Microbiology</i> , 2009, 75, 2139-2147.	3.1	61
111	Analysis of Ten <i>Brucella</i> Genomes Reveals Evidence for Horizontal Gene Transfer Despite a Preferred Intracellular Lifestyle. <i>Journal of Bacteriology</i> , 2009, 191, 3569-3579.	2.2	103
112	Multiple whole-genome alignments without a reference organism. <i>Genome Research</i> , 2009, 19, 682-689.	5.5	63
113	CSA: An efficient algorithm to improve circular DNA multiple alignment. <i>BMC Bioinformatics</i> , 2009, 10, 230.	2.6	37
114	Context-driven discovery of gene cassettes in mobile integrons using a computational grammar. <i>BMC Bioinformatics</i> , 2009, 10, 281.	2.6	17
115	CASSIOPE: An expert system for conserved regions searches. <i>BMC Bioinformatics</i> , 2009, 10, 284.	2.6	9
116	Maximum independent sets of commuting and noninterfering inversions. <i>BMC Bioinformatics</i> , 2009, 10, S6.	2.6	7
117	Co-evolution of genomes and plasmids within <i>Chlamydia trachomatis</i> and the emergence in Sweden of a new variant strain. <i>BMC Genomics</i> , 2009, 10, 239.	2.8	119
118	Comparative genomic analyses of <i>Streptococcus mutans</i> provide insights into chromosomal shuffling and species-specific content. <i>BMC Genomics</i> , 2009, 10, 358.	2.8	72
119	Insertion sequence content reflects genome plasticity in strains of the root nodule actinobacterium <i>Frankia</i> . <i>BMC Genomics</i> , 2009, 10, 468.	2.8	34
120	Comparative analysis of two <i>Neisseria gonorrhoeae</i> genome sequences reveals evidence of mobilization of <i>Correia Repeat Enclosed Elements</i> and their role in regulation. <i>BMC Genomics</i> , 2009, 10, 70.	2.8	29
121	Contributions to selected phenotypic characteristics of large species- and lineage-specific genomic regions in <i>Listeria monocytogenes</i> . <i>Food Microbiology</i> , 2009, 26, 212-223.	4.2	22
122	A framework for phylogenetic sequence alignment. <i>Plant Systematics and Evolution</i> , 2009, 282, 127-149.	0.9	45
123	Plasmids captured in <i>C. metallidurans</i> CH34: defining the PromA family of broad-host-range plasmids. <i>Antonie Van Leeuwenhoek</i> , 2009, 96, 193-204.	1.7	67
124	Computational Biology Methods and Their Application to the Comparative Genomics of Endocellular Symbiotic Bacteria of Insects. <i>Biological Procedures Online</i> , 2009, 11, 52-78.	2.9	6
125	GO4genome: A Prokaryotic Phylogeny Based on Genome Organization. <i>Journal of Molecular Evolution</i> , 2009, 68, 550-562.	1.8	4
126	Comparative genomics-guided loop-mediated isothermal amplification for characterization of <i>Pseudomonas syringae</i> pv. <i>phaseolicola</i> . <i>Journal of Applied Microbiology</i> , 2009, 107, 717-726.	3.1	13

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127	A single regulatory gene is sufficient to alter bacterial host range. <i>Nature</i> , 2009, 458, 215-218.	27.8	177
128	Genomic analysis of multiple Roseophage SIO1 strains. <i>Environmental Microbiology</i> , 2009, 11, 2863-2873.	3.8	64
129	Comparative analysis of the widespread and conserved PBl ϕ -like viruses infecting <i>Pseudomonas aeruginosa</i> . <i>Environmental Microbiology</i> , 2009, 11, 2874-2883.	3.8	85
130	Genome analysis of <i>Bacillus amyloliquefaciens</i> FZB42 reveals its potential for biocontrol of plant pathogens. <i>Journal of Biotechnology</i> , 2009, 140, 27-37.	3.8	372
131	Comparative studies of <i>Campylobacter jejuni</i> genomic diversity reveal the importance of core and dispensable genes in the biology of this enigmatic food-borne pathogen. <i>Current Opinion in Biotechnology</i> , 2009, 20, 158-165.	6.6	19
132	Genome flexibility in <i>Neisseria meningitidis</i> . <i>Vaccine</i> , 2009, 27, B103-B111.	3.8	47
133	The genome and proteome of a virulent <i>Escherichia coli</i> O157:H7 bacteriophage closely resembling <i>Salmonella</i> phage Felix O1. <i>Virology Journal</i> , 2009, 6, 41.	3.4	34
134	<i>Brucella</i> . , 2009, , 1-64.		5
135	Cytogenetics and Molecular Data in Snakes: A Phylogenetic Approach. <i>Cytogenetic and Genome Research</i> , 2009, 127, 128-142.	1.1	43
136	Decoding Synteny Blocks and Large-Scale Duplications in Mammalian and Plant Genomes. <i>Lecture Notes in Computer Science</i> , 2009, , 220-232.	1.3	9
137	A Novel Heuristic for Local Multiple Alignment of Interspersed DNA Repeats. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2009, 6, 180-189.	3.0	14
138	MizBee: A Multiscale Synteny Browser. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2009, 15, 897-904.	4.4	127
139	3D Genome Tuner: Compare Multiple Circular Genomes in a 3D Context. <i>Genomics, Proteomics and Bioinformatics</i> , 2009, 7, 143-146.	6.9	1
140	Multiple Alignment of DNA Sequences with MAFFT. <i>Methods in Molecular Biology</i> , 2009, 537, 39-64.	0.9	1,145
141	Genomic Sequencing Reveals Regulatory Mutations and Recombinational Events in the Widely Used MC4100 Lineage of <i>Escherichia coli</i> K-12. <i>Journal of Bacteriology</i> , 2009, 191, 4025-4029.	2.2	98
142	Chromosomal diversity in <i>Lactococcus lactis</i> and the origin of dairy starter cultures. <i>Genome Biology and Evolution</i> , 2010, 2, 729-44.	2.5	90
143	The Sequence of a 1.8-Mb Bacterial Linear Plasmid Reveals a Rich Evolutionary Reservoir of Secondary Metabolic Pathways. <i>Genome Biology and Evolution</i> , 2010, 2, 212-224.	2.5	193
145	Complete Genome Sequence of the Fire Blight Pathogen <i>Erwinia amylovora</i> CFBP 1430 and Comparison to Other <i>Erwinia</i> spp.. <i>Molecular Plant-Microbe Interactions</i> , 2010, 23, 384-393.	2.6	156

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147	Comparative genomics of green sulfur bacteria. <i>Photosynthesis Research</i> , 2010, 104, 137-152.	2.9	12
148	Comparative genomics of pAKD4, the prototype IncP-1 ϕ plasmid with a complete backbone. <i>Plasmid</i> , 2010, 63, 98-107.	1.4	20
149	Improving de novo sequence assembly using machine learning and comparative genomics for overlap correction. <i>BMC Bioinformatics</i> , 2010, 11, 33.	2.6	16
150	MS4 - Multi-Scale Selector of Sequence Signatures: An alignment-free method for classification of biological sequences. <i>BMC Bioinformatics</i> , 2010, 11, 406.	2.6	8
151	Automatic detection of anchor points for multiple sequence alignment. <i>BMC Bioinformatics</i> , 2010, 11, 445.	2.6	6
152	Pan-genome sequence analysis using Panseq: an online tool for the rapid analysis of core and accessory genomic regions. <i>BMC Bioinformatics</i> , 2010, 11, 461.	2.6	249
153	BIGSdb: Scalable analysis of bacterial genome variation at the population level. <i>BMC Bioinformatics</i> , 2010, 11, 595.	2.6	2,074
154	High-throughput genome sequencing of two <i>Listeria monocytogenes</i> clinical isolates during a large foodborne outbreak. <i>BMC Genomics</i> , 2010, 11, 120.	2.8	306
155	<i>Legionella pneumophila</i> pangenome reveals strain-specific virulence factors. <i>BMC Genomics</i> , 2010, 11, 181.	2.8	161
156	Complete genome sequence of the fire blight pathogen <i>Erwinia pyrifoliae</i> DSM 12163T and comparative genomic insights into plant pathogenicity. <i>BMC Genomics</i> , 2010, 11, 2.	2.8	57
157	A scenario of mitochondrial genome evolution in maize based on rearrangement events. <i>BMC Genomics</i> , 2010, 11, 233.	2.8	44
158	Genome comparison of the epiphytic bacteria <i>Erwinia billingiae</i> and <i>E. tasmaniensis</i> with the pear pathogen <i>E. pyrifoliae</i> . <i>BMC Genomics</i> , 2010, 11, 393.	2.8	92
159	Markedly different genome arrangements between serotype a strains and serotypes b or c strains of <i>Aggregatibacter actinomycetemcomitans</i> . <i>BMC Genomics</i> , 2010, 11, 489.	2.8	17
160	Comparative genomics of the bacterial genus <i>Listeria</i> : Genome evolution is characterized by limited gene acquisition and limited gene loss. <i>BMC Genomics</i> , 2010, 11, 688.	2.8	174
161	Analysis of genomic differences among <i>Clostridium botulinum</i> type A1 strains. <i>BMC Genomics</i> , 2010, 11, 725.	2.8	21
162	Genetic and phenotypic diversity in <i>Burkholderia</i> : contributions by prophage and phage-like elements. <i>BMC Microbiology</i> , 2010, 10, 202.	3.3	45
163	Characterization of JG024, a <i>Pseudomonas aeruginosa</i> PB1-like broad host range phage under simulated infection conditions. <i>BMC Microbiology</i> , 2010, 10, 301.	3.3	81
164	A highly conserved gene island of three genes on chromosome 3B of hexaploid wheat: diverse gene function and genomic structure maintained in a tightly linked block. <i>BMC Plant Biology</i> , 2010, 10, 98.	3.6	16

#	ARTICLE	IF	CITATIONS
166	Global gene expression profile of <i>Orientia tsutsugamushi</i> . <i>Proteomics</i> , 2010, 10, 1699-1715.	2.2	26
167	ANALYSES OF THE COMPLETE CHLOROPLAST GENOME SEQUENCES OF TWO MEMBERS OF THE PELAGOPHYCEAE: <i>AUREOCOCCUS ANOPHAGEFFERENS</i> CCMP1984 AND <i>AUREOUMBRA LAGUNENSIS</i> CCMP1507 ¹ . <i>Journal of Phycology</i> , 2010, 46, 602-615.	2.3	32
168	Visualizing genomes: techniques and challenges. <i>Nature Methods</i> , 2010, 7, S5-S15.	19.0	146
169	Detecting genomic islands using bioinformatics approaches. <i>Nature Reviews Microbiology</i> , 2010, 8, 373-382.	28.6	257
170	Annotation and overview of the <i>Pseudomonas savastanoi</i> pv. <i>savastanoi</i> NCPPB 3335 draft genome reveals the virulence gene complement of a tumour-inducing pathogen of woody hosts. <i>Environmental Microbiology</i> , 2010, 12, 1604-1620.	3.8	80
171	Análisis comparativo de seis genomas del complejo <i>Mycobacterium tuberculosis</i> . <i>Biomedica</i> , 2010, 30, 23.	0.7	2
172	Complete Genome Sequence of the Multiresistant Taxonomic Outlier <i>Pseudomonas aeruginosa</i> PA7. <i>PLoS ONE</i> , 2010, 5, e8842.	2.5	236
173	<i>Shewanella</i> spp. Genomic Evolution for a Cold Marine Lifestyle and In-Situ Explosive Biodegradation. <i>PLoS ONE</i> , 2010, 5, e9109.	2.5	76
174	Sequencing and Genetic Variation of Multidrug Resistance Plasmids in <i>Klebsiella pneumoniae</i> . <i>PLoS ONE</i> , 2010, 5, e10141.	2.5	52
175	The Complete Plastid Genomes of the Two "Dinotoms" <i>Durinskia baltica</i> and <i>Kryptoperidinium foliaceum</i> . <i>PLoS ONE</i> , 2010, 5, e10711.	2.5	89
176	Conjugative Botulinum Neurotoxin-Encoding Plasmids in <i>Clostridium botulinum</i> . <i>PLoS ONE</i> , 2010, 5, e11087.	2.5	48
177	Murasaki: A Fast, Parallelizable Algorithm to Find Anchors from Multiple Genomes. <i>PLoS ONE</i> , 2010, 5, e12651.	2.5	30
178	Identification of Mendel's White Flower Character. <i>PLoS ONE</i> , 2010, 5, e13230.	2.5	135
179	Population Genetic Analysis of <i>Propionibacterium acnes</i> Identifies a Subpopulation and Epidemic Clones Associated with Acne. <i>PLoS ONE</i> , 2010, 5, e12277.	2.5	233
180	Host-Interactive Genes in Amerindian <i>Helicobacter pylori</i> Diverge from Their Old World Homologs and Mediate Inflammatory Responses. <i>Journal of Bacteriology</i> , 2010, 192, 3078-3092.	2.2	50
181	Inference of Homologous Recombination in Bacteria Using Whole-Genome Sequences. <i>Genetics</i> , 2010, 186, 1435-1449.	2.9	155
182	Comparative Genomic Characterization of <i>Actinobacillus pleuropneumoniae</i> . <i>Journal of Bacteriology</i> , 2010, 192, 5625-5636.	2.2	59
183	Evolutionary dynamics of <i>Clostridium difficile</i> over short and long time scales. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 7527-7532.	7.1	346

#	ARTICLE	IF	CITATIONS
184	Differential Gene Retention in Plastids of Common Recent Origin. <i>Molecular Biology and Evolution</i> , 2010, 27, 1530-1537.	8.9	102
187	The Genetic Basis of Laboratory Adaptation in <i>Caulobacter crescentus</i> . <i>Journal of Bacteriology</i> , 2010, 192, 3678-3688.	2.2	166
188	Virulence Factors Encoded by <i>Legionella longbeachae</i> Identified on the Basis of the Genome Sequence Analysis of Clinical Isolate D-4968. <i>Journal of Bacteriology</i> , 2010, 192, 1030-1044.	2.2	58
189	A computational genomics pipeline for prokaryotic sequencing projects. <i>Bioinformatics</i> , 2010, 26, 1819-1826.	4.1	71
190	genoPlotR: comparative gene and genome visualization in R. <i>Bioinformatics</i> , 2010, 26, 2334-2335.	4.1	651
191	A milieu of regulatory elements in the epidermal differentiation complex syntenic block: implications for atopic dermatitis and psoriasis. <i>Human Molecular Genetics</i> , 2010, 19, 1453-1460.	2.9	92
192	Different Phylogenomic Approaches to Resolve the Evolutionary Relationships among Model Fish Species. <i>Molecular Biology and Evolution</i> , 2010, 27, 2757-2774.	8.9	18
193	Cassis: detection of genomic rearrangement breakpoints. <i>Bioinformatics</i> , 2010, 26, 1897-1898.	4.1	22
194	A Novel Technique for Detecting Putative Horizontal Gene Transfer in the Sequence Space. <i>Journal of Computational Biology</i> , 2010, 17, 1535-1548.	1.6	2
195	The Chloroplast Genome Sequence of Mungbean (<i>Vigna radiata</i>) Determined by High-throughput Pyrosequencing: Structural Organization and Phylogenetic Relationships. <i>DNA Research</i> , 2010, 17, 11-22.	3.4	198
196	Emergence of a New Multidrug-Resistant Serotype X Variant in an Epidemic Clone of <i>Shigella flexneri</i> . <i>Journal of Clinical Microbiology</i> , 2010, 48, 419-426.	3.9	104
197	mGenomeSubtractor: a web-based tool for parallel in silico subtractive hybridization analysis of multiple bacterial genomes. <i>Nucleic Acids Research</i> , 2010, 38, W194-W200.	14.5	74
198	Analysis of the <i>Legionella longbeachae</i> Genome and Transcriptome Uncovers Unique Strategies to Cause Legionnaires' Disease. <i>PLoS Genetics</i> , 2010, 6, e1000851.	3.5	143
199	Evolution of an X-Linked Primate-Specific Micro RNA Cluster. <i>Molecular Biology and Evolution</i> , 2010, 27, 671-683.	8.9	64
200	SNPS IN THE HIV-1 TATA BOX AND THE AIDS PANDEMIC. <i>Journal of Bioinformatics and Computational Biology</i> , 2010, 08, 607-625.	0.8	19
201	The solution space of genome sequence alignment and LIS graph decomposition. , 2010, , .		0
202	Comparative Analysis of Plasmids in the Genus <i>Listeria</i> . <i>PLoS ONE</i> , 2010, 5, e12511.	2.5	110
203	Complete Genomic Sequence of Bacteriophage Felix O1. <i>Viruses</i> , 2010, 2, 710-730.	3.3	72

#	ARTICLE	IF	CITATIONS
204	Complex prokaryotic genome structure: rapid evolution of chromosome II. <i>Genome</i> , 2010, 53, 675-687.	2.0	18
205	DRIMM-Synten: decomposing genomes into evolutionary conserved segments. <i>Bioinformatics</i> , 2010, 26, 2509-2516.	4.1	78
206	Genomic differences between the food-grade <i>Staphylococcus carnosus</i> and pathogenic staphylococcal species. <i>International Journal of Medical Microbiology</i> , 2010, 300, 104-108.	3.6	22
207	Genomic and transcriptomic studies in <i>Mycobacterium avium</i> subspecies <i>paratuberculosis</i> . <i>Veterinary Immunology and Immunopathology</i> , 2010, 138, 303-311.	1.2	8
208	Identification of lytic bacteriophage MmP1, assigned to a new member of T7-like phages infecting <i>Morganella morganii</i> . <i>Genomics</i> , 2010, 96, 167-172.	2.9	19
209	Genomic Databases and Resources at the National Center for Biotechnology Information. <i>Methods in Molecular Biology</i> , 2010, 609, 17-44.	0.9	17
210	Structure and dynamics of the pan-genome of <i>Streptococcus pneumoniae</i> and closely related species. <i>Genome Biology</i> , 2010, 11, R107.	8.8	321
211	Small variable segments constitute a major type of diversity of bacterial genomes at the species level. <i>Genome Biology</i> , 2010, 11, R45.	9.6	17
212	Genomic characterization of the <i>Yersinia</i> genus. <i>Genome Biology</i> , 2010, 11, R1.	9.6	103
213	Multilocus Sequence Typing of <i>Clostridium difficile</i> . <i>Journal of Clinical Microbiology</i> , 2010, 48, 770-778.	3.9	399
214	Visual comparison for information visualization. <i>Information Visualization</i> , 2011, 10, 289-309.	1.9	417
215	Evolution and Spread of a Multidrug-Resistant <i>Proteus mirabilis</i> Clone with Chromosomal AmpC-Type Cephalosporinases in Europe. <i>Antimicrobial Agents and Chemotherapy</i> , 2011, 55, 2735-2742.	3.2	52
217	Recent Trends in Molecular Phylogenetic Analysis: Where to Next?. <i>Journal of Heredity</i> , 2011, 102, 130-138.	2.4	85
218	Pathogen comparative genomics in the next-generation sequencing era: genome alignments, pangenomics and metagenomics. <i>Briefings in Functional Genomics</i> , 2011, 10, 322-333.	2.7	41
219	Development and evaluation of a loop-mediated isothermal amplification assay for rapid detection and identification of <i>Pectobacterium atrosepticum</i> . <i>Canadian Journal of Plant Pathology</i> , 2011, 33, 447-457.	1.4	26
220	Characterization of the complete chloroplast genome of <i>Hevea brasiliensis</i> reveals genome rearrangement, RNA editing sites and phylogenetic relationships. <i>Gene</i> , 2011, 475, 104-112.	2.2	92
221	Identifying and characterizing a member of the RhopH1/Clag family in <i>Plasmodium vivax</i> . <i>Gene</i> , 2011, 481, 17-23.	2.2	7
222	Short communication: The complete genome sequence of <i>Bifidobacterium animalis</i> subspecies <i>animalis</i> ATCC 2527T and comparative analysis of growth in milk with <i>B. animalis</i> subspecies <i>lactis</i> DSM 10140T. <i>Journal of Dairy Science</i> , 2011, 94, 5864-5870.	3.4	10

#	ARTICLE	IF	CITATIONS
223	Sequence Surveyor: Leveraging Overview for Scalable Genomic Alignment Visualization. IEEE Transactions on Visualization and Computer Graphics, 2011, 17, 2392-2401.	4.4	38
224	PoPoolation: A Toolbox for Population Genetic Analysis of Next Generation Sequencing Data from Pooled Individuals. PLoS ONE, 2011, 6, e15925.	2.5	556
225	Using Genomic Sequencing for Classical Genetics in E. coli K12. PLoS ONE, 2011, 6, e16717.	2.5	56
226	Sequencing and Comparative Genome Analysis of Two Pathogenic Streptococcus gallolyticus Subspecies: Genome Plasticity, Adaptation and Virulence. PLoS ONE, 2011, 6, e20519.	2.5	41
227	Microbial Diversity in the Midguts of Field and Lab-Reared Populations of the European Corn Borer Ostrinia nubilalis. PLoS ONE, 2011, 6, e21751.	2.5	71
228	Evolutionary Genomics of a Temperate Bacteriophage in an Obligate Intracellular Bacteria (Wolbachia). PLoS ONE, 2011, 6, e24984.	2.5	45
229	Structural and Content Diversity of Mitochondrial Genome in Beet: A Comparative Genomic Analysis. Genome Biology and Evolution, 2011, 3, 723-736.	2.5	67
230	Chloroplast genome sequences from total DNA for plant identification. Plant Biotechnology Journal, 2011, 9, 328-333.	8.3	316
231	Rickettsial evolution in the light of comparative genomics. Biological Reviews, 2011, 86, 379-405.	10.4	219
232	Adherence and motility characteristics of clinical Acinetobacter baumannii isolates. FEMS Microbiology Letters, 2011, 323, 44-51.	1.8	168
233	Comparative genomics and phylogeny of the IncI1 plasmids: A common plasmid type among porcine enterotoxigenic Escherichia coli. Plasmid, 2011, 66, 144-151.	1.4	66
234	Everything at once: Comparative analysis of the genomes of bacterial pathogens. Veterinary Microbiology, 2011, 153, 13-26.	1.9	12
235	Horizontal gene transfer in Histophilus somni and its role in the evolution of pathogenic strain 2336, as determined by comparative genomic analyses. BMC Genomics, 2011, 12, 570.	2.8	34
236	Closely related Campylobacter jejuni strains from different sources reveal a generalist rather than a specialist lifestyle. BMC Genomics, 2011, 12, 584.	2.8	101
237	Complete genome sequence of the lytic Pseudomonas fluorescens phage ÎBB-PF7A. Virology Journal, 2011, 8, 142.	3.4	11
238	The evolution of chloroplast genes and genomes in ferns. Plant Molecular Biology, 2011, 76, 251-261.	3.9	87
239	Complete genomic sequence of the Lactobacillus temperate phage LF1. Archives of Virology, 2011, 156, 1909-1912.	2.1	11
240	Interplay of recombination and selection in the genomes of Chlamydia trachomatis. Biology Direct, 2011, 6, 28.	4.6	70

#	ARTICLE	IF	CITATIONS
241	nocoRNAc: Characterization of non-coding RNAs in prokaryotes. BMC Bioinformatics, 2011, 12, 40.	2.6	39
242	The rise and fall of breakpoint reuse depending on genome resolution. BMC Bioinformatics, 2011, 12, S1.	2.6	19
243	Genomic lineages of <i>Rhizobium etli</i> revealed by the extent of nucleotide polymorphisms and low recombination. BMC Evolutionary Biology, 2011, 11, 305.	3.2	40
244	<i>Mycoplasma mycoides</i> , from "mycoides Small Colony" to "capri". A microevolutionary perspective. BMC Genomics, 2011, 12, 114.	2.8	64
245	Investigation of the human pathogen <i>Acinetobacter baumannii</i> under iron limiting conditions. BMC Genomics, 2011, 12, 126.	2.8	215
246	Shotgun sequencing of <i>Yersinia enterocolitica</i> strain W22703 (biotype 2, serotype O:9): genomic evidence for oscillation between invertebrates and mammals. BMC Genomics, 2011, 12, 168.	2.8	33
247	Characterization and genome sequencing of two <i>Propionibacterium acnes</i> phages displaying pseudolysogeny. BMC Genomics, 2011, 12, 198.	2.8	34
248	Comparative genome analysis and genome-guided physiological analysis of <i>Roseobacter litoralis</i> . BMC Genomics, 2011, 12, 324.	2.8	54
249	Complete genome and comparative analysis of <i>Streptococcus gallolyticus</i> subsp. <i>gallolyticus</i> , an emerging pathogen of infective endocarditis. BMC Genomics, 2011, 12, 400.	2.8	41
250	BLAST Ring Image Generator (BRIG): simple prokaryote genome comparisons. BMC Genomics, 2011, 12, 402.	2.8	2,691
251	Attenuation of virulence in an apicomplexan hemoparasite results in reduced genome diversity at the population level. BMC Genomics, 2011, 12, 410.	2.8	31
252	Within-species lateral genetic transfer and the evolution of transcriptional regulation in <i>Escherichia coli</i> and <i>Shigella</i> . BMC Genomics, 2011, 12, 532.	2.8	28
253	Sequence of the hyperplastic genome of the naturally competent <i>Thermus scotoductus</i> SA-01. BMC Genomics, 2011, 12, 577.	2.8	49
254	Sequencing and Characterization of <i>Pseudomonas aeruginosa</i> phage JG004. BMC Microbiology, 2011, 11, 102.	3.3	60
255	Hypervirulent <i>Chlamydia trachomatis</i> Clinical Strain Is a Recombinant between Lymphogranuloma Venereum (L ₂) and D Lineages. MBio, 2011, 2, e00045-11.	4.1	100
256	Using inversion signatures to generate draft genome sequence scaffolds. , 2011, , .		1
257	Evidence-Based Annotation of Transcripts and Proteins in the Sulfate-Reducing Bacterium <i>Desulfovibrio vulgaris</i> Hildenborough. Journal of Bacteriology, 2011, 193, 5716-5727.	2.2	28
258	Genome of Multidrug-Resistant Uropathogenic <i>Escherichia coli</i> Strain NA114 from India. Journal of Bacteriology, 2011, 193, 4272-4273.	2.2	63

#	ARTICLE	IF	CITATIONS
259	Mauve Assembly Metrics. <i>Bioinformatics</i> , 2011, 27, 2756-2757.	4.1	108
260	Comparative Genomic Analysis of <i>Acinetobacter oleivorans</i> DR1 To Determine Strain-Specific Genomic Regions and Gentisate Biodegradation. <i>Applied and Environmental Microbiology</i> , 2011, 77, 7418-7424.	3.1	27
261	Using Single-Nucleotide Polymorphisms To Discriminate Disease-Associated from Carried Genomes of <i>Neisseria meningitidis</i> . <i>Journal of Bacteriology</i> , 2011, 193, 3633-3641.	2.2	5
262	Genome Sequence of <i>Vibrio rotiferianus</i> Strain DAT722. <i>Journal of Bacteriology</i> , 2011, 193, 3381-3382.	2.2	16
263	Complete Genome Sequence of the Nicotine-Degrading <i>Pseudomonas putida</i> Strain S16. <i>Journal of Bacteriology</i> , 2011, 193, 5541-5542.	2.2	60
264	Major Families of Multiresistant Plasmids from Geographically and Epidemiologically Diverse <i>Staphylococci</i> . <i>G3: Genes, Genomes, Genetics</i> , 2011, 1, 581-591.	1.8	92
265	An alternative approach to multiple genome comparison. <i>Nucleic Acids Research</i> , 2011, 39, e101-e101.	14.5	3
266	Pan-genome of the dominant human gut-associated archaeon, <i>Methanobrevibacter smithii</i> , studied in twins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 4599-4606.	7.1	221
267	Long-Range and Targeted Ectopic Recombination between the Two Homeologous Chromosomes 11 and 12 in <i>Oryza</i> Species. <i>Molecular Biology and Evolution</i> , 2011, 28, 3139-3150.	8.9	23
268	Whole-Genome Sequence of <i>Streptococcus pseudopneumoniae</i> Isolate IS7493. <i>Journal of Bacteriology</i> , 2011, 193, 6102-6103.	2.2	20
269	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.	2.2	42
270	Complete Genome Sequence of <i>Bacillus subtilis</i> BSn5, an Endophytic Bacterium of <i>Amorphophallus konjac</i> with Antimicrobial Activity for the Plant Pathogen <i>Erwinia carotovora</i> subsp. <i>carotovora</i> . <i>Journal of Bacteriology</i> , 2011, 193, 2070-2071.	2.2	97
271	Birth and death of genes linked to chromosomal inversion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 1501-1506.	7.1	62
272	Complete Genome Sequences of <i>Brucella melitensis</i> Strains M28 and M5-90, with Different Virulence Backgrounds. <i>Journal of Bacteriology</i> , 2011, 193, 2904-2905.	2.2	20
273	ORIGINAL RESEARCH: Comparative constraint-based model development for thermophilic hydrogen production. <i>Industrial Biotechnology</i> , 2011, 7, 63-82.	0.8	4
274	Complete Genome Sequence of the Bacterium <i>Porphyromonas gingivalis</i> TDC60, Which Causes Periodontal Disease. <i>Journal of Bacteriology</i> , 2011, 193, 4259-4260.	2.2	54
275	<i>Neisseria meningitidis</i> is structured in clades associated with restriction modification systems that modulate homologous recombination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 4494-4499.	7.1	198
276	SyMAP v3.4: a turnkey synteny system with application to plant genomes. <i>Nucleic Acids Research</i> , 2011, 39, e68-e68.	14.5	304

#	ARTICLE	IF	CITATIONS
277	Genome Sequences of Three <i>Acinetobacter baumannii</i> Strains Assigned to the Multilocus Sequence Typing Genotypes ST2, ST25, and ST78. <i>Journal of Bacteriology</i> , 2011, 193, 2359-2360.	2.2	28
278	Mutation of a Broadly Conserved Operon (RL3499-RL3502) from <i>Rhizobium leguminosarum</i> Biovar <i>viciae</i> Causes Defects in Cell Morphology and Envelope Integrity. <i>Journal of Bacteriology</i> , 2011, 193, 2684-2694.	2.2	24
279	The Adherence Locus of Enterotoxigenic <i>Escherichia coli</i> Is Regulated by Cyclic AMP Receptor Protein. <i>Journal of Bacteriology</i> , 2011, 193, 1369-1376.	2.2	10
280	Broad-Host-Range Plasmids from Agricultural Soils Have IncP-1 Backbones with Diverse Accessory Genes. <i>Applied and Environmental Microbiology</i> , 2011, 77, 7975-7983.	3.1	96
281	The pleiotropic regulator AdpAch is required for natamycin biosynthesis and morphological differentiation in <i>Streptomyces chattanoogensis</i> . <i>Microbiology (United Kingdom)</i> , 2011, 157, 1300-1311.	1.8	48
282	Complete Genome Sequence of <i>Bacillus amyloliquefaciens</i> TA208, a Strain for Industrial Production of Guanosine and Ribavirin. <i>Journal of Bacteriology</i> , 2011, 193, 3142-3143.	2.2	16
283	A Theoretical Model for Whole Genome Alignment. <i>Journal of Computational Biology</i> , 2011, 18, 705-728.	1.6	2
284	Quantifying Nonvertical Inheritance in the Evolution of <i>Legionella pneumophila</i> . <i>Molecular Biology and Evolution</i> , 2011, 28, 985-1001.	8.9	47
285	Neisseria Base: a comparative genomics database for <i>Neisseria meningitidis</i> . <i>Database: the Journal of Biological Databases and Curation</i> , 2011, 2011, bar035.	3.0	9
286	Conserved small RNAs govern replication and incompatibility of a diverse new plasmid family from marine bacteria. <i>Nucleic Acids Research</i> , 2011, 39, 1004-1013.	14.5	40
287	Computational inference of grammars for larger-than-gene structures from annotated gene sequences. <i>Bioinformatics</i> , 2011, 27, 791-796.	4.1	6
288	Recombination and Population Structure in <i>Salmonella enterica</i> . <i>PLoS Genetics</i> , 2011, 7, e1002191.	3.5	135
289	Cactus: Algorithms for genome multiple sequence alignment. <i>Genome Research</i> , 2011, 21, 1512-1528.	5.5	245
290	Transformation of Natural Genetic Variation into <i>Haemophilus Influenzae</i> Genomes. <i>PLoS Pathogens</i> , 2011, 7, e1002151.	4.7	75
291	Mugsy: fast multiple alignment of closely related whole genomes. <i>Bioinformatics</i> , 2011, 27, 334-342.	4.1	444
293	A Novel Computational Method Identifies Intra- and Inter-Species Recombination Events in <i>Staphylococcus aureus</i> and <i>Streptococcus pneumoniae</i> . <i>PLoS Computational Biology</i> , 2012, 8, e1002668.	3.2	9
294	Whole Genome Sequencing Reveals Local Transmission Patterns of <i>Mycobacterium bovis</i> in Sympatric Cattle and Badger Populations. <i>PLoS Pathogens</i> , 2012, 8, e1003008.	4.7	173
295	Genome Sequence of a Serotype b Non-JP2 <i>Aggregatibacter actinomycetemcomitans</i> Strain, ANH9381, from a Periodontally Healthy Individual. <i>Journal of Bacteriology</i> , 2012, 194, 1837-1837.	2.2	6

#	ARTICLE	IF	CITATIONS
296	i-ADHoRe 3.0â€”fast and sensitive detection of genomic homology in extremely large data sets. Nucleic Acids Research, 2012, 40, e11-e11.	14.5	192
297	Draft Genome Sequence of <i>Corynebacterium diphtheriae</i> Biovar Intermedius NCTC 5011. Journal of Bacteriology, 2012, 194, 4738-4738.	2.2	19
298	Genome-Wide Survey of Mutual Homologous Recombination in a Highly Sexual Bacterial Species. Genome Biology and Evolution, 2012, 4, 628-640.	2.5	34
299	Using Sybil for interactive comparative genomics of microbes on the web. Bioinformatics, 2012, 28, 160-166.	4.1	53
300	Single-cell sequencing provides clues about the host interactions of segmented filamentous bacteria (SFB). Genome Research, 2012, 22, 1107-1119.	5.5	108
301	Characterization of the ELPhIS Prophage from <i>Salmonella enterica</i> Serovar Enteritidis Strain LK5. Applied and Environmental Microbiology, 2012, 78, 1785-1793.	3.1	23
302	After the bottleneck: Genome-wide diversification of the <i>Mycobacterium tuberculosis</i> complex by mutation, recombination, and natural selection. Genome Research, 2012, 22, 721-734.	5.5	141
303	Insight into the Transmission Biology and Species-Specific Functional Capabilities of Tsetse (Diptera: Tj ETQq1 1 0.784314 rgBT /Overlo	4.1	105
304	Using Comparative Genomics for Inquiry-Based Learning to Dissect Virulence of <i>Escherichia coli</i> O157:H7 and <i>Yersinia pestis</i> . CBE Life Sciences Education, 2012, 11, 81-93.	2.3	15
305	GenomeRing: alignment visualization based on SuperGenome coordinates. Bioinformatics, 2012, 28, i7-i15.	4.1	41
306	Comparative chloroplast genomics between <i>Euglena viridis</i> and <i>Euglena gracilis</i> (Euglenophyta). Phycologia, 2012, 51, 711-718.	1.4	21
307	Complete DNA Sequence Analysis of Enterohemorrhagic <i>Escherichia coli</i> Plasmid pO157_2 in Î²-Glucuronidase-Positive <i>E. coli</i> O157:H7 Reveals a Novel Evolutionary Path. Journal of Bacteriology, 2012, 194, 3457-3463.	2.2	31
308	Genomic characterization of the <i>Bacillus cereus</i> sensu lato species: Backdrop to the evolution of <i>Bacillus anthracis</i> . Genome Research, 2012, 22, 1512-1524.	5.5	148
309	Transcriptional Analysis of a Dehalococcoides-Containing Microbial Consortium Reveals Prophage Activation. Applied and Environmental Microbiology, 2012, 78, 1178-1186.	3.1	34
310	FSL J1-208, a Virulent Uncommon Phylogenetic Lineage IV <i>Listeria monocytogenes</i> Strain with a Small Chromosome Size and a Putative Virulence Plasmid Carrying Internalin-Like Genes. Applied and Environmental Microbiology, 2012, 78, 1876-1889.	3.1	43
311	Impact of Loci Nature on Estimating Recombination and Mutation Rates in <i>Chlamydia trachomatis</i> . G3: Genes, Genomes, Genetics, 2012, 2, 761-768.	1.8	12
312	Whole-Genome Sequence of the Human Pathogen <i>Legionella pneumophila</i> Serogroup 12 Strain 570-CO-H. Journal of Bacteriology, 2012, 194, 1613-1614.	2.2	21
313	Genomic analysis of <i>Pseudomonas putida</i> : genes in a genome island are crucial for nicotine degradation. Scientific Reports, 2012, 2, 377.	3.3	69

#	ARTICLE	IF	CITATIONS
314	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.	2.5	43
315	Polyclonality of Concurrent Natural Populations of <i>Alteromonas macleodii</i> . <i>Genome Biology and Evolution</i> , 2012, 4, 1360-1374.	2.5	57
316	Role of IncP-1 ² Plasmids pWDL7:: <i>rfp</i> and pNB8c in Chloroaniline Catabolism as Determined by Genomic and Functional Analyses. <i>Applied and Environmental Microbiology</i> , 2012, 78, 828-838.	3.1	45
317	Complete Mitochondrial and Plastid Genomes of the Green Microalga <i>Trebouxia phyceae</i> sp. Strain MX-AZ01 Isolated from a Highly Acidic Geothermal Lake. <i>Eukaryotic Cell</i> , 2012, 11, 1417-1418.	3.4	20
318	Genome Sequence of the Persistent <i>Salmonella enterica</i> subsp. <i>enterica</i> Serotype Senftenberg Strain SS209. <i>Journal of Bacteriology</i> , 2012, 194, 2385-2386.	2.2	8
319	Genome Sequence of the Invasive <i>Salmonella enterica</i> subsp. <i>enterica</i> Serotype Enteritidis Strain LA5. <i>Journal of Bacteriology</i> , 2012, 194, 2387-2388.	2.2	12
320	Draft Genome Sequence of <i>Lactobacillus gigeriorum</i> CRBIP 24.85 ^T , Isolated from a Chicken Crop. <i>Journal of Bacteriology</i> , 2012, 194, 5973-5973.	2.2	0
321	Complete Genome Sequence of the Serotype k <i>Streptococcus mutans</i> Strain LJ23. <i>Journal of Bacteriology</i> , 2012, 194, 2754-2755.	2.2	20
322	Genome Sequence of the Moderately Halotolerant, Arsenite-Oxidizing Bacterium <i>Pseudomonas stutzeri</i> TS44. <i>Journal of Bacteriology</i> , 2012, 194, 4473-4474.	2.2	22
323	Non-contiguous finished genome sequence and description of <i>Paenibacillus senegalensis</i> sp. nov.. <i>Standards in Genomic Sciences</i> , 2012, 7, 70-81.	1.5	66
324	Phylogeny rather than ecology or lifestyle biases the construction of <i>Escherichia coli</i> & “ <i>Shigella</i> ” genetic exchange communities. <i>Open Biology</i> , 2012, 2, 120112.	3.6	42
325	Whole-Genome Sequences of <i>Bacillus subtilis</i> and Close Relatives. <i>Journal of Bacteriology</i> , 2012, 194, 2378-2379.	2.2	52
326	Phylogenetic Analysis of Non-O157 Shiga Toxin-Producing <i>Escherichia coli</i> Strains by Whole-Genome Sequencing. <i>Journal of Clinical Microbiology</i> , 2012, 50, 4123-4127.	3.9	39
327	Mitochondrial genome variability within the <i>Candida parapsilosis</i> species complex. <i>Mitochondrion</i> , 2012, 12, 514-519.	3.4	20
328	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.	7.3	66
329	Sequencing papaya X and Y ^h chromosomes reveals molecular basis of incipient sex chromosome evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 13710-13715.	7.1	264
330	Evolution of the Chloroplast Genome in Photosynthetic Euglenoids: A Comparison of <i>Eutreptia viridis</i> and <i>Euglena gracilis</i> (Euglenophyta). <i>Protist</i> , 2012, 163, 832-843.	1.5	33
331	Pneumococcal genome sequencing tracks a vaccine escape variant formed through a multi-fragment recombination event. <i>Nature Genetics</i> , 2012, 44, 352-355.	21.4	144

#	ARTICLE	IF	CITATIONS
332	Gene-RiViT: A visualization tool for comparative analysis of gene neighborhoods in prokaryotes. , 2012, , ,		3
333	Horizontal Transfer of PAH Catabolism Genes in <i>Mycobacterium</i> : Evidence from Comparative Genomics and Isolated Pyrene-Degrading Bacteria. Environmental Science & Technology, 2012, 46, 99-106.	10.0	71
334	Miniature Inverted-Repeat Transposable Elements (MITEs) Have Been Accumulated through Amplification Bursts and Play Important Roles in Gene Expression and Species Diversity in <i>Oryza sativa</i> . Molecular Biology and Evolution, 2012, 29, 1005-1017.	8.9	191
335	Complete cpDNA genome sequence of <i>Smilax china</i> and phylogenetic placement of Liliales " Influences of gene partitions and taxon sampling. Molecular Phylogenetics and Evolution, 2012, 64, 545-562.	2.7	49
336	Tracking a Hospital Outbreak of Carbapenem-Resistant <i>Klebsiella pneumoniae</i> with Whole-Genome Sequencing. Science Translational Medicine, 2012, 4, 148ra116.	12.4	781
337	Transforming clinical microbiology with bacterial genome sequencing. Nature Reviews Genetics, 2012, 13, 601-612.	16.3	684
338	Mapping single molecule sequencing reads using basic local alignment with successive refinement (BLASR): application and theory. BMC Bioinformatics, 2012, 13, 238.	2.6	1,075
339	Genomic and Phylogenetic Characterization of Brazilian Yellow Fever Virus Strains. Journal of Virology, 2012, 86, 13263-13271.	3.4	41
340	Prokaryote Genome Fluidity: Toward a System Approach of the Mobilome. Methods in Molecular Biology, 2012, 804, 57-80.	0.9	41
341	Population Genomics of <i>Chlamydia trachomatis</i> : Insights on Drift, Selection, Recombination, and Population Structure. Molecular Biology and Evolution, 2012, 29, 3933-3946.	8.9	94
342	Rapid detection and antimicrobial resistance gene profiling of <i>Yersinia pestis</i> using pyrosequencing technology. Journal of Microbiological Methods, 2012, 90, 228-234.	1.6	21
343	Development of species-, strain- and antibiotic biosynthesis-specific quantitative PCR assays for <i>Pantoea agglomerans</i> as tools for biocontrol monitoring. Journal of Microbiological Methods, 2012, 90, 315-320.	1.6	24
344	Comparative analysis of the Hrp pathogenicity island of <i>Rubus</i> - and <i>Spiraeoideae</i> -infecting <i>Erwinia amylovora</i> strains identifies the IT region as a remnant of an integrative conjugative element. Gene, 2012, 504, 6-12.	2.2	16
345	<i>Phaeobacter gallaeciensis</i> genomes from globally opposite locations reveal high similarity of adaptation to surface life. ISME Journal, 2012, 6, 2229-2244.	9.8	143
346	SIS: a program to generate draft genome sequence scaffolds for prokaryotes. BMC Bioinformatics, 2012, 13, 96.	2.6	29
347	A phylogenomic analysis of <i>Escherichia coli</i> / <i>Shigella</i> group: implications of genomic features associated with pathogenicity and ecological adaptation. BMC Evolutionary Biology, 2012, 12, 174.	3.2	72
348	A genome-wide study of recombination rate variation in <i>Bartonella henselae</i> . BMC Evolutionary Biology, 2012, 12, 65.	3.2	18
349	A comparative genomics perspective on the genetic content of the alkaliphilic haloarchaeon <i>Natrialba magadii</i> ATCC 43099T. BMC Genomics, 2012, 13, 165.	2.8	36

#	ARTICLE	IF	CITATIONS
350	Mitochondrial genome evolution in species belonging to the <i>Phialocephala fortinii</i> s.l. - <i>Acephala applanata</i> species complex. BMC Genomics, 2012, 13, 166.	2.8	49
351	Impact of homologous and non-homologous recombination in the genomic evolution of <i>Escherichia coli</i> . BMC Genomics, 2012, 13, 256.	2.8	141
352	High resolution clustering of <i>Salmonella enterica</i> serovar Montevideo strains using a next-generation sequencing approach. BMC Genomics, 2012, 13, 32.	2.8	140
353	Genetic changes during a laboratory adaptive evolution process that allowed fast growth in glucose to an <i>Escherichia coli</i> strain lacking the major glucose transport system. BMC Genomics, 2012, 13, 385.	2.8	45
354	Comparative genomic analysis of <i>Geobacter sulfurreducens</i> KN400, a strain with enhanced capacity for extracellular electron transfer and electricity production. BMC Genomics, 2012, 13, 471.	2.8	36
355	Sequencing of the core MHC region of black grouse (<i>Tetrao tetrix</i>) and comparative genomics of the galliform MHC. BMC Genomics, 2012, 13, 553.	2.8	29
356	Genome sequencing of ovine isolates of <i>Mycobacterium avium</i> subspecies paratuberculosis offers insights into host association. BMC Genomics, 2012, 13, 89.	2.8	54
357	Complete genome sequence of <i>Enterococcus faecium</i> strain TX16 and comparative genomic analysis of <i>Enterococcus faecium</i> genomes. BMC Microbiology, 2012, 12, 135.	3.3	126
358	Investigations into genome diversity of <i>Haemophilus influenzae</i> using whole genome sequencing of clinical isolates and laboratory transformants. BMC Microbiology, 2012, 12, 273.	3.3	39
359	Genomes-based phylogeny of the genus <i>Xanthomonas</i> . BMC Microbiology, 2012, 12, 43.	3.3	71
360	Endemic bacteriophages: a cautionary tale for evaluation of bacteriophage therapy and other interventions for infection control in animals. Virology Journal, 2012, 9, 207.	3.4	24
361	The highly dynamic CRISPR1 system of <i>Streptococcus agalactiae</i> controls the diversity of its mobilome. Molecular Microbiology, 2012, 85, 1057-1071.	2.5	153
362	Condition-Dependent Transcriptome Reveals High-Level Regulatory Architecture in <i>Bacillus subtilis</i> . Science, 2012, 335, 1103-1106.	12.6	809
363	Evolution of Multipartite Genomes in Prokaryotes. , 2012, , 301-323.		5
364	Replacing and Additive Horizontal Gene Transfer in <i>Streptococcus</i> . Molecular Biology and Evolution, 2012, 29, 3309-3320.	8.9	33
365	Fighting Outbreaks with Bacterial Genomics: Case Review and Workflow Proposal. Public Health Genomics, 2012, 15, 341-351.	1.0	10
366	High-throughput bacterial genome sequencing: an embarrassment of choice, a world of opportunity. Nature Reviews Microbiology, 2012, 10, 599-606.	28.6	367
367	Comparison of genome diversity of <i>Brucella</i> spp. field isolates using Universal Bio-signature Detection Array and whole genome sequencing reveals limitations of current diagnostic methods. Gene, 2012, 509, 142-148.	2.2	9

#	ARTICLE	IF	CITATIONS
368	Whole-Genome Alignment. <i>Methods in Molecular Biology</i> , 2012, 855, 237-257.	0.9	27
370	A multiplex real-time PCR assay for the detection and differentiation of <i>Francisella tularensis</i> subspecies. <i>Journal of Medical Microbiology</i> , 2012, 61, 1525-1531.	1.8	17
371	Bacteriophages with the Ability to Degrade Uropathogenic <i>Escherichia Coli</i> Biofilms. <i>Viruses</i> , 2012, 4, 471-487.	3.3	94
372	Multiple genome comparison based on overlap regions of pairwise local alignments. <i>BMC Bioinformatics</i> , 2012, 13, S7.	2.6	6
373	Whole genome sequencing of the fish pathogen <i>Francisella noatunensis</i> subsp. <i>orientalis</i> Toba04 gives novel insights into <i>Francisella</i> evolution and pathogenecity. <i>BMC Genomics</i> , 2012, 13, 598.	2.8	31
374	Genetic structure of community acquired methicillin-resistant <i>Staphylococcus aureus</i> USA300. <i>BMC Genomics</i> , 2012, 13, 508.	2.8	24
375	New Insights into the Bacterial Fitness-Associated Mechanisms Revealed by the Characterization of Large Plasmids of an Avian Pathogenic <i>E. coli</i> . <i>PLoS ONE</i> , 2012, 7, e29481.	2.5	24
376	The Highly Virulent 2006 Norwegian EHEC O103:H25 Outbreak Strain Is Related to the 2011 German O104:H4 Outbreak Strain. <i>PLoS ONE</i> , 2012, 7, e31413.	2.5	29
377	A Novel <i>Escherichia coli</i> O157:H7 Clone Causing a Major Hemolytic Uremic Syndrome Outbreak in China. <i>PLoS ONE</i> , 2012, 7, e36144.	2.5	61
378	Optimizing Read Mapping to Reference Genomes to Determine Composition and Species Prevalence in Microbial Communities. <i>PLoS ONE</i> , 2012, 7, e36427.	2.5	48
379	The Molecular Mechanism of Action of the CR6261-Azichromycin Combination Found through Computational Analysis. <i>PLoS ONE</i> , 2012, 7, e37790.	2.5	1
380	Comparative Geno-Plasticity Analysis of <i>Mycoplasma bovis</i> HB0801 (Chinese Isolate). <i>PLoS ONE</i> , 2012, 7, e38239.	2.5	71
381	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.	2.5	37
382	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.	2.5	61
383	An Integrated Pipeline for de Novo Assembly of Microbial Genomes. <i>PLoS ONE</i> , 2012, 7, e42304.	2.5	436
384	Tertiary Endosymbiosis in Two Dinotoms Has Generated Little Change in the Mitochondrial Genomes of Their Dinoflagellate Hosts and Diatom Endosymbionts. <i>PLoS ONE</i> , 2012, 7, e43763.	2.5	47
385	Survey of Endosymbionts in the <i>Diaphorina citri</i> Metagenome and Assembly of a <i>Wolbachia</i> wDi Draft Genome. <i>PLoS ONE</i> , 2012, 7, e50067.	2.5	77
386	Conveniently Pre-Tagged and Pre-Packaged: Extended Molecular Identification and Metagenomics Using Complete Metazoan Mitochondrial Genomes. <i>PLoS ONE</i> , 2012, 7, e51263.	2.5	14

#	ARTICLE	IF	CITATIONS
387	Lineage-specific Virulence Determinants of <i>Haemophilus influenzae</i> Biogroup aegyptius. Emerging Infectious Diseases, 2012, 18, 449-457.	4.3	22
388	Case Study of Sequence Capture Enrichment Technology: Identification of Variation Underpinning Developmental Syndromes in an Amniote Model. Genes, 2012, 3, 233-247.	2.4	7
389	In Silico Characterization and Molecular Evolutionary Analysis of a Novel Superfamily of Fungal Effector Proteins. Molecular Biology and Evolution, 2012, 29, 3371-3384.	8.9	90
390	Insights into salt tolerance from the genome of <i>Thellungiella salsuginea</i> . Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 12219-12224.	7.1	272
391	Chloroplast genome sequence confirms distinctness of Australian and Asian wild rice. Ecology and Evolution, 2012, 2, 211-217.	1.9	84
392	Nucleosomes Suppress Spontaneous Mutations Base-Specifically in Eukaryotes. Science, 2012, 335, 1235-1238.	12.6	90
393	The Draft Genome Sequence of <i>Corynebacterium diphtheriae</i> bv. mitis NCTC 3529 Reveals Significant Diversity between the Primary Disease-Causing Biovars. Journal of Bacteriology, 2012, 194, 3269-3269.	2.2	16
394	Accurate Identification of <i>Candida parapsilosis</i> (Sensu Lato) by Use of Mitochondrial DNA and Real-Time PCR. Journal of Clinical Microbiology, 2012, 50, 2310-2314.	3.9	28
395	Whole genome shotgun sequencing of one Colombian clinical isolate of <i>Mycobacterium tuberculosis</i> reveals DosR regulon gene deletions. FEMS Microbiology Letters, 2012, 330, 113-120.	1.8	20
396	Comparative genomic analysis of <i>Salmonella enterica</i> subsp. <i>enterica</i> serovar Weltevreden foodborne strains with other serovars. International Journal of Food Microbiology, 2012, 155, 247-256.	4.7	16
397	Alignment of multiple complete genomes suggests that gene rearrangements may contribute towards the speciation of <i>Mycobacteria</i> . Infection, Genetics and Evolution, 2012, 12, 819-826.	2.3	16
398	Expansion of the IncX plasmid family for improved identification and typing of novel plasmids in drug-resistant Enterobacteriaceae. Plasmid, 2012, 68, 43-50.	1.4	260
399	Lipopolysaccharide biosynthesis genes discriminate between <i>Rubus</i> and <i>Spiraeoideae</i> infective genotypes of <i>Erwinia amylovora</i> . Molecular Plant Pathology, 2012, 13, 975-984.	4.2	16
400	The metagenome of the marine anammox bacterium <i>Candidatus Scalindua profunda</i> illustrates the versatility of this globally important nitrogen cycle bacterium. Environmental Microbiology, 2013, 15, 1275-1289.	3.8	246
401	Comparative genome characterization of <i>Achromobacter</i> members reveals potential genetic determinants facilitating the adaptation to a pathogenic lifestyle. Applied Microbiology and Biotechnology, 2013, 97, 6413-6425.	3.6	45
402	Dissection of a major QTL for seed colour and fibre content in <i>Brassica napus</i> reveals colocalization with candidate genes for phenylpropanoid biosynthesis and flavonoid deposition. Plant Breeding, 2013, 132, 382-389.	1.9	46
403	Tool for rapid annotation of microbial SNPs (TRAMS): a simple program for rapid annotation of genomic variation in prokaryotes. Antonie Van Leeuwenhoek, 2013, 104, 431-434.	1.7	15
404	Genomic characterization provides new insight into <i>Salmonella</i> phage diversity. BMC Genomics, 2013, 14, 481.	2.8	80

#	ARTICLE	IF	CITATIONS
405	Comparative genomics of <i>Salmonella enterica</i> serovars Derby and Mbandaka, two prevalent serovars associated with different livestock species in the UK. BMC Genomics, 2013, 14, 365.	2.8	45
406	Reductive evolution in <i>Streptococcus agalactiae</i> and the emergence of a host adapted lineage. BMC Genomics, 2013, 14, 252.	2.8	81
407	Comparative genomic analyses of <i>Mycoplasma hyopneumoniae</i> pathogenic 168 strain and its high-passaged attenuated strain. BMC Genomics, 2013, 14, 80.	2.8	49
408	High quality de novo sequencing and assembly of the <i>Saccharomyces arboricolus</i> genome. BMC Genomics, 2013, 14, 69.	2.8	87
409	Comparative genome analysis of <i>Spiroplasma melliferum</i> IPMB4A, a honeybee-associated bacterium. BMC Genomics, 2013, 14, 22.	2.8	118
410	Draft genome sequence of the male-killing <i>Wolbachia</i> strain wBol1 reveals recent horizontal gene transfers from diverse sources. BMC Genomics, 2013, 14, 20.	2.8	65
411	Comparative genome analysis of an avirulent and two virulent strains of avian <i>Pasteurella multocida</i> reveals candidate genes involved in fitness and pathogenicity. BMC Microbiology, 2013, 13, 106.	3.3	40
412	“Marseilleviridae”, a new family of giant viruses infecting amoebae. Archives of Virology, 2013, 158, 915-920.	2.1	106
413	Long-term strain improvements accumulate mutations in regulatory elements responsible for hyper-production of cellulolytic enzymes. Scientific Reports, 2013, 3, 1569.	3.3	104
414	Genome Sequencing of <i>Giardia lamblia</i> Genotypes A2 and B Isolates (DH and GS) and Comparative Analysis with the Genomes of Genotypes A1 and E (WB and Pig). Genome Biology and Evolution, 2013, 5, 2498-2511.	2.5	83
415	Truncation and Sequence Shuffling of Segment 6 Generate Replication-Competent Neuraminidase-Negative Influenza H5N1 Viruses. Journal of Virology, 2013, 87, 13556-13568.	3.4	10
416	An alignment-free test for recombination. Bioinformatics, 2013, 29, 3121-3127.	4.1	8
417	Genome sequencing and comparative genomics of honey bee microsporidia, <i>Nosema apis</i> reveal novel insights into host-parasite interactions. BMC Genomics, 2013, 14, 451.	2.8	61
418	Comparative analysis of the complete genome of an epidemic hospital sequence type 203 clone of vancomycin-resistant <i>Enterococcus faecium</i> . BMC Genomics, 2013, 14, 595.	2.8	50
419	Comparative genomics of actinomycetes with a focus on natural product biosynthetic genes. BMC Genomics, 2013, 14, 611.	2.8	175
420	inTB - a data integration platform for molecular and clinical epidemiological analysis of tuberculosis. BMC Bioinformatics, 2013, 14, 264.	2.6	7
421	Microbes, metagenomes and marine mammals: enabling the next generation of scientist to enter the genomic era. BMC Genomics, 2013, 14, 600.	2.8	27
422	Comparative genomics of <i>Campylobacter concisus</i> isolates reveals genetic diversity and provides insights into disease association. BMC Genomics, 2013, 14, 585.	2.8	39

#	ARTICLE	IF	CITATIONS
423	Genetic variability of mutans streptococci revealed by wide whole-genome sequencing. BMC Genomics, 2013, 14, 430.	2.8	31
424	Two Rapidly Evolving Genes Contribute to Male Fitness in Drosophila. Journal of Molecular Evolution, 2013, 77, 246-259.	1.8	6
425	Streptococcal collagen-like protein A and general stress protein 24 are immunomodulating virulence factors of group A Streptococcus. FASEB Journal, 2013, 27, 2633-2643.	0.5	18
426	Comparison of Genomes of Brucella melitensis M28 and the B. melitensis M5-90 Derivative Vaccine Strain Highlights the Translation Elongation Factor Tu Gene <i>tuf2</i> as an Attenuation-Related Gene. Infection and Immunity, 2013, 81, 2812-2818.	2.2	18
427	The evolutionary landscape of the Mycobacterium tuberculosis genome. Gene, 2013, 518, 187-193.	2.2	8
428	Intraspecific comparative genomics of Candida albicans mitochondria reveals non-coding regions under neutral evolution. Infection, Genetics and Evolution, 2013, 14, 302-312.	2.3	19
429	Real-Time Sequencing To Decipher the Molecular Mechanism of Resistance of a Clinical Pan-Drug-Resistant Acinetobacter baumannii Isolate from Marseille, France. Antimicrobial Agents and Chemotherapy, 2013, 57, 592-596.	3.2	70
430	Bioinformatics for microbial genotyping of equine encephalitis viruses, orthopoxviruses, and hantaviruses. Journal of Virological Methods, 2013, 193, 112-120.	2.1	3
431	Complete genome sequence of the endosymbiont Blattabacterium from the cockroach Nauphoeta cinerea (Blattodea: Blaberidae). Genomics, 2013, 102, 479-483.	2.9	20
432	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 E. coli isolates. Plasmid, 2013, 69, 127-137.	1.4	35
433	Evaluation of whole-genome sequencing as a genotyping tool for Campylobacter jejuni in comparison with pulsed-field gel electrophoresis and flaA typing. Poultry Science, 2013, 92, 573-580.	3.4	25
434	Bioinformatics Approaches in Studying Microbial Diversity. , 2013, , 119-140.		1
435	Identification and characterization of a periplasmic trilactone esterase, <i>Cee</i> , revealed unique features of ferric enterobactin acquisition in <i>Campylobacter</i> . Molecular Microbiology, 2013, 87, 594-608.	2.5	42
436	Tracing Patterns of Chloroplast Evolution in Euglenoids: Contributions from <i>Colacium vesiculosum</i> and <i>Strombomonas acuminata</i> (Euglenophyta). Journal of Eukaryotic Microbiology, 2013, 60, 214-221.	1.7	25
437	Genome-assisted development of nuclear intergenic sequence markers for entomopathogenic fungi of the <i>Metarhizium anisopliae</i> species complex. Molecular Ecology Resources, 2013, 13, 210-217.	4.8	56
438	Organellar genome, nuclear ribosomal DNA repeat unit, and microsatellites isolated from a small-scale of 454 GS FLX sequencing on two mosses. Molecular Phylogenetics and Evolution, 2013, 66, 1089-1094.	2.7	23
439	High-Resolution Transcriptome Maps Reveal Strain-Specific Regulatory Features of Multiple Campylobacter jejuni Isolates. PLoS Genetics, 2013, 9, e1003495.	3.5	260
440	Genome-Wide Comparison of Medieval and Modern <i>Mycobacterium leprae</i> . Science, 2013, 341, 179-183.	12.6	313

#	ARTICLE	IF	CITATIONS
441	Whole genome sequencing identifies zoonotic transmission of MRSA isolates with the novel <i>mecA</i> homologue <i>mecC</i> . EMBO Molecular Medicine, 2013, 5, 509-515.	6.9	192
442	Comprehensive discovery and characterization of small RNAs in <i>Corynebacterium glutamicum</i> ATCC 13032. BMC Genomics, 2013, 14, 714.	2.8	61
443	STAR: ultrafast universal RNA-seq aligner. Bioinformatics, 2013, 29, 15-21.	4.1	35,376
444	Genome Sequence of the Group III <i>Clostridium botulinum</i> Strain Eklund-C. Genome Announcements, 2013, 1, e0004413.	0.8	5
445	Draft Genome Sequence of <i>Vibrio mimicus</i> Strain CAIM 602 T. Genome Announcements, 2013, 1, e0008413.	0.8	4
446	Draft Genome Sequence of MKD8, a Conjugal Recipient <i>Mycobacterium smegmatis</i> Strain. Genome Announcements, 2013, 1, e0014813.	0.8	8
447	Genome Sequence of <i>Salmonella bongori</i> Strain N268-08, a Rare Clinical Isolate. Genome Announcements, 2013, 1, .	0.8	2
448	Draft Genome Sequence of <i>Lactobacillus hominis</i> Strain CRBIP 24.179 T , Isolated from Human Intestine. Genome Announcements, 2013, 1, .	0.8	1
449	A Conserved Apomixis-Specific Polymorphism Is Correlated with Exclusive Exonuclease Expression in Premeiotic Ovules of Apomictic <i>Boechera</i> Species. Plant Physiology, 2013, 163, 1660-1672.	4.8	71
450	The Conserved Chimeric Transcript UPGRADE2 Is Associated with Unreduced Pollen Formation and Is Exclusively Found in Apomictic <i>Boechera</i> Species. Plant Physiology, 2013, 163, 1640-1659.	4.8	31
451	Complete Sequence of pOZ176, a 500-Kilobase IncP-2 Plasmid Encoding IMP-9-Mediated Carbapenem Resistance, from Outbreak Isolate <i>Pseudomonas aeruginosa</i> 96. Antimicrobial Agents and Chemotherapy, 2013, 57, 3775-3782.	3.2	73
452	Genome Sequence of an Epidemic Isolate of <i>Mycobacterium abscessus</i> subsp. <i>bolletii</i> from Rio de Janeiro, Brazil. Genome Announcements, 2013, 1, .	0.8	9
453	Draft Genome Sequence of <i>Geobacillus thermoleovorans</i> Strain B23. Genome Announcements, 2013, 1, .	0.8	7
454	Comparative Analysis of <i>Chlamydia psittaci</i> Genomes Reveals the Recent Emergence of a Pathogenic Lineage with a Broad Host Range. MBio, 2013, 4, .	4.1	90
455	Deciphering the Cryptic Genome: Genome-wide Analyses of the Rice Pathogen <i>Fusarium fujikuroi</i> Reveal Complex Regulation of Secondary Metabolism and Novel Metabolites. PLoS Pathogens, 2013, 9, e1003475.	4.7	406
456	The Subtelomeric <i>kipu</i> Satellite Repeat from <i>Phaseolus vulgaris</i> : Lessons Learned from the Genome Analysis of the Andean Genotype G19833. Frontiers in Plant Science, 2013, 4, 109.	3.6	39
457	De Novo ORFs in <i>Drosophila</i> Are Important to Organismal Fitness and Evolved Rapidly from Previously Non-coding Sequences. PLoS Genetics, 2013, 9, e1003860.	3.5	124
458	Whole Genome Sequencing versus Traditional Genotyping for Investigation of a <i>Mycobacterium tuberculosis</i> Outbreak: A Longitudinal Molecular Epidemiological Study. PLoS Medicine, 2013, 10, e1001387.	8.4	425

#	ARTICLE	IF	CITATIONS
459	Replicon-Dependent Bacterial Genome Evolution: The Case of <i>Sinorhizobium meliloti</i> . <i>Genome Biology and Evolution</i> , 2013, 5, 542-558.	2.5	94
460	Characterization of the Genome of the Dairy <i>Lactobacillus helveticus</i> Bacteriophage ϕ AQ113. <i>Applied and Environmental Microbiology</i> , 2013, 79, 4712-4718.	3.1	24
461	Genomic Evolution of the Pathogenic <i>Wolbachia</i> Strain, wMelPop. <i>Genome Biology and Evolution</i> , 2013, 5, 2189-2204.	2.5	96
462	Genomic Diversity of "Deep Ecotype" <i>Alteromonas macleodii</i> Isolates: Evidence for Pan-Mediterranean Clonal Frames. <i>Genome Biology and Evolution</i> , 2013, 5, 1220-1232.	2.5	71
463	Progressive genome-wide introgression in agricultural <i>Campylobacter coli</i> . <i>Molecular Ecology</i> , 2013, 22, 1051-1064.	3.9	128
464	Whole-Genome Draft Sequences of 26 Enterohemorrhagic <i>Escherichia coli</i> O157:H7 Strains. <i>Genome Announcements</i> , 2013, 1, e0013412.	0.8	31
465	Comparative genomics of Japanese <i>Erwinia pyrifoliae</i> strain Ejp617 with closely related erwinias. <i>Genome</i> , 2013, 56, 83-90.	2.0	5
466	Nucleotide sequence alignment using sparse coding and belief propagation. , 2013, 2013, 588-91.		1
467	H-NS Plays a Role in Expression of <i>Acinetobacter baumannii</i> Virulence Features. <i>Infection and Immunity</i> , 2013, 81, 2574-2583.	2.2	100
468	Genome Sequencing Identifies Two Nearly Unchanged Strains of Persistent <i>Listeria monocytogenes</i> Isolated at Two Different Fish Processing Plants Sampled 6 Years Apart. <i>Applied and Environmental Microbiology</i> , 2013, 79, 2944-2951.	3.1	110
469	Non-contiguous finished genome sequence and description of <i>Clostridium dakarense</i> sp. nov.. <i>Standards in Genomic Sciences</i> , 2013, 9, 14-27.	1.5	45
470	Non-contiguous finished genome sequence and description of <i>Nosocomiicoccus massiliensis</i> sp. nov.. <i>Standards in Genomic Sciences</i> , 2013, 9, 205-219.	1.5	18
471	Non-contiguous finished genome sequence and description of <i>Holdemania massiliensis</i> sp. nov.. <i>Standards in Genomic Sciences</i> , 2013, 9, 395-409.	1.5	25
472	Non contiguous-finished genome sequence and description of <i>Peptoniphilus grossensis</i> sp. nov.. <i>Standards in Genomic Sciences</i> , 2012, 7, 320-330.	1.5	34
473	Non contiguous-finished genome sequence and description of <i>Peptoniphilus senegalensis</i> sp. nov.. <i>Standards in Genomic Sciences</i> , 2013, 7, 370-381.	1.5	38
474	Non contiguous-finished genome sequence and description of <i>Enorma massiliensis</i> gen. nov., sp. nov., a new member of the Family <i>Coriobacteriaceae</i> . <i>Standards in Genomic Sciences</i> , 2013, 8, 290-305.	1.5	37
475	Non contiguous-finished genome sequence and description of <i>Bacillus massiliosenegalensis</i> sp. nov.. <i>Standards in Genomic Sciences</i> , 2013, 8, 264-278.	1.5	33
476	Non contiguous-finished genome sequence and description of <i>Dielma fastidiosa</i> gen. nov., sp. nov., a new member of the Family <i>Erysipelotrichaceae</i> . <i>Standards in Genomic Sciences</i> , 2013, 8, 336-351.	1.5	52

#	ARTICLE	IF	CITATIONS
477	Non-contiguous finished genome sequence and description of <i>Kallipyga massiliensis</i> gen. nov., sp. nov., a new member of the family Clostridiales Incertae Sedis XI. Standards in Genomic Sciences, 2013, 8, 500-515.	1.5	23
478	Genome sequence and description of <i>Timonella senegalensis</i> gen. nov., sp. nov., a new member of the suborder Micrococcinae. Standards in Genomic Sciences, 2013, 8, 318-335.	1.5	32
479	Non-contiguous finished genome sequence and description of <i>Bacillus massilioanorexius</i> sp. nov.. Standards in Genomic Sciences, 2013, 8, 465-479.	1.5	24
480	Large-scale multiple sequence alignment visualization through gradient vector flow analysis. , 2013, , .		4
481	Comparative Genomics of Multiple Strains of <i>Pseudomonas cannabina</i> pv. <i>alisalensis</i> , a Potential Model Pathogen of Both Monocots and Dicots. PLoS ONE, 2013, 8, e59366.	2.5	34
482	On the Evolutionary History, Population Genetics and Diversity among Isolates of <i>Salmonella</i> Enteritidis PFGE Pattern JEGX01.0004. PLoS ONE, 2013, 8, e55254.	2.5	146
483	Comparative Genomic Analysis of <i>Mycobacterium tuberculosis</i> Drug Resistant Strains from Russia. PLoS ONE, 2013, 8, e56577.	2.5	42
484	Evolution of Red Algal Plastid Genomes: Ancient Architectures, Introns, Horizontal Gene Transfer, and Taxonomic Utility of Plastid Markers. PLoS ONE, 2013, 8, e59001.	2.5	112
485	Genome Sequence of <i>Lactobacillus pentosus</i> KCA1: Vaginal Isolate from a Healthy Premenopausal Woman. PLoS ONE, 2013, 8, e59239.	2.5	50
486	Defining the Sequence Elements and Candidate Genes for the Coloboma Mutation. PLoS ONE, 2013, 8, e60267.	2.5	4
487	Adaptability and Persistence of the Emerging Pathogen <i>Bordetella petrii</i> . PLoS ONE, 2013, 8, e65102.	2.5	17
488	The Plastid Genome of the Red Macroalga <i>Grateloupia taiwanensis</i> (Halymeniaceae). PLoS ONE, 2013, 8, e68246.	2.5	26
489	TCW: Transcriptome Computational Workbench. PLoS ONE, 2013, 8, e69401.	2.5	17
490	Genome Annotation of <i>Burkholderia</i> sp. SJ98 with Special Focus on Chemotaxis Genes. PLoS ONE, 2013, 8, e70624.	2.5	9
491	Comparative Genome Analysis of <i>Mycobacterium avium</i> Revealed Genetic Diversity in Strains that Cause Pulmonary and Disseminated Disease. PLoS ONE, 2013, 8, e71831.	2.5	75
492	Normal Mutation Rate Variants Arise in a Mutator (Mut S) <i>Escherichia coli</i> Population. PLoS ONE, 2013, 8, e72963.	2.5	37
493	Virulence Potential and Genome-Wide Characterization of Drug Resistant <i>Streptococcus pneumoniae</i> Clones Selected In Vivo by the 7-Valent Pneumococcal Conjugate Vaccine. PLoS ONE, 2013, 8, e74867.	2.5	13
494	Comparative Genomic Analyses of <i>Streptococcus pseudopneumoniae</i> Provide Insight into Virulence and Commensalism Dynamics. PLoS ONE, 2013, 8, e65670.	2.5	21

#	ARTICLE	IF	CITATIONS
495	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.	2.5	107
496	Evolutionary Genomics and Adaptive Evolution of the Hedgehog Gene Family (Shh, Ihh and Dhh) in Vertebrates. <i>PLoS ONE</i> , 2014, 9, e74132.	2.5	27
497	Genomics of Sponge-Associated <i>Streptomyces</i> spp. Closely Related to <i>Streptomyces albus</i> J1074: Insights into Marine Adaptation and Secondary Metabolite Biosynthesis Potential. <i>PLoS ONE</i> , 2014, 9, e96719.	2.5	51
498	<i>Marinobacter salarius</i> sp. nov. and <i>Marinobacter similis</i> sp. nov., Isolated from Sea Water. <i>PLoS ONE</i> , 2014, 9, e106514.	2.5	39
499	New Insights into <i>Dehalococcoides mccartyi</i> Metabolism from a Reconstructed Metabolic Network-Based Systems-Level Analysis of <i>D. mccartyi</i> Transcriptomes. <i>PLoS ONE</i> , 2014, 9, e94808.	2.5	14
500	Genomes of Two New Ammonia-Oxidizing Archaea Enriched from Deep Marine Sediments. <i>PLoS ONE</i> , 2014, 9, e96449.	2.5	32
501	The 203 kbp Mitochondrial Genome of the Phytopathogenic Fungus <i>Sclerotinia borealis</i> Reveals Multiple Invasions of Introns and Genomic Duplications. <i>PLoS ONE</i> , 2014, 9, e107536.	2.5	93
502	Conserved Gene Order and Expanded Inverted Repeats Characterize Plastid Genomes of <i>Thalassiosirales</i> . <i>PLoS ONE</i> , 2014, 9, e107854.	2.5	44
503	Exploring the Genes of Yerba Mate (<i>Ilex paraguariensis</i> A. St.-Hil.) by NGS and De Novo Transcriptome Assembly. <i>PLoS ONE</i> , 2014, 9, e109835.	2.5	19
504	Local Similarity Search to Find Gene Indicators in Mitochondrial Genomes. <i>Biology</i> , 2014, 3, 220-242.	2.8	1
505	Complete Genome Sequence of <i>Klebsiella pneumoniae</i> Strain ATCC 43816 KPPR1, a Rifampin-Resistant Mutant Commonly Used in Animal, Genetic, and Molecular Biology Studies. <i>Genome Announcements</i> , 2014, 2, .	0.8	52
506	Inference of the Properties of the Recombination Process from Whole Bacterial Genomes. <i>Genetics</i> , 2014, 196, 253-265.	2.9	41
507	Whole-Genome Sequencing for Rapid and Accurate Identification of Bacterial Transmission Pathways. <i>Methods in Microbiology</i> , 2014, 41, 123-152.	0.8	4
508	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.	3.3	3
509	Phylogenetic Analyses on the Diversity of <i>Aspergillus fumigatus</i> Sensu Lato Based on Five Orthologous Loci. <i>Mycopathologia</i> , 2014, 178, 163-176.	3.1	9
510	Comparative analysis of surface-exposed virulence factors of <i>Acinetobacter baumannii</i> . <i>BMC Genomics</i> , 2014, 15, 1020.	2.8	149
511	Genome organisation of the <i>Acinetobacter</i> lytic phage ZZ1 and comparison with other T4-like <i>Acinetobacter</i> phages. <i>BMC Genomics</i> , 2014, 15, 793.	2.8	14
512	Complete genome sequence of bacteriophage vB_YenP_AP5 which infects <i>Yersinia enterocolitica</i> serotype O:3. <i>Virology Journal</i> , 2014, 11, 188.	3.4	20

#	ARTICLE	IF	CITATIONS
513	Genome analysis of <i>Campylobacter jejuni</i> strains isolated from a waterborne outbreak. BMC Genomics, 2014, 15, 768.	2.8	40
514	Insights into the history of a bacterial group II intron remnant from the genomes of the nitrogen-fixing symbionts <i>Sinorhizobium meliloti</i> and <i>Sinorhizobium medicae</i> . Heredity, 2014, 113, 306-315.	2.6	13
515	Potential impact on kidney infection: a whole-genome analysis of <i>Leptospira santarosai</i> serovar Shermani. Emerging Microbes and Infections, 2014, 3, 1-11.	6.5	12
516	Annotation of a hybrid partial genome of the coffee rust (<i>Hemileia vastatrix</i>) contributes to the gene repertoire catalog of the Pucciniales. Frontiers in Plant Science, 2014, 5, 594.	3.6	34
517	Draft Genome Sequences of the Onion Center Rot Pathogen <i>Pantoea ananatis</i> PA4 and Maize Brown Stalk Rot Pathogen <i>P. ananatis</i> BD442. Genome Announcements, 2014, 2, .	0.8	7
518	Gene Arrangement Convergence, Diverse Intron Content, and Genetic Code Modifications in Mitochondrial Genomes of Sphaeropleales (Chlorophyta). Genome Biology and Evolution, 2014, 6, 2170-2180.	2.5	37
519	Evolution and Comparative Genomics of <i>Campylobacter jejuni</i> ST-677 Clonal Complex. Genome Biology and Evolution, 2014, 6, 2424-2438.	2.5	21
520	Comparative Genomic Analysis of N ₂ -Fixing and Non-N ₂ -Fixing <i>Paenibacillus</i> spp.: Organization, Evolution and Expression of the Nitrogen Fixation Genes. PLoS Genetics, 2014, 10, e1004231.	3.5	117
521	Bacterial gene neighborhood investigation environment: A large-scale genome visualization for big displays. , 2014, , .		1
522	Symbionts Commonly Provide Broad Spectrum Resistance to Viruses in Insects: A Comparative Analysis of <i>Wolbachia</i> Strains. PLoS Pathogens, 2014, 10, e1004369.	4.7	226
523	Whole-Genome Sequencing of the Nonproteolytic <i>Bacillus anthracis</i> V770-NP1-R Strain Reveals Multiple Mutations in Peptidase Loci. Genome Announcements, 2014, 2, .	0.8	7
524	Genome Sequence of a Presumptive <i>Mannheimia haemolytica</i> Strain with an A1/A6-Cross-Reactive Serotype from a White-Tailed Deer (<i>Odocoileus virginianus</i>). Genome Announcements, 2014, 2, .	0.8	2
525	Draft Genome Sequence of a Multidrug-Resistant <i>Acinetobacter baumannii</i> PKAB07 Clinical Strain from India Belonging to Sequence Type 195. Genome Announcements, 2014, 2, .	0.8	6
526	Whole-Genome Sequencing of Streptomycin-Resistant <i>Mycobacterium tuberculosis</i> Isolate VRFCWCF MRTB 180 Reveals Novel and Potential Mutations for Resistance. Genome Announcements, 2014, 2, .	0.8	2
527	Finished Genome Sequence of the Laboratory Strain <i>Escherichia coli</i> K-12 RV308 (ATCC 31608). Genome Announcements, 2014, 2, .	0.8	2
528	The mitochondrial and chloroplast genomes of the haptophyte <i>Chrysochromulina tobin</i> contain unique repeat structures and gene profiles. BMC Genomics, 2014, 15, 604.	2.8	30
529	Alignathon: a competitive assessment of whole-genome alignment methods. Genome Research, 2014, 24, 2077-2089.	5.5	102
530	Complete Genome Sequences of <i>Bacillus subtilis</i> subsp. <i>subtilis</i> Laboratory Strains JH642 (AG174) and AG1839. Genome Announcements, 2014, 2, .	0.8	45

#	ARTICLE	IF	CITATIONS
531	A Shared Population of Epidemic Methicillin-Resistant <i>Staphylococcus aureus</i> 15 Circulates in Humans and Companion Animals. <i>MBio</i> , 2014, 5, e00985-13.	4.1	95
532	Finished Genome Sequence of <i>Escherichia coli</i> K-12 Strain HMS174 (ATCC 47011). <i>Genome Announcements</i> , 2014, 2, .	0.8	4
533	Genomic insights into the rapid emergence and evolution of MDR in <i>Staphylococcus pseudintermedius</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, 997-1007.	3.0	77
534	A novel plasmid pEA68 of <i>Erwinia amylovora</i> and the description of a new family of plasmids. <i>Archives of Microbiology</i> , 2014, 196, 891-899.	2.2	9
535	Revolutionizing Prokaryotic Systematics Through Next-Generation Sequencing. <i>Methods in Microbiology</i> , 2014, , 75-101.	0.8	7
536	Next-Gen phylogeography of rainforest trees: exploring landscape-level cpDNA variation from whole-genome sequencing. <i>Molecular Ecology Resources</i> , 2014, 14, 199-208.	4.8	34
537	Complete genome sequence of the bacteriophage YMC/09/04/R1988 MRSA BP: a lytic phage from a methicillin-resistant <i>Staphylococcus aureus</i> isolate. <i>FEMS Microbiology Letters</i> , 2014, 359, 144-146.	1.8	7
538	The marine bacterium <i>Marinobacter hydrocarbonoclasticus</i> SP17 degrades a wide range of lipids and hydrocarbons through the formation of oleolytic biofilms with distinct gene expression profiles. <i>FEMS Microbiology Ecology</i> , 2014, 90, 816-831.	2.7	56
539	Uncovering a Glycosyltransferase Provides Insights into the Glycosylation Step during Macrolactin and Bacillaene Biosynthesis. <i>ChemBioChem</i> , 2014, 15, 2747-2753.	2.6	19
540	Population Structure of KPC-Producing <i>Klebsiella pneumoniae</i> Isolates from Midwestern U.S. Hospitals. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 4961-4965.	3.2	78
541	Genetic Diversity of <i>Salmonella</i> Pathogenicity Islands SPI-5 and SPI-6 in <i>Salmonella</i> Newport. <i>Foodborne Pathogens and Disease</i> , 2014, 11, 798-807.	1.8	13
542	Genome skimming by shotgun sequencing helps resolve the phylogeny of a pantropical tree family. <i>Molecular Ecology Resources</i> , 2014, 14, 966-975.	4.8	102
543	Origin and Evolution of European Community-Acquired Methicillin-Resistant <i>Staphylococcus aureus</i> . <i>MBio</i> , 2014, 5, e01044-14.	4.1	112
544	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.	0.9	3
545	Widespread expression of conserved small RNAs in small symbiont genomes. <i>ISME Journal</i> , 2014, 8, 2490-2502.	9.8	47
546	Evidence for a single loss of mineralized teeth in the common avian ancestor. <i>Science</i> , 2014, 346, 1254390.	12.6	99
547	An <i>In Vitro</i> Deletion in <i>ribE</i> Encoding Lumazine Synthase Contributes to Nitrofurantoin Resistance in <i>Escherichia coli</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 7225-7233.	3.2	32
548	Comparative genomics reveals insights into avian genome evolution and adaptation. <i>Science</i> , 2014, 346, 1311-1320.	12.6	895

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549	Diversity and genomic insights into the uncultured <i>Clostridium</i> from the human microbiota. <i>Environmental Microbiology</i> , 2014, 16, 2635-2643.	3.8	55
550	Genome-guided insights into the versatile metabolic capabilities of the mercaptosuccinate-utilizing <i>Proteobacterium</i> strain <i>Bacteroides</i> . <i>Environmental Microbiology</i> , 2014, 16, 3370-3386.	3.8	13
551	NextGen sequencing reveals short double crossovers contribute disproportionately to genetic diversity in <i>Toxoplasma gondii</i> . <i>BMC Genomics</i> , 2014, 15, 1168.	2.8	17
552	Genome sequence of <i>Erinnyis ello</i> granulovirus (ErelGV), a natural cassava hornworm pesticide and the first sequenced sphingid-infecting betabaculovirus. <i>BMC Genomics</i> , 2014, 15, 856.	2.8	23
553	Comparative genomics of the major fungal agents of human and animal Sporotrichosis: <i>Sporothrix schenckii</i> and <i>Sporothrix brasiliensis</i> . <i>BMC Genomics</i> , 2014, 15, 943.	2.8	121
554	Intraspecies comparison of <i>Streptomyces pratensis</i> genomes reveals high levels of recombination and gene conservation between strains of disparate geographic origin. <i>BMC Genomics</i> , 2014, 15, 970.	2.8	46
555	Comparative analyses of <i>Legionella</i> species identifies genetic features of strains causing Legionnaires' disease. <i>Genome Biology</i> , 2014, 15, 505.	8.8	82
556	The Harvest suite for rapid core-genome alignment and visualization of thousands of intraspecific microbial genomes. <i>Genome Biology</i> , 2014, 15, 524.	8.8	1,428
557	Widespread differences in cortex DNA methylation of the <i>CNTNAP2</i> gene between humans and chimpanzees. <i>Epigenetics</i> , 2014, 9, 533-545.	2.7	30
558	Mining the <i>Pseudomonas</i> Genome. <i>Methods in Molecular Biology</i> , 2014, 1149, 417-432.	0.9	4
559	Phytoplasma Genomes: Evolution Through Mutually Complementary Mechanisms, Gene Loss and Horizontal Acquisition. , 2014, , 235-271.		22
560	Genome Sequencing of a Mung Bean Plant Growth Promoting Strain of <i>P. aeruginosa</i> with Biocontrol Ability. <i>International Journal of Genomics</i> , 2014, 2014, 1-10.	1.6	12
561	Novel Three-Component Rieske Non-Heme Iron Oxygenase System Catalyzing the <i>N</i> -Dealkylation of Chloroacetanilide Herbicides in Sphingomonads DC-6 and DC-2. <i>Applied and Environmental Microbiology</i> , 2014, 80, 5078-5085.	3.1	90
562	Using Arabidopsis-Related Model Species (ARMS): Growth, Genetic Transformation, and Comparative Genomics. <i>Methods in Molecular Biology</i> , 2014, 1062, 27-51.	0.9	8
563	Comparative Analysis of the Full Genome of <i>Helicobacter pylori</i> Isolate Sahul64 Identifies Genes of High Divergence. <i>Journal of Bacteriology</i> , 2014, 196, 1073-1083.	2.2	25
564	Assembly and analysis of a male sterile rubber tree mitochondrial genome reveals DNA rearrangement events and a novel transcript. <i>BMC Plant Biology</i> , 2014, 14, 45.	3.6	53
565	Previously Undescribed Plasmids Recovered from Activated Sludge Confer Tetracycline Resistance and Phenotypic Changes to <i>Acinetobacter oleivorans</i> DR1. <i>Microbial Ecology</i> , 2014, 67, 369-379.	2.8	12
566	CodaChrome: a tool for the visualization of proteome conservation across all fully sequenced bacterial genomes. <i>BMC Genomics</i> , 2014, 15, 65.	2.8	3

#	ARTICLE	IF	CITATIONS
567	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.	2.8	109
568	Genomic comparison of sporeforming bacilli isolated from milk. <i>BMC Genomics</i> , 2014, 15, 26.	2.8	27
569	Narrow-Host-Range Bacteriophages That Infect <i>Rhizobium etli</i> Associate with Distinct Genomic Types. <i>Applied and Environmental Microbiology</i> , 2014, 80, 446-454.	3.1	59
570	Genomic analysis of <i>Pseudomonas aeruginosa</i> PA96, the host of carbapenem resistance plasmid pOZ176. <i>FEMS Microbiology Letters</i> , 2014, 356, 212-216.	1.8	9
571	Characterization of <i>Euglenaformis</i> gen. nov. and the chloroplast genome of <i>Euglena proxima</i> (Euglenophyta). <i>Phycologia</i> , 2014, 53, 66-73.	1.4	36
572	To settle or to move? The interplay between two classes of cyclic lipopeptides in the biocontrol strain <i>Pseudomonas</i> CMR12a. <i>Environmental Microbiology</i> , 2014, 16, 2282-2300.	3.8	78
573	Genetic Characteristics and Pathogenic Mechanisms of Periodontal Pathogens. <i>Advances in Dental Research</i> , 2014, 26, 15-22.	3.6	34
574	Origin and Evolution of B Chromosomes in the Cichlid Fish <i>Astatotilapia latifasciata</i> Based on Integrated Genomic Analyses. <i>Molecular Biology and Evolution</i> , 2014, 31, 2061-2072.	8.9	112
575	Microevolution of <i>Renibacterium salmoninarum</i> : evidence for intercontinental dissemination associated with fish movements. <i>ISME Journal</i> , 2014, 8, 746-756.	9.8	32
576	Genomic analysis of three sponge-associated <i>Arthrobacter</i> Antarctic strains, inhibiting the growth of <i>Burkholderia cepacia</i> complex bacteria by synthesizing volatile organic compounds. <i>Microbiological Research</i> , 2014, 169, 593-601.	5.3	38
577	A single nucleotide in the promoter region modulates the expression of the β -lactamase OXA-61 in <i>Campylobacter jejuni</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2014, 69, 1215-1223.	3.0	57
578	<i>Streptococcus pneumoniae</i> Arginine Synthesis Genes Promote Growth and Virulence in Pneumococcal Meningitis. <i>Journal of Infectious Diseases</i> , 2014, 209, 1781-1791.	4.0	23
579	A lack of genetic basis for biovar differentiation in clinically important <i>Corynebacterium diphtheriae</i> from whole genome sequencing. <i>Infection, Genetics and Evolution</i> , 2014, 21, 54-57.	2.3	43
580	Complete genome sequence of Courdo11 virus, a member of the family Mimiviridae. <i>Virus Genes</i> , 2014, 48, 218-223.	1.6	21
581	β -Acetolactate synthase of <i>Lactococcus lactis</i> contributes to pH homeostasis in acid stress conditions. <i>International Journal of Food Microbiology</i> , 2014, 188, 99-107.	4.7	38
582	<i>Streptococcus agalactiae</i> clones infecting humans were selected and fixed through the extensive use of tetracycline. <i>Nature Communications</i> , 2014, 5, 4544.	12.8	208
583	Genomic analysis of a phage and prophage from a <i>Bacillus thuringiensis</i> strain. <i>Journal of General Virology</i> , 2014, 95, 751-761.	2.9	9
584	The genome of the <i>Erwinia amylovora</i> phage PhiEaH1 reveals greater diversity and broadens the applicability of phages for the treatment of fire blight. <i>FEMS Microbiology Letters</i> , 2014, 350, 25-27.	1.8	31

#	ARTICLE	IF	CITATIONS
585	The <i>Vibrio cholerae</i> type VI secretion system employs diverse effector modules for intraspecific competition. <i>Nature Communications</i> , 2014, 5, 3549.	12.8	211
586	Comparative genomic analyses reveal a lack of a substantial signature of host adaptation in <i>Rhodococcus equi</i> (â€Prescottella equiâ€™™). <i>Pathogens and Disease</i> , 2014, 71, 352-356.	2.0	11
587	Spontaneously Induced Prophages in <i>Lactobacillus gasseri</i> Contribute to Horizontal Gene Transfer. <i>Applied and Environmental Microbiology</i> , 2014, 80, 3508-3517.	3.1	62
588	Genomic Insights into the Evolutionary Origin of <i>Xanthomonas axonopodis</i> pv. <i>citri</i> and Its Ecological Relatives. <i>Applied and Environmental Microbiology</i> , 2014, 80, 6266-6279.	3.1	36
589	Complete genome sequence of the Gram-negative probiotic <i>Escherichia coli</i> strain Nissle 1917. <i>Journal of Biotechnology</i> , 2014, 187, 106-107.	3.8	76
590	Nextâ€™generation sequencing, <i>scp</i> FISH mapping and syntenyâ€™based modeling reveal mechanisms of decreasing dysploidy in <i>Cucumis</i> . <i>Plant Journal</i> , 2014, 77, 16-30.	5.7	90
591	High diversity of beta-lactamases in the General Hospital Vienna verified by whole genome sequencing and statistical analysis. <i>Infection, Genetics and Evolution</i> , 2014, 27, 408-417.	2.3	9
592	Prevalence and mapping of a plasmid encoding a type IV secretion system in <i>Acinetobacter baumannii</i> . <i>Genomics</i> , 2014, 104, 215-223.	2.9	23
593	Unveiling viralâ€™host interactions within the â€™microbial dark matterâ€™™. <i>Nature Communications</i> , 2014, 5, 4542.	12.8	69
594	Recombination drives genome evolution in outbreak-related <i>Legionella pneumophila</i> isolates. <i>Nature Genetics</i> , 2014, 46, 1205-1211.	21.4	76
595	Mitochondrial Phylogenomics of Early Land Plants: Mitigating the Effects of Saturation, Compositional Heterogeneity, and Codon-Usage Bias. <i>Systematic Biology</i> , 2014, 63, 862-878.	5.6	108
596	Chromosomal Rearrangement Features of <i>Yersinia pestis</i> Strains from Natural Plague Foci in China. <i>American Journal of Tropical Medicine and Hygiene</i> , 2014, 91, 722-728.	1.4	4
597	Evolution of Resistance to a Last-Resort Antibiotic in <i>Staphylococcus aureus</i> via Bacterial Competition. <i>Cell</i> , 2014, 158, 1060-1071.	28.9	178
598	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.	3.6	5
599	Analysis of the <i>Pantoea ananatis</i> pan-genome reveals factors underlying its ability to colonize and interact with plant, insect and vertebrate hosts. <i>BMC Genomics</i> , 2014, 15, 404.	2.8	127
600	Comparative genomic analysis of <i>Mycobacterium tuberculosis</i> clinical isolates. <i>BMC Genomics</i> , 2014, 15, 469.	2.8	33
601	Genomes of <i>Alteromonas australica</i> , a world apart. <i>BMC Genomics</i> , 2014, 15, 483.	2.8	45
602	Complete nucleotide sequence of pRS218, a large virulence plasmid, that augments pathogenic potential of meningitis-associated <i>Escherichia coli</i> strain RS218. <i>BMC Microbiology</i> , 2014, 14, 203.	3.3	34

#	ARTICLE	IF	CITATIONS
603	Immunoglobulin A Coating Identifies Colitogenic Bacteria in Inflammatory Bowel Disease. <i>Cell</i> , 2014, 158, 1000-1010.	28.9	982
604	In silico identification of potential virulence genes in 1,3-propanediol producer <i>Klebsiella pneumoniae</i> . <i>Journal of Biotechnology</i> , 2014, 189, 9-14.	3.8	11
605	An algebraic view of bacterial genome evolution. <i>Journal of Mathematical Biology</i> , 2014, 69, 1693-1718.	1.9	12
606	Genomic characterization of a <i>Helicobacter pylori</i> isolate from a patient with gastric cancer in China. <i>Gut Pathogens</i> , 2014, 6, 5.	3.4	6
607	Genetic Diversity and Evolution of <i>Salmonella enterica</i> Serovar Enteritidis Strains with Different Phage Types. <i>Journal of Clinical Microbiology</i> , 2014, 52, 1490-1500.	3.9	26
608	AOBA: Recognizing Object Behavior in Pervasive Urban Management. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2014, 26, 2625-2638.	5.7	2
609	Nitrogen-Fixing Rhizobial Strains Isolated from Common Bean Seeds: Phylogeny, Physiology, and Genome Analysis. <i>Applied and Environmental Microbiology</i> , 2014, 80, 5644-5654.	3.1	48
610	New Insights into Dissemination and Variation of the Health Care-Associated Pathogen <i>Acinetobacter baumannii</i> from Genomic Analysis. <i>MBio</i> , 2014, 5, e00963-13.	4.1	184
611	A Survey Sequence Comparison of <i>Saccharum</i> Genotypes Reveals Allelic Diversity Differences. <i>Tropical Plant Biology</i> , 2014, 7, 71-83.	1.9	14
612	Superinfection exclusion reveals heteroimmunity between <i>Pseudomonas aeruginosa</i> temperate phages. <i>Journal of Microbiology</i> , 2014, 52, 515-520.	2.8	3
613	Genome alignment with graph data structures: a comparison. <i>BMC Bioinformatics</i> , 2014, 15, 99.	2.6	32
614	Genomic and metabolic comparison with <i>Dickeya dadantii</i> 3937 reveals the emerging <i>Dickeya solani</i> potato pathogen to display distinctive metabolic activities and T5SS/T6SS-related toxin repertoire. <i>BMC Genomics</i> , 2014, 15, 283.	2.8	61
615	A high resolution map of mammalian X chromosome fragile regions assessed by large-scale comparative genomics. <i>Mammalian Genome</i> , 2014, 25, 618-635.	2.2	5
616	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.	4.1	67
617	Mitochondrial Genome Sequences and Comparative Genomics of <i>Achlya hypogyna</i> and <i>Thraustotheca clavata</i> . <i>Journal of Eukaryotic Microbiology</i> , 2014, 61, 146-154.	1.7	12
618	Genomic Heterogeneity and Ecological Speciation within One Subspecies of <i>Bacillus subtilis</i> . <i>Applied and Environmental Microbiology</i> , 2014, 80, 4842-4853.	3.1	44
619	Draft genome sequences of Terra1 and Terra2 viruses, new members of the family Mimiviridae isolated from soil. <i>Virology</i> , 2014, 452-453, 125-132.	2.4	22
620	Comparative genomics of oral isolates of <i>Streptococcus mutans</i> by in silico genome subtraction does not reveal accessory DNA associated with severe early childhood caries. <i>Infection, Genetics and Evolution</i> , 2014, 21, 269-278.	2.3	18

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621	A Novel Angular Dioxygenase Gene Cluster Encoding 3-Phenoxybenzoate 1â€²,2â€²-Dioxygenase in <i>Sphingobium wenxiniae</i> JZ-1. <i>Applied and Environmental Microbiology</i> , 2014, 80, 3811-3818.	3.1	30
622	Functional type 2 photosynthetic reaction centers found in the rare bacterial phylum Gemmatimonadetes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 7795-7800.	7.1	220
623	The mitochondrial genome of the red alga <i>Kappaphycus striatus</i> (â€œGreen Sacolâ€ variety): Complete nucleotide sequence, genome structure and organization, and comparative analysis. <i>Marine Genomics</i> , 2014, 18, 155-161.	1.1	20
624	Non-contiguous finished genome sequence and description of <i>Clostridium saudii</i> sp. nov. <i>Standards in Genomic Sciences</i> , 2014, 9, 8.	1.5	15
625	Identifying Pathogenicity Islands in Bacterial Pathogenomics Using Computational Approaches. <i>Pathogens</i> , 2014, 3, 36-56.	2.8	78
626	Genomic characterization of Î•RS603, a filamentous bacteriophage that is infectious to the phytopathogen <i>Ralstonia solanacearum</i> . <i>Microbiology and Immunology</i> , 2014, 58, 697-700.	1.4	18
627	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.	1.8	11
628	Whole Genome Sequence of Polyresistant <i>Mycobacterium tuberculosis</i> CWCFVRF PRTB 19 Sputum Isolate from Chennai, India, Closely Clustering with East African Indian 5 Genogroup. <i>Genome Announcements</i> , 2014, 2, .	0.8	2
629	Draft Genome Sequence of Multidrug-Resistant <i>Mycobacterium tuberculosis</i> Strain CWCFVRF MDRTB 670, Isolated from the Sputum of a Patient from Chennai, India, with Clinically Suspected Tuberculosis. <i>Genome Announcements</i> , 2014, 2, .	0.8	4
630	Draft genome sequence of <i>Gluconobacter thailandicus</i> NBRC 3257. <i>Standards in Genomic Sciences</i> , 2014, 9, 614-623.	1.5	12
631	Non-contiguous finished genome sequence and description of <i>Collinsella massiliensis</i> sp. nov.. <i>Standards in Genomic Sciences</i> , 2014, 9, 1144-1158.	1.5	13
632	Non-contiguous finished genome sequence and description of <i>Corynebacterium jeddahense</i> sp. nov.. <i>Standards in Genomic Sciences</i> , 2014, 9, 987-1002.	1.5	11
633	Genome sequence and description of <i>Nesterenkonia massiliensis</i> sp. nov. strain NP1T. <i>Standards in Genomic Sciences</i> , 2014, 9, 866-882.	1.5	18
634	Non-contiguous finished genome sequence and description of <i>Alistipes ihumii</i> sp. nov.. <i>Standards in Genomic Sciences</i> , 2014, 9, 1221-1235.	1.5	48
635	Non contiguous-finished genome sequence and description of <i>Enorma timonensis</i> sp. nov.. <i>Standards in Genomic Sciences</i> , 2014, 9, 970-986.	1.5	10
636	Genome sequence and description of <i>Bacteroides timonensis</i> sp. nov.. <i>Standards in Genomic Sciences</i> , 2014, 9, 1181-1197.	1.5	10
637	Non contiguous-finished genome sequence and description of <i>Clostridium jeddahense</i> sp. nov.. <i>Standards in Genomic Sciences</i> , 2014, 9, 1003-1019.	1.5	26
638	Genomic analysis of <i>Skermanella stibiirensistens</i> type strain SB22T. <i>Standards in Genomic Sciences</i> , 2014, 9, 1211-1220.	1.5	14

#	ARTICLE	IF	CITATIONS
639	Complete Genome Sequence of the Multiresistant <i>Acinetobacter baumannii</i> Strain AbH12O-A2, Isolated during a Large Outbreak in Spain. <i>Genome Announcements</i> , 2014, 2, .	0.8	19
640	Identification and characterization of accessory genomes in bacterial species based on genome comparison and metagenomic recruitment. , 2014, , .		0
641	Noncontiguous finished genome sequence and description of <i>Paenibacillus antibiotrophicus</i> sp. nov. GD11T, the type strain of <i>Paenibacillus antibiotrophicus</i> . <i>New Microbes and New Infections</i> , 2015, 8, 137-147.	1.6	5
642	Noncontiguous finished genome sequence and description of <i>Weeksellia massiliensis</i> sp. nov.. <i>New Microbes and New Infections</i> , 2015, 8, 89-98.	1.6	12
643	Comparative genomics of <i>Pseudomonas fluorescens</i> subclade III strains from human lungs. <i>BMC Genomics</i> , 2015, 16, 1032.	2.8	15
644	<i>Clostridium polynesiense</i> sp. nov., a new member of the human gut microbiota in French Polynesia. <i>Anaerobe</i> , 2015, 36, 79-87.	2.1	4
645	Supergroup C <i>Wolbachia</i> , mutualist symbionts of filarial nematodes, have a distinct genome structure. <i>Open Biology</i> , 2015, 5, 150099.	3.6	38
646	Genomic analysis of a ginger pathogen <i>Bacillus pumilus</i> providing the understanding to the pathogenesis and the novel control strategy. <i>Scientific Reports</i> , 2015, 5, 10259.	3.3	29
647	Comparative genomics <i>Lactobacillus reuteri</i> from sourdough reveals adaptation of an intestinal symbiont to food fermentations. <i>Scientific Reports</i> , 2015, 5, 18234.	3.3	65
648	Four novel algal virus genomes discovered from Yellowstone Lake metagenomes. <i>Scientific Reports</i> , 2015, 5, 15131.	3.3	44
649	The post-vaccine microevolution of invasive <i>Streptococcus pneumoniae</i> . <i>Scientific Reports</i> , 2015, 5, 14952.	3.3	36
650	Revisiting the reference genomes of human pathogenic <i>Cryptosporidium</i> species: reannotation of <i>C. parvum</i> Iowa and a new <i>C. hominis</i> reference. <i>Scientific Reports</i> , 2015, 5, 16324.	3.3	44
651	Phylogeny Inference of Closely Related Bacterial Genomes: Combining the Features of Both Overlapping Genes and Collinear Genomic Regions. <i>Evolutionary Bioinformatics</i> , 2015, 11s2, EBO.S33491.	1.2	3
652	BactoGeNIE: a large-scale comparative genome visualization for big displays. <i>BMC Bioinformatics</i> , 2015, 16, S6.	2.6	10
653	A platform for leveraging next generation sequencing for routine microbiology and public health use. <i>Health Information Science and Systems</i> , 2015, 3, S7.	5.2	7
654	Deep sequencing analysis of the heterogeneity of seed and commercial lots of the bacillus Calmette-Guérin (BCG) tuberculosis vaccine substrain Tokyo-172. <i>Scientific Reports</i> , 2015, 5, 17827.	3.3	10
655	Noncontiguous finished genome sequence and description of <i>Necropsobacter massiliensis</i> sp. nov.. <i>New Microbes and New Infections</i> , 2015, 8, 41-50.	1.6	8
656	Genome analysis and in vivo virulence of porcine extraintestinal pathogenic <i>Escherichia coli</i> strain PCN033. <i>BMC Genomics</i> , 2015, 16, 717.	2.8	63

#	ARTICLE	IF	CITATIONS
657	Genome analysis of <i>Daldinia eschscholtzii</i> strains UM 1400 and UM 1020, wood-decaying fungi isolated from human hosts. BMC Genomics, 2015, 16, 966.	2.8	16
658	Non contiguous-finished genome sequence and description of <i>Bacillus jeddahensis</i> sp. nov.. Standards in Genomic Sciences, 2015, 10, 47.	1.5	22
659	Draft genome sequence of <i>Cellulomonas carbonis</i> T26T and comparative analysis of six <i>Cellulomonas</i> genomes. Standards in Genomic Sciences, 2015, 10, 104.	1.5	5
660	Draft Genome Sequence of <i>Halostagnicola</i> sp. A56, an Extremely Halophilic Archaeon Isolated from the Andaman Islands. Genome Announcements, 2015, 3, .	0.8	3
661	Draft Genome Sequence of <i>Pedobacter</i> sp. Strain Hv1, an Isolate from Medicinal Leech Mucosal Castings. Genome Announcements, 2015, 3, .	0.8	0
662	Fatty acid kinase A is an important determinant of biofilm formation in <i>Staphylococcus aureus</i> USA300. BMC Genomics, 2015, 16, 861.	2.8	26
663	The genome of <i>Dasychira pudibunda</i> nucleopolyhedrovirus (DapuNPV) reveals novel genetic connection between baculoviruses infecting moths of the Lymantriidae family. BMC Genomics, 2015, 16, 759.	2.8	11
664	Comparison of <i>Xenorhabdus bovienii</i> bacterial strain genomes reveals diversity in symbiotic functions. BMC Genomics, 2015, 16, 889.	2.8	22
665	Comparative genome analysis identifies two large deletions in the genome of highly-passaged attenuated <i>Streptococcus agalactiae</i> strain YM001 compared to the parental pathogenic strain HN016. BMC Genomics, 2015, 16, 897.	2.8	21
666	Phylogenetic patterns of gene rearrangements in four mitochondrial genomes from the green algal family Hydrodictyaceae (<i>Sphaeropleales</i> , <i>Chlorophyceae</i>). BMC Genomics, 2015, 16, 826.	2.8	11
667	Exploring the genomic traits of fungus-feeding bacterial genus <i>Collimonas</i> . BMC Genomics, 2015, 16, 1103.	2.8	57
668	<i>Brachyspira suanatina</i> sp. nov., an enteropathogenic intestinal spirochaete isolated from pigs and mallards: genomic and phenotypic characteristics. BMC Microbiology, 2015, 15, 208.	3.3	39
669	Non-contiguous finished genome sequence and description of <i>Clostridium ihumii</i> sp. nov.. Standards in Genomic Sciences, 2015, 10, 63.	1.5	11
670	Draft genome sequence of <i>Halomonas meridiana</i> R1t3 isolated from the surface microbiota of the Caribbean Elkhorn coral <i>Acropora palmata</i> . Standards in Genomic Sciences, 2015, 10, 75.	1.5	19
671	Genomic information of the arsenic-resistant bacterium <i>Lysobacter arseniciresistens</i> type strain ZS79T and comparison of <i>Lysobacter</i> draft genomes. Standards in Genomic Sciences, 2015, 10, 88.	1.5	6
672	Chloroplast Genome Evolution in the Euglenaceae. Journal of Eukaryotic Microbiology, 2015, 62, 773-785.	1.7	35
673	A quantitative hybridization approach using 17 <i>scp</i> DNA markers for identification and clustering analysis of <i>Ralstonia solanacearum</i> . Plant Pathology, 2015, 64, 1270-1283.	2.4	2
674	Draft Genome Sequences of Two South African <i>Bacillus anthracis</i> Strains. Genome Announcements, 2015, 3, .	0.8	6

#	ARTICLE	IF	CITATIONS
675	Draft Genome Sequences of the Fish Pathogen <i>Vibrio harveyi</i> Strains VH2 and VH5. <i>Genome Announcements</i> , 2015, 3, .	0.8	6
676	Phage ϕ Pan70, a Putative Temperate Phage, Controls <i>Pseudomonas aeruginosa</i> in Planktonic, Biofilm and Burn Mouse Model Assays. <i>Viruses</i> , 2015, 7, 4602-4623.	3.3	42
677	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.	3.9	43
678	Genomic Resources of Three <i>Pulsatilla</i> Species Reveal Evolutionary Hotspots, Species-Specific Sites and Variable Plastid Structure in the Family Ranunculaceae. <i>International Journal of Molecular Sciences</i> , 2015, 16, 22258-22279.	4.1	25
679	Best practices for evaluating single nucleotide variant calling methods for microbial genomics. <i>Frontiers in Genetics</i> , 2015, 6, 235.	2.3	160
680	Unravelling the genome of long chain N-acylhomoserine lactone-producing <i>Acinetobacter</i> sp. strain GG2 and identification of its quorum sensing synthase gene. <i>Frontiers in Microbiology</i> , 2015, 6, 240.	3.5	16
681	Whole-genome comparative analysis of virulence genes unveils similarities and differences between endophytes and other symbiotic bacteria. <i>Frontiers in Microbiology</i> , 2015, 6, 419.	3.5	31
682	Genomic comparison of closely related Giant Viruses supports an accordion-like model of evolution. <i>Frontiers in Microbiology</i> , 2015, 6, 593.	3.5	41
683	Genome sequencing reveals a new lineage associated with lablab bean and genetic exchange between <i>Xanthomonas axonopodis</i> pv. <i>phaseoli</i> and <i>Xanthomonas fuscans</i> subsp. <i>fuscans</i> . <i>Frontiers in Microbiology</i> , 2015, 6, 1080.	3.5	29
684	A New Zamilon-like Virophage Partial Genome Assembled from a Bioreactor Metagenome. <i>Frontiers in Microbiology</i> , 2015, 6, 1308.	3.5	20
685	A Census of Nuclear Cyanobacterial Recruits in the Plant Kingdom. <i>PLoS ONE</i> , 2015, 10, e0120527.	2.5	1
686	Comparative Genomics of a <i>Helicobacter pylori</i> Isolate from a Chinese Yunnan Naxi Ethnic Aborigine Suggests High Genetic Divergence and Phage Insertion. <i>PLoS ONE</i> , 2015, 10, e0120659.	2.5	9
687	Genome-Guided Analysis of Physiological Capacities of <i>Tepidanaerobacter acetatoxydans</i> Provides Insights into Environmental Adaptations and Syntrophic Acetate Oxidation. <i>PLoS ONE</i> , 2015, 10, e0121237.	2.5	28
688	Comparative Genome Analyses of <i>Serratia marcescens</i> FS14 Reveals Its High Antagonistic Potential. <i>PLoS ONE</i> , 2015, 10, e0123061.	2.5	51
689	The Plastid Genome of the Cryptomonad <i>Teleaulax amphioxieia</i> . <i>PLoS ONE</i> , 2015, 10, e0129284.	2.5	30
690	Novel <i>recA</i> -Independent Horizontal Gene Transfer in <i>Escherichia coli</i> K-12. <i>PLoS ONE</i> , 2015, 10, e0130813.	2.5	12
691	Genome Sequence Analysis of the Naphthenic Acid Degrading and Metal Resistant Bacterium <i>Cupriavidus gilardii</i> CR3. <i>PLoS ONE</i> , 2015, 10, e0132881.	2.5	44
692	Comparative Transcriptome Analysis Reveals Cool Virulence Factors of <i>Ralstonia solanacearum</i> Race 3 Biovar 2. <i>PLoS ONE</i> , 2015, 10, e0139090.	2.5	43

#	ARTICLE	IF	CITATIONS
693	Deciphering the conserved genetic loci implicated in plant disease control through comparative genomics of <i>Bacillus amyloliquefaciens</i> subsp. <i>plantarum</i> . <i>Frontiers in Plant Science</i> , 2015, 6, 631.	3.6	52
694	An Effective Big Data Supervised Imbalanced Classification Approach for Ortholog Detection in Related Yeast Species. <i>BioMed Research International</i> , 2015, 2015, 1-12.	1.9	17
695	Population structure of <i>Neisseria gonorrhoeae</i> based on whole genome data and its relationship with antibiotic resistance. <i>PeerJ</i> , 2015, 3, e806.	2.0	67
696	Targeting DnaN for tuberculosis therapy using novel griselimycins. <i>Science</i> , 2015, 348, 1106-1112.	12.6	262
697	Detection and Genomic Characterization of Motility in <i>Lactobacillus curvatus</i> : Confirmation of Motility in a Species outside the <i>Lactobacillus salivarius</i> Clade. <i>Applied and Environmental Microbiology</i> , 2015, 81, 1297-1308.	3.1	67
698	Genome sequencing reveals novel deletions associated with secondary resistance to pyrazinamide in MDR <i>Mycobacterium tuberculosis</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, 2511-2514.	3.0	21
699	Mechanisms of solvent resistance mediated by interplay of cellular factors in <i>Pseudomonas putida</i> . <i>FEMS Microbiology Reviews</i> , 2015, 39, 555-566.	8.6	143
700	dipSPAdes: Assembler for Highly Polymorphic Diploid Genomes. <i>Journal of Computational Biology</i> , 2015, 22, 528-545.	1.6	69
701	The genomes of closely related <i>Pantoea ananatis</i> maize seed endophytes having different effects on the host plant differ in secretion system genes and mobile genetic elements. <i>Frontiers in Microbiology</i> , 2015, 6, 440.	3.5	85
702	Next-generation sequencing approach for connecting secondary metabolites to biosynthetic gene clusters in fungi. <i>Frontiers in Microbiology</i> , 2015, 5, 774.	3.5	80
703	Full genome SNP-based phylogenetic analysis reveals the origin and global spread of <i>Brucella melitensis</i> . <i>BMC Genomics</i> , 2015, 16, 93.	2.8	72
704	Comparative genomic analysis reveals occurrence of genetic recombination in virulent <i>Cryptosporidium hominis</i> subtypes and telomeric gene duplications in <i>Cryptosporidium parvum</i> . <i>BMC Genomics</i> , 2015, 16, 320.	2.8	74
705	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.	2.5	31
706	Structure, evolution and functional inference on the Mildew Locus O (MLO) gene family in three cultivated <i>Cucurbitaceae</i> spp.. <i>BMC Genomics</i> , 2015, 16, 1112.	2.8	45
707	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.	2.5	20
708	Distinctive Genome Reduction Rates Revealed by Genomic Analyses of Two <i>Coxiella</i> -Like Endosymbionts in Ticks. <i>Genome Biology and Evolution</i> , 2015, 7, 1779-1796.	2.5	140
709	Draft Genome Sequence of Isolate <i>Staphylococcus aureus</i> LHSKB Clinical, Isolated from an Infected Hip. <i>Genome Announcements</i> , 2015, 3, .	0.8	2
710	Draft Genome Sequences of Two Clinical Isolates of <i>Mycobacterium tuberculosis</i> from Sputum of Kazakh Patients. <i>Genome Announcements</i> , 2015, 3, .	0.8	4

#	ARTICLE	IF	CITATIONS
711	Draft Genome Sequence of <i>Stenotrophomonas maltophilia</i> Strain UV74 Reveals Extensive Variability within Its Genomic Group. <i>Genome Announcements</i> , 2015, 3, .	0.8	5
712	Draft Genome Sequences of <i>Vibrio alginolyticus</i> Strains V1 and V2, Opportunistic Marine Pathogens. <i>Genome Announcements</i> , 2015, 3, .	0.8	20
713	Draft Genome Sequence of the Biofilm-Hyperproducing <i>Acinetobacter baumannii</i> Clinical Strain MAR002. <i>Genome Announcements</i> , 2015, 3, .	0.8	6
714	Genome Sequence and Annotation of a Human Infection Isolate of <i>Escherichia coli</i> O26:H11 Involved in a Raw Milk Cheese Outbreak. <i>Genome Announcements</i> , 2015, 3, .	0.8	10
715	Population genomics reveals additive and replacing horizontal gene transfers in the emerging pathogen <i>Dickeya solani</i> . <i>BMC Genomics</i> , 2015, 16, 788.	2.8	63
716	<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.	2.5	30
717	Rise of Microbial Culturomics: Noncontiguous Finished Genome Sequence and Description of <i>Beduini massiliensis</i> gen. nov., sp. nov.. <i>OMICS A Journal of Integrative Biology</i> , 2015, 19, 766-776.	2.0	15
719	Draft Genome Sequence of the Commercial Biocontrol Strain <i>Pantoea agglomerans</i> P10c. <i>Genome Announcements</i> , 2015, 3, .	0.8	29
720	The <i>Bacillus cereus</i> Group. , 2015, , 1041-1078.		5
721	Phylogenomics characterization of a highly virulent <i>Edwardsiella</i> strain ET080813T encoding two distinct T3SS and three T6SS gene clusters: Propose a novel species as <i>Edwardsiella anguillarum</i> sp. nov.. <i>Systematic and Applied Microbiology</i> , 2015, 38, 36-47.	2.8	126
722	Comparative Analysis of Asteraceae Chloroplast Genomes: Structural Organization, RNA Editing and Evolution. <i>Plant Molecular Biology Reporter</i> , 2015, 33, 1526-1538.	1.8	65
723	Genome assembly and annotation of a <i>Drosophila simulans</i> strain from Madagascar. <i>Molecular Ecology Resources</i> , 2015, 15, 372-381.	4.8	46
724	Ecology and genomic features of infection with <i>Mycobacterium avium</i> subspecies <i>paratuberculosis</i> in Egypt. <i>Microbiology (United Kingdom)</i> , 2015, 161, 807-818.	1.8	27
725	Complete genome sequence of a filamentous bacteriophage, RS611, that infects the phytopathogen <i>Ralstonia solanacearum</i> . <i>Archives of Virology</i> , 2015, 160, 865-867.	2.1	7
726	<i>Fast and accurate estimation of evolutionary distances between closely related genomes</i> . <i>Bioinformatics</i> , 2015, 31, 1169-1175.	4.1	89
727	Polymerase chain reaction-based serotyping of pathogenic bacteria in food. <i>Journal of Microbiological Methods</i> , 2015, 110, 18-26.	1.6	25
728	Identification and monitoring of nitrification and denitrification genes in <i>Klebsiella pneumoniae</i> EGD-HP19-C for its ability to perform heterotrophic nitrification and aerobic denitrification. <i>Functional and Integrative Genomics</i> , 2015, 15, 63-76.	3.5	77
729	Is Sequence Alignment an Art or a Science?. <i>Systematic Botany</i> , 2015, 40, 14-26.	0.5	25

#	ARTICLE	IF	CITATIONS
730	Molecular and serological in-herd prevalence of <i>Anaplasma marginale</i> infection in Texas cattle. Preventive Veterinary Medicine, 2015, 119, 1-9.	1.9	34
731	Genomic and phenotypic differentiation among <i>Methanosarcina mazei</i> populations from Columbia River sediment. ISME Journal, 2015, 9, 2191-2205.	9.8	42
732	The broad-host-range plasmid pSFA231 isolated from petroleum-contaminated sediment represents a new member of the PromA plasmid family. Frontiers in Microbiology, 2014, 5, 777.	3.5	32
733	Gene Amplification and Sequencing for Bacterial Identification. Methods in Microbiology, 2015, 42, 433-464.	0.8	10
734	Genomic Tools for the Study of <i>Azospirillum</i> and Other Plant Growth-Promoting Rhizobacteria. , 2015, , 83-97.		1
735	Exploring Vertical Transmission of Bifidobacteria from Mother to Child. Applied and Environmental Microbiology, 2015, 81, 7078-7087.	3.1	191
736	Genetic profiles of <i>Propionibacterium acnes</i> and identification of a unique transposon with novel insertion sequences in sarcoid and non-sarcoid isolates. Scientific Reports, 2015, 5, 9832.	3.3	12
737	Genome-Assisted Development of a Diagnostic Protocol for Distinguishing High Virulence <i>Pseudomonas syringae</i> pv. tomato Strains. Plant Disease, 2015, 99, 527-534.	1.4	10
738	In silico identification of AMPylating enzymes and study of their divergent evolution. Scientific Reports, 2015, 5, 10804.	3.3	32
739	Characterization of Three <i>Mycobacterium</i> spp. with Potential Use in Bioremediation by Genome Sequencing and Comparative Genomics. Genome Biology and Evolution, 2015, 7, 1871-1886.	2.5	17
740	Exceptional reduction of the plastid genome of saguaro cactus (<i>Carnegiea gigantea</i>): Loss of the <i>ndh</i> gene suite and inverted repeat. American Journal of Botany, 2015, 102, 1115-1127.	1.7	137
741	Worldwide Population Structure, Long-Term Demography, and Local Adaptation of <i>Helicobacter pylori</i> . Genetics, 2015, 200, 947-963.	2.9	65
742	Differential RNA-seq (dRNA-seq) for annotation of transcriptional start sites and small RNAs in <i>Helicobacter pylori</i> . Methods, 2015, 86, 89-101.	3.8	47
743	Whole-Genome Sequence Analysis and Genome-Wide Virulence Gene Identification of <i>Riemerella anatipestifer</i> Strain Yb2. Applied and Environmental Microbiology, 2015, 81, 5093-5102.	3.1	35
744	Proteny: discovering and visualizing statistically significant syntenic clusters at the proteome level. Bioinformatics, 2015, 31, 3437-3444.	4.1	6
745	Genome Sequence of the <i>Drosophila melanogaster</i> Male-Killing Spiroplasma Strain MSRO Endosymbiont. MBio, 2015, 6, .	4.1	60
746	A naturally occurring <i>prfA</i> truncation in a <i>Listeria monocytogenes</i> field strain contributes to reduced replication and cell-to-cell spread. Veterinary Microbiology, 2015, 179, 91-101.	1.9	37
747	Genomic Avenue to Avian Colisepticemia. MBio, 2015, 6, .	4.1	59

#	ARTICLE	IF	CITATIONS
748	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.	2.8	19
749	Ecophysiological diversity of a novel member of the genus <i>Alteromonas</i> , and description of <i>Alteromonas mediterranea</i> sp. nov.. <i>Antonie Van Leeuwenhoek</i> , 2015, 107, 119-132.	1.7	44
750	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.	2.8	22
751	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.	2.8	105
752	Comparative genome analysis of <i>Pediococcus damnosus</i> LMG 28219, a strain well-adapted to the beer environment. <i>BMC Genomics</i> , 2015, 16, 267.	2.8	26
753	Genome sequencing and comparative genomics provides insights on the evolutionary dynamics and pathogenic potential of different H-serotypes of Shiga toxin-producing <i>Escherichia coli</i> O104. <i>BMC Microbiology</i> , 2015, 15, 83.	3.3	24
754	Complete plastome sequence of <i>Thalictrum coreanum</i> (Ranunculaceae) and transfer of the <i>rpl32</i> gene to the nucleus in the ancestor of the subfamily <i>Thalicthroideae</i> . <i>BMC Plant Biology</i> , 2015, 15, 40.	3.6	71
755	Bioinformatic analysis of phage AB3, a phiKMV-like virus infecting <i>Acinetobacter baumannii</i> . <i>Genetics and Molecular Research</i> , 2015, 14, 190-198.	0.2	7
756	Single-molecule sequencing reveals the molecular basis of multidrug-resistance in ST772 methicillin-resistant <i>Staphylococcus aureus</i> . <i>BMC Genomics</i> , 2015, 16, 388.	2.8	24
757	IonGAP: integrative bacterial genome analysis for Ion Torrent sequence data. <i>Bioinformatics</i> , 2015, 31, 2870-2873.	4.1	12
758	Identifying a potential receptor for the antibacterial peptide of sponge <i>Axinella donnani</i> endosymbiont. <i>Gene</i> , 2015, 566, 166-174.	2.2	3
759	Sequencing and characterizing the genome of <i>Estrella lausannensis</i> as an undergraduate project: training students and biological insights. <i>Frontiers in Microbiology</i> , 2015, 6, 101.	3.5	32
760	Characterization of a new Vi-like <i>Erwinia amylovora</i> bacteriophage phiEa2809. <i>FEMS Microbiology Letters</i> , 2015, 362, .	1.8	18
761	Origin and domestication of papaya Y^h chromosome. <i>Genome Research</i> , 2015, 25, 524-533.	5.5	87
762	Use of Whole-Genome Phylogeny and Comparisons for Development of a Multiplex PCR Assay To Identify Sequence Type 36 <i>Vibrio parahaemolyticus</i> . <i>Journal of Clinical Microbiology</i> , 2015, 53, 1864-1872.	3.9	21
763	The Pathogen of the Great Barrier Reef Sponge <i>Rhopaloeides odorabile</i> Is a New Strain of <i>Pseudoalteromonas agarivorans</i> Containing Abundant and Diverse Virulence-Related Genes. <i>Marine Biotechnology</i> , 2015, 17, 463-478.	2.4	51
764	Genomic characterization of Italian <i>Clostridium botulinum</i> group I strains. <i>Infection, Genetics and Evolution</i> , 2015, 36, 62-71.	2.3	24
765	The lanthipeptides of <i>Bacillus methylotrophicus</i> and their association with genomic islands. <i>Systematic and Applied Microbiology</i> , 2015, 38, 525-533.	2.8	10

#	ARTICLE	IF	CITATIONS
766	Whole-Genome Sequences of Eight <i>Campylobacter jejuni</i> Isolates from Wild Birds. <i>Genome Announcements</i> , 2015, 3, .	0.8	6
767	Nanoarchaeota, Their Sulfolobales Host, and Nanoarchaeota Virus Distribution across Yellowstone National Park Hot Springs. <i>Applied and Environmental Microbiology</i> , 2015, 81, 7860-7868.	3.1	63
768	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.	2.8	27
769	<i>Virgibacillus senegalensis</i> sp. nov., a new moderately halophilic bacterium isolated from human gut. <i>New Microbes and New Infections</i> , 2015, 8, 116-126.	1.6	12
770	Isolation and characterization of a native avirulent strain of <i>Streptococcus suis</i> serotype 2: a perspective for vaccine development. <i>Scientific Reports</i> , 2015, 5, 9835.	3.3	19
771	Lifestyle Evolution in Cyanobacterial Symbionts of Sponges. <i>MBio</i> , 2015, 6, e00391-15.	4.1	103
772	Hypermutator <i>Salmonella</i> Heidelberg induces an early cell death in epithelial cells. <i>Veterinary Microbiology</i> , 2015, 180, 65-74.	1.9	4
773	Genome Sequencing of Multiple Isolates Highlights Subtelomeric Genomic Diversity within <i>Fusarium fujikuroi</i> . <i>Genome Biology and Evolution</i> , 2015, 7, 3062-3069.	2.5	36
774	Multiple Genetic Mutations Associated with Polymyxin Resistance in <i>Acinetobacter baumannii</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 7899-7902.	3.2	35
775	<i>Burkholderia kirstenboschensis</i> sp. nov. nodulates papilionoid legumes indigenous to South Africa. <i>Systematic and Applied Microbiology</i> , 2015, 38, 545-554.	2.8	68
776	YOC, A new strategy for pairwise alignment of collinear genomes. <i>BMC Bioinformatics</i> , 2015, 16, 111.	2.6	8
777	The chloroplast genomes of <i>Bryopsis plumosa</i> and <i>Tydemania expeditiones</i> (Bryopsidales.) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	2.8	63
778	Draft Genome Sequence of the <i>Streptococcus pneumoniae</i> Avery Strain A66. <i>Genome Announcements</i> , 2015, 3, .	0.8	10
779	Buying in to bioinformatics: an introduction to commercial sequence analysis software. <i>Briefings in Bioinformatics</i> , 2015, 16, 700-709.	6.5	36
780	Whole-Genome Sequencing Identifies Emergence of a Quinolone Resistance Mutation in a Case of <i>Stenotrophomonas maltophilia</i> Bacteremia. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 7117-7120.	3.2	24
781	<i>Bordetella pertussis</i> evolution in the (functional) genomics era. <i>Pathogens and Disease</i> , 2015, 73, ftv064.	2.0	25
782	It Is Not All about Single Nucleotide Polymorphisms: Comparison of Mobile Genetic Elements and Deletions in <i>Listeria monocytogenes</i> Genomes Links Cases of Hospital-Acquired Listeriosis to the Environmental Source. <i>Journal of Clinical Microbiology</i> , 2015, 53, 3492-3500.	3.9	24
783	A protocol for targeted enrichment of intron-containing sequence markers for recent radiations: A phylogenomic example from <i>Heuchera</i> (Saxifragaceae). <i>Applications in Plant Sciences</i> , 2015, 3, 1500039.	2.1	99

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784	Comparative Genomics of Environmental and Clinical <i>Stenotrophomonas maltophilia</i> Strains with Different Antibiotic Resistance Profiles. <i>Genome Biology and Evolution</i> , 2015, 7, 2484-2505.	2.5	90
785	Draft Genome Sequence of <i>Thermus</i> sp. Isolate 2.9, Obtained from a Hot Water Spring Located in Salta, Argentina. <i>Genome Announcements</i> , 2015, 3, .	0.8	6
786	An Exploration into Fern Genome Space. <i>Genome Biology and Evolution</i> , 2015, 7, 2533-2544.	2.5	85
787	Genomic Epidemiology of <i>Clostridium botulinum</i> Isolates from Temporally Related Cases of Infant Botulism in New South Wales, Australia. <i>Journal of Clinical Microbiology</i> , 2015, 53, 2846-2853.	3.9	9
788	<i>Sinorhizobium meliloti</i> Phage Î M9 Defines a New Group of T4 Superfamily Phages with Unusual Genomic Features but a Common T=16 Capsid. <i>Journal of Virology</i> , 2015, 89, 10945-10958.	3.4	29
789	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.	3.0	13
790	Complete Genome Sequence of the Nonpathogenic Soil-Dwelling Bacterium <i>Clostridium sporogenes</i> Strain NCIMB 10696. <i>Genome Announcements</i> , 2015, 3, .	0.8	4
791	Draft genomic sequence of a selenite-reducing bacterium, <i>Paenirhodobacter ensiensis</i> DW2-9T. <i>Standards in Genomic Sciences</i> , 2015, 10, 38.	1.5	4
792	Mutations and genomic islands can explain the strain dependency of sugar utilization in 21 strains of <i>Propionibacterium freudenreichii</i> . <i>BMC Genomics</i> , 2015, 16, 296.	2.8	30
793	Transcriptional profiles of <i>Haloferax mediterranei</i> based on nitrogen availability. <i>Journal of Biotechnology</i> , 2015, 193, 100-107.	3.8	19
794	Environmental Surveillance for Toxigenic <i>Vibrio cholerae</i> in Surface Waters of Haiti. <i>American Journal of Tropical Medicine and Hygiene</i> , 2015, 92, 118-125.	1.4	20
795	Bacteriophage Resistance Mechanisms in the Fish Pathogen <i>Flavobacterium psychrophilum</i> : Linking Genomic Mutations to Changes in Bacterial Virulence Factors. <i>Applied and Environmental Microbiology</i> , 2015, 81, 1157-1167.	3.1	95
796	Genomic analyses of <i>Clostridium perfringens</i> isolates from five toxinotypes. <i>Research in Microbiology</i> , 2015, 166, 255-263.	2.1	71
797	Ten years of pan-genome analyses. <i>Current Opinion in Microbiology</i> , 2015, 23, 148-154.	5.1	498
798	Integration of genomic and proteomic analyses in the classification of the Siphoviridae family. <i>Virology</i> , 2015, 477, 144-154.	2.4	52
799	Molecular methods for serovar determination of <i>Salmonella</i> . <i>Critical Reviews in Microbiology</i> , 2015, 41, 309-325.	6.1	76
800	<scp>POY</scp> version 5: phylogenetic analysis using dynamic homologies under multiple optimality criteria. <i>Cladistics</i> , 2015, 31, 189-196.	3.3	74
801	Genomic and Transcriptomic Analyses of Colistin-Resistant Clinical Isolates of <i>Klebsiella pneumoniae</i> Reveal Multiple Pathways of Resistance. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 536-543.	3.2	185

#	ARTICLE	IF	CITATIONS
802	Effects of Actin-Like Proteins Encoded by Two <i>Bacillus pumilus</i> Phages on Unstable Lysogeny, Revealed by Genomic Analysis. <i>Applied and Environmental Microbiology</i> , 2015, 81, 339-350.	3.1	21
803	Genomic overview of the phytopathogen <i>Pectobacterium wasabiae</i> strain RNS 08.42.1A suggests horizontal acquisition of quorum-sensing genes. <i>Genetica</i> , 2015, 143, 241-252.	1.1	7
804	Insights into structural variations and genome rearrangements in prokaryotic genomes. <i>Bioinformatics</i> , 2015, 31, 1-9.	4.1	58
805	Complete genome of the multidrug-resistant <i>Acinetobacter baumannii</i> strain KBN10P02143 isolated from Korea. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2016, 111, 355-358.	1.6	4
807	The Complete Genome of <i>Brucella Suis</i> 019 Provides Insights on Cross-Species Infection. <i>Genes</i> , 2016, 7, 7.	2.4	13
808	Genetic Characterization and Comparative Genome Analysis of <i>Brucella melitensis</i> Isolates from India. <i>International Journal of Genomics</i> , 2016, 2016, 1-13.	1.6	12
809	A Brazilian <i>Marseillevirus</i> Is the Founding Member of a Lineage in Family <i>Marseilleviridae</i> . <i>Viruses</i> , 2016, 8, 76.	3.3	74
810	TP53 copy number expansion is associated with the evolution of increased body size and an enhanced DNA damage response in elephants. <i>ELife</i> , 2016, 5, .	6.0	191
811	Evolution and Diversity of the Antimicrobial Resistance Associated Mobilome in <i>Streptococcus suis</i> : A Probable Mobile Genetic Elements Reservoir for Other <i>Streptococci</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2016, 6, 118.	3.9	75
812	Comparative Genomics of Two ST 195 Carbapenem-Resistant <i>Acinetobacter baumannii</i> with Different Susceptibility to Polymyxin Revealed Underlying Resistance Mechanism. <i>Frontiers in Microbiology</i> , 2015, 6, 1445.	3.5	40
813	Recombination Does Not Hinder Formation or Detection of Ecological Species of <i>Synechococcus</i> Inhabiting a Hot Spring Cyanobacterial Mat. <i>Frontiers in Microbiology</i> , 2015, 6, 1540.	3.5	16
814	Novel Virophages Discovered in a Freshwater Lake in China. <i>Frontiers in Microbiology</i> , 2016, 7, 5.	3.5	48
815	Comparative Genomic Analysis of the ICESa2603 Family ICEs and Spread of <i>erm</i> (B)- and <i>tet</i> (O)-Carrying Transferable 89K-Subtype ICEs in Swine and Bovine Isolates in China. <i>Frontiers in Microbiology</i> , 2016, 7, 55.	3.5	38
816	Microevolution Analysis of <i>Bacillus coahuilensis</i> Unveils Differences in Phosphorus Acquisition Strategies and Their Regulation. <i>Frontiers in Microbiology</i> , 2016, 7, 58.	3.5	17
817	Multiple ESBL-Producing <i>Escherichia coli</i> Sequence Types Carrying Quinolone and Aminoglycoside Resistance Genes Circulating in Companion and Domestic Farm Animals in Mwanza, Tanzania, Harbor Commonly Occurring Plasmids. <i>Frontiers in Microbiology</i> , 2016, 7, 142.	3.5	63
818	Genetic Evidence for O-Specific Antigen as Receptor of <i>Pseudomonas aeruginosa</i> Phage K8 and Its Genomic Analysis. <i>Frontiers in Microbiology</i> , 2016, 7, 252.	3.5	22
819	Genomic Insights into a New <i>Citrobacter koseri</i> Strain Revealed Gene Exchanges with the Virulence-Associated <i>Yersinia pestis</i> pPCP1 Plasmid. <i>Frontiers in Microbiology</i> , 2016, 7, 340.	3.5	13
820	Integrating DNA Methylation and Gene Expression Data in the Development of the Soybean- <i>Bradyrhizobium</i> N2-Fixing Symbiosis. <i>Frontiers in Microbiology</i> , 2016, 7, 518.	3.5	32

#	ARTICLE	IF	CITATIONS
822	Genome and Transcriptome Sequences Reveal the Specific Parasitism of the Nematophagous <i>Purpureocillium lilacinum</i> 36-1. <i>Frontiers in Microbiology</i> , 2016, 7, 1084.	3.5	33
823	Identification of Novel Genomic Islands in Liverpool Epidemic Strain of <i>Pseudomonas aeruginosa</i> Using Segmentation and Clustering. <i>Frontiers in Microbiology</i> , 2016, 7, 1210.	3.5	57
824	Production of the Bioactive Compounds Violacein and Indolmycin Is Conditional in a <i>maeA</i> Mutant of <i>Pseudoalteromonas luteoviolacea</i> S4054 Lacking the Malic Enzyme. <i>Frontiers in Microbiology</i> , 2016, 7, 1461.	3.5	18
825	Co-diversification of <i>Enterococcus faecium</i> Core Genomes and PBP5: Evidences of <i>pbp5</i> Horizontal Transfer. <i>Frontiers in Microbiology</i> , 2016, 7, 1581.	3.5	34
826	Comparative Functional Genomic Analysis of Two <i>Vibrio</i> Phages Reveals Complex Metabolic Interactions with the Host Cell. <i>Frontiers in Microbiology</i> , 2016, 7, 1807.	3.5	16
827	Intraclonal Genome Stability of the Metallo- β -lactamase SPM-1-producing <i>Pseudomonas aeruginosa</i> ST277, an Endemic Clone Disseminated in Brazilian Hospitals. <i>Frontiers in Microbiology</i> , 2016, 7, 1946.	3.5	37
828	Comparative Genomic Analysis of Two Serotype 1/2b <i>Listeria monocytogenes</i> Isolates from Analogous Environmental Niches Demonstrates the Influence of Hypervariable Hotspots in Defining Pathogenesis. <i>Frontiers in Nutrition</i> , 2016, 3, 54.	3.7	4
829	Comparative Analysis of the Chloroplast Genomic Information of <i>Cunninghamia lanceolata</i> (Lamb.) Hook with Sibling Species from the Genera <i>Cryptomeria</i> D. Don, <i>Taiwania</i> Hayata, and <i>Calocedrus</i> Kurz. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1084.	4.1	23
830	H-NS Facilitates Sequence Diversification of Horizontally Transferred DNAs during Their Integration in Host Chromosomes. <i>PLoS Genetics</i> , 2016, 12, e1005796.	3.5	25
831	Comparative Genome Analysis Provides Insights into the Pathogenicity of <i>Flavobacterium psychrophilum</i> . <i>PLoS ONE</i> , 2016, 11, e0152515.	2.5	41
832	Mutation-Driven Divergence and Convergence Indicate Adaptive Evolution of the Intracellular Human-Restricted Pathogen, <i>Bartonella bacilliformis</i> . <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004712.	3.0	19
833	Molecular and Genomic Characterization of <i>Vibrio mimicus</i> Isolated from a Frozen Shrimp Processing Facility in Mexico. <i>PLoS ONE</i> , 2016, 11, e0144885.	2.5	13
834	The Formulation of Bacteriophage in a Semi Solid Preparation for Control of <i>Propionibacterium acnes</i> Growth. <i>PLoS ONE</i> , 2016, 11, e0151184.	2.5	49
835	De Novo Assembly of Human Herpes Virus Type 1 (HHV-1) Genome, Mining of Non-Canonical Structures and Detection of Novel Drug-Resistance Mutations Using Short- and Long-Read Next Generation Sequencing Technologies. <i>PLoS ONE</i> , 2016, 11, e0157600.	2.5	43
836	A Cytolethal Distending Toxin Variant from <i>Aggregatibacter actinomycetemcomitans</i> with an Aberrant CdtB That Lacks the Conserved Catalytic Histidine 160. <i>PLoS ONE</i> , 2016, 11, e0159231.	2.5	5
837	The Complete Chloroplast Genome Sequence of a Relict Conifer <i>Glyptostrobus pensilis</i> : Comparative Analysis and Insights into Dynamics of Chloroplast Genome Rearrangement in Cupressophytes and Pinaceae. <i>PLoS ONE</i> , 2016, 11, e0161809.	2.5	26
838	Comparative Genomic and Phenotypic Characterization of Pathogenic and Non-Pathogenic Strains of <i>Xanthomonas arboricola</i> Reveals Insights into the Infection Process of Bacterial Spot Disease of Stone Fruits. <i>PLoS ONE</i> , 2016, 11, e0161977.	2.5	31
839	In-silico prediction and deep-DNA sequencing validation indicate phase variation in 115 <i>Neisseria meningitidis</i> genes. <i>BMC Genomics</i> , 2016, 17, 843.	2.8	22

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840	RNA-seq of <i>Ranunculus sceleratus</i> and Identification of Orthologous Genes among Four <i>Ranunculus</i> Species. <i>Frontiers in Plant Science</i> , 2016, 7, 732.	3.6	5
841	Chloroplast Genome Sequence of <i>Pigeonpea</i> (<i>Cajanus cajan</i> (L.) Millspaugh) and <i>Cajanus scarabaeoides</i> (L.) Thouars: Genome Organization and Comparison with Other Legumes. <i>Frontiers in Plant Science</i> , 2016, 7, 1847.	3.6	34
842	Comparative structural analysis of Bru1 region homeologs in <i>Saccharum spontaneum</i> and <i>S. officinarum</i> . <i>BMC Genomics</i> , 2016, 17, 446.	2.8	8
843	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.	3.8	72
844	mcr-1.2, a New mcr Variant Carried on a Transferable Plasmid from a Colistin-Resistant KPC Carbapenemase-Producing <i>Klebsiella pneumoniae</i> Strain of Sequence Type 512. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 5612-5615.	3.2	165
845	<i>Yersinia enterocolitica</i> -Specific Infection by Bacteriophages TG1 and ÎR1-RT Is Dependent on Temperature-Regulated Expression of the Phage Host Receptor OmpF. <i>Applied and Environmental Microbiology</i> , 2016, 82, 5340-5353.	3.1	44
846	Identification of Polymorphisms Associated with Drought Adaptation QTL in <i>Brassica napus</i> by Resequencing. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 793-803.	1.8	39
847	Complete Genome Sequence of <i>Corynebacterium pseudotuberculosis</i> Strain PA01, Isolated from Sheep in Pará, Brazil. <i>Genome Announcements</i> , 2016, 4, .	0.8	4
848	Temperate phages promote colicin-dependent fitness of <i>Salmonella enterica</i> serovar Typhimurium. <i>Environmental Microbiology</i> , 2016, 18, 1591-1603.	3.8	35
849	Inflated organelle genomes and a circular-mapping mtDNA probably existed at the origin of coloniality in volvocine green algae. <i>European Journal of Phycology</i> , 2016, 51, 369-377.	2.0	20
850	<i>Saccharomyces eubayanus</i> and <i>Saccharomyces arboricola</i> reside in North Island native New Zealand forests. <i>Environmental Microbiology</i> , 2016, 18, 1137-1147.	3.8	64
851	Characterization of a novel <i>Achromobacter xylosoxidans</i> specific siphoviruse: phiAxp-1. <i>Scientific Reports</i> , 2016, 6, 21943.	3.3	19
852	Whole Genome Comparison of <i>Thermus</i> sp. NMX2.A1 Reveals Principal Carbon Metabolism Differences with Closest Relation <i>Thermus scotoductus</i> SA-01. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2791-2797.	1.8	5
853	Draft Genome Sequence of Biocontrol Agent <i>Bacillus cereus</i> UW85. <i>Genome Announcements</i> , 2016, 4, .	0.8	19
854	<i>Chlamydia trachomatis</i> from Australian Aboriginal people with trachoma are polyphyletic composed of multiple distinctive lineages. <i>Nature Communications</i> , 2016, 7, 10688.	12.8	42
855	Whole-Genome Sequencing Applied to the Molecular Epidemiology of Shiga Toxin-Producing <i>Escherichia coli</i> O157:H7 in Argentina. <i>Genome Announcements</i> , 2016, 4, .	0.8	5
856	Homologous Recombination within Large Chromosomal Regions Facilitates Acquisition of Î²-Lactam and Vancomycin Resistance in <i>Enterococcus faecium</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 5777-5786.	3.2	31
857	<i>Salmonella</i> Degrades the Host Glycocalyx Leading to Altered Infection and Glycan Remodeling. <i>Scientific Reports</i> , 2016, 6, 29525.	3.3	66

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858	Changes in pathogenicity and immunogenicity of <i>Mycoplasma mycoides</i> subsp. <i>mycoides</i> strains revealed by comparative genomics analysis. <i>Scientific Reports</i> , 2016, 6, 19081.	3.3	5
859	An account of Genomic Islands of zoonotic origin <i>Staphylococcus aureus</i> genomes – In silico approach. , 2016, , .		0
860	Genomic analysis of nontypeable pneumococci causing invasive pneumococcal disease in South Africa, 2003–2013. <i>BMC Genomics</i> , 2016, 17, 470.	2.8	15
861	Genome-wide analysis of chromosomal import patterns after natural transformation of <i>Helicobacter pylori</i> . <i>Nature Communications</i> , 2016, 7, 11995.	12.8	59
862	Delta-proteobacterial SAR324 group in hydrothermal plumes on the South Mid-Atlantic Ridge. <i>Scientific Reports</i> , 2016, 6, 22842.	3.3	21
863	MTGpick allows robust identification of genomic islands from a single genome. <i>Briefings in Bioinformatics</i> , 2016, 19, bbw118.	6.5	34
864	Comparative genomics of mitochondria in chlorarachniophyte algae: endosymbiotic gene transfer and organellar genome dynamics. <i>Scientific Reports</i> , 2016, 6, 21016.	3.3	23
865	Complete Genome Sequence of a <i>Bohle iridovirus</i> Isolate from Ornate Burrowing Frogs (<i>Tj ETQq1 1 0.784314 rgBT /Overlock</i>	0.8	12
866	(Meta)genomic insights into the pathogenome of <i>Cellulosimicrobium cellulans</i> . <i>Scientific Reports</i> , 2016, 6, 25527.	3.3	20
867	Use of single molecule sequencing for comparative genomics of an environmental and a clinical isolate of <i>Clostridium difficile</i> ribotype 078. <i>BMC Genomics</i> , 2016, 17, 1020.	2.8	11
868	Genomic diversity of bacteriophages infecting the fish pathogen <i>Flavobacterium psychrophilum</i> . <i>FEMS Microbiology Letters</i> , 2016, 363, fnw272.	1.8	29
869	Comparative genomics reveals <i>Lysinibacillus sphaericus</i> group comprises a novel species. <i>BMC Genomics</i> , 2016, 17, 709.	2.8	18
870	Draft Genome Sequences of Five Clinical Strains of <i>Brucella melitensis</i> Isolated from Patients Residing in Kuwait. <i>Genome Announcements</i> , 2016, 4, .	0.8	7
871	Structural and functional organization of the plasmid regulons of <i>Rhizobium leguminosarum</i> symbiotic genes. <i>Microbiology</i> , 2016, 85, 708-716.	1.2	2
872	Complete Genome Sequence of a New Megavirus Family Member Isolated from an Inland Water Lake for the First Time in India. <i>Genome Announcements</i> , 2016, 4, .	0.8	9
873	Draft genome sequence of <i>Psychrobacter</i> sp. ENNN9_III, a strain isolated from water in a polluted temperate estuarine system (Ria de Aveiro , Portugal). <i>Genomics Data</i> , 2016, 8, 21-24.	1.3	0
874	High-quality genome sequence and description of <i>Chryseobacterium senegalense</i> sp. nov.. <i>New Microbes and New Infections</i> , 2016, 10, 93-100.	1.6	4
875	Noncontiguous finished genome sequence and description of <i>Planococcus massiliensis</i> sp. nov., a moderately halophilic bacterium isolated from the human gut. <i>New Microbes and New Infections</i> , 2016, 10, 36-46.	1.6	14

#	ARTICLE	IF	CITATIONS
876	Complete genome sequence of <i>Halanaeroarchaeum sulfurreducens</i> ™ M27-SA2, a sulfur-reducing and acetate-oxidizing haloarchaeon from the deep-sea hypersaline anoxic lake Medee. Standards in Genomic Sciences, 2016, 11, 35.	1.5	15
877	The genome and genetics of a high oxidative stress tolerant <i>Serratia</i> sp. LCN16 isolated from the plant parasitic nematode <i>Bursaphelenchus xylophilus</i> . BMC Genomics, 2016, 17, 301.	2.8	18
878	Geographic isolates of <i>Lymantria dispar</i> multiple nucleopolyhedrovirus: Genome sequence analysis and pathogenicity against European and Asian gypsy moth strains. Journal of Invertebrate Pathology, 2016, 137, 10-22.	3.2	19
879	<i>In Vivo</i> Application of Bacteriophage as a Potential Therapeutic Agent To Control OXA-66-Like Carbapenemase-Producing <i>Acinetobacter baumannii</i> Strains Belonging to Sequence Type 357. Applied and Environmental Microbiology, 2016, 82, 4200-4208.	3.1	49
880	Gene and whole genome analyses reveal that the mycobacterial strain JS 623 is not a member of the species <i>Mycobacterium smegmatis</i> . Microbial Biotechnology, 2016, 9, 269-274.	4.2	2
881	Characterisation of worldwide <i>Helicobacter pylori</i> strains reveals genetic conservation and essentiality of serine protease HtrA. Molecular Microbiology, 2016, 99, 925-944.	2.5	70
882	PacBio SMRT assembly of a complex multi-replicon genome reveals chlorocatechol degradative operon in a region of genome plasticity. Gene, 2016, 586, 239-247.	2.2	22
883	<i>Risunbinella massiliensis</i> sp. nov., a new member of Thermoactinomycetaceae isolated from human gut. Antonie Van Leeuwenhoek, 2016, 109, 773-784.	1.7	8
884	Complete Genome Sequence of <i>Bacillus subtilis</i> Strain CU1050, Which Is Sensitive to Phage SP1 ² . Genome Announcements, 2016, 4, .	0.8	6
885	Enhancing the Sweetness of Yoghurt through Metabolic Remodeling of Carbohydrate Metabolism in <i>Streptococcus thermophilus</i> and <i>Lactobacillus delbrueckii</i> subsp. <i>bulgaricus</i> . Applied and Environmental Microbiology, 2016, 82, 3683-3692.	3.1	61
886	Mechanisms Involved in Acquisition of <i>bla</i> _{NDM} Genes by <i>IncA/C</i> ₂ and <i>IncFII</i> _Y Plasmids. Antimicrobial Agents and Chemotherapy, 2016, 60, 4082-4088.	3.2	49
887	Non contiguous-finished genome sequence and description of <i>Microbacterium gorillae</i> sp. nov.. Standards in Genomic Sciences, 2016, 11, 32.	1.5	24
888	Improved Complete Genome Sequence of the Extremely Radioresistant Bacterium <i>Deinococcus radiodurans</i> R1 Obtained Using PacBio Single-Molecule Sequencing. Genome Announcements, 2016, 4, .	0.8	26
889	Genomic Comparison of <i>Campylobacter</i> spp. and Their Potential for Zoonotic Transmission between Birds, Primates, and Livestock. Applied and Environmental Microbiology, 2016, 82, 7165-7175.	3.1	73
890	A systematic study of the whole genome sequence of <i>Amycolatopsis methanolica</i> strain 239 T provides an insight into its physiological and taxonomic properties which correlate with its position in the genus. Synthetic and Systems Biotechnology, 2016, 1, 169-186.	3.7	29
891	Software-based analysis of bacteriophage genomes, physical ends, and packaging strategies. BMC Genomics, 2016, 17, 679.	2.8	87
892	Genomic diversification of marine cyanophages into stable ecotypes. Environmental Microbiology, 2016, 18, 4240-4253.	3.8	44
893	Complete genome sequence of <i>Fictibacillus phosphorivorans</i> G25-29, a strain toxic to nematodes. Journal of Biotechnology, 2016, 239, 20-22.	3.8	8

#	ARTICLE	IF	CITATIONS
894	Characterization of <i>Pseudomonas aeruginosa</i> phage K5 genome and identification of its receptor related genes. Journal of Basic Microbiology, 2016, 56, 1344-1353.	3.3	12
895	An alphabaculovirus isolated from dead <i>Lymantria dispar</i> larvae shows high genetic similarity to baculovirus previously isolated from <i>Lymantria monacha</i> – An example of adaptation to a new host. Journal of Invertebrate Pathology, 2016, 139, 56-66.	3.2	11
896	Comparative genomic evidence for duplication of TLR1 subfamily and miiuy croaker TLR1 perceives LPS stimulation via MyD88 and TIRAP. Fish and Shellfish Immunology, 2016, 56, 336-348.	3.6	39
897	Evidence for an Opportunistic and Endophytic Lifestyle of the Bursaphelenchus xylophilus-Associated Bacteria Serratia marcescens PWN146 Isolated from Wilting Pinus pinaster. Microbial Ecology, 2016, 72, 669-681.	2.8	22
898	Vibrio natriegens as a fast-growing host for molecular biology. Nature Methods, 2016, 13, 849-851.	19.0	203
899	CRISPR Diversity and Microevolution in <i>Clostridium difficile</i> . Genome Biology and Evolution, 2016, 8, 2841-2855.	2.5	60
900	Characterisation of a novel integrative and conjugative element ICESsD9 carrying erm(B) and tet(O) resistance determinants in Streptococcus suis, and the distribution of ICESsD9-like elements in clinical isolates. Journal of Global Antimicrobial Resistance, 2016, 7, 13-18.	2.2	17
901	Genome-wide analyses of chitin synthases identify horizontal gene transfers towards bacteria and allow a robust and unifying classification into fungi. BMC Evolutionary Biology, 2016, 16, 252.	3.2	43
902	Genome Sequence of a Ranavirus Isolated from Pike-Perch <i>Sander lucioperca</i> . Genome Announcements, 2016, 4, .	0.8	11
903	Speciation driven by hybridization and chromosomal plasticity in a wild yeast. Nature Microbiology, 2016, 1, 15003.	13.3	161
904	Patient-Specific <i>Bacteroides</i> Genome Variants in Pouchitis. MBio, 2016, 7, .	4.1	38
905	Comparative genomics of European avian pathogenic E. Coli (APEC). BMC Genomics, 2016, 17, 960.	2.8	84
906	Ancestral Gene Flow and Parallel Organellar Genome Capture Result in Extreme Phylogenomic Discord in a Lineage of Angiosperms. Systematic Biology, 2017, 66, syw083.	5.6	132
907	MSAViewer: interactive JavaScript visualization of multiple sequence alignments. Bioinformatics, 2016, 32, 3501-3503.	4.1	156
908	Isolation and complete genome sequencing of Mimivirus bombay , a Giant Virus in sewage of Mumbai, India. Genomics Data, 2016, 9, 1-3.	1.3	16
909	Genome-sequence analysis of Acinetobacter johnsonii MB44 reveals potential nematode-virulent factors. SpringerPlus, 2016, 5, 986.	1.2	15
910	Comparison of a Modern and FossilPithovirusReveals Its Genetic Conservation and Evolution. Genome Biology and Evolution, 2016, 8, 2333-2339.	2.5	53
911	Tessaracoccus massiliensis sp. nov., a new bacterial species isolated from the human gut. New Microbes and New Infections, 2016, 13, 3-12.	1.6	8

#	ARTICLE	IF	CITATIONS
912	Complete Genome Sequence of <i>Moraxella osloensis</i> Strain KMC41, a Producer of 4-Methyl-3-Hexenoic Acid, a Major Malodor Compound in Laundry. Genome Announcements, 2016, 4, .	0.8	8
913	A genomic view of food-related and probiotic Enterococcus strains. DNA Research, 2017, 24, dsw043.	3.4	38
914	Genomic Sequence of a Ranavirus Isolated from Short-Finned Eel (<i>Anguilla australis</i>). Genome Announcements, 2016, 4, .	0.8	10
915	Whole genome sequencing revealed host adaptation-focused genomic plasticity of pathogenic <i>Leptospira</i> . Scientific Reports, 2016, 6, 20020.	3.3	86
916	Phenotypic differentiation of <i>Streptococcus pyogenes</i> populations is induced by recombination-driven gene-specific sweeps. Scientific Reports, 2016, 6, 36644.	3.3	24
917	Parallel evolution of highly conserved plastid genome architecture in red seaweeds and seed plants. BMC Biology, 2016, 14, 75.	3.8	72
918	An assemblage of Frankia Cluster II strains from California contains the canonical nod genes and also the sulfotransferase gene nodH. BMC Genomics, 2016, 17, 796.	2.8	97
919	Computational pan-genomics: status, promises and challenges. Briefings in Bioinformatics, 2018, 19, bbw089.	6.5	207
920	Complete Genome Sequence of the Endophytic Biocontrol Strain <i>Bacillus velezensis</i> CC09. Genome Announcements, 2016, 4, .	0.8	19
921	Organization and characteristics of the major histocompatibility complex class II region in the Yangtze finless porpoise (<i>Neophocaena asiaeorientalis asiaeorientalis</i>). Scientific Reports, 2016, 6, 22471.	3.3	35
922	Quantum changes in <i>Helicobacter pylori</i> gene expression accompany host-adaptation. DNA Research, 2017, 24, dsw046.	3.4	8
923	Evidence for the sexual origin of heterokaryosis in arbuscular mycorrhizal fungi. Nature Microbiology, 2016, 1, 16033.	13.3	137
924	CRISPR System Acquisition and Evolution of an Obligate Intracellular <i>Chlamydia</i> -Related Bacterium. Genome Biology and Evolution, 2016, 8, 2376-2386.	2.5	23
925	European derived <i>Saccharomyces cerevisiae</i> colonisation of New Zealand vineyards aided by humans. FEMS Yeast Research, 2016, 16, fow091.	2.3	29
926	Identification and molecular characterization of bacteriophage phiAxp-2 of <i>Achromobacter xylosoxidans</i> . Scientific Reports, 2016, 6, 34300.	3.3	14
927	Genomic Evolution of Two <i>Acinetobacter baumannii</i> Clinical Strains from ST-2 Clones Isolated in 2000 and 2010 (ST-2_clon_2000 and ST-2_clon_2010). Genome Announcements, 2016, 4, .	0.8	6
928	Separate F-Type Plasmids Have Shaped the Evolution of the <i>H</i> 30 Subclone of <i>Escherichia coli</i> Sequence Type 131. MSphere, 2016, 1, .	2.9	98
929	Comparing three complete mitochondrial genomes of the moss genus <i>Orthotrichum</i> Hedw.. Mitochondrial DNA Part B: Resources, 2016, 1, 168-170.	0.4	8

#	ARTICLE	IF	CITATIONS
930	Genomic Sequencing of Ranaviruses Isolated from Turbot (<i>Scophthalmus maximus</i>) and Atlantic Cod (<i>Gadus morhua</i>) Tj ETQq0 0 0 rgBT /Overlock 10	0.8	6
931	Reclassification of the taxonomic status of SEMIA3007 isolated in Mexico B-11A Mex as <i>Rhizobium leguminosarum</i> bv. <i>viciae</i> by bioinformatic tools. BMC Microbiology, 2016, 16, 260.	3.3	5
932	Draft Genome Sequence of 11399, a Transformable Citrus-Pathogenic Strain of <i>Xylella fastidiosa</i> . Genome Announcements, 2016, 4, .	0.8	12
933	SIMBA: a web tool for managing bacterial genome assembly generated by Ion PGM sequencing technology. BMC Bioinformatics, 2016, 17, 456.	2.6	8
934	Genomic insights from whole genome sequencing of four clonal outbreak <i>Campylobacter jejuni</i> assessed within the global <i>C. jejuni</i> population. BMC Genomics, 2016, 17, 990.	2.8	28
935	Comparative genomics analyses revealed two virulent <i>Listeria monocytogenes</i> strains isolated from ready-to-eat food. Gut Pathogens, 2016, 8, 65.	3.4	15
936	Whole-genome sequencing and comparative genomic analysis of <i>Escherichia coli</i> O91 strains isolated from symptomatic and asymptomatic human carriers. Gut Pathogens, 2016, 8, 57.	3.4	2
937	Genome sequence of a commensal bacterium, <i>Enterococcus faecalis</i> CBA7120, isolated from a Korean fecal sample. Gut Pathogens, 2016, 8, 62.	3.4	9
938	Complete genome sequence of <i>Methanoculleus bourgensis</i> strain MAB1, the syntrophic partner of mesophilic acetate-oxidising bacteria (SAOB). Standards in Genomic Sciences, 2016, 11, 80.	1.5	44
939	Mitogenome of the extinct helmeted musk ox, <i>Bootherium bombifrons</i> . Mitochondrial DNA Part B: Resources, 2016, 1, 862-863.	0.4	3
940	The complete chloroplast genome of <i>Gracilariopsis lemaneiformis</i> (Rhodophyta) gives new insight into the evolution of family Gracilariaceae. Journal of Phycology, 2016, 52, 441-450.	2.3	43
941	Draft Genome of <i>Shewanella frigidimarina</i> Ag06-30, a Marine Bacterium Isolated from Potter Peninsula, King George Island, Antarctica. Genome Announcements, 2016, 4, .	0.8	1
942	Draft Genome Sequence of White Spot Syndrome Virus Isolated from Cultured <i>Litopenaeus vannamei</i> in Mexico. Genome Announcements, 2016, 4, .	0.8	20
943	Influence of Host Ecology and Behavior on <i>Campylobacter jejuni</i> Prevalence and Environmental Contamination Risk in a Synanthropic Wild Bird Species. Applied and Environmental Microbiology, 2016, 82, 4811-4820.	3.1	33
944	The plasmid-mediated evolution of the mycobacterial ESX (Type VII) secretion systems. BMC Evolutionary Biology, 2016, 16, 62.	3.2	61
945	High-quality draft genome sequence and description of <i>Haemophilus massiliensis</i> sp. nov.. Standards in Genomic Sciences, 2016, 11, 31.	1.5	47
946	Complete genome sequence and genomic characterization of <i>Microcystis panniformis</i> FACHB 1757 by third-generation sequencing. Standards in Genomic Sciences, 2016, 11, 11.	1.5	19
947	Synteny Portal: a web-based application portal for synteny block analysis. Nucleic Acids Research, 2016, 44, W35-W40.	14.5	42

#	ARTICLE	IF	CITATIONS
948	Resilience of microbial communities in a simulated drinking water distribution system subjected to disturbances: role of conditionally rare taxa and potential implications for antibiotic-resistant bacteria. <i>Environmental Science: Water Research and Technology</i> , 2016, 2, 645-657.	2.4	48
949	Genomic and Phenotypic Analyses Reveal the Emergence of an Atypical <i>Salmonella enterica</i> Serovar Senftenberg Variant in China. <i>Journal of Clinical Microbiology</i> , 2016, 54, 2014-2022.	3.9	14
950	Circulation of clonal populations of fluoroquinolone-resistant CTX-M-15-producing <i>Escherichia coli</i> ST410 in humans and animals in Germany. <i>International Journal of Antimicrobial Agents</i> , 2016, 47, 457-465.	2.5	107
951	High-quality genome sequence and description of <i>Paenibacillus dakarensis</i> sp. nov.. <i>New Microbes and New Infections</i> , 2016, 10, 132-141.	1.6	10
952	The gene cortex controls mimicry and crypsis in butterflies and moths. <i>Nature</i> , 2016, 534, 106-110.	27.8	212
953	Noncontiguous finished genome sequence and description of <i>Gabonia massiliensis</i> gen. nov., sp. nov.. <i>New Microbes and New Infections</i> , 2016, 9, 35-44.	1.6	11
954	Genome sequence and description of <i>Anaerosalibacter massiliensis</i> sp. nov.. <i>New Microbes and New Infections</i> , 2016, 10, 66-76.	1.6	125
955	Noncontiguous finished genome sequence and description of <i>Nocardioides massiliensis</i> sp. nov. CD13T. <i>New Microbes and New Infections</i> , 2016, 10, 47-57.	1.6	6
956	Computational methods for predicting genomic islands in microbial genomes. <i>Computational and Structural Biotechnology Journal</i> , 2016, 14, 200-206.	4.1	54
957	The complete chloroplast genome sequence of <i>Abies nephrolepis</i> (Pinaceae: Abietoideae). <i>Journal of Asia-Pacific Biodiversity</i> , 2016, 9, 245-249.	0.4	16
958	A predicted T4 secretion system and conserved DNA-repeats identified in a subset of related <i>Arthrobacter</i> plasmids. <i>Microbiological Research</i> , 2016, 191, 32-37.	5.3	18
959	Noncontiguous finished genome sequence and description of <i>Kallipyga gabonensis</i> sp. nov.. <i>New Microbes and New Infections</i> , 2016, 9, 15-23.	1.6	7
960	Non-contiguous finished genome sequence and description of <i>Streptococcus varani</i> sp. nov.. <i>New Microbes and New Infections</i> , 2016, 11, 93-102.	1.6	1
961	A novel strain of cynomolgus macaque cytomegalovirus: implications for host-virus co-evolution. <i>BMC Genomics</i> , 2016, 17, 277.	2.8	11
962	Whole-genome optical mapping reveals a mis-assembly between two rRNA operons of <i>Corynebacterium pseudotuberculosis</i> strain 1002. <i>BMC Genomics</i> , 2016, 17, 315.	2.8	17
963	Draft genome sequence of non-shiga toxin-producing <i>Escherichia coli</i> O157 NCCP15738. <i>Gut Pathogens</i> , 2016, 8, 13.	3.4	4
964	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
965	Birth of Four Chimeric Plastid Gene Clusters in Japanese Umbrella Pine. <i>Genome Biology and Evolution</i> , 2016, 8, 1776-1784.	2.5	46

#	ARTICLE	IF	CITATIONS
966	The chloroplast genome of <i>Phacus orbicularis</i> (Euglenophyceae): an initial datum point for the phacaceae. <i>Journal of Phycology</i> , 2016, 52, 404-411.	2.3	12
967	Draft Genome Sequence of Vancomycin-Susceptible, Ampicillin-Intermediate Enterococcus faecium Strain D344RRF. <i>Genome Announcements</i> , 2016, 4, .	0.8	2
968	Evolution of Nine Microsatellite Loci in the Fungus <i>Fusarium oxysporum</i> . <i>Journal of Molecular Evolution</i> , 2016, 82, 27-37.	1.8	3
969	Identifying Potential Mechanisms Enabling Acidophily in the Ammonia-Oxidizing Archaeon <i>Candidatus Nitrosotalea devanatterra</i> . <i>Applied and Environmental Microbiology</i> , 2016, 82, 2608-2619.	3.1	117
970	Genome analysis of <i>Listeria ivanovii</i> strain G770 that caused a deadly aortic prosthesis infection. <i>New Microbes and New Infections</i> , 2016, 10, 87-92.	1.6	20
971	Comparative Genomic Analyses of the <i>Moraxella catarrhalis</i> Serosensitive and Seroresistant Lineages Demonstrate Their Independent Evolution. <i>Genome Biology and Evolution</i> , 2016, 8, 955-974.	2.5	20
972	Complete chloroplast genome sequences of <i>Eucommia ulmoides</i> : genome structure and evolution. <i>Tree Genetics and Genomes</i> , 2016, 12, 1.	1.6	53
973	Genomic characterization of <i>Pasteurella multocida</i> HB01, a serotype A bovine isolate from China. <i>Gene</i> , 2016, 581, 85-93.	2.2	36
974	Comparative genome analyses of novel <i>Mangrovimonas</i> -like strains isolated from estuarine mangrove sediments reveal xylan and arabinan utilization genes. <i>Marine Genomics</i> , 2016, 25, 115-121.	1.1	12
975	Complete Genome Sequence of Nonhemolytic <i>Streptococcus agalactiae</i> Serotype V Strain 1, Isolated from the Buccal Cavity of a Canine. <i>Genome Announcements</i> , 2016, 4, .	0.8	1
976	The genome of an Encephalitozoon cuniculi type III strain reveals insights into the genetic diversity and mode of reproduction of a ubiquitous vertebrate pathogen. <i>Heredity</i> , 2016, 116, 458-465.	2.6	16
977	Analysis of the role of the LH92_11085 gene of a biofilm hyper-producing <i>Acinetobacter baumannii</i> strain on biofilm formation and attachment to eukaryotic cells. <i>Virulence</i> , 2016, 7, 443-455.	4.4	52
978	A novel chimeric prophage vB_LdeS-phijB from commercial <i>Lactobacillus delbrueckii</i> subsp. <i>bulgaricus</i> . <i>Journal of Industrial Microbiology and Biotechnology</i> , 2016, 43, 681-689.	3.0	11
979	Characterization of the temperate phage vB_RleM_PPF1 and its site-specific integration into the <i>Rhizobium leguminosarum</i> F1 genome. <i>Molecular Genetics and Genomics</i> , 2016, 291, 349-362.	2.1	7
980	A Combinatorial Kin Discrimination System in <i>Bacillus subtilis</i> . <i>Current Biology</i> , 2016, 26, 733-742.	3.9	103
981	Rapid Emergence and Evolution of <i>Staphylococcus aureus</i> Clones Harboring <i>fusC</i> -Containing Staphylococcal Cassette Chromosome Elements. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 2359-2365.	3.2	41
982	Draft Genome Sequence of <i>Acinetobacter bereziniae</i> HPC229, a Carbapenem-Resistant Clinical Strain from Argentina Harboring <i>bla</i> _{NDM-1} . <i>Genome Announcements</i> , 2016, 4, .	0.8	9
983	On Identifying Minimal Absent and Unique Words: An Efficient Scheme. <i>Cognitive Computation</i> , 2016, 8, 603-613.	5.2	2

#	ARTICLE	IF	CITATIONS
984	The <i>Mycobacterium phlei</i> genome: expectations and surprises. <i>Genome Biology and Evolution</i> , 2016, 8, evw049.	2.5	11
985	High-quality genome sequencing and description of <i>Dermabacter indicis</i> sp. nov.. <i>New Microbes and New Infections</i> , 2016, 11, 59-67.	1.6	6
986	Intraspecies Transfer of the Chromosomal <i>Acinetobacter baumannii</i> <i>bla</i> NDM-1 Carbapenemase Gene. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 3032-3040.	3.2	65
987	Comparative genomic study of three species within the genus <i>Ornithinibacillus</i> , reflecting the adaption to different habitats. <i>Gene</i> , 2016, 578, 25-31.	2.2	6
988	Intraspecific variation within and across complete organellar genomes and nuclear ribosomal repeats in a moss. <i>Molecular Phylogenetics and Evolution</i> , 2016, 96, 195-199.	2.7	13
989	Evidence for the critical role of a secondary site <i>rpoB</i> mutation in the compensatory evolution and successful transmission of an MDR tuberculosis outbreak strain. <i>Journal of Antimicrobial Chemotherapy</i> , 2016, 71, 324-332.	3.0	33
990	Degradation of Benzene by <i>Pseudomonas veronii</i> 1YdBTEX2 and 1YB2 Is Catalyzed by Enzymes Encoded in Distinct Catabolism Gene Clusters. <i>Applied and Environmental Microbiology</i> , 2016, 82, 167-173.	3.1	18
991	Comparative mitochondrial genome analysis of <i>Pythium insidiosum</i> and related oomycete species provides new insights into genetic variation and phylogenetic relationships. <i>Gene</i> , 2016, 575, 34-41.	2.2	11
992	Microbial bioinformatics for food safety and production. <i>Briefings in Bioinformatics</i> , 2016, 17, 283-292.	6.5	53
993	The chloroplast genome of the marine green macroalga <i>Ulva fasciata</i> Delile (Ulvophyceae, Tj ETQq1 1 0.784314 rgBT /Overload	0.7	
994	The Chloroplast Genome of <i>Euglena mutabilis</i> "Cluster Arrangement, Intron Analysis, and Intragenomic Trends. <i>Journal of Eukaryotic Microbiology</i> , 2017, 64, 31-44.	1.7	13
995	Population genomic insights into variation and evolution of <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> . <i>Scientific Reports</i> , 2017, 7, 40694.	3.3	45
996	Adaptation of genetically monomorphic bacteria: evolution of copper resistance through multiple horizontal gene transfers of complex and versatile mobile genetic elements. <i>Molecular Ecology</i> , 2017, 26, 2131-2149.	3.9	53
997	Comparative genomic analysis of three white spot syndrome virus isolates of different virulence. <i>Virus Genes</i> , 2017, 53, 249-258.	1.6	28
998	Genomic and metabolic traits endow <i>Bacillus velezensis</i> CC09 with a potential biocontrol agent in control of wheat powdery mildew disease. <i>Microbiological Research</i> , 2017, 196, 89-94.	5.3	80
999	<i>Rubeoparvulum massiliense</i> gen. nov., sp. nov., a new bacterial genus isolated from the human gut of a Senegalese infant with severe acute malnutrition. <i>New Microbes and New Infections</i> , 2017, 15, 49-60.	1.6	8
1000	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.	1.4	6
1001	<i>Paenibacillus phocaensis</i> sp. nov., isolated from the gut microbiota of a healthy infant. <i>New Microbes and New Infections</i> , 2017, 16, 13-24.	1.6	4

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1002	A <i>Clostridium difficile</i> Lineage Endemic to Costa Rican Hospitals Is Multidrug Resistant by Acquisition of Chromosomal Mutations and Novel Mobile Genetic Elements. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	3.2	32
1003	Genomic analysis of a <i>Streptococcus pyogenes</i> strain causing endocarditis in a child. <i>New Microbes and New Infections</i> , 2017, 17, 1-6.	1.6	2
1004	Whole-Genome Sequences of <i>Mycobacterium tuberculosis</i> TB282 and TB284, a Widespread and a Unique Strain, Respectively, Identified in a Previous Study of Tuberculosis Transmission in Central Los Angeles, California, USA. <i>Genome Announcements</i> , 2017, 5, .	0.8	0
1005	Genome Sequencing of the Behavior Manipulating Virus LbFV Reveals a Possible New Virus Family. <i>Genome Biology and Evolution</i> , 2016, 8, 3718-3739.	2.5	21
1006	Complete-genome sequencing elucidates outbreak dynamics of CA-MRSA USA300 (ST8-spa t008) in an academic hospital of Paramaribo, Republic of Suriname. <i>Scientific Reports</i> , 2017, 7, 41050.	3.3	33
1007	Interaction of <i>Cutibacterium</i> (formerly <i>Propionibacterium</i>) <i>acnes</i> with bone cells: a step toward understanding bone and joint infection development. <i>Scientific Reports</i> , 2017, 7, 42918.	3.3	42
1008	A Natural Chimeric <i>Pseudomonas</i> Bacteriocin with Novel Pore-Forming Activity Parasitizes the Ferrichrome Transporter. <i>MBio</i> , 2017, 8, .	4.1	24
1009	Comparative genomics of Crohn's disease-associated adherent-invasive <i>Escherichia coli</i> . <i>Gut</i> , 2017, 66, 1382-1389.	12.1	114
1010	Genomic characterization of <i>Ensifer aridi</i> , a proposed new species of nitrogen-fixing rhizobium recovered from Asian, African and American deserts. <i>BMC Genomics</i> , 2017, 18, 85.	2.8	34
1011	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.	3.8	48
1012	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
1013	The Plastid Genome of <i>Polytoma uvella</i> Is the Largest Known among Colorless Algae and Plants and Reflects Contrasting Evolutionary Paths to Nonphotosynthetic Lifestyles. <i>Plant Physiology</i> , 2017, 173, 932-943.	4.8	33
1014	Shrimp AHPND-causing plasmids encoding the PirAB toxins as mediated by pirAB-Tn903 are prevalent in various <i>Vibrio</i> species. <i>Scientific Reports</i> , 2017, 7, 42177.	3.3	106
1015	Draft Genome Sequence of an Erythromycin-Resistant <i>Propionibacterium acnes</i> Isolate Recovered from Folliculitis of the Scalp. <i>Genome Announcements</i> , 2017, 5, .	0.8	3
1016	<i>Escherichia coli</i> sequence type 73 as a cause of community acquired urinary tract infection in men and women in Rio de Janeiro, Brazil. <i>Diagnostic Microbiology and Infectious Disease</i> , 2017, 88, 69-74.	1.8	13
1017	Draft Genome Sequence of the Tumor-Targeting <i>Salmonella enterica</i> Serovar Typhimurium Strain SL7207. <i>Genome Announcements</i> , 2017, 5, .	0.8	8
1018	Ecological and Evolutionary Insights into <i>Xanthomonas citri</i> Pathovar Diversity. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	41
1019	Curious bivalves: Systematic utility and unusual properties of anomalodesmatan mitochondrial genomes. <i>Molecular Phylogenetics and Evolution</i> , 2017, 110, 60-72.	2.7	24

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1020	Sputum DNA sequencing in cystic fibrosis: non-invasive access to the lung microbiome and to pathogen details. <i>Microbiome</i> , 2017, 5, 20.	11.1	100
1021	<i>Inediibacterium massiliense</i> gen. nov., sp. nov., a new bacterial species isolated from the gut microbiota of a severely malnourished infant. <i>Antonie Van Leeuwenhoek</i> , 2017, 110, 737-750.	1.7	12
1022	Phylogenomic relationship of feijoa (<i>Acca sellowiana</i> (O.Berg) Burret) with other Myrtaceae based on complete chloroplast genome sequences. <i>Genetica</i> , 2017, 145, 163-174.	1.1	27
1023	Phylogenomics of <i>Trypanosoma cruzi</i> : Few evidence of TcI/TcII mosaicism in TcIII challenges the hypothesis of an ancient TcI/TcII hybridization. <i>Infection, Genetics and Evolution</i> , 2017, 50, 25-27.	2.3	2
1024	Comparative genome analysis reveals important genetic differences among serotype O1 and serotype O2 strains of <i>Y.Âruckeri</i> and provides insights into host adaptation and virulence. <i>MicrobiologyOpen</i> , 2017, 6, e00460.	3.0	18
1025	Draft Genome Sequence of <i>Corynebacterium pseudotuberculosis</i> Strain PA06 Isolated from a Subauricular Abscess in an Ovine Host. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
1026	Structural and functional genomics analysis of methyltransferase genes and networks associate to understand antibiotic resistance inside the pangenome of <i>Pseudomonas aeruginosa</i> . <i>IFMBE Proceedings</i> , 2017, , 702-705.	0.3	1
1027	A Locus Encoding Variable Defense Systems against Invading DNA Identified in <i>Streptococcus suis</i> . <i>Genome Biology and Evolution</i> , 2017, 9, 1000-1012.	2.5	17
1028	A comparison of the adaptations of strains of <i>Lymantria dispar</i> multiple nucleopolyhedrovirus to hosts from spatially isolated populations. <i>Journal of Invertebrate Pathology</i> , 2017, 146, 41-46.	3.2	12
1029	Genome-Wide Abolishment of Mobile Genetic Elements Using Genome Shuffling and CRISPR/Cas-Assisted MAGE Allows the Efficient Stabilization of a Bacterial Chassis. <i>ACS Synthetic Biology</i> , 2017, 6, 1471-1483.	3.8	55
1030	Primates, Lice and Bacteria: Speciation and Genome Evolution in the Symbionts of Hominid Lice. <i>Molecular Biology and Evolution</i> , 2017, 34, 1743-1757.	8.9	51
1031	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.	1.4	12
1032	Draft Genome Sequences of 18 Psychrotolerant and 2 Thermotolerant Strains Representative of Particular Ecotypes in the <i>Bacillus cereus</i> Group. <i>Genome Announcements</i> , 2017, 5, .	0.8	4
1033	Draft Genome Sequence of <i>Mycobacterium ulcerans</i> S4018 Isolated from a Patient with an Active Buruli Ulcer in Benin, Africa. <i>Genome Announcements</i> , 2017, 5, .	0.8	4
1034	Comparative Genome Analyses of <i>Vibrio anguillarum</i> Strains Reveal a Link with Pathogenicity Traits. <i>MSystems</i> , 2017, 2, .	3.8	58
1035	Comparative Genomics of the Ectomycorrhizal Sister Species <i>Rhizopogon vinicolor</i> and <i>Rhizopogon vesiculosus</i> (Basidiomycota: Boletales) Reveals a Divergence of the Mating Type <i>B</i> Locus. <i>Genes, Genomes, Genetics</i> , 2017, 7, 1775-1789.	1.8	17
1036	Pelagic and benthic communities of the Antarctic ecosystem of Potter Cove: Genomics and ecological implications. <i>Marine Genomics</i> , 2017, 33, 1-11.	1.1	23
1037	Mitochondrial Recombination and Introgression during Speciation by Hybridization. <i>Molecular Biology and Evolution</i> , 2017, 34, 1947-1959.	8.9	57

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1038	Whole genome sequencing and functional features of UMX-103: a new <i>Bacillus</i> strain with biosurfactant producing capability. <i>Genes and Genomics</i> , 2017, 39, 877-886.	1.4	2
1039	Inactivation of Transcriptional Regulators during Within-Household Evolution of <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2017, 199, .	2.2	10
1040	Pacmanvirus, a New Giant Icosahedral Virus at the Crossroads between Asfarviridae and Faustoviruses. <i>Journal of Virology</i> , 2017, 91, .	3.4	99
1041	<i>Pseudomonas aeruginosa</i> adaptation and diversification in the non-cystic fibrosis bronchiectasis lung. <i>European Respiratory Journal</i> , 2017, 49, 1602108.	6.7	75
1042	The genome sequence of <i>Agrotis segetum</i> granulovirus, isolate AgseGV-DA, reveals a new Betabaculovirus species of a slow killing granulovirus. <i>Journal of Invertebrate Pathology</i> , 2017, 146, 58-68.	3.2	6
1043	Noncontiguous finished genome sequence and description of <i>Streptococcus timonensis</i> sp. nov. isolated from the human stomach. <i>New Microbes and New Infections</i> , 2017, 15, 77-88.	1.6	7
1044	Large-Scale Sequence Comparison. <i>Methods in Molecular Biology</i> , 2017, 1525, 191-224.	0.9	3
1045	Nanopore sequencing data analysis: state of the art, applications and challenges. <i>Briefings in Bioinformatics</i> , 2018, 19, 1256-1272.	6.5	91
1046	<i>Cedratvirus lausannensis</i> “digging into <i>Pithoviridae</i> diversity. <i>Environmental Microbiology</i> , 2017, 19, 4022-4034.	3.8	36
1047	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.	3.8	27
1048	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.	1.8	49
1049	Comparative and functional genomics of the <i>Lactococcus lactis</i> taxon; insights into evolution and niche adaptation. <i>BMC Genomics</i> , 2017, 18, 267.	2.8	117
1050	Distinct Biological Potential of <i>Streptococcus gordonii</i> and <i>Streptococcus sanguinis</i> Revealed by Comparative Genome Analysis. <i>Scientific Reports</i> , 2017, 7, 2949.	3.3	28
1051	Single-virus genomics reveals hidden cosmopolitan and abundant viruses. <i>Nature Communications</i> , 2017, 8, 15892.	12.8	165
1052	Persistent <i>Listeria monocytogenes</i> strains isolated from mussel production facilities form more biofilm but are not linked to specific genetic markers. <i>International Journal of Food Microbiology</i> , 2017, 256, 45-53.	4.7	50
1053	Dataset of the transcribed 45S ribosomal RNA sequence of the tree crop “ <i>eyerba mate</i> ”. <i>Data in Brief</i> , 2017, 12, 649-651.	1.0	0
1054	Whole-Genome Sequence of <i>Corynebacterium pseudotuberculosis</i> PA04, Isolated from the Lymph Node of a Sheep in the Amazon, Brazil. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
1055	Complete Genome Sequence of an Aquaculture-Associated Phage, FL-1, Infecting <i>Flavobacterium</i> spp. <i>Genome Announcements</i> , 2017, 5, .	0.8	1

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1056	Draft Genome Sequence of <i>Pseudomonas chlororaphis</i> ATCC 9446, a Nonpathogenic Bacterium with Bioremediation and Industrial Potential. <i>Genome Announcements</i> , 2017, 5, .	0.8	6
1057	Comparative analyses of whole genome sequences of <i>Leishmania infantum</i> isolates from humans and dogs in northeastern Brazil. <i>International Journal for Parasitology</i> , 2017, 47, 655-665.	3.1	32
1058	A New Natural Product Analog of Blasticidin S Reveals Cellular Uptake Facilitated by the NorA Multidrug Transporter. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	3.2	10
1059	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.	3.0	80
1060	Giant viruses with an expanded complement of translation system components. <i>Science</i> , 2017, 356, 82-85.	12.6	234
1061	Evolutionary Origin of the Staphylococcal Cassette Chromosome <i>mec</i> (SCC <i>mec</i>). <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	3.2	64
1062	Deep genomic analysis of the <i>Chlorella sorokiniana</i> SAG 211-8k chloroplast. <i>European Journal of Phycology</i> , 2017, 52, 320-329.	2.0	3
1063	Genome-wide analysis of a avirulent and reveal the strain induces pro-TECTIVE immunity against challenge with virulent <i>Streptococcus suis</i> Serotype 2. <i>BMC Microbiology</i> , 2017, 17, 67.	3.3	7
1064	Networking in microbes: conjugative elements and plasmids in the genus <i>Alteromonas</i> . <i>BMC Genomics</i> , 2017, 18, 36.	2.8	39
1065	Draft Genome Sequence of <i>Bacillus licheniformis</i> Strain YNP1-TSU Isolated from Whiterock Springs in Yellowstone National Park. <i>Genome Announcements</i> , 2017, 5, .	0.8	5
1066	Identification of Strain-Specific Sequences That Distinguish a <i>Mycoplasma gallisepticum</i> Vaccine Strain from Field Isolates. <i>Journal of Clinical Microbiology</i> , 2017, 55, 244-252.	3.9	14
1067	Insight into the Genome of <i>Brochothrix thermosphacta</i> , a Problematic Meat Spoilage Bacterium. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	61
1068	Comparative analysis of chloroplast DNA sequences of <i>Codonopsis lanceolata</i> and <i>Platycodon grandiflorus</i> and application in development of molecular markers. <i>Applied Biological Chemistry</i> , 2017, 60, 23-31.	1.9	2
1069	Comparative genome analysis of multiple vancomycin-resistant <i>Enterococcus faecium</i> isolated from two fatal cases. <i>Infection, Genetics and Evolution</i> , 2017, 49, 55-65.	2.3	3
1070	Comparative genome analyses of <i>Mycobacterium avium</i> reveal genomic features of its subspecies and strains that cause progression of pulmonary disease. <i>Scientific Reports</i> , 2017, 7, 39750.	3.3	62
1071	Expansion of inverted repeat does not decrease substitution rates in <i>Pelargonium</i> plastid genomes. <i>New Phytologist</i> , 2017, 214, 842-851.	7.3	99
1072	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.	1.9	30
1073	Noncontiguous finished genome sequence and description of <i>Fusobacterium massiliense</i> sp. nov. isolated from human duodenum. <i>New Microbes and New Infections</i> , 2017, 16, 3-12.	1.6	2

#	ARTICLE	IF	CITATIONS
1074	Transition from heterothallism to homothallism is hypothesised to have facilitated speciation among emerging Botryosphaeriaceae wheat-pathogens. Fungal Genetics and Biology, 2017, 109, 36-45.	2.1	8
1075	Plasticity of the <i>MFS1</i> Promoter Leads to Multidrug Resistance in the Wheat Pathogen <i>Zymoseptoria tritici</i> . MSphere, 2017, 2, .	2.9	75
1076	Expression of a Peptidoglycan Hydrolase from Lytic Bacteriophages Atu_ph02 and Atu_ph03 Triggers Lysis of <i>Agrobacterium tumefaciens</i> . Applied and Environmental Microbiology, 2017, 83, .	3.1	25
1077	Comparative Phenotypic and Genotypic Analysis of <i>Edwardsiella</i> Isolates from Different Hosts and Geographic Origins, with Emphasis on Isolates Formerly Classified as <i>E. tarda</i> , and Evaluation of Diagnostic Methods. Journal of Clinical Microbiology, 2017, 55, 3466-3491.	3.9	70
1078	Comparative genomics of <i>Lactobacillus kefirianofaciens</i> ZW3 and related members of <i>Lactobacillus</i> . spp reveal adaptations to dairy and gut environments. Scientific Reports, 2017, 7, 12827.	3.3	33
1079	Genomic divergence within non-photosynthetic cyanobacterial endosymbionts in rhopalodiacean diatoms. Scientific Reports, 2017, 7, 13075.	3.3	17
1080	Genomic Sequencing of Ranaviruses Isolated from Edible Frogs (<i>Pelophylax esculentus</i>). Genome Announcements, 2017, 5, .	0.8	4
1081	Evolutionary Comparisons of the Chloroplast Genome in Lauraceae and Insights into Loss Events in the Magnoliids. Genome Biology and Evolution, 2017, 9, 2354-2364.	2.5	70
1082	Draft Genome Sequences of Seven <i>Streptococcus agalactiae</i> Strains Isolated from <i>Camelus dromedarius</i> at the Horn of Africa. Genome Announcements, 2017, 5, .	0.8	8
1083	Complete Genome Sequences of Three <i>Xanthomonas citri</i> Strains from Texas. Genome Announcements, 2017, 5, .	0.8	7
1084	Typing and comparative genome analysis of <i>Brucella melitensis</i> isolated from Lebanon. FEMS Microbiology Letters, 2017, 364, .	1.8	11
1085	Microbial taxonomy in the era of OMICS: application of DNA sequences, computational tools and techniques. Antonie Van Leeuwenhoek, 2017, 110, 1357-1371.	1.7	54
1086	Structure, proteome and genome of <i>Sinorhizobium meliloti</i> phage Î M5: A virus with LUZ24-like morphology and a highly mosaic genome. Journal of Structural Biology, 2017, 200, 343-359.	2.8	17
1087	Complete genome analysis of <i>Lactobacillus fermentum</i> SK152 from kimchi reveals genes associated with its antimicrobial activity. FEMS Microbiology Letters, 2017, 364, .	1.8	20
1088	Molecular epidemiology of Epizootic haematopoietic necrosis virus (EHNV). Virology, 2017, 511, 320-329.	2.4	2
1089	Environmental vibrios represent a source of antagonistic compounds that inhibit pathogenic <i>Vibrio cholerae</i> and <i>Vibrio parahaemolyticus</i> strains. MicrobiologyOpen, 2017, 6, e00504.	3.0	9
1090	A Serendipitous Mutation Reveals the Severe Virulence Defect of a <i>Klebsiella pneumoniae</i> <i>fepB</i> Mutant. MSphere, 2017, 2, .	2.9	29
1091	Comparative whole genome analysis of three consecutive <i>Salmonella diarizonae</i> isolates. International Journal of Medical Microbiology, 2017, 307, 542-551.	3.6	10

#	ARTICLE	IF	CITATIONS
1092	Colonic Spirochetes: What Has Genomics Taught Us?. Current Topics in Microbiology and Immunology, 2017, 415, 273-294.	1.1	5
1093	Ancestral acquisitions, gene flow and multiple evolutionary trajectories of the type three secretion system and effectors in <i>Xanthomonas</i> plant pathogens. Molecular Ecology, 2017, 26, 5939-5952.	3.9	56
1094	Comparative Genomic and Regulatory Analyses of Natamycin Production of <i>Streptomyces lydicus</i> A02. Scientific Reports, 2017, 7, 9114.	3.3	20
1095	Evolutionary Dynamics of Cryptophyte Plastid Genomes. Genome Biology and Evolution, 2017, 9, 1859-1872.	2.5	51
1096	Identification of the <i>hcb</i> Gene Operon Involved in Catalyzing Aerobic Hexachlorobenzene Dechlorination in <i>Nocardioides</i> sp. Strain PD653. Applied and Environmental Microbiology, 2017, 83, .	3.1	16
1097	Noncontiguous finished genome sequences and description of <i>Bacillus massili-glaciei</i> , <i>Bacillus mediterraneensis</i> , <i>Bacillus massilnigeriensis</i> , <i>Bacillus phocaeensis</i> and <i>Bacillus tuaregi</i> , five new species identified by culturomics. New Microbes and New Infections, 2017, 19, 45-59.	1.6	4
1098	soxRS induces colistin hetero-resistance in <i>Enterobacter asburiae</i> and <i>Enterobacter cloacae</i> by regulating the <i>acrAB-tolC</i> efflux pump. Journal of Antimicrobial Chemotherapy, 2017, 72, 2715-2721.	3.0	56
1099	A comparative genome analysis of <i>Cercospora soja</i> with other members of the pathogen genus <i>Mycosphaerella</i> on different plant hosts. Genomics Data, 2017, 13, 54-63.	1.3	15
1100	<i>Dakarella massiliensis</i> gen. nov., sp. nov., strain ND3T: a new bacterial genus isolated from the female genital tract. New Microbes and New Infections, 2017, 18, 38-46.	1.6	5
1101	Noncontiguous finished genome sequences and descriptions of <i>Paenibacillus bouchesdurhonensis</i> , <i>Paenibacillus rubinfantis</i> , <i>Paenibacillus senegalimassiliensis</i> and <i>Paenibacillus tuaregi</i> identified by culturomics. New Microbes and New Infections, 2017, 20, 1-13.		1
1102	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.	2.3	23
1103	Genome Sequencing of Steroid Producing Bacteria Using Ion Torrent Technology and a Reference Genome. Methods in Molecular Biology, 2017, 1645, 45-58.	0.9	0
1104	Population genomics reveals a candidate gene involved in bumble bee pigmentation. Ecology and Evolution, 2017, 7, 3406-3413.	1.9	13
1105	Origin and evolutionary history of freshwater Rhodophyta: further insights based on phylogenomic evidence. Scientific Reports, 2017, 7, 2934.	3.3	25
1106	Genomic insights into the virulence and salt tolerance of <i>Staphylococcus equorum</i> . Scientific Reports, 2017, 7, 5383.	3.3	34
1107	On the brink: the highly reduced plastomes of nonphotosynthetic Ericaceae. New Phytologist, 2017, 216, 254-266.	7.3	46
1108	Development of a new real-time quantitative PCR assay for the detection of <i>Staphylococcus aureus</i> genotype B in cow milk, targeting the new gene <i>adlb</i> . Journal of Dairy Science, 2017, 100, 7834-7845.	3.4	20
1109	Genetic analysis of a PER-2-producing <i>Shewanella</i> sp. strain harbouring a variety of mobile genetic elements and antibiotic resistance determinants. Journal of Global Antimicrobial Resistance, 2017, 11, 81-86.	2.2	10

#	ARTICLE	IF	CITATIONS
1110	A novel viral lineage distantly related to herpesviruses discovered within fish genome sequence data. <i>Virus Evolution</i> , 2017, 3, vex016.	4.9	20
1111	Ranavirus phylogenomics: Signatures of recombination and inversions among bullfrog ranaculture isolates. <i>Virology</i> , 2017, 511, 330-343.	2.4	50
1112	Whole genome comparative analysis of four Georgian grape cultivars. <i>Molecular Genetics and Genomics</i> , 2017, 292, 1377-1389.	2.1	9
1113	Complete mitochondrial genome of the freshwater red alga <i>Lympha mucosa</i> (Rhodophyta). <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 707-708.	0.4	2
1114	Complete Genome Sequences of 12 Isolates of <i>Listeria monocytogenes</i> Belonging to Serotypes 1/2a, 1/2b, and 4b Obtained from Food Products and Food-Processing Environments in Canada. <i>Genome Announcements</i> , 2017, 5, .	0.8	0
1115	The natural product carolacton inhibits folate-dependent C1 metabolism by targeting FdD/MTHFD. <i>Nature Communications</i> , 2017, 8, 1529.	12.8	66
1116	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
1117	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.	2.4	22
1118	The food-borne pathogen <i>Campylobacter jejuni</i> responds to the bile salt deoxycholate with countermeasures to reactive oxygen species. <i>Scientific Reports</i> , 2017, 7, 15455.	3.3	27
1119	Ammonia-oxidising archaea living at low pH: Insights from comparative genomics. <i>Environmental Microbiology</i> , 2017, 19, 4939-4952.	3.8	107
1120	Genome sequence and analysis of <i>Escherichia coli</i> production strain LS5218. <i>Metabolic Engineering Communications</i> , 2017, 5, 78-83.	3.6	9
1121	Genome-wide detection of genetic loci associated with soybean aphid resistance in soybean germplasm PI 603712. <i>Euphytica</i> , 2017, 213, 1.	1.2	10
1122	Whole genome sequence analysis; an improved technology that identifies underlying genotypic differences between closely related <i>Listeria monocytogenes</i> strains. <i>Innovative Food Science and Emerging Technologies</i> , 2017, 44, 89-96.	5.6	8
1123	The complete chloroplast genome sequence of tung tree (<i>Vernicia fordii</i>): Organization and phylogenetic relationships with other angiosperms. <i>Scientific Reports</i> , 2017, 7, 1869.	3.3	38
1124	Parallel Evolution of Two Clades of an Atlantic-Endemic Pathogenic Lineage of <i>Vibrio parahaemolyticus</i> by Independent Acquisition of Related Pathogenicity Islands. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	27
1125	Comparative Genomics of Two Sequential <i>Candida glabrata</i> Clinical Isolates. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2413-2426.	1.8	62
1126	Draft Genome Sequence of <i>Pseudomonas koreensis</i> CI12, a <i>Bacillus cereus</i> "Hitchhiker" from the Soybean Rhizosphere. <i>Genome Announcements</i> , 2017, 5, .	0.8	10
1127	Molecular Mechanism and Genetic Determinants of Buprofezin Degradation. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	14

#	ARTICLE	IF	CITATIONS
1128	Cleaning and Disinfection of Biofilms Composed of <i>Listeria monocytogenes</i> and Background Microbiota from Meat Processing Surfaces. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	111
1129	The Proline Variant of the W[F/L/M][T/S]R Cyclic Di-GMP Binding Motif Suppresses Dependence on Signal Association for Regulator Function. <i>Journal of Bacteriology</i> , 2017, 199, .	2.2	12
1130	Complete chloroplast genome of <i>Gracilaria firma</i> (Gracilariaceae, Rhodophyta), with discussion on the use of chloroplast phylogenomics in the subclass Rhodymeniophycidae. <i>BMC Genomics</i> , 2017, 18, 40.	2.8	29
1131	Transcriptomic buffering of cryptic genetic variation contributes to meningococcal virulence. <i>BMC Genomics</i> , 2017, 18, 282.	2.8	14
1132	sRNAs as possible regulators of retrotransposon activity in <i>Cryptococcus gattii</i> VGII. <i>BMC Genomics</i> , 2017, 18, 294.	2.8	1
1133	Complete sequence and comparative genomic analysis of eight native <i>Pseudomonas syringae</i> plasmids belonging to the pPT23A family. <i>BMC Genomics</i> , 2017, 18, 365.	2.8	23
1134	Hierarchical genomic analysis of carried and invasive serogroup A <i>Neisseria meningitidis</i> during the 2011 epidemic in Chad. <i>BMC Genomics</i> , 2017, 18, 398.	2.8	15
1135	Lost in plasmids: next generation sequencing and the complex genome of the tick-borne pathogen <i>Borrelia burgdorferi</i> . <i>BMC Genomics</i> , 2017, 18, 422.	2.8	83
1136	Comparative genomic analysis of Shiga toxin-producing and non-Shiga toxin-producing <i>Escherichia coli</i> O157 isolated from outbreaks in Korea. <i>Gut Pathogens</i> , 2017, 9, 7.	3.4	3
1137	Complete genome sequence of <i>Clostridium perfringens</i> CBA7123 isolated from a faecal sample from Korea. <i>Gut Pathogens</i> , 2017, 9, 32.	3.4	4
1138	Mitogenomic analyses support the recent division of the genus <i>Orthotrichum</i> (Orthotrichaceae,) Tj ETQq0 0 0 rgBT./Overlock, 10 Tf 50 3	3.3	31
1139	Detection of the cryptic prophage-like molecule pBtic235 in <i>Bacillus thuringiensis</i> subsp. israelensis. <i>Research in Microbiology</i> , 2017, 168, 319-330.	2.1	19
1140	Comparative Genomics Reveals the Diversity of Restriction-Modification Systems and DNA Methylation Sites in <i>Listeria monocytogenes</i> . <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	31
1141	The FhaB/FhaC two-partner secretion system is involved in adhesion of <i>Acinetobacter baumannii</i> AbH12O-A2 strain. <i>Virulence</i> , 2017, 8, 959-974.	4.4	72
1142	Comparative genomics of extrachromosomal elements in <i>Bacillus thuringiensis</i> subsp. israelensis. <i>Research in Microbiology</i> , 2017, 168, 331-344.	2.1	28
1143	Genome comparison and physiological characterization of eight <i>Streptococcus thermophilus</i> strains isolated from Italian dairy products. <i>Food Microbiology</i> , 2017, 63, 47-57.	4.2	34
1144	Improved production of propionic acid using genome shuffling. <i>Biotechnology Journal</i> , 2017, 12, 1600120.	3.5	23
1145	Comparative genome analysis of two <i>Streptococcus phocae</i> subspecies provides novel insights into pathogenicity. <i>Marine Genomics</i> , 2017, 31, 53-61.	1.1	6

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1146	Synten Explorer: An Interactive Visualization Application for Teaching Genome Evolution. IEEE Transactions on Visualization and Computer Graphics, 2017, 23, 711-720.	4.4	7
1147	The complete chloroplast genome sequence of <i>Glycyrrhiza lepidota</i> (Nutt.) Pursh - An American wild licorice. Journal of Crop Science and Biotechnology, 2017, 20, 295-303.	1.5	10
1149	Structured Populations of <i>Sulfolobus acidocaldarius</i> with Susceptibility to Mobile Genetic Elements. Genome Biology and Evolution, 2017, 9, 1699-1710.	2.5	17
1150	Integrated Genomic and Proteomic Analyses of High-level Chloramphenicol Resistance in <i>Campylobacter jejuni</i> . Scientific Reports, 2017, 7, 16973.	3.3	12
1151	<i>Epichloa</i> hybrida, sp. nov., an emerging model system for investigating fungal allopolyploidy. Mycologia, 2017, 109, 1-15.	1.9	43
1152	Revealing the genomic differences between two subgroups in <i>Lactobacillus gasseri</i> . Bioscience of Microbiota, Food and Health, 2017, 36, 155-159.	1.8	8
1153	The complete genome sequence of <i>Ensifer meliloti</i> strain CCMM B554 (FSM-MA), a highly effective nitrogen-fixing microsymbiont of <i>Medicago truncatula</i> Gaertn. Standards in Genomic Sciences, 2017, 12, 75.	1.5	3
1154	Genetic Drift and Indel Mutation in the Evolution of Yeast Mitochondrial Genome Size. Genome Biology and Evolution, 2017, 9, 3088-3099.	2.5	31
1155	Draft Genome Sequence of <i>Myroides</i> sp. N17-2, a Multidrug-Resistant Bacterium Isolated from Radiation-Polluted Soils. Genome Announcements, 2017, 5, .	0.8	2
1156	Determination of Nucleopolyhedrovirus™ Taxonomic Position. , 2017, , .		1
1157	Genome analysis of <i>E. coli</i> isolated from Crohn's disease patients. BMC Genomics, 2017, 18, 544.	2.8	37
1158	Genomic Analysis of <i>Bacillus licheniformis</i> CBA7126 Isolated from a Human Fecal Sample. Frontiers in Pharmacology, 2017, 8, 724.	3.5	10
1159	Genomic Analysis of a Pathogenic Bacterium, <i>Paenibacillus sordellii</i> CBA7122 Containing the Highest Number of rRNA Operons, Isolated from a Human Stool Sample. Frontiers in Pharmacology, 2017, 8, 840.	3.5	27
1160	The Chloroplast Genome of <i>Passiflora edulis</i> (Passifloraceae) Assembled from Long Sequence Reads: Structural Organization and Phylogenomic Studies in Malpighiales. Frontiers in Plant Science, 2017, 8, 334.	3.6	79
1161	Comparative Analysis of <i>Ralstonia solanacearum</i> Methylobacter. Frontiers in Plant Science, 2017, 8, 504.	3.6	13
1162	A Dynamic Tandem Repeat in Monocotyledons Inferred from a Comparative Analysis of Chloroplast Genomes in Melanthiaceae. Frontiers in Plant Science, 2017, 8, 693.	3.6	13
1163	Comparative Genomics of <i>Ralstonia solanacearum</i> Identifies Candidate Genes Associated with Cool Virulence. Frontiers in Plant Science, 2017, 8, 1565.	3.6	25
1164	XCAVATOR: accurate detection and genotyping of copy number variants from second and third generation whole-genome sequencing experiments. BMC Genomics, 2017, 18, 747.	2.8	29

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1165	Complete Genome Sequences of Two Strains of the Meat Spoilage Bacterium <i>Brochothrix thermosphacta</i> Isolated from Ground Chicken. <i>Genome Announcements</i> , 2017, 5, .	0.8	3
1166	Chloroplast Genome Sequence of Clusterbean (<i>Cyamopsis tetragonoloba</i> L.): Genome Structure and Comparative Analysis. <i>Genes</i> , 2017, 8, 212.	2.4	46
1167	Complete Chloroplast Genome of <i>Pinus massoniana</i> (Pinaceae): Gene Rearrangements, Loss of <i>ndh</i> Genes, and Short Inverted Repeats Contraction, Expansion. <i>Molecules</i> , 2017, 22, 1528.	3.8	33
1168	Variation in the Genetic Repertoire of Viruses Infecting <i>Micromonas pusilla</i> Reflects Horizontal Gene Transfer and Links to Their Environmental Distribution. <i>Viruses</i> , 2017, 9, 116.	3.3	15
1169	Stumbling across the Same Phage: Comparative Genomics of Widespread Temperate Phages Infecting the Fish Pathogen <i>Vibrio anguillarum</i> . <i>Viruses</i> , 2017, 9, 122.	3.3	43
1170	Deciphering Single Nucleotide Polymorphisms and Evolutionary Trends in Isolates of the <i>Cydia pomonella</i> granulovirus. <i>Viruses</i> , 2017, 9, 227.	3.3	16
1171	Generation of Small Colony Variants in Biofilms by <i>Escherichia coli</i> Harboring a Conjugative F Plasmid. <i>Microbes and Environments</i> , 2017, 32, 40-46.	1.6	21
1172	Comparative Analysis of the Complete Chloroplast Genome of Four Endangered Herbals of <i>Notopterygium</i> . <i>Genes</i> , 2017, 8, 124.	2.4	54
1173	Comparative Genomics of <i>Mycoplasma bovis</i> Strains Reveals That Decreased Virulence with Increasing Passages Might Correlate with Potential Virulence-Related Factors. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 177.	3.9	39
1174	<i>Bacillus thuringiensis</i> and <i>Bacillus weihenstephanensis</i> Inhibit the Growth of Phytopathogenic <i>Verticillium</i> Species. <i>Frontiers in Microbiology</i> , 2016, 7, 2171.	3.5	74
1175	Genomic Analysis of a New Serovar of <i>Leptospira weilii</i> Serogroup Manhao. <i>Frontiers in Microbiology</i> , 2017, 8, 149.	3.5	18
1176	Effect of Temperature on the Prevalence of <i>Saccharomyces non cerevisiae</i> Species against a <i>S. cerevisiae</i> Wine Strain in Wine Fermentation: Competition, Physiological Fitness, and Influence in Final Wine Composition. <i>Frontiers in Microbiology</i> , 2017, 8, 150.	3.5	90
1177	Characterization of Potential Polysaccharide Utilization Systems in the Marine Bacteroidetes <i>Gramella flava</i> JLT2011 Using a Multi-Omics Approach. <i>Frontiers in Microbiology</i> , 2017, 8, 220.	3.5	57
1178	An In vitro Study of Bio-Control and Plant Growth Promotion Potential of <i>Salicaceae</i> Endophytes. <i>Frontiers in Microbiology</i> , 2017, 8, 386.	3.5	126
1179	Evidence for Contemporary Switching of the O-Antigen Gene Cluster between Shiga Toxin-Producing <i>Escherichia coli</i> Strains Colonizing Cattle. <i>Frontiers in Microbiology</i> , 2017, 8, 424.	3.5	13
1180	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.	3.5	38
1181	Comparative Genomics and Transcriptional Analysis of <i>Flavobacterium columnare</i> Strain ATCC 49512. <i>Frontiers in Microbiology</i> , 2017, 8, 588.	3.5	46
1182	Genomics Reveals a Unique Clone of <i>Burkholderia cenocepacia</i> Harboring an Actively Excising Novel Genomic Island. <i>Frontiers in Microbiology</i> , 2017, 8, 590.	3.5	24

#	ARTICLE	IF	CITATIONS
1183	A Genotypic Analysis of Five <i>P. aeruginosa</i> Strains after Biofilm Infection by Phages Targeting Different Cell Surface Receptors. <i>Frontiers in Microbiology</i> , 2017, 8, 1229.	3.5	41
1184	Complete Mitochondrial Genome of <i>Phytophthora nicotianae</i> and Identification of Molecular Markers for the Oomycetes. <i>Frontiers in Microbiology</i> , 2017, 8, 1484.	3.5	22
1185	Genome Plasticity and Polymorphisms in Critical Genes Correlate with Increased Virulence of Dutch Outbreak-Related <i>Coxiella burnetii</i> Strains. <i>Frontiers in Microbiology</i> , 2017, 8, 1526.	3.5	26
1186	New Insights into the Diversity of the Genus <i>Faecalibacterium</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 1790.	3.5	71
1187	pirABvp-Bearing <i>Vibrio parahaemolyticus</i> and <i>Vibrio campbellii</i> Pathogens Isolated from the Same AHPND-Affected Pond Possess Highly Similar Pathogenic Plasmids. <i>Frontiers in Microbiology</i> , 2017, 8, 1859.	3.5	66
1188	Complete Genome Sequence of <i>Vibrio campbellii</i> LMB 29 Isolated from Red Drum with Four Native Megaplasms. <i>Frontiers in Microbiology</i> , 2017, 8, 2035.	3.5	38
1189	Double-Face Meets the Bacterial World: The Opportunistic Pathogen <i>Stenotrophomonas maltophilia</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 2190.	3.5	66
1190	Comparative Genomics of a Bovine <i>Mycobacterium tuberculosis</i> Isolate and Other Strains Reveals Its Potential Mechanism of Bovine Adaptation. <i>Frontiers in Microbiology</i> , 2017, 8, 2500.	3.5	11
1191	Severe infections emerge from commensal bacteria by adaptive evolution. <i>ELife</i> , 2017, 6, .	6.0	93
1192	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.	1.6	18
1193	Comparative analyses of plastid genomes from fourteen <i>Cornales</i> species: inferences for phylogenetic relationships and genome evolution. <i>BMC Genomics</i> , 2017, 18, 956.	2.8	40
1194	Genomic divergence and cohesion in a species of pelagic freshwater bacteria. <i>BMC Genomics</i> , 2017, 18, 794.	2.8	14
1195	Bacteriophages are the major drivers of <i>Shigella flexneri</i> serotype 1c genome plasticity: a complete genome analysis. <i>BMC Genomics</i> , 2017, 18, 722.	2.8	10
1196	Legionnairesâ€™ Disease Outbreak Caused by Endemic Strain of <i>Legionella pneumophila</i> , New York, New York, USA, 2015. <i>Emerging Infectious Diseases</i> , 2017, 23, 1784-1791.	4.3	33
1197	The First Chloroplast Genome Sequence of <i>Boswellia sacra</i> , a Resin-Producing Plant in Oman. <i>PLoS ONE</i> , 2017, 12, e0169794.	2.5	19
1198	Comparative Genome Sequencing Reveals Within-Host Genetic Changes in <i>Neisseria meningitidis</i> during Invasive Disease. <i>PLoS ONE</i> , 2017, 12, e0169892.	2.5	26
1199	Genomic confirmation of vancomycin-resistant <i>Enterococcus</i> transmission from deceased donor to liver transplant recipient. <i>PLoS ONE</i> , 2017, 12, e0170449.	2.5	16
1200	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.	2.5	27

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1201	Comparative genomics of two super-shedder isolates of <i>Escherichia coli</i> O157:H7. <i>PLoS ONE</i> , 2017, 12, e0182940.	2.5	19
1202	The complete chloroplast genome sequences of three <i>Adenophora</i> species and comparative analysis with <i>Campanuloid</i> species (<i>Campanulaceae</i>). <i>PLoS ONE</i> , 2017, 12, e0183652.	2.5	19
1203	The mitochondrial genome of the plant-pathogenic fungus <i>Stemphylium lycopersici</i> uncovers a dynamic structure due to repetitive and mobile elements. <i>PLoS ONE</i> , 2017, 12, e0185545.	2.5	52
1204	Prevalence of binary toxin positive <i>Clostridium difficile</i> in diarrhoeal humans in the absence of epidemic ribotype 027. <i>PLoS ONE</i> , 2017, 12, e0187658.	2.5	11
1205	Isolation and characterization of a N4-like lytic bacteriophage infecting <i>Vibrio splendidus</i> , a pathogen of fish and bivalves. <i>PLoS ONE</i> , 2017, 12, e0190083.	2.5	33
1206	Promiscuous signaling by a regulatory system unique to the pandemic PMEN1 pneumococcal lineage. <i>PLoS Pathogens</i> , 2017, 13, e1006339.	4.7	38
1207	The Use of Next-Generation Sequencing in the Identification of a Fastidious Pathogen: A Lesson From a Clinical Setup. <i>Evolutionary Bioinformatics</i> , 2017, 13, 117693431668607.	1.2	17
1208	Comparative genomics of the tardigrades <i>Hypsibius dujardini</i> and <i>Ramazzottius varieornatus</i> . <i>PLoS Biology</i> , 2017, 15, e2002266.	5.6	170
1209	Anaerobically Grown <i>Escherichia coli</i> Has an Enhanced Mutation Rate and Distinct Mutational Spectra. <i>PLoS Genetics</i> , 2017, 13, e1006570.	3.5	60
1210	First insights in the variability of <i>Borrelia recurrentis</i> genomes. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005865.	3.0	14
1211	Expression and evolutionary patterns of mycobacteriophage D29 and its temperate close relatives. <i>BMC Microbiology</i> , 2017, 17, 225.	3.3	24
1212	Alignment-free sequence comparison: benefits, applications, and tools. <i>Genome Biology</i> , 2017, 18, 186.	8.8	371
1213	Genome characterization of a novel binary toxin-positive strain of <i>Clostridium difficile</i> and comparison with the epidemic 027 and 078 strains. <i>Gut Pathogens</i> , 2017, 9, 42.	3.4	15
1214	A VP24-truncated isolate of white spot syndrome virus is inefficient in per os infection. <i>Veterinary Research</i> , 2017, 48, 87.	3.0	15
1215	Genome sequencing and analysis of the first spontaneous Nanosilver resistant bacterium <i>Proteus mirabilis</i> strain SCDR1. <i>Antimicrobial Resistance and Infection Control</i> , 2017, 6, 119.	4.1	16
1216	High-quality draft genome sequence of a biofilm forming lignocellulolytic <i>Aspergillus niger</i> strain ATCC 10864. <i>Standards in Genomic Sciences</i> , 2017, 12, 37.	1.5	10
1217	Complete genome sequence of <i>Thermotoga</i> sp. strain RQ7. <i>Standards in Genomic Sciences</i> , 2017, 12, 62.	1.5	9
1218	Draft genome sequence of <i>Bacillus velezensis</i> 2A-2B strain: a rhizospheric inhabitant of <i>Sporobolus airoides</i> (Torr.) Torr., with antifungal activity against root rot causing phytopathogens. <i>Standards in Genomic Sciences</i> , 2017, 12, 73.	1.5	26

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1219	Complete genome sequence analysis of <i>Archaeoglobus fulgidus</i> strain 7324 (DSM 8774), a hyperthermophilic archaeal sulfate reducer from a North Sea oil field. <i>Standards in Genomic Sciences</i> , 2017, 12, 79.	1.5	19
1220	NucDiff: in-depth characterization and annotation of differences between two sets of DNA sequences. <i>BMC Bioinformatics</i> , 2017, 18, 338.	2.6	43
1221	Whole genome sequencing for the molecular characterization of carbapenem-resistant <i>Klebsiella pneumoniae</i> strains isolated at the Italian ASST Fatebenefratelli Sacco Hospital, 2012–2014. <i>BMC Infectious Diseases</i> , 2017, 17, 666.	2.9	33
1222	The genomic sequence of <i>Exiguobacterium chiriqhucha</i> str. N139 reveals a species that thrives in cold waters and extreme environmental conditions. <i>PeerJ</i> , 2017, 5, e3162.	2.0	27
1223	Complete Genome Sequences of Two Geographically Distinct <i>Legionella micdadei</i> Clinical Isolates. <i>Genome Announcements</i> , 2017, 5, .	0.8	0
1224	Draft Genome Sequences of Seven 4-Formylaminoxyvinylglycine Producers Belonging to the <i>Pseudomonas fluorescens</i> Species Complex. <i>Genome Announcements</i> , 2017, 5, .	0.8	6
1225	Comparative genomic analysis of <i>Acinetobacter</i> strains isolated from murine colonic crypts. <i>BMC Genomics</i> , 2017, 18, 525.	2.8	14
1226	Approaches for in silico finishing of microbial genome sequences. <i>Genetics and Molecular Biology</i> , 2017, 40, 553-576.	1.3	17
1227	Draft Genome Sequence of <i>Micrococcus luteus</i> (Schroeter) Cohn (ATCC 12698). <i>Genome Announcements</i> , 2017, 5, .	0.8	2
1228	Draft Genome Sequences of Two Highly Erythromycin-Resistant <i>Streptococcus gallolyticus</i> subsp. <i>gallolyticus</i> Isolates Containing a Novel Tn 916 -Like Element, Tn 6331. <i>Genome Announcements</i> , 2017, 5, .	0.8	7
1229	Draft Genome Sequence of <i>Flavobacterium johnsoniae</i> CI04, an Isolate from the Soybean Rhizosphere. <i>Genome Announcements</i> , 2017, 5, .	0.8	5
1230	A GRASP-Based Heuristic for the Sorting by Length-Weighted Inversions Problem. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 352-363.	3.0	3
1231	Evaluating the use of whole-genome sequencing for outbreak investigations in the lack of closely related reference genome. <i>Infection, Genetics and Evolution</i> , 2018, 59, 1-6.	2.3	7
1232	Coexistence of <i>mcr-1</i> , <i>bla</i> KPC-2 and two copies of <i>fosA3</i> in a clinical <i>Escherichia coli</i> strain isolated from urine. <i>Infection, Genetics and Evolution</i> , 2018, 60, 77-79.	2.3	9
1233	Complete Sequence of the IncA/C ₁ Plasmid pCf587 Carrying <i>bla</i> _{PER-2} from <i>Citrobacter freundii</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	3.2	9
1234	Culture-Facilitated Comparative Genomics of the Facultative Symbiont <i>Hamiltonella defensa</i> . <i>Genome Biology and Evolution</i> , 2018, 10, 786-802.	2.5	37
1235	Considerations for Visualizing Comparison. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2018, 24, 413-423.	4.4	118
1236	Emergence, transmission and phylogeny of methicillin-resistant <i>Staphylococcus aureus</i> sequence type 8 (USA300) in Taiwan. <i>Journal of Hospital Infection</i> , 2018, 100, 355-358.	2.9	13

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1237	<i>Peptoniphilus lacydonensis</i> sp. nov., a new human-associated species isolated from a patient with chronic refractory sinusitis. <i>New Microbes and New Infections</i> , 2018, 23, 61-69.	1.6	14
1238	Novel sequencing technologies to support industrial biotechnology. <i>FEMS Microbiology Letters</i> , 2018, 365, .	1.8	15
1239	Genomic analysis of oral <i>Campylobacter concisus</i> strains identified a potential bacterial molecular marker associated with active Crohn's disease. <i>Emerging Microbes and Infections</i> , 2018, 7, 1-14.	6.5	25
1240	Safety assessment and functional properties of four enterococci strains isolated from regional Argentinean cheese. <i>International Journal of Food Microbiology</i> , 2018, 277, 1-9.	4.7	16
1241	Comparative genome and transcriptome analysis reveal the medicinal basis and environmental adaptation of artificially cultivated <i>Taiwanofungus camphoratus</i> . <i>Mycological Progress</i> , 2018, 17, 871-883.	1.4	9
1242	T Cell-Independent Gamma Interferon and B Cells Cooperate To Prevent Mortality Associated with Disseminated <i>Chlamydia muridarum</i> Genital Tract Infection. <i>Infection and Immunity</i> , 2018, 86, .	2.2	18
1243	riboSeed: leveraging prokaryotic genomic architecture to assemble across ribosomal regions. <i>Nucleic Acids Research</i> , 2018, 46, e68-e68.	14.5	10
1244	Comparison of closely related, uncultivated <i>Coxiella</i> tick endosymbiont population genomes reveals clues about the mechanisms of symbiosis. <i>Environmental Microbiology</i> , 2018, 20, 1751-1764.	3.8	33
1245	Evolution of the Plastid Genomes in Diatoms. <i>Advances in Botanical Research</i> , 2018, 85, 129-155.	1.1	51
1246	Raising the Stakes: Loss of Efflux Pump Regulation Decreases Meropenem Susceptibility in <i>Burkholderia pseudomallei</i> . <i>Clinical Infectious Diseases</i> , 2018, 67, 243-250.	5.8	34
1247	Draft genome sequence of <i>Penicillium chrysogenum</i> strain HKF2, a fungus with potential for production of prebiotic synthesizing enzymes. <i>3 Biotech</i> , 2018, 8, 106.	2.2	11
1248	Potato late blight field resistance from QTL dPI09c is conferred by the NB-LRR gene R8. <i>Journal of Experimental Botany</i> , 2018, 69, 1545-1555.	4.8	56
1249	Bacteriophages of the Urinary Microbiome. <i>Journal of Bacteriology</i> , 2018, 200, .	2.2	70
1250	Genetic characterization and modification of a bioethanol-producing yeast strain. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 2213-2223.	3.6	5
1251	A Genome Comparison of T7-like Podoviruses That Infect <i>Caulobacter crescentus</i> . <i>Current Microbiology</i> , 2018, 75, 760-765.	2.2	4
1252	Intragenomic Variability Between the Chloroplast Genomes of <i>Trachelomonas grandis</i> and <i>Trachelomonas volvocina</i> and Phylogenomic Analysis of Phototrophic Euglenoids. <i>Journal of Eukaryotic Microbiology</i> , 2018, 65, 648-660.	1.7	3
1253	The genome sequence of a new strain of <i>Mycobacterium ulcerans</i> ecovar <i>Liflandii</i> , emerging as a sturgeon pathogen. <i>Aquaculture</i> , 2018, 489, 141-147.	3.5	17
1254	Comparative Genomics for Prokaryotes. <i>Methods in Molecular Biology</i> , 2018, 1704, 55-78.	0.9	15

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1255	Genome Rearrangement Analysis: Cut and Join Genome Rearrangements and Gene Cluster Preserving Approaches. <i>Methods in Molecular Biology</i> , 2018, 1704, 261-289.	0.9	5
1256	Taxonomomic description of four new <i>Clostridium</i> species isolated from human gut: <i>Clostridium amazonitimonense</i> TM , <i>Clostridium merdae</i> TM , <i>Clostridium massilidielmoense</i> TM and <i>Clostridium nigeriense</i> TM . <i>New Microbes and New Infections</i> , 2018, 21, 128-139.	1.6	28
1257	Patterns of Genomic Variation in the Opportunistic Pathogen <i>Candida glabrata</i> Suggest the Existence of Mating and a Secondary Association with Humans. <i>Current Biology</i> , 2018, 28, 15-27.e7.	3.9	114
1258	Successive Emergence of Ceftazidime-Avibactam Resistance through Distinct Genomic Adaptations in <i>bla</i> _{KPC-2} -Harboring <i>Klebsiella pneumoniae</i> Sequence Type 307 Isolates. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	3.2	162
1259	Methylation in <i>Mycobacterium tuberculosis</i> is lineage specific with associated mutations present globally. <i>Scientific Reports</i> , 2018, 8, 160.	3.3	31
1260	Clinical and molecular features of MDR livestock-associated MRSA ST9 with staphylococcal cassette chromosome <i>mecXII</i> in humans. <i>Journal of Antimicrobial Chemotherapy</i> , 2018, 73, 33-40.	3.0	47
1261	Microbial culturomics to isolate halophilic bacteria from table salt: genome sequence and description of the moderately halophilic bacterium <i>Bacillus salis</i> sp. nov.. <i>New Microbes and New Infections</i> , 2018, 23, 28-38.	1.6	4
1262	Transfer of a <i>bla</i> CTX-M-1-carrying plasmid between different <i>Escherichia coli</i> strains within the human gut explored by whole genome sequencing analyses. <i>Scientific Reports</i> , 2018, 8, 280.	3.3	28
1263	Weak Epistasis May Drive Adaptation in Recombining Bacteria. <i>Genetics</i> , 2018, 208, 1247-1260.	2.9	51
1264	Draft Genome Sequences of <i>Pseudomonas putida</i> UV4 and UV4/95, Toluene Dioxygenase-Expressing Producers of <i>cis</i> -1,2-Dihydrodiols. <i>Genome Announcements</i> , 2018, 6, .	0.8	4
1265	<i>Staphylococcus aureus</i> undergoes major transcriptional reorganization during growth with <i>Enterococcus faecalis</i> in milk. <i>Food Microbiology</i> , 2018, 73, 17-28.	4.2	15
1266	Genomic diversity and distribution of <i>Bifidobacterium longum</i> subsp. <i>longum</i> across the human lifespan. <i>Scientific Reports</i> , 2018, 8, 85.	3.3	99
1267	Complete genome sequence of <i>Tsukamurella</i> sp. MH1: A wide-chain length alkane-degrading actinomycete. <i>Journal of Biotechnology</i> , 2018, 268, 1-5.	3.8	5
1268	The putative functions of lysogeny in mediating the survivorship of <i>Escherichia coli</i> in seawater and marine sediment. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	2.7	6
1269	Genomic analysis and immune response in a murine mastitis model of vB_EcoM-UFV13, a potential biocontrol agent for use in dairy cows. <i>Scientific Reports</i> , 2018, 8, 6845.	3.3	26
1270	Comparative genomic and metabolic analysis of three <i>Lactobacillus paracasei</i> cheese isolates reveals considerable genomic differences in strains from the same niche. <i>BMC Genomics</i> , 2018, 19, 205.	2.8	29
1271	Comparative genomics of the wheat fungal pathogen <i>Pyrenophora tritici-repentis</i> reveals chromosomal variations and genome plasticity. <i>BMC Genomics</i> , 2018, 19, 279.	2.8	56
1272	Development of race-specific molecular marker for <i>Xanthomonas campestris</i> pv. <i>campestris</i> race 3, the causal agent of black rot of crucifers. <i>Canadian Journal of Plant Science</i> , 2018, 98, 1119-1125.	0.9	12

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1273	Draft genome sequence of <i>Fermentimonas caenicola</i> strain SIT8, isolated from the human gut. <i>Standards in Genomic Sciences</i> , 2018, 13, 8.	1.5	7
1274	Draft Genome Sequences of Four <i>Parasaccharibacter apium</i> Strains Isolated from Honey Bees. <i>Genome Announcements</i> , 2018, 6, .	0.8	9
1275	Ancient DNA study reveals HLA susceptibility locus for leprosy in medieval Europeans. <i>Nature Communications</i> , 2018, 9, 1569.	12.8	67
1276	Male-killing toxin in a bacterial symbiont of <i>Drosophila</i> . <i>Nature</i> , 2018, 557, 252-255.	27.8	111
1277	A new strategy to infer circularity applied to four new complete frog mitogenomes. <i>Ecology and Evolution</i> , 2018, 8, 4011-4018.	1.9	15
1278	Draft Genome Sequences of 12 Clinical and Environmental Methicillin-Resistant <i>Staphylococcus pseudintermedius</i> Strains Isolated from a Veterinary Teaching Hospital in Washington State. <i>Genome Announcements</i> , 2018, 6, .	0.8	0
1279	Genomic characterization of <i>Nitrospirillum amazonense</i> strain CBAmC, a nitrogen-fixing bacterium isolated from surface-sterilized sugarcane stems. <i>Molecular Genetics and Genomics</i> , 2018, 293, 997-1016.	2.1	17
1280	Morphologic and Genomic Analyses of New Isolates Reveal a Second Lineage of Cedratviruses. <i>Journal of Virology</i> , 2018, 92, .	3.4	21
1281	Complete genome sequence of <i>Bacillus velezensis</i> QST713: A biocontrol agent that protects <i>Agaricus bisporus</i> crops against the green mould disease. <i>Journal of Biotechnology</i> , 2018, 278, 10-19.	3.8	67
1282	Molecular basis for the structural diversity in serogroup O2-antigen polysaccharides in <i>Klebsiella pneumoniae</i> . <i>Journal of Biological Chemistry</i> , 2018, 293, 4666-4679.	3.4	42
1283	Molecular Characterization of OXA-198 Carbapenemase-Producing <i>Pseudomonas aeruginosa</i> Clinical Isolates. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	3.2	23
1284	<i>In Vitro</i> Culture of the Insect Endosymbiont <i>Spiroplasma poulsonii</i> Highlights Bacterial Genes Involved in Host-Symbiont Interaction. <i>MBio</i> , 2018, 9, .	4.1	51
1285	Isolation and identification of <i>Salmonella pullorum</i> bacteriophage YSP2 and its use as a therapy for chicken diarrhea. <i>Virus Genes</i> , 2018, 54, 446-456.	1.6	25
1286	Genome variation in nine co-occurring toxic <i>Cylindrospermopsis raciborskii</i> strains. <i>Harmful Algae</i> , 2018, 73, 157-166.	4.8	35
1287	A Novel <i>Glaesserella</i> sp. Isolated from Pigs with Severe Respiratory Infections Has a Mosaic Genome with Virulence Factors Putatively Acquired by Horizontal Transfer. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	17
1288	Draft Genome Sequences of 11 <i>Salmonella enterica</i> Seroovar Typhimurium Strains Isolated from Human Systemic and Nonsystemic Sites in Brazil. <i>Genome Announcements</i> , 2018, 6, .	0.8	2
1289	Large Diversity of Nonstandard Genes and Dynamic Evolution of Chloroplast Genomes in Siphonous Green Algae (Bryopsidales, Chlorophyta). <i>Genome Biology and Evolution</i> , 2018, 10, 1048-1061.	2.5	27
1290	Microbial Culturomics Application for Global Health: Noncontiguous Finished Genome Sequence and Description of <i>Pseudomonas massiliensis</i> Strain CB-1 ^T sp. nov. in Brazil. <i>OMICS A Journal of Integrative Biology</i> , 2018, 22, 164-175.	2.0	6

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1291	<i>Bacillus kwashiorkori</i> sp. nov., a new bacterial species isolated from a malnourished child using culturomics. <i>MicrobiologyOpen</i> , 2018, 7, e00535.	3.0	6
1292	The <i>Linum usitatissimum</i> L. plastome reveals atypical structural evolution, new editing sites, and the phylogenetic position of Linaceae within Malpighiales. <i>Plant Cell Reports</i> , 2018, 37, 307-328.	5.6	43
1293	Planctomycetes attached to algal surfaces: Insight into their genomes. <i>Genomics</i> , 2018, 110, 231-238.	2.9	39
1294	Comparative Genomic Analyses of <i>Clavibacter michiganensis</i> subsp. <i>insidiosus</i> and Pathogenicity on <i>Medicago truncatula</i> . <i>Phytopathology</i> , 2018, 108, 172-185.	2.2	15
1295	Characterisation of <i>Lactococcus lactis</i> isolates from herbs, fruits and vegetables for use as biopreservatives against <i>Listeria monocytogenes</i> in cheese. <i>Food Control</i> , 2018, 85, 472-483.	5.5	41
1296	The first complete organellar genomes of an Antarctic red alga, <i>Pyropia endiviifolia</i> : insights into its genome architecture and phylogenetic position within genus <i>Pyropia</i> (Bangiales, Rhodophyta). <i>Journal of Oceanology and Limnology</i> , 2018, 36, 1315-1328.	1.3	12
1297	The complete chloroplast genome sequence of <i>Dodonaea viscosa</i> : comparative and phylogenetic analyses. <i>Genetica</i> , 2018, 146, 101-113.	1.1	54
1298	Complete plastid genome sequences of three tropical <i>Alseodaphne</i> trees in the family Lauraceae. <i>Holzforschung</i> , 2018, 72, 337-345.	1.9	23
1299	Challenges of <i>Francisella</i> classification exemplified by an atypical clinical isolate. <i>Diagnostic Microbiology and Infectious Disease</i> , 2018, 90, 241-247.	1.8	3
1300	Genome-Wide Identification of Fitness Factors in Mastitis-Associated <i>Escherichia coli</i> . <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	21
1301	The genetic basis underlying variation in production of the flavour compound diacetyl by <i>Lactobacillus rhamnosus</i> strains in milk. <i>International Journal of Food Microbiology</i> , 2018, 265, 30-39.	4.7	23
1302	HomBlocks: A multiple-alignment construction pipeline for organelle phylogenomics based on locally collinear block searching. <i>Genomics</i> , 2018, 110, 18-22.	2.9	183
1303	From plants to nematodes: <i>Serratia grimesii</i> BXF1 genome reveals an adaptation to the modulation of multi-species interactions. <i>Microbial Genomics</i> , 2018, 4, .	2.0	19
1304	Genomic Alterations of <i>Staphylococcus aureus</i> ATCC 25923 after Prolonged Passage in the Laboratory. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	1
1305	Using Core Genome Alignments To Assign Bacterial Species. <i>MSystems</i> , 2018, 3, .	3.8	54
1306	Draft Genome Sequence of <i>Rhizobium</i> sp. Strain T2.30D-1.1, Isolated from 538.5 Meters Deep on the Subsurface of the Iberian Pyrite Belt. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	5
1307	Identification and characterization of novel conserved RNA structures in <i>Drosophila</i> . <i>BMC Genomics</i> , 2018, 19, 899.	2.8	6
1308	Closed Genome Sequence of <i>Salmonella enterica</i> Serovar Richmond Strain CFSAN000191, Obtained with Nanopore Sequencing. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	4

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1309	Complete Genome Sequence of <i>Marinobacter flavimaris</i> LMG 23834 ^T , Which Is Potentially Useful in Bioremediation. <i>Genome Announcements</i> , 2018, 6, .	0.8	3
1310	Closed Genome Sequences of Two <i>Clostridium botulinum</i> Strains Obtained by Nanopore Sequencing. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	13
1311	Evolution of six novel ORFs in the plastome of <i>Mankyua chejuense</i> and phylogeny of eusporangiate ferns. <i>Scientific Reports</i> , 2018, 8, 16466.	3.3	10
1312	Comparative genomics of <i>Botryosphaeria dothidea</i> and <i>B. kuwatsukai</i> , causal agents of apple ring rot, reveals both species expansion of pathogenicity-related genes and variations in virulence gene content during speciation. <i>IMA Fungus</i> , 2018, 9, 243-257.	3.8	37
1313	A Nonribosomal Peptide Synthase Gene Driving Virulence in <i>Mycobacterium tuberculosis</i> . <i>MSphere</i> , 2018, 3, .	2.9	20
1314	Impacts of horizontal gene transfer on the compact genome of the clavulanic acid-producing <i>Streptomyces</i> strain F613-1. <i>3 Biotech</i> , 2018, 8, 472.	2.2	3
1315	Visualization-assisted binning of metagenome assemblies reveals potential new pathogenic profiles in idiopathic travelers' diarrhea. <i>Microbiome</i> , 2018, 6, 201.	11.1	20
1316	Combinatorial Loss of the Enzymatic Activities of Viral Uracil-DNA Glycosylase and Viral dUTPase Impairs Murine Gammaherpesvirus Pathogenesis and Leads to Increased Recombination-Based Deletion in the Viral Genome. <i>MBio</i> , 2018, 9, .	4.1	11
1317	Position and Content Paradigms in Genome Rearrangements: The Wild and Crazy World of Permutations in Genomics. <i>Bulletin of Mathematical Biology</i> , 2018, 80, 3227-3246.	1.9	13
1318	Nonmutational mechanism of inheritance in the Archaeon <i>Sulfolobus solfataricus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 12271-12276.	7.1	8
1319	Gene inversion potentiates bacterial evolvability and virulence. <i>Nature Communications</i> , 2018, 9, 4662.	12.8	61
1320	Presence of an <i>Agrobacterium</i> -Type Tumor-Inducing Plasmid in <i>Neorhizobium</i> sp. NCHU2750 and the Link to Phytopathogenicity. <i>Genome Biology and Evolution</i> , 2018, 10, 3188-3195.	2.5	13
1321	Genetic Loci Associated With Fluoride Resistance in <i>Streptococcus mutans</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 3093.	3.5	16
1322	Genome Sequences and Comparative Analysis of Two Extended-Spectrum Extensively-Drug Resistant <i>Mycobacterium tuberculosis</i> Strains. <i>Frontiers in Pharmacology</i> , 2018, 9, 1492.	3.5	2
1323	High-Quality Draft Genome Sequence of <i>Xanthomonas</i> sp. Strain CPBF 424, a Walnut-Pathogenic Strain with Atypical Features. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	7
1324	High-Quality Draft Genome Sequence of <i>Xanthomonas arboricola</i> pv. <i>juglandis</i> CPBF 1521, Isolated from Leaves of a Symptomatic Walnut Tree in Portugal without a Past of Phytosanitary Treatment. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	5
1325	Comparative analysis of <i>Faecalibacterium prausnitzii</i> genomes shows a high level of genome plasticity and warrants separation into new species-level taxa. <i>BMC Genomics</i> , 2018, 19, 931.	2.8	78
1326	Loss of Bacitracin Resistance Due to a Large Genomic Deletion among <i>Bacillus anthracis</i> Strains. <i>MSystems</i> , 2018, 3, .	3.8	9

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1327	Clinical, immunological and bacteriological characteristics of H7N9 patients nosocomially co-infected by <i>Acinetobacter Baumannii</i> : a case control study. <i>BMC Infectious Diseases</i> , 2018, 18, 664.	2.9	8
1328	Sequencing of organellar genomes of <i>Gymnomitrium concinnatum</i> (Jungermanniales) revealed the first exception in the structure and gene order of evolutionary stable liverworts mitogenomes. <i>BMC Plant Biology</i> , 2018, 18, 321.	3.6	21
1329	Emergence of a dalbavancin induced glycopeptide/lipoglycopeptide non-susceptible <i>Staphylococcus aureus</i> during treatment of a cardiac device-related endocarditis. <i>Emerging Microbes and Infections</i> , 2018, 7, 1-10.	6.5	50
1330	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.	3.5	17
1331	High throughput ANI analysis of 90K prokaryotic genomes reveals clear species boundaries. <i>Nature Communications</i> , 2018, 9, 5114.	12.8	2,816
1332	The <i>afc</i> antifungal activity cluster, which is under tight regulatory control of <i>ShvR</i> , is essential for transition from intracellular persistence of <i>Burkholderia cenocepacia</i> to acute pro-inflammatory infection. <i>PLoS Pathogens</i> , 2018, 14, e1007473.	4.7	13
1333	Intergeneric Relationships within the Early-Diverging Angiosperm Family Nymphaeaceae Based on Chloroplast Phylogenomics. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3780.	4.1	11
1334	SWPhylo – A Novel Tool for Phylogenomic Inferences by Comparison of Oligonucleotide Patterns and Integration of Genome-Based and Gene-Based Phylogenetic Trees. <i>Evolutionary Bioinformatics</i> , 2018, 14, 117693431875929.	1.2	2
1335	Species Identification of <i>Conyza bonariensis</i> Assisted by Chloroplast Genome Sequencing. <i>Frontiers in Genetics</i> , 2018, 9, 374.	2.3	24
1336	Punctuated plastome reduction and host-parasite horizontal gene transfer in the holoparasitic plant genus <i>Aphyllon</i> . <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018, 285, 20181535.	2.6	25
1337	Comparing Two <i>Mycobacterium tuberculosis</i> Genomes from Chinese Immigrants with Native Genomes Using Mauve Alignments. <i>Tuberculosis and Respiratory Diseases</i> , 2018, 81, 216.	1.8	4
1338	Implications of <i>stx</i> loss for clinical diagnostics of Shiga toxin-producing <i>Escherichia coli</i> . <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2018, 37, 2361-2370.	2.9	17
1339	Complete genome sequence of <i>Kocuria rhizophila</i> BT304, isolated from the small intestine of castrated beef cattle. <i>Gut Pathogens</i> , 2018, 10, 42.	3.4	5
1340	A Cotransformation Method To Identify a Restriction-Modification Enzyme That Reduces Conjugation Efficiency in <i>Campylobacter jejuni</i> . <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	2
1341	Comparison of Highly and Weakly Virulent <i>Dickeya solani</i> Strains, With a View on the Pangenome and Panregulon of This Species. <i>Frontiers in Microbiology</i> , 2018, 9, 1940.	3.5	50
1342	S-plot2: Rapid Visual and Statistical Analysis of Genomic Sequences. <i>Evolutionary Bioinformatics</i> , 2018, 14, 117693431879735.	1.2	8
1343	Plastid genome analysis of three Nemaliophycidae red algal species suggests environmental adaptation for iron limited habitats. <i>PLoS ONE</i> , 2018, 13, e0196995.	2.5	9
1344	Comparative genomics of cocci-shaped <i>Sporosarcina</i> strains with diverse spatial isolation. <i>BMC Genomics</i> , 2018, 19, 310.	2.8	9

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1345	Complete Chloroplast Genome Sequence of Broomcorn Millet (<i>Panicum miliaceum</i> L.) and Comparative Analysis with Other Panicoideae Species. <i>Agronomy</i> , 2018, 8, 159.	3.0	14
1346	Function of BriC peptide in the pneumococcal competence and virulence portfolio. <i>PLoS Pathogens</i> , 2018, 14, e1007328.	4.7	44
1347	Characterization of a <i>Salmonella</i> Enteritidis bacteriophage showing broad lytic activity against Gram-negative enteric bacteria. <i>Journal of Microbiology</i> , 2018, 56, 917-925.	2.8	22
1348	Prophage-driven genomic structural changes promote <i>Bartonella</i> vertical evolution. <i>Genome Biology and Evolution</i> , 2018, 10, 3089-3103.	2.5	13
1349	Genome sequencing and functional analysis of an environmental isolate <i>Escherichia coli</i> Cont-1 revealed its genetic basis of arsenic-transformation and niche adaptation. <i>Ecological Genetics and Genomics</i> , 2018, 9, 34-42.	0.5	1
1350	Capsular Switching and ICE Transformation Occurred in Human <i>Streptococcus agalactiae</i> ST19 With High Pathogenicity to Fish. <i>Frontiers in Veterinary Science</i> , 2018, 5, 281.	2.2	3
1351	Complete genome of streamlined marine actinobacterium <i>Pontimonas salivibrio</i> strain CL-TW6T adapted to coastal planktonic lifestyle. <i>BMC Genomics</i> , 2018, 19, 625.	2.8	10
1352	Complete genome sequence reveals evolutionary dynamics of an emerging and variant pathovar of <i>Xanthomonas euvesicatoria</i> . <i>Genome Biology and Evolution</i> , 2018, 10, 3104-3109.	2.5	8
1353	Desiccation tolerance in <i>Acinetobacter baumannii</i> is mediated by the two-component response regulator BfmR. <i>PLoS ONE</i> , 2018, 13, e0205638.	2.5	67
1354	Whole-Genome Sequence of the Novel <i>Antarctobacter heliothermus</i> Strain SMS3, Found in Association with the Marine Diatom <i>Skeletonema marinoi</i> . <i>Journal of Genomics</i> , 2018, 6, 113-116.	0.9	4
1355	Genome Analysis of the Yeast M14, an Industrial Brewing Yeast Strain Widely Used in China. <i>Journal of the American Society of Brewing Chemists</i> , 2018, 76, 223-235.	1.1	1
1356	High genomic variability in the plant pathogenic bacterium <i>Pectobacterium parmentieri</i> deciphered from de novo assembled complete genomes. <i>BMC Genomics</i> , 2018, 19, 751.	2.8	28
1357	Mitochondrial and Plastid Genomes from Coralline Red Algae Provide Insights into the Incongruent Evolutionary Histories of Organelles. <i>Genome Biology and Evolution</i> , 2018, 10, 2961-2972.	2.5	29
1358	Tracking key virulence loci encoding aerobactin and salmochelin siderophore synthesis in <i>Klebsiella pneumoniae</i> . <i>Genome Medicine</i> , 2018, 10, 77.	8.2	153
1359	In vivo evolution of drug-resistant <i>Mycobacterium tuberculosis</i> in patients during long-term treatment. <i>BMC Genomics</i> , 2018, 19, 640.	2.8	18
1360	The Energy-Coupling Factor Transporter Module EcfAA TM , a Novel Candidate for the Genetic Basis of Fatty Acid-Auxotrophic Small-Colony Variants of <i>Staphylococcus aureus</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 1863.	3.5	12
1361	A New Freshwater Cyanosiphovirus Harboring Integrase. <i>Frontiers in Microbiology</i> , 2018, 9, 2204.	3.5	26
1362	Novel diagnostic marker genes differentiate <i>Saccharomyces</i> with respect to their potential application. <i>Journal of the Institute of Brewing</i> , 2018, 124, 416-424.	2.3	2

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1363	High and Variable Rates of Repeat-Mediated Mitochondrial Genome Rearrangement in a Genus of Plants. <i>Molecular Biology and Evolution</i> , 2018, 35, 2773-2785.	8.9	60
1364	Characterizing Mobilized Virulence Factors and Multidrug Resistance Genes in Carbapenemase-Producing <i>Klebsiella pneumoniae</i> in a Sri Lankan Hospital. <i>Frontiers in Microbiology</i> , 2018, 9, 2044.	3.5	13
1365	Nanopore sequencing and full genome de novo assembly of human cytomegalovirus TB40/E reveals clonal diversity and structural variations. <i>BMC Genomics</i> , 2018, 19, 577.	2.8	17
1366	Genome sequences and description of novel exopolysaccharides producing species <i>Komagataeibacter pomaceti</i> sp. nov. and reclassification of <i>Komagataeibacter kombuchae</i> (Dutta and Gachhui 2007) Yamada et al., 2013 as a later heterotypic synonym of <i>Komagataeibacter hansenii</i> (Gossel et al. 1983) Yamada et al., 2013. <i>Systematic and Applied Microbiology</i> , 2018, 41, 581-592.	2.8	46

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1381	Characterization of the mitochondrial genomes of three species in the ectomycorrhizal genus <i>Cantharellus</i> and phylogeny of Agaricomycetes. <i>International Journal of Biological Macromolecules</i> , 2018, 118, 756-769.	7.5	43
1382	A clone of the emergent <i>Streptococcus pyogenes</i> emm89 clade responsible for a large outbreak in a post-surgery oncology unit in France. <i>Medical Microbiology and Immunology</i> , 2018, 207, 287-296.	4.8	10
1383	Genomic analysis of a <i>Raoultella ornithinolytica</i> strain causing prosthetic joint infection in an immunocompetent patient. <i>Scientific Reports</i> , 2018, 8, 9462.	3.3	10
1384	Intragenomic chloroplast genome comparison in the genus <i>Euglena</i> (Phylum: Euglenophyta) with annotated chloroplast genomes of <i>Euglena hiemalis</i> and <i>Euglena clara</i> . <i>Journal of Applied Phycology</i> , 2018, 30, 3167-3177.	2.8	2
1385	The origin and remolding of genomic islands of differentiation in the European sea bass. <i>Nature Communications</i> , 2018, 9, 2518.	12.8	86
1386	Whole genome comparison of two <i>Starmerella bacillaris</i> strains with other wine yeasts uncovers genes involved in modulating important winemaking traits. <i>FEMS Yeast Research</i> , 2018, 18, .	2.3	15
1387	Rapid Detection of <i>Candida auris</i> Based on Loop-Mediated Isothermal Amplification (LAMP). <i>Journal of Clinical Microbiology</i> , 2018, 56, .	3.9	46
1388	Draft Genome Sequence of a White Spot Syndrome Virus Isolate Obtained in Ecuador. <i>Genome Announcements</i> , 2018, 6, .	0.8	16
1389	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.	2.5	30
1390	Characterization and comparative mitogenomic analysis of six newly sequenced mitochondrial genomes from ectomycorrhizal fungi (<i>Russula</i>) and phylogenetic analysis of the Agaricomycetes. <i>International Journal of Biological Macromolecules</i> , 2018, 119, 792-802.	7.5	67
1391	Distinctive characters of <i>Nostoc</i> genomes in cyanolichens. <i>BMC Genomics</i> , 2018, 19, 434.	2.8	30
1392	Otitis in a cat associated with <i>Corynebacterium provencense</i> . <i>BMC Veterinary Research</i> , 2018, 14, 200.	1.9	5
1393	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.	4.7	20
1394	Mesophilic Sporeformers Identified in Whey Powder by Using Shotgun Metagenomic Sequencing. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	15
1395	Emergence of a vanG-carrying and multidrug resistant ICE in zoonotic pathogen <i>Streptococcus suis</i> . <i>Veterinary Microbiology</i> , 2018, 222, 109-113.	1.9	14
1396	Whole genome sequencing and identification of <i>Bacillus endophyticus</i> and <i>B. anthracis</i> isolated from anthrax outbreaks in South Africa. <i>BMC Microbiology</i> , 2018, 18, 67.	3.3	11
1397	Comparative Chloroplast Genomics of Dipsacales Species: Insights Into Sequence Variation, Adaptive Evolution, and Phylogenetic Relationships. <i>Frontiers in Plant Science</i> , 2018, 9, 689.	3.6	110
1398	Horse Y chromosome assembly displays unique evolutionary features and putative stallion fertility genes. <i>Nature Communications</i> , 2018, 9, 2945.	12.8	56

#	ARTICLE	IF	CITATIONS
1399	SNP hot-spots in the clam parasite QPX. BMC Genomics, 2018, 19, 486.	2.8	2
1400	Genetic Separation of <i>Listeria monocytogenes</i> Causing Central Nervous System Infections in Animals. Frontiers in Cellular and Infection Microbiology, 2018, 8, 20.	3.9	22
1401	Phylogeny of <i>Vibrio vulnificus</i> from the Analysis of the Core-Genome: Implications for Intra-Species Taxonomy. Frontiers in Microbiology, 2017, 8, 2613.	3.5	50
1402	Orpheovirus IHUMI-LCC2: A New Virus among the Giant Viruses. Frontiers in Microbiology, 2017, 8, 2643.	3.5	70
1403	Phase Variable Expression of a Single Phage Receptor in <i>Campylobacter jejuni</i> NCTC12662 Influences Sensitivity Toward Several Diverse CPS-Dependent Phages. Frontiers in Microbiology, 2018, 9, 82.	3.5	31
1404	Exploring the Genomic Traits of Non-toxigenic <i>Vibrio parahaemolyticus</i> Strains Isolated in Southern Chile. Frontiers in Microbiology, 2018, 9, 161.	3.5	37
1405	<i>Pantoea ananatis</i> Genetic Diversity Analysis Reveals Limited Genomic Diversity as Well as Accessory Genes Correlated with Onion Pathogenicity. Frontiers in Microbiology, 2018, 9, 184.	3.5	48
1406	Comparative Genomics of Environmental and Clinical <i>Burkholderia cenocepacia</i> Strains Closely Related to the Highly Transmissible Epidemic ET12 Lineage. Frontiers in Microbiology, 2018, 9, 383.	3.5	16
1407	Genomic Structural Variations Affecting Virulence During Clonal Expansion of <i>Pseudomonas syringae</i> pv. <i>actinidiae</i> Biovar 3 in Europe. Frontiers in Microbiology, 2018, 9, 656.	3.5	18
1408	A Novel <i>mcr-1</i> Variant Carried by an IncI2-Type Plasmid Identified From a Multidrug Resistant Enterotoxigenic <i>Escherichia coli</i> . Frontiers in Microbiology, 2018, 9, 815.	3.5	12
1409	The PL6-Family Plasmids of <i>Haloquadratum</i> Are Virus-Related. Frontiers in Microbiology, 2018, 9, 1070.	3.5	3
1410	Comparative Genomics Reveals Evidence of Genome Reduction and High Extracellular Protein Degradation Potential in <i>Kangiella</i> . Frontiers in Microbiology, 2018, 9, 1224.	3.5	11
1411	Clinical <i>Staphylococcus argenteus</i> Develops to Small Colony Variants to Promote Persistent Infection. Frontiers in Microbiology, 2018, 9, 1347.	3.5	20
1412	â€ˆCandidatus <i>Aquirickettsiella gammari</i> â€™™ (Gammaproteobacteria: Legionellales: Coxiellaceae): A bacterial pathogen of the freshwater crustacean <i>Gammarus fossarum</i> (Malacostraca: Amphipoda). Journal of Invertebrate Pathology, 2018, 156, 41-53.	3.2	23
1413	<i>Bacillus safensis</i> FO-36b and <i>Bacillus pumilus</i> SAFR-032: a whole genome comparison of two spacecraft assembly facility isolates. BMC Microbiology, 2018, 18, 57.	3.3	16
1414	Physiological and Comparative Genomic Analysis of <i>Arthrobacter</i> sp. SRS-W-1-2016 Provides Insights on Niche Adaptation for Survival in Uraniferous Soils. Genes, 2018, 9, 31.	2.4	42
1415	The Unexplored Diversity of Pleolipoviruses: The Surprising Case of Two Viruses with Identical Major Structural Modules. Genes, 2018, 9, 131.	2.4	8
1416	Understanding plastome evolution in Hemiparasitic Santalales: Complete chloroplast genomes of three species, <i>Dendrotrophe varians</i> , <i>Helixanthera parasitica</i> , and <i>Macrosolen cochinchinensis</i> . PLoS ONE, 2018, 13, e0200293.	2.5	32

#	ARTICLE	IF	CITATIONS
1417	<i>Fusobacterium</i> Genomics Using MinION and Illumina Sequencing Enables Genome Completion and Correction. <i>MSphere</i> , 2018, 3, .	2.9	23
1418	Whole-Genome Comparison Reveals Heterogeneous Divergence and Mutation Hotspots in Chloroplast Genome of <i>Eucommia ulmoides</i> Oliver. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1037.	4.1	30
1419	Comparative Plastid Genomes of <i>Primula</i> Species: Sequence Divergence and Phylogenetic Relationships. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1050.	4.1	43
1420	<i>Pseudomonas</i> PB1-Like Phages: Whole Genomes from Metagenomes Offer Insight into an Abundant Group of Bacteriophages. <i>Viruses</i> , 2018, 10, 331.	3.3	23
1421	An integrative, multi-omics approach towards the prioritization of <i>Klebsiella pneumoniae</i> drug targets. <i>Scientific Reports</i> , 2018, 8, 10755.	3.3	50
1422	Cell-Derived Viral Genes Evolve under Stronger Purifying Selection in Rhadinoviruses. <i>Journal of Virology</i> , 2018, 92, .	3.4	3
1423	<i>Anaerococcus jeddahensis</i> sp. nov., a New Bacterial Species Isolated From Healthy Nomadic Bedouin Woman From Saudi Arabia. <i>Current Microbiology</i> , 2018, 75, 1419-1428.	2.2	6
1424	Genome comparison of different <i>Zymomonas mobilis</i> strains provides insights on conservation of the evolution. <i>PLoS ONE</i> , 2018, 13, e0195994.	2.5	6
1425	Novel multidomain, multifunctional glycoside hydrolases from highly lignocellulolytic <i>Caldicellulosiruptor</i> species. <i>AIChE Journal</i> , 2018, 64, 4218-4228.	3.6	19
1426	Population genomics of hypervirulent <i>Klebsiella pneumoniae</i> clonal-group 23 reveals early emergence and rapid global dissemination. <i>Nature Communications</i> , 2018, 9, 2703.	12.8	205
1427	The first plastid genome of a filamentous taxon <i>Bangia</i> sp. OUCPT-01 in the Bangiales. <i>Scientific Reports</i> , 2018, 8, 10688.	3.3	6
1428	Analysis of Phylogenetic Variation of <i>Stenotrophomonas maltophilia</i> Reveals Human-Specific Branches. <i>Frontiers in Microbiology</i> , 2018, 9, 806.	3.5	39
1429	Complete Genome Sequence of <i>Clostridium kluyveri</i> JZZ Applied in Chinese Strong-Flavor Liquor Production. <i>Current Microbiology</i> , 2018, 75, 1429-1433.	2.2	11
1430	SssP1, a <i>Streptococcus suis</i> Fimbria-Like Protein Transported by the SecY2/A2 System, Contributes to Bacterial Virulence. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	16
1431	Comparative mitochondrial genomics of cryptophyte algae: gene shuffling and dynamic mobile genetic elements. <i>BMC Genomics</i> , 2018, 19, 275.	2.8	23
1432	The genome sequence of a SNP type 3K strain of <i>Mycobacterium leprae</i> isolated from a seventh-century Hungarian case of lepromatous leprosy. <i>International Journal of Osteoarchaeology</i> , 2018, 28, 439-447.	1.2	13
1433	Gene loss and genome rearrangement in the plastids of five Hemiparasites in the family Orobanchaceae. <i>BMC Plant Biology</i> , 2018, 18, 30.	3.6	72
1434	The reporting of a <i>Bacillus anthracis</i> B-clade strain in South Africa after more than 20 years. <i>BMC Research Notes</i> , 2018, 11, 264.	1.4	3

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1435	Chloroplast genome analyses and genomic resource development for epilithic sister genera <i>Oresitrophe</i> and <i>Mukdenia</i> (Saxifragaceae), using genome skimming data. <i>BMC Genomics</i> , 2018, 19, 235.	2.8	106
1436	Comparative genomics and systematics of <i>Betaphycus</i> , <i>Eucheuma</i> , and <i>Kappaphycus</i> (Solieriaceae:). <i>Tj ETQq1 1 0.784314 rgBT /Overl</i>	2.8	11
1437	Genome sequencing and functional characterization of the non-pathogenic <i>Klebsiella pneumoniae</i> KpGe bacteria. <i>Microbes and Infection</i> , 2018, 20, 293-301.	1.9	28
1438	xenoGI: reconstructing the history of genomic island insertions in clades of closely related bacteria. <i>BMC Bioinformatics</i> , 2018, 19, 32.	2.6	12
1439	Elucidation of the anti-hyperammonemic mechanism of <i>Lactobacillus amylovorus</i> JBD401 by comparative genomic analysis. <i>BMC Genomics</i> , 2018, 19, 292.	2.8	12
1440	Larger Than Life: Isolation and Genomic Characterization of a Jumbo Phage That Infects the Bacterial Plant Pathogen, <i>Agrobacterium tumefaciens</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 1861.	3.5	23
1441	Characterization of the Complete Chloroplast Genomes of <i>Buddleja colvilei</i> and <i>B. sessilifolia</i> : Implications for the Taxonomy of <i>Buddleja</i> L.. <i>Molecules</i> , 2018, 23, 1248.	3.8	17
1442	The genome of a prasinoviruses-related freshwater virus reveals unusual diversity of phycodnaviruses. <i>BMC Genomics</i> , 2018, 19, 49.	2.8	10
1443	Genomic mapping of ST85 blaNDM-1 and blaOXA-94 producing <i>Acinetobacter baumannii</i> isolates from Syrian Civil War Victims. <i>International Journal of Infectious Diseases</i> , 2018, 74, 100-108.	3.3	23
1444	Three Distinct Contact-Dependent Growth Inhibition Systems Mediate Interbacterial Competition by the Cystic Fibrosis Pathogen <i>Burkholderia dolosa</i> . <i>Journal of Bacteriology</i> , 2018, 200, .	2.2	19
1445	Comparative Genome Analysis of 2 <i>Mycobacterium Tuberculosis</i> Strains from Pakistan: Insights Globally Into Drug Resistance, Virulence, and Niche Adaptation. <i>Evolutionary Bioinformatics</i> , 2018, 14, 117693431879025.	1.2	3
1446	Tracking microevolution events among ST11 carbapenemase-producing hypervirulent <i>Klebsiella pneumoniae</i> outbreak strains. <i>Emerging Microbes and Infections</i> , 2018, 7, 1-8.	6.5	65
1447	The complete methylome of an entomopathogenic bacterium reveals the existence of loci with unmethylated Adenines. <i>Scientific Reports</i> , 2018, 8, 12091.	3.3	27
1448	Linking genotype and phenotype in an economically viable propionic acid biosynthesis process. <i>Biotechnology for Biofuels</i> , 2018, 11, 224.	6.2	10
1449	Comparative genomic analysis of multidrug-resistant <i>Streptococcus pneumoniae</i> isolates. <i>Infection and Drug Resistance</i> , 2018, Volume 11, 659-670.	2.7	7
1450	What's the Difference?. , 2018, , .		14
1451	Cooperative Metabolic Adaptations in the Host Can Favor Asymptomatic Infection and Select for Attenuated Virulence in an Enteric Pathogen. <i>Cell</i> , 2018, 175, 146-158.e15.	28.9	127
1452	Comparison between complete genomes of an isolate of <i>Pseudomonas syringae</i> pv. <i>actinidiae</i> from Japan and a New Zealand isolate of the pandemic lineage. <i>Scientific Reports</i> , 2018, 8, 10915.	3.3	23

#	ARTICLE	IF	CITATIONS
1453	Near-Complete Genome Sequence of <i>Pseudomonas palleroniana</i> MAB3, a Beneficial 1-Aminocyclopropane-1-Carboxylate Deaminase-Producing Bacterium Able To Promote the Growth of Mushrooms and Plants. <i>Genome Announcements</i> , 2018, 6, .	0.8	3
1454	Positions 299 and 302 of the GerAA subunit are important for function of the GerA spore germination receptor in <i>Bacillus subtilis</i> . <i>PLoS ONE</i> , 2018, 13, e0198561.	2.5	7
1455	Next-Generation lineage discovery: A case study of tuberous <i>Claytonia</i> L.. <i>American Journal of Botany</i> , 2018, 105, 536-548.	1.7	15
1456	Genomic comparisons of <i>Rhizobium</i> species using in silico AFLP-PCR, endonuclease restriction, and AMPylating enzymes. <i>Electronic Journal of Biotechnology</i> , 2018, 34, 67-75.	2.2	0
1457	Comparison of genomes and proteomes of four whole genome-sequenced <i>Campylobacter jejuni</i> from different phylogenetic backgrounds. <i>PLoS ONE</i> , 2018, 13, e0190836.	2.5	7
1458	Genomic differences between nasal <i>Staphylococcus aureus</i> from hog slaughterhouse workers and their communities. <i>PLoS ONE</i> , 2018, 13, e0193820.	2.5	11
1459	Diversity of CTX-M-1-producing <i>E. coli</i> from German food samples and genetic diversity of the bla CTX-M-1 region on IncI1 ST3 plasmids. <i>Veterinary Microbiology</i> , 2018, 221, 98-104.	1.9	54
1460	Genome Rearrangement Shapes <i>Prochlorococcus</i> Ecological Adaptation. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	17
1461	Microbial genomic island discovery, visualization and analysis. <i>Briefings in Bioinformatics</i> , 2019, 20, 1685-1698.	6.5	86
1462	Complete Genome Sequence of <i>Actinosynnema pretiosum</i> X47, An Industrial Strain that Produces the Antibiotic Ansamitocin AP-3. <i>Current Microbiology</i> , 2019, 76, 954-958.	2.2	6
1463	<i>Passiflora</i> plastome sequencing reveals widespread genomic rearrangements. <i>Journal of Systematics and Evolution</i> , 2019, 57, 1-14.	3.1	61
1464	Noncontiguous finished genome sequence and description of <i>Intestinimonas massiliensis</i> sp. nov strain <scp>GD</scp>2^T, the second <i>Intestinimonas</i> species cultured from the human gut. <i>MicrobiologyOpen</i> , 2019, 8, e00621.	3.0	19
1465	Genome Alignment. , 2019, , 268-283.		0
1466	Genome Sequence and Antifungal Activity of Two Niche-Sharing <i>Pseudomonas protegens</i> Related Strains Isolated from Hydroponics. <i>Microbial Ecology</i> , 2019, 77, 1025-1035.	2.8	2
1467	Accurate multiple alignment of distantly related genome sequences using filtered spaced word matches as anchor points. <i>Bioinformatics</i> , 2019, 35, 211-218.	4.1	11
1468	Plastid Genomes of Five Species of Riverweeds (Podostemaceae): Structural Organization and Comparative Analysis in Malpighiales. <i>Frontiers in Plant Science</i> , 2019, 10, 1035.	3.6	43
1469	Morphologic and genomic characterization of a broad host range <i>Salmonella enterica</i> serovar Pullorum lytic phage vB_SPuM_SP116. <i>Microbial Pathogenesis</i> , 2019, 136, 103659.	2.9	24
1470	Genomic and Ecogenomic Characterization of <i>Proteus mirabilis</i> Bacteriophages. <i>Frontiers in Microbiology</i> , 2019, 10, 1783.	3.5	13

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1471	Phylogenetic, genomic, and biogeographic characterization of a novel and ubiquitous marine invertebrate-associated Rickettsiales parasite, <i>Candidatus</i> Aquarickettsia rohweri, gen. nov., sp. nov. ISME Journal, 2019, 13, 2938-2953.	9.8	82
1472	Thirteen New Plastid Genomes from Mixotrophic and Autotrophic Species Provide Insights into Heterotrophy Evolution in Neottieae Orchids. Genome Biology and Evolution, 2019, 11, 2457-2467.	2.5	26
1473	Elucidating Viral Communities During a Phytoplankton Bloom on the West Antarctic Peninsula. Frontiers in Microbiology, 2019, 10, 1014.	3.5	28
1474	Genomic Polymorphism Associated with the Emergence of Virulent Isolates of Mycobacterium bovis in the Nile Delta. Scientific Reports, 2019, 9, 11657.	3.3	17
1475	Shared Pathogenomic Patterns Characterize a New Phylotype, Revealing Transition toward Host-Adaptation Long before Speciation of Mycobacterium tuberculosis. Genome Biology and Evolution, 2019, 11, 2420-2438.	2.5	29
1476	Development of gene-based molecular markers tagging low alkaloid pauper locus in white lupin (Lupinus albus L.). Journal of Applied Genetics, 2019, 60, 269-281.	1.9	17
1477	Engineered Interspecies Amino Acid Cross-Feeding Increases Population Evenness in a Synthetic Bacterial Consortium. MSystems, 2019, 4, .	3.8	39
1478	Comparison of single-nucleotide variants identified by Illumina and Oxford Nanopore technologies in the context of a potential outbreak of Shiga toxin-producing Escherichia coli. GigaScience, 2019, 8, .	6.4	42
1479	Frog Virus 3 Genomes Reveal Prevalent Recombination between Ranavirus Lineages and Their Origins in Canada. Journal of Virology, 2019, 93, .	3.4	20
1480	Complete genome and plasmid sequence of a novel Bacillus sp. BD59S, a parasporal protein synthesizing bacterium. 3 Biotech, 2019, 9, 318.	2.2	1
1481	Dual Role of <i>gnaA</i> in Antibiotic Resistance and Virulence in Acinetobacter baumannii. Antimicrobial Agents and Chemotherapy, 2019, 63, .	3.2	23
1482	Defining the human gut host-phage network through single-cell viral tagging. Nature Microbiology, 2019, 4, 2192-2203.	13.3	95
1483	The complete mitochondrial genomes of five important medicinal Ganoderma species: Features, evolution, and phylogeny. International Journal of Biological Macromolecules, 2019, 139, 397-408.	7.5	62
1484	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. Journal of Applied Microbiology, 2019, 127, 1511-1520.	3.1	15
1485	The importance of genome sequence quality to microbial comparative genomics. BMC Genomics, 2019, 20, 662.	2.8	35
1486	Whole-Genome Alignment. Methods in Molecular Biology, 2019, 1910, 121-147.	0.9	5
1487	Efficient merging of genome profile alignments. Bioinformatics, 2019, 35, i71-i80.	4.1	1
1488	Closed Genome Sequences of Three Salmonella enterica Strains Belonging to Serovars Saintpaul, Weltevreden, and Thompson, Isolated from Mexico. Microbiology Resource Announcements, 2019, 8, .	0.6	4

#	ARTICLE	IF	CITATIONS
1489	Extensive chloroplast genome rearrangement amongst three closely related <i>Halamphora</i> spp. (Bacillariophyceae), and evidence for rapid evolution as compared to land plants. <i>PLoS ONE</i> , 2019, 14, e0217824.	2.5	16
1490	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.	2.5	13
1491	Functional genome annotation depicts probiotic properties of <i>Bacillus velezensis</i> FTC01. <i>Gene</i> , 2019, 713, 143971.	2.2	22
1492	Chromosome-Level Alpaca Reference Genome VicPac3.1 Improves Genomic Insight Into the Biology of New World Camelids. <i>Frontiers in Genetics</i> , 2019, 10, 586.	2.3	19
1493	Quorum Quenching Enzyme APTM01, an Acylhomoserine-Lactone Acylase from Marine Bacterium of <i>Pseudoalteromonas tetradonis</i> Strain MQS005. <i>Current Microbiology</i> , 2019, 76, 1387-1397.	2.2	10
1494	Resistome and a Novel <i>NDM-1</i> -Harboring Plasmid of an <i>Acinetobacter haemolyticus</i> Strain from a Children's Hospital in Puebla, Mexico. <i>Microbial Drug Resistance</i> , 2019, 25, 1023-1031.	2.0	27
1495	Insights From the Genome Sequence of <i>Mycobacterium paragordoniae</i> , a Potential Novel Live Vaccine for Preventing Mycobacterial Infections: The Putative Role of Type VII Secretion Systems for an Intracellular Lifestyle Within Free-Living Environmental Predators. <i>Frontiers in Microbiology</i> , 2019, 10, 1524.	3.5	8
1496	High colonization rate of a novel carbapenem-resistant <i>Klebsiella</i> lineage among migratory birds at Qinghai Lake, China. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 2895-2903.	3.0	21
1497	Mycoheterotrophic <i>Epirixanthes</i> (Polygalaceae) has a typical angiosperm mitogenome but unorthodox plastid genomes. <i>Annals of Botany</i> , 2019, 124, 791-807.	2.9	14
1498	Differentiations in Gene Content and Expression Response to Virulence Induction Between Two <i>Agrobacterium</i> Strains. <i>Frontiers in Microbiology</i> , 2019, 10, 1554.	3.5	25
1499	geneCo: a visualized comparative genomic method to analyze multiple genome structures. <i>Bioinformatics</i> , 2019, 35, 5303-5305.	4.1	19
1500	Nanopore sequencing for fast determination of plasmids, phages, virulence markers, and antimicrobial resistance genes in Shiga toxin-producing <i>Escherichia coli</i> . <i>PLoS ONE</i> , 2019, 14, e0220494.	2.5	86
1501	Retrospective Analysis of Archived Pyrazinamide Resistant <i>Mycobacterium tuberculosis</i> Complex Isolates from Uganda—Evidence of Interspecies Transmission. <i>Microorganisms</i> , 2019, 7, 221.	3.6	6
1502	Comparative genomics of <i>Mycobacterium mucogenicum</i> and <i>Mycobacterium neoaurum</i> clade members emphasizing tRNA and non-coding RNA. <i>BMC Evolutionary Biology</i> , 2019, 19, 124.	3.2	10
1503	Plastid genome evolution in tribe Desmodieae (Fabaceae: Papilionoideae). <i>PLoS ONE</i> , 2019, 14, e0218743.	2.5	23
1504	Terpene Synthase Genes Originated from Bacteria through Horizontal Gene Transfer Contribute to Terpenoid Diversity in Fungi. <i>Scientific Reports</i> , 2019, 9, 9223.	3.3	31
1505	Comparative genomic analyses of <i>Mycoplasma synoviae</i> vaccine strain MS-H and its wild-type parent strain 86079/7NS: implications for the identification of virulence factors and applications in diagnosis of <i>M. synoviae</i> . <i>Avian Pathology</i> , 2019, 48, 537-548.	2.0	14
1506	Comparative Genome Analysis of Uropathogenic <i>Morganella morganii</i> Strains. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 167.	3.9	30

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1507	Biological properties and genomics analysis of vB_KpnS_GH-K3, a Klebsiella phage with a putative depolymerase-like protein. <i>Virus Genes</i> , 2019, 55, 696-706.	1.6	26
1508	Penicillin-Binding Protein Typing, Antibiotic Resistance Gene Identification, and Molecular Phylogenetic Analysis of Meropenem-Resistant <i>Streptococcus pneumoniae</i> Serotype 19A-CC3111 Strains in Japan. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	13
1509	Whole genome analysis of <i>Aspergillus sojae</i> SMF 134 supports its merits as a starter for soybean fermentation. <i>Journal of Microbiology</i> , 2019, 57, 874-883.	2.8	16
1510	Deletion of the major <i>Escherichia coli</i> multidrug transporter AcrB reveals transporter plasticity and redundancy in bacterial cells. <i>PLoS ONE</i> , 2019, 14, e0218828.	2.5	15
1511	The complete chloroplast genome of pearl millet (<i>Pennisetum glaucum</i> (L.) R. Br.) and comparative analysis within the family poaceae. <i>Cereal Research Communications</i> , 2019, 47, 1-10.	1.6	3
1512	Differential efficiency of wild type rhizogenic strains for rol gene transformation of plants. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 6657-6672.	3.6	20
1513	Genomic analysis of the four ecologically distinct cactus host populations of <i>Drosophila mojavensis</i> . <i>BMC Genomics</i> , 2019, 20, 732.	2.8	17
1514	A new PacBio genome sequence of an Australian <i>Pyrenophora tritici-repentis</i> race 1 isolate. <i>BMC Research Notes</i> , 2019, 12, 642.	1.4	12
1515	Can Insertion Sequences Proliferation Influence Genomic Plasticity? Comparative Analysis of <i>Acinetobacter baumannii</i> Sequence Type 78, a Persistent Clone in Italian Hospitals. <i>Frontiers in Microbiology</i> , 2019, 10, 2080.	3.5	23
1516	Adaptive Evolution of <i>Sphingobium hydrophobicum</i> C1T in Electronic Waste Contaminated River Sediment. <i>Frontiers in Microbiology</i> , 2019, 10, 2263.	3.5	7
1517	De Novo Assembly Discovered Novel Structures in Genome of Plastids and Revealed Divergent Inverted Repeats in <i>Mammillaria</i> (Cactaceae, Caryophyllales). <i>Plants</i> , 2019, 8, 392.	3.5	28
1518	Amphibian skin-associated Pigmentiphaga: Genome sequence and occurrence across geography and hosts. <i>PLoS ONE</i> , 2019, 14, e0223747.	2.5	8
1519	The complete mitochondrial genome sequence of the medicinal fungus <i>Inonotus obliquus</i> (Hymenochaetaceae, Basidiomycota). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3504-3506.	0.4	5
1520	Phenotypic characteristics contributing to the enhanced growth of <i>Escherichia coli</i> bloom strains. <i>Environmental Microbiology Reports</i> , 2019, 11, 817-824.	2.4	1
1521	Comparative Mitochondrial Genome Analysis of Two Ectomycorrhizal Fungi (<i>Rhizopogon</i>) Reveals Dynamic Changes of Intron and Phylogenetic Relationships of the Subphylum Agaricomycotina. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5167.	4.1	65
1522	<i>lptG</i> contributes to changes in membrane permeability and the emergence of multidrug hypersusceptibility in a cystic fibrosis isolate of <i>Pseudomonas aeruginosa</i> . <i>MicrobiologyOpen</i> , 2019, 8, e844.	3.0	6
1523	The architecture of the <i>Plasmodiophora brassicae</i> nuclear and mitochondrial genomes. <i>Scientific Reports</i> , 2019, 9, 15753.	3.3	17
1524	The PATRIC Bioinformatics Resource Center: expanding data and analysis capabilities. <i>Nucleic Acids Research</i> , 2020, 48, D606-D612.	14.5	552

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1525	Bioinformatics for Marine Products: An Overview of Resources, Bottlenecks, and Perspectives. <i>Marine Drugs</i> , 2019, 17, 576.	4.6	26
1526	Evolutionary Dynamics of Transferred Sequences Between Organellar Genomes in <i>Cucurbita</i> . <i>Journal of Molecular Evolution</i> , 2019, 87, 327-342.	1.8	4
1527	Gene Composition as a Potential Barrier to Large Recombinations in the Bacterial Pathogen <i>Klebsiella pneumoniae</i> . <i>Genome Biology and Evolution</i> , 2019, 11, 3240-3251.	2.5	18
1528	Himalayan <i>Saccharomyces eubayanus</i> Genome Sequences Reveal Genetic Markers Explaining Heterotic Maltotriose Consumption by <i>Saccharomyces pastorianus</i> Hybrids. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	21
1529	Draft genome sequence of <i>Bacillus paralicheniformis</i> TRQ65, a biological control agent and plant growth-promoting bacterium isolated from wheat (<i>Triticum turgidum</i> subsp. <i>durum</i>) rhizosphere in the Yaqui Valley, Mexico. <i>3 Biotech</i> , 2019, 9, 436.	2.2	32
1530	Molecular tools for the characterization of seizure susceptibility in genetic rodent models of epilepsy. <i>Epilepsy and Behavior</i> , 2021, 121, 106594.	1.7	6
1531	Comparative Study on A Novel Pathogen of European Seabass. Diversity of <i>Aeromonas veronii</i> in the Aegean Sea. <i>Microorganisms</i> , 2019, 7, 504.	3.6	13
1532	Characterization of a Novel <i>Thermobifida fusca</i> Bacteriophage P318. <i>Viruses</i> , 2019, 11, 1042.	3.3	0
1533	Multiplex PCR for genotyping <i>Flavobacterium columnare</i> . <i>Journal of Fish Diseases</i> , 2019, 42, 1531-1542.	1.9	17
1534	Large Phenotypic and Genetic Diversity of Prophages Induced from the Fish Pathogen <i>Vibrio anguillarum</i> . <i>Viruses</i> , 2019, 11, 983.	3.3	19
1535	gapFinisher: A reliable gap filling pipeline for SSPACE-LongRead scaffold output. <i>PLoS ONE</i> , 2019, 14, e0216885.	2.5	14
1536	Plastid Genomes of Carnivorous Plants <i>Drosera rotundifolia</i> and <i>Nepenthes ventrata</i> Reveal Evolutionary Patterns Resembling Those Observed in Parasitic Plants. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4107.	4.1	13
1537	Production of WW males lacking the masculine Z chromosome and mining the <i>Macrobrachium rosenbergii</i> genome for sex-chromosomes. <i>Scientific Reports</i> , 2019, 9, 12408.	3.3	25
1538	Identification of Novel Bacteriophages with Therapeutic Potential That Target <i>Enterococcus faecalis</i> . <i>Infection and Immunity</i> , 2019, 87, .	2.2	50
1539	Comparative genomics of 11 complete chloroplast genomes of Senecioneae (Asteraceae) species: DNA barcodes and phylogenetics. , 2019, 60, 17.		29
1540	Draft Assembly of <i>Phytophthora capsici</i> from Long-Read Sequencing Uncovers Complexity. <i>Molecular Plant-Microbe Interactions</i> , 2019, 32, 1559-1563.	2.6	33
1541	Comparative genomics of <i>Aeromonas veronii</i> : Identification of a pathotype impacting aquaculture globally. <i>PLoS ONE</i> , 2019, 14, e0221018.	2.5	50
1542	Investigation into limiting dilution and tick transmissibility phenotypes associated with attenuation of the S24 vaccine strain. <i>Parasites and Vectors</i> , 2019, 12, 419.	2.5	4

#	ARTICLE	IF	CITATIONS
1543	A novel salt-tolerant genotype illuminates the sucrose gene evolution in freshwater bloom-forming cyanobacterium <i>Microcystis aeruginosa</i> . FEMS Microbiology Letters, 2019, 366, .	1.8	5
1544	Phylogenomic and epidemiological insights into two clinical <i>Mycobacterium bovis</i> BCG strains circulating in South Africa. International Journal of Infectious Diseases, 2019, 87, 32-38.	3.3	2
1545	Characteristics and Complete Genome Analysis of <i>Bacillus asahii</i> OM18, a Bacterium in Relation to Soil Fertility in Alkaline Soils Under Long-Term Organic Manure Amendment. Current Microbiology, 2019, 76, 1512-1519.	2.2	4
1546	A hybrid sub-lineage of <i>Listeria monocytogenes</i> comprising hypervirulent isolates. Nature Communications, 2019, 10, 4283.	12.8	76
1547	Comparative Genomics and Phylogenomic Analysis of the Genus <i>Salinivibrio</i> . Frontiers in Microbiology, 2019, 10, 2104.	3.5	23
1548	Genome Mining and Comparative Pathogenomic Analysis of An Endemic Methicillin-Resistant <i>Staphylococcus Aureus</i> (MRSA) Clone, ST612-CC8-t1257-SCCmec_IVd(2B), Isolated in South Africa. Pathogens, 2019, 8, 166.	2.8	9
1549	Assembly and comparative analyses of the mitochondrial genome of <i>Castanospermum australe</i> (Papilionoideae, Leguminosae). Australian Systematic Botany, 2019, 32, 484-494.	0.9	4
1550	An African <i>Salmonella</i> Typhimurium ST313 sublineage with extensive drug-resistance and signatures of host adaptation. Nature Communications, 2019, 10, 4280.	12.8	80
1551	Whole genome sequencing of a ST2594 MRSA strain causing non-mucosal preoperative colonization and low-grade postoperative infection. Antonie Van Leeuwenhoek, 2019, 112, 961-964.	1.7	1
1552	The Genome Sequence of M228, a Chinese Isolate of <i>Pseudomonas syringae</i> pv. <i>actinidiae</i> , Illustrates Insertion Sequence Element Mobility. Microbiology Resource Announcements, 2019, 8, .	0.6	7
1553	Whole-genome sequencing data-based modeling for the investigation of an outbreak of community-associated methicillin-resistant <i>Staphylococcus aureus</i> in a neonatal intensive care unit in Hong Kong. European Journal of Clinical Microbiology and Infectious Diseases, 2019, 38, 563-573.	2.9	23
1554	Megaphages infect <i>Prevotella</i> and variants are widespread in gut microbiomes. Nature Microbiology, 2019, 4, 693-700.	13.3	141
1555	The complete mitochondrial genome sequence of the edible mushroom <i>Stropharia rugosoannulata</i> (Strophariaceae, Basidiomycota). Mitochondrial DNA Part B: Resources, 2019, 4, 570-572.	0.4	3
1556	Plastid Genomes from Diverse Glaucophyte Genera Reveal a Largely Conserved Gene Content and Limited Architectural Diversity. Genome Biology and Evolution, 2019, 11, 174-188.	2.5	16
1557	Transcriptional Reprogramming of Rice Cells by <i>Xanthomonas oryzae</i> TALEs. Frontiers in Plant Science, 2019, 10, 162.	3.6	38
1558	Rational construction of genome-reduced and high-efficient industrial <i>Streptomyces</i> chassis based on multiple comparative genomic approaches. Microbial Cell Factories, 2019, 18, 16.	4.0	55
1559	Comparative analysis reveals the Genomic Islands in <i>Pasteurella multocida</i> population genetics: on Symbiosis and adaptability. BMC Genomics, 2019, 20, 63.	2.8	9
1560	Design and Preclinical Development of a Phage Product for the Treatment of Antibiotic-Resistant <i>Staphylococcus aureus</i> Infections. Viruses, 2019, 11, 88.	3.3	109

#	ARTICLE	IF	CITATIONS
1561	Virulence Characteristics and an Action Mode of Antibiotic Resistance in Multidrug-Resistant <i>Pseudomonas aeruginosa</i> . <i>Scientific Reports</i> , 2019, 9, 487.	3.3	59
1562	Dissecting the Evolutionary Development of the Species <i>Bifidobacterium animalis</i> through Comparative Genomics Analyses. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	11
1563	Genome analysis of <i>Salmonella enterica</i> subsp. <i>diarizonae</i> isolates from invasive human infections reveals enrichment of virulence-related functions in lineage ST1256. <i>BMC Genomics</i> , 2019, 20, 99.	2.8	24
1564	Detecting useful genetic markers and reconstructing the phylogeny of an important medicinal resource plant, <i>Artemisia selengensis</i> , based on chloroplast genomics. <i>PLoS ONE</i> , 2019, 14, e0211340.	2.5	43
1565	Preventive effect of the phage VB-SavM-JYL01 on rabbit necrotizing pneumonia caused by <i>Staphylococcus aureus</i> . <i>Veterinary Microbiology</i> , 2019, 229, 72-80.	1.9	31
1566	Comparative genomic analysis of subspecies of <i>Pantoea stewartii</i> reveals distinct variations. <i>Journal of Plant Pathology</i> , 2019, 101, 997-1004.	1.2	1
1567	The complete organelle genomes of <i>Physochlaina orientalis</i> : Insights into short sequence repeats across seed plant mitochondrial genomes. <i>Molecular Phylogenetics and Evolution</i> , 2019, 137, 274-284.	2.7	19
1568	The implication of plastid transcriptome analysis in petaloid monocotyledons: A case study of <i>Lilium lancifolium</i> (Liliaceae, Liliales). <i>Scientific Reports</i> , 2019, 9, 6662.	3.3	3
1569	Draft Genome Sequence of <i>Rhodoplanes</i> sp. Strain T2.26MG-98, Isolated from 492.6 Meters Deep on the Subsurface of the Iberian Pyrite Belt. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	8
1570	Global Biogeographic Distribution Patterns of Thermoacidophilic Verrucomicrobia Methanotrophs Suggest Allopatric Evolution. <i>Frontiers in Microbiology</i> , 2019, 10, 1129.	3.5	31
1571	Successful treatment and digestive decolonisation of a patient with osteitis caused by a carbapenemase-producing <i>Klebsiella pneumoniae</i> isolate harbouring both NDM-1 and OXA-48 enzymes. <i>Journal of Global Antimicrobial Resistance</i> , 2019, 18, 225-229.	2.2	9
1572	Genetic and Phenotypic Features of a Novel <i>Acinetobacter</i> Species, Strain A47, Isolated From the Clinical Setting. <i>Frontiers in Microbiology</i> , 2019, 10, 1375.	3.5	4
1573	Isolation and Characterization T4- and T7-Like Phages that Infect the Bacterial Plant Pathogen <i>Agrobacterium tumefaciens</i> . <i>Viruses</i> , 2019, 11, 528.	3.3	9
1574	Microbial characterization of heavy metal resistant bacterial strains isolated from an electroplating wastewater treatment plant. <i>Ecotoxicology and Environmental Safety</i> , 2019, 181, 472-480.	6.0	49
1575	An <i>In Vitro</i> Enrichment Strategy for Formulating Synergistic Synbiotics. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	15
1576	Comparative genomic analysis of <i>Pectobacterium carotovorum</i> subsp. <i>brasiliense</i> SX309 provides novel insights into its genetic and phenotypic features. <i>BMC Genomics</i> , 2019, 20, 486.	2.8	29
1577	Characterization of a bacteriophage with broad host range against strains of <i>Pseudomonas aeruginosa</i> isolated from domestic animals. <i>BMC Microbiology</i> , 2019, 19, 134.	3.3	35
1578	Enrichment of G4DNA and a Large Inverted Repeat Coincide in the Mitochondrial Genomes of <i>Termitomyces</i> . <i>Genome Biology and Evolution</i> , 2019, 11, 1857-1869.	2.5	23

#	ARTICLE	IF	CITATIONS
1579	Genomic analysis and lactose transporter expression in <i>Kluyveromyces marxianus</i> CCT 7735. <i>Fungal Biology</i> , 2019, 123, 687-697.	2.5	4
1580	Antimicrobial activity of bioactive starch packaging films against <i>Listeria monocytogenes</i> and reconstituted meat microbiota on ham. <i>International Journal of Food Microbiology</i> , 2019, 305, 108253.	4.7	37
1581	Temperate Bacteriophages from Chronic <i>Pseudomonas aeruginosa</i> Lung Infections Show Disease-Specific Changes in Host Range and Modulate Antimicrobial Susceptibility. <i>MSystems</i> , 2019, 4, .	3.8	38
1582	A mitochondrial genome phylogeny of Mytilidae (Bivalvia: Mytilida). <i>Molecular Phylogenetics and Evolution</i> , 2019, 139, 106533.	2.7	41
1583	Whole-genome sequencing reveals recent and frequent genetic recombination between clonal lineages of <i>Cryphonectria parasitica</i> in western Europe. <i>Fungal Genetics and Biology</i> , 2019, 130, 122-133.	2.1	16
1584	Diversification of <i>Vibrio anguillarum</i> Driven by the Bacteriophage CHOED. <i>Frontiers in Microbiology</i> , 2019, 10, 1396.	3.5	11
1586	Genomic sequencing of <i>Troides aeacus</i> nucleopolyhedrovirus (TraeNPV) from golden birdwing larvae (<i>Troides aeacus formosanus</i>) to reveal defective <i>Autographa californica</i> NPV genomic features. <i>BMC Genomics</i> , 2019, 20, 419.	2.8	5
1587	Extremely diverse structural organization in the complete mitochondrial genome of seedless <i>Phoenix dactylifera</i> L. <i>Vegetos</i> , 2019, 32, 92-97.	1.5	3
1588	Comparative Genomics of <i>Thiohalobacter thiocyanaticus</i> HRh1T and <i>Guyparkeria</i> sp. SCN-R1, Halophilic Chemolithoautotrophic Sulfur-Oxidizing Gammaproteobacteria Capable of Using Thiocyanate as Energy Source. <i>Frontiers in Microbiology</i> , 2019, 10, 898.	3.5	20
1589	Complete plastid genome of <i>Kappaphycus alvarezii</i> : insights of large-scale rearrangements among Florideophyceae plastid genomes. <i>Journal of Applied Phycology</i> , 2019, 31, 3997-4005.	2.8	9
1590	Genetic characterization of susceptible and multi-drug resistant <i>Mannheimia haemolytica</i> isolated from high-risk stocker calves prior to and after antimicrobial metaphylaxis. <i>Veterinary Microbiology</i> , 2019, 235, 110-117.	1.9	11
1591	Improving End-User Trust in the Quality of Commercial Probiotic Products. <i>Frontiers in Microbiology</i> , 2019, 10, 739.	3.5	109
1592	Pacbio Sequencing Reveals Identical Organelle Genomes between American Cranberry (<i>Vaccinium</i>) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	2.4	12
1593	De novo genome sequencing and secretome analysis of <i>Tilletia indica</i> inciting Karnal bunt of wheat provides pathogenesis-related genes. <i>3 Biotech</i> , 2019, 9, 219.	2.2	19
1594	Comparative Analysis of the Two <i>Acinetobacter baumannii</i> Multilocus Sequence Typing (MLST) Schemes. <i>Frontiers in Microbiology</i> , 2019, 10, 930.	3.5	133
1595	Omics-based comparative analysis of putative mobile genetic elements in <i>Lactococcus lactis</i> . <i>FEMS Microbiology Letters</i> , 2019, 366, .	1.8	4
1596	Genome characterization of an extensively drug-resistant <i>Streptococcus pneumoniae</i> serotype 11A strain. <i>Microbiology and Immunology</i> , 2019, 63, 206-212.	1.4	0
1597	Antarctic <i>Streptomyces fildesensis</i> So13.3 strain as a promising source for antimicrobials discovery. <i>Scientific Reports</i> , 2019, 9, 7488.	3.3	27

#	ARTICLE	IF	CITATIONS
1598	Mobile genetic elements explain size variation in the mitochondrial genomes of four closely-related <i>Armillaria</i> species. <i>BMC Genomics</i> , 2019, 20, 351.	2.8	49
1599	Breaking Free: The Genomics of Allopolyploidy-Facilitated Niche Expansion in White Clover. <i>Plant Cell</i> , 2019, 31, 1466-1487.	6.6	89
1600	The Complete Chloroplast Genome of <i>Euphrasia regelii</i> , Pseudogenization of <i>ndh</i> Genes and the Phylogenetic Relationships Within <i>Orobanchaceae</i> . <i>Frontiers in Genetics</i> , 2019, 10, 444.	2.3	31
1601	Guarani Virophage, a New Sputnik-Like Isolate From a Brazilian Lake. <i>Frontiers in Microbiology</i> , 2019, 10, 1003.	3.5	19
1602	Comparative Genomic Analysis of <i>Lactobacillus plantarum</i> : An Overview. <i>International Journal of Genomics</i> , 2019, 2019, 1-11.	1.6	45
1603	Chromosomal genome assembly of the ethanol production strain CBS 11270 indicates a highly dynamic genome structure in the yeast species <i>Brettanomyces bruxellensis</i> . <i>PLoS ONE</i> , 2019, 14, e0215077.	2.5	8
1604	The Canoe-eMLST Program: An Approach for the Calculation of Canonical Extended Multi-Locus Sequence Typing, Making Comparison of Genetic Differences Among Bunches of Bacterial Strains. <i>Microorganisms</i> , 2019, 7, 98.	3.6	2
1605	Extended insight into the <i>Mycobacterium chelonae-abscessus</i> complex through whole genome sequencing of <i>Mycobacterium salmoniphilum</i> outbreak and <i>Mycobacterium salmoniphilum</i> -like strains. <i>Scientific Reports</i> , 2019, 9, 4603.	3.3	12
1606	Strain- and Species-Level Variation in the Microbiome of Diabetic Wounds Is Associated with Clinical Outcomes and Therapeutic Efficacy. <i>Cell Host and Microbe</i> , 2019, 25, 641-655.e5.	11.0	192
1607	Comparative Genomic Analysis of the Virulence Plasmid from <i>Salmonella enterica</i> Subspecies <i>enterica</i> Serovar <i>Enteritidis</i> . <i>Russian Journal of Genetics</i> , 2019, 55, 144-153.	0.6	3
1608	The complete chloroplast genome sequence of <i>Rubus coreanus</i> , an excellent diseases-resistant resource. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 216-217.	0.4	5
1609	Post-transcriptional Regulation of FLOWERING LOCUS T Modulates Heat-Dependent Source-Sink Development in Potato. <i>Current Biology</i> , 2019, 29, 1614-1624.e3.	3.9	58
1610	The bacteriocin from the prophylactic candidate <i>Streptococcus suis</i> 90-1330 is widely distributed across <i>S. suis</i> isolates and appears encoded in an integrative and conjugative element. <i>PLoS ONE</i> , 2019, 14, e0216002.	2.5	8
1611	Complete genome sequence of fowl adenovirus-8b UPM04217 isolate associated with the inclusion body hepatitis disease in commercial broiler chickens in Malaysia reveals intermediate evolution. <i>VirusDisease</i> , 2019, 30, 426-432.	2.0	6
1612	Illumina sequencing of clinical samples for virus detection in a public health laboratory. <i>Scientific Reports</i> , 2019, 9, 5409.	3.3	34
1613	Phage-Encoded LuxR-Type Receptors Responsive to Host-Produced Bacterial Quorum-Sensing Autoinducers. <i>MBio</i> , 2019, 10, .	4.1	46
1614	Isolation and Bacteriocin-Related Typing of <i>Streptococcus dentisani</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 110.	3.9	28
1615	Genome sequence and description of <i>Traorella massiliensis</i> gen. nov., sp. nov., a new bacterial genus isolated from human left colon. <i>New Microbes and New Infections</i> , 2019, 29, 100520.	1.6	2

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1616	Complete chloroplast genome of <i>Anathallis obovata</i> (Orchidaceae: Pleurothallidinae). <i>Revista Brasileira De Botanica</i> , 2019, 42, 345-352.	1.3	3
1617	Trapping the Enemy: <i>Vermamoeba vermiformis</i> Circumvents Faustovirus Mariensis Dissemination by Enclosing Viral Progeny inside Cysts. <i>Journal of Virology</i> , 2019, 93, .	3.4	20
1618	Genome Features and Secondary Metabolites Biosynthetic Potential of the Class Ktedonobacteria. <i>Frontiers in Microbiology</i> , 2019, 10, 893.	3.5	61
1619	Accurate high throughput alignment via line sweep-based seed processing. <i>Nature Communications</i> , 2019, 10, 1939.	12.8	11
1620	The complete chloroplast genome sequences of four <i>Viola</i> species (Violaceae) and comparative analyses with its congeneric species. <i>PLoS ONE</i> , 2019, 14, e0214162.	2.5	35
1621	Characterizing the Biology of Lytic Bacteriophage vB_EaeM_ItEap-3 Infecting Multidrug-Resistant <i>Enterobacter aerogenes</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 420.	3.5	43
1622	Genomic characterization of an atypical enteropathogenic <i>Escherichia coli</i> strain isolated in Fujian province, China. <i>Science China Life Sciences</i> , 2019, 62, 1261-1263.	4.9	0
1623	Phylogenetic Studies on the Prodigiosin Biosynthetic Operon. <i>Current Microbiology</i> , 2019, 76, 597-606.	2.2	9
1624	Inference of Convergent Gene Acquisition Among <i>Pseudomonas syringae</i> Strains Isolated From Watermelon, Cantaloupe, and Squash. <i>Frontiers in Microbiology</i> , 2019, 10, 270.	3.5	17
1625	Comparative analysis of the mitochondrial genomes of <i>Orthonectida</i> : insights into the evolution of an invertebrate parasite species. <i>Molecular Genetics and Genomics</i> , 2019, 294, 715-727.	2.1	18
1626	Using WGS to identify antibiotic resistance genes and predict antimicrobial resistance phenotypes in MDR <i>Acinetobacter baumannii</i> in Tanzania. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 1484-1493.	3.0	46
1627	Genome Sequence of <i>Rhizobium jaguaris</i> CCGE525 ^T , a Strain Isolated from <i>Calliandra grandiflora</i> Nodules from a Rain Forest in Mexico. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	3
1628	Identification of <i>Streptococcus pneumoniae</i> by a real-time PCR assay targeting SP2020. <i>Scientific Reports</i> , 2019, 9, 3285.	3.3	53
1629	Complete genome sequencing of <i>Lactobacillus plantarum</i> CAUH2 reveals a novel plasmid pCAUH203 associated with oxidative stress tolerance. <i>3 Biotech</i> , 2019, 9, 116.	2.2	8
1630	FLOWERING LOCUS T, GIGANTEA, SEPALLATA, and FRIGIDA homologs are candidate genes involved in white lupin (<i>Lupinus albus</i> L.) early flowering. <i>Molecular Breeding</i> , 2019, 39, 1.	2.1	24
1631	Insight into the genome and brackish water adaptation strategies of toxic and bloom-forming Baltic Sea <i>Dolichospermum</i> sp. UHCC 0315. <i>Scientific Reports</i> , 2019, 9, 4888.	3.3	14
1632	Metabolic analyses reveal common adaptations in two invasive <i>Haemophilus influenzae</i> strains. <i>Pathogens and Disease</i> , 2019, 77, .	2.0	9
1633	Conserved and specific features of <i>Streptococcus pyogenes</i> and <i>Streptococcus agalactiae</i> transcriptional landscapes. <i>BMC Genomics</i> , 2019, 20, 236.	2.8	30

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1634	A Novel Chimeric Mitochondrial Gene Confers Cytoplasmic Effects on Seed Oil Content in Polyploid Rapeseed (<i>Brassica napus</i>). <i>Molecular Plant</i> , 2019, 12, 582-596.	8.3	26
1635	Nanopore ultra-long read sequencing technology for antimicrobial resistance detection in <i>Mannheimia haemolytica</i> . <i>Journal of Microbiological Methods</i> , 2019, 159, 138-147.	1.6	22
1636	Gen2Epi: an automated whole-genome sequencing pipeline for linking full genomes to antimicrobial susceptibility and molecular epidemiological data in <i>Neisseria gonorrhoeae</i> . <i>BMC Genomics</i> , 2019, 20, 165.	2.8	8
1637	Genomic and metagenomic signatures of giant viruses are ubiquitous in water samples from sewage, inland lake, waste water treatment plant, and municipal water supply in Mumbai, India. <i>Scientific Reports</i> , 2019, 9, 3690.	3.3	9
1638	The Genome of <i>Drosophila innubila</i> Reveals Lineage-Specific Patterns of Selection in Immune Genes. <i>Molecular Biology and Evolution</i> , 2019, 36, 1405-1417.	8.9	37
1639	Complete Genome Sequences of Two Isolates of <i>Fusobacterium necrophorum</i> subsp. <i>funduliforme</i> , Obtained from Blood from Patients with Lemierre's Syndrome. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	0
1640	Characterization of the emerging multidrug-resistant <i>Salmonella enterica</i> serovar Indiana strains in China. <i>Emerging Microbes and Infections</i> , 2019, 8, 29-39.	6.5	23
1641	Impact of a bathing tradition on shared gut microbes among Japanese families. <i>Scientific Reports</i> , 2019, 9, 4380.	3.3	16
1642	Fine-Tuning of E Activation Suppresses Multiple Assembly-Defective Mutations in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2019, 201, .	2.2	6
1643	Extended Spectrum Beta-Lactamase-Producing Gram-Negative Bacteria Recovered From an Amazonian Lake Near the City of Belém, Brazil. <i>Frontiers in Microbiology</i> , 2019, 10, 364.	3.5	38
1644	Sequencing the Obligate Intracellular <i>Rhombodochlamydia helvetica</i> within Its Tick Host <i>Ixodes ricinus</i> to Investigate Their Symbiotic Relationship. <i>Genome Biology and Evolution</i> , 2019, 11, 1334-1344.	2.5	21
1645	Impact of antibiotic treatment and host innate immune pressure on enterococcal adaptation in the human bloodstream. <i>Science Translational Medicine</i> , 2019, 11, .	12.4	32
1646	Comparative genomic analysis unravels the transmission pattern and intra-species divergence of acute hepatopancreatic necrosis disease (AHPND)-causing <i>Vibrio parahaemolyticus</i> strains. <i>Molecular Genetics and Genomics</i> , 2019, 294, 1007-1022.	2.1	14
1647	Biological and molecular characterization of two <i>Anticarsia gemmatilis</i> multiple nucleopolyhedrovirus clones exhibiting contrasting virulence. <i>Journal of Invertebrate Pathology</i> , 2019, 164, 23-31.	3.2	3
1648	Don't overlook the little guy: An evaluation of the frequency of small plasmids co-conjugating with larger carbapenemase gene containing plasmids. <i>Plasmid</i> , 2019, 103, 1-8.	1.4	36
1649	Biological characteristics and genome-wide sequence analysis of endophytic nitrogen-fixing bacteria <i>Klebsiella variicola</i> GN02. <i>Biotechnology and Biotechnological Equipment</i> , 2019, 33, 108-117.	1.3	15
1650	First clinical isolate of <i>Escherichia coli</i> harboring <i>mcr-1</i> gene in Mexico. <i>PLoS ONE</i> , 2019, 14, e0214648.	2.5	23
1651	Probiotic Potential and Safety Evaluation of <i>Enterococcus faecalis</i> OB14 and OB15, Isolated From Traditional Tunisian Testouri Cheese and Rigouta, Using Physiological and Genomic Analysis. <i>Frontiers in Microbiology</i> , 2019, 10, 881.	3.5	81

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1652	Genomic analysis of the aggressive tree pathogen <i>Ceratocystis albifundus</i> . <i>Fungal Biology</i> , 2019, 123, 351-363.	2.5	11
1653	An efficient genomic signature ranking method for genomic island prediction from a single genome. <i>Journal of Theoretical Biology</i> , 2019, 467, 142-149.	1.7	9
1654	Host Resistance, Genomics and Population Dynamics in a <i>Salmonella</i> Enteritidis and Phage System. <i>Viruses</i> , 2019, 11, 188.	3.3	16
1655	The chloroplast genome of the marine microalga <i>Tisochrysis lutea</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 253-255.	0.4	11
1656	A linear nonribosomal octapeptide from <i>Fusarium graminearum</i> facilitates cell-to-cell invasion of wheat. <i>Nature Communications</i> , 2019, 10, 922.	12.8	74
1657	An N-nitrosating metalloenzyme constructs the pharmacophore of streptozotocin. <i>Nature</i> , 2019, 566, 94-99.	27.8	108
1658	Genome Analysis of <i>Shigella flexneri</i> Serotype 3b Strain SFL1520 Reveals Significant Horizontal Gene Acquisitions Including a Multidrug Resistance Cassette. <i>Genome Biology and Evolution</i> , 2019, 11, 776-785.	2.5	9
1659	CAMISIM: simulating metagenomes and microbial communities. <i>Microbiome</i> , 2019, 7, 17.	11.1	117
1660	Resource Concentration Modulates the Fate of Dissimilated Nitrogen in a Dual-Pathway Actinobacterium. <i>Frontiers in Microbiology</i> , 2019, 10, 3.	3.5	20
1661	The complete plastome of real yellow wood (<i>Podocarpus latifolius</i>): gene organization and comparison with related species. <i>Holzforschung</i> , 2019, 73, 525-536.	1.9	2
1662	<i>Pseudomonas</i> Diversity Within Urban Freshwaters. <i>Frontiers in Microbiology</i> , 2019, 10, 195.	3.5	16
1663	Genome Analyses of a New <i>Mycoplasma</i> Species from the Scorpion <i>Centruroides vittatus</i> . <i>C3: Genes, Genomes, Genetics</i> , 2019, 9, 993-997.	1.8	2
1664	Sequencing of Capsicum Organellar Genomes. <i>Compendium of Plant Genomes</i> , 2019, , 153-172.	0.5	0
1665	Combining Strengths for Multi-genome Visual Analytics Comparison. <i>Bioinformatics and Biology Insights</i> , 2019, 13, 117793221882512.	2.0	1
1666	Identification and molecular characterization of <i>Serratia marcescens</i> phages vB_SmaA_2050H1 and vB_SmaM_2050HW. <i>Archives of Virology</i> , 2019, 164, 1085-1094.	2.1	11
1667	Phylogenomic characterization of red seabream iridovirus from Florida pompano <i>Trachinotus carolinus</i> maricultured in the Caribbean Sea. <i>Archives of Virology</i> , 2019, 164, 1209-1212.	2.1	9
1668	Bacteriophages of the Human Gut: The “Known Unknown” of the Microbiome. <i>Cell Host and Microbe</i> , 2019, 25, 195-209.	11.0	436
1669	Genome Sequence of the Plant Growth-Promoting Rhizobacterium <i>Pantoea agglomerans</i> C1. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	12

#	ARTICLE	IF	CITATIONS
1670	Bacterial phylogeny in the Cayley graph. Discrete Mathematics, Algorithms and Applications, 2019, 11, 1950059.	0.6	4
1671	Comparative Genomic Analysis of <i>Rhodococcus equi</i> : An Insight into Genomic Diversity and Genome Evolution. International Journal of Genomics, 2019, 2019, 1-14.	1.6	7
1672	Aquatic Hemiptera in Southwest Cameroon: Biodiversity of Potential Reservoirs of Mycobacterium ulcerans and Multiple Wolbachia Sequence Types Revealed by Metagenomics. Diversity, 2019, 11, 225.	1.7	2
1673	Draft Genome Sequence of Bacillus lehensis M136, Isolated from the Manleluag Hyperalkaline Spring in Pangasinan, Philippines. Microbiology Resource Announcements, 2019, 8, .	0.6	0
1674	Whole-Genome Sequencing of a Salmonella enterica subsp. enterica Seroovar Infantis Strain Isolated from Broiler Chicken in Peru. Microbiology Resource Announcements, 2019, 8, .	0.6	25
1675	Genome Sequence of an Aspergillus flavus CA14 Strain That Is Widely Used in Gene Function Studies. Microbiology Resource Announcements, 2019, 8, .	0.6	4
1676	Whole-Genome Sequence of Rickettsia parkeri Strain Atlantic Rainforest, Isolated from a Colombian Tick. Microbiology Resource Announcements, 2019, 8, .	0.6	9
1677	Complete Genome Sequence of Pseudomonas aeruginosa Reference Strain PAK. Microbiology Resource Announcements, 2019, 8, .	0.6	26
1678	Draft Genome Sequence of Heavy Metal-Resistant Aeromonas veronii CTe-01, Isolated from a Peruvian Wastewater Treatment Plant. Microbiology Resource Announcements, 2019, 8, .	0.6	3
1679	Has gene expression neofunctionalization in the fire ant antennae contributed to queen discrimination behavior?. Ecology and Evolution, 2019, 9, 12754-12766.	1.9	6
1680	Twelve complete chloroplast genomes of wild peanuts: great genetic resources and a better understanding of Arachis phylogeny. BMC Plant Biology, 2019, 19, 504.	3.6	16
1681	Genomic Analysis of Fluoroquinolone- and Tetracycline-Resistant <i>Campylobacter jejuni</i> Sequence Type 6964 in Humans and Poultry, New Zealand, 2014–2016. Emerging Infectious Diseases, 2019, 25, 2226-2234.	4.3	27
1682	De novo Assembly of the Brugia malayi Genome Using Long Reads from a Single MinION Flowcell. Scientific Reports, 2019, 9, 19521.	3.3	9
1683	Characterization of the mitochondrial genome of the pathogenic fungus Scytalidium auriculariicola (Leotiomyces) and insights into its phylogenetics. Scientific Reports, 2019, 9, 17447.	3.3	21
1684	Genetic Diversity of Composite Enterotoxigenic Staphylococcus epidermidis Pathogenicity Islands. Genome Biology and Evolution, 2019, 11, 3498-3509.	2.5	21
1685	Characterization of antibiotic resistance genes in the species of the rumen microbiota. Nature Communications, 2019, 10, 5252.	12.8	68
1686	Complete plastid genome of Suriana maritima L. (Surianaceae) and its implications in phylogenetic reconstruction of Fabales. Journal of Genetics, 2019, 98, 1.	0.7	1
1687	Comparative genomics of Mycoplasma pneumoniae isolated from children with pneumonia: South Korea, 2010–2016. BMC Genomics, 2019, 20, 910.	2.8	7

#	ARTICLE	IF	CITATIONS
1688	VCGIDB: A Database and Web Resource for the Genomic Islands from <i>Vibrio cholerae</i> . <i>Pathogens</i> , 2019, 8, 261.	2.8	5
1689	deltaRpk: an R package for a rapid detection of differential gene presence between related bacterial genomes. <i>BMC Bioinformatics</i> , 2019, 20, 621.	2.6	3
1690	Transduction as a Potential Dissemination Mechanism of a Clonal qnrB19-Carrying Plasmid Isolated From <i>Salmonella</i> of Multiple Serotypes and Isolation Sources. <i>Frontiers in Microbiology</i> , 2019, 10, 2503.	3.5	12
1691	Complete genome sequence analysis of a lytic <i>Shigella flexneri</i> vB_SfIS-ISF001 bacteriophage. <i>Turkish Journal of Biology</i> , 2019, 43, 99-112.	0.8	15
1692	Modification of the genome topology network and its application to the comparison of group B <i>Streptococcus</i> genomes. <i>BMC Genomics</i> , 2019, 20, 886.	2.8	0
1693	Search for Ancestral Features in Genomes of <i>Rhizobium leguminosarum</i> bv. <i>viciae</i> Strains Isolated from the Relict Legume <i>Vavilovia formosa</i> . <i>Genes</i> , 2019, 10, 990.	2.4	8
1694	Genomic and evolutionary features of two AHPND positive <i>Vibrio parahaemolyticus</i> strains isolated from shrimp (<i>Penaeus monodon</i>) of south-west Bangladesh. <i>BMC Microbiology</i> , 2019, 19, 270.	3.3	15
1695	Isolation and Characterization of a Novel <i>Klebsiella pneumoniae</i> N4-like Bacteriophage KP8. <i>Viruses</i> , 2019, 11, 1115.	3.3	13
1696	Chromosome-level genome assembly for giant panda provides novel insights into Carnivora chromosome evolution. <i>Genome Biology</i> , 2019, 20, 267.	8.8	31
1697	Prophages in <i>Lactobacillus reuteri</i> Are Associated with Fitness Trade-Offs but Can Increase Competitiveness in the Gut Ecosystem. <i>Applied and Environmental Microbiology</i> , 2019, 86, .	3.1	44
1698	Gclust: A Parallel Clustering Tool for Microbial Genomic Data. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 496-502.	6.9	7
1699	Interaction of <i>Phthorimaea operculella</i> granulovirus with a <i>Nosema</i> sp. microsporidium in larvae of <i>Phthorimaea operculella</i> . <i>Journal of Invertebrate Pathology</i> , 2019, 160, 76-86.	3.2	3
1700	A Cryptic Non-Inducible Prophage Confers Phage-Immunity on the <i>Streptococcus thermophilus</i> M17PTZA496. <i>Viruses</i> , 2019, 11, 7.	3.3	26
1701	A novel integrative conjugative element mediates transfer of multi-drug resistance between <i>Streptococcus suis</i> strains of different serotypes. <i>Veterinary Microbiology</i> , 2019, 229, 110-116.	1.9	23
1702	Phoenix phylogeny, and analysis of genetic variation in a diverse collection of date palm (<i>Phoenix</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	3.7	27
1703	Understanding the Evolution of Mitochondrial Genomes in Phaeophyceae Inferred from Mitogenomes of <i>Ishige okamurae</i> (Ishigeales) and <i>Dictyopteris divaricata</i> (Dictyotales). <i>Journal of Molecular Evolution</i> , 2019, 87, 16-26.	1.8	10
1704	A Remote <i>cis</i> -Regulatory Region Is Required for <i>NIN</i> Expression in the Pericycle to Initiate Nodule Primordium Formation in <i>Medicago truncatula</i> . <i>Plant Cell</i> , 2019, 31, 68-83.	6.6	101
1705	Diversity and distribution of <i>Klebsiella</i> capsules in <i>Escherichia coli</i> . <i>Environmental Microbiology Reports</i> , 2019, 11, 107-117.	2.4	15

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1706	Draft Genome Sequences of <i>Proteus mirabilis</i> K1609 and K670: A Model Strains for Territoriality Examination. <i>Current Microbiology</i> , 2019, 76, 144-152.	2.2	3
1707	Discrimination of <i>Mycobacterium leprae</i> and <i>Mycobacterium haemophilum</i> in Clinical Isolates and Specimens by Multiplex PCR Assay and Prediction of Drug Susceptibility. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	3.9	3
1708	Evaluating the evolution and function of the dynamic Venom Y protein in ectoparasitoid wasps. <i>Insect Molecular Biology</i> , 2019, 28, 499-508.	2.0	5
1709	Common and distinctive adaptive traits expressed in <i>Dickeya dianthicola</i> and <i>Dickeya solani</i> pathogens when exploiting potato plant host. <i>Environmental Microbiology</i> , 2019, 21, 1004-1018.	3.8	42
1710	The Complete Plastid Genome of <i>Magnolia zenii</i> and Genetic Comparison to Magnoliaceae species. <i>Molecules</i> , 2019, 24, 261.	3.8	38
1711	Characterization and Genome Analysis of <i>Staphylococcus aureus</i> Podovirus CSA13 and Its Anti-Biofilm Capacity. <i>Viruses</i> , 2019, 11, 54.	3.3	28
1712	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.	2.4	11
1713	Genome mining reveals the origin of a bald phenotype and a cryptic nucleocidin gene cluster in <i>Streptomyces asterosporus</i> DSM 41452. <i>Journal of Biotechnology</i> , 2019, 292, 23-31.	3.8	21
1714	Phage defense mechanisms and their genomic and phenotypic implications in the fish pathogen <i>Vibrio anguillarum</i> . <i>FEMS Microbiology Ecology</i> , 2019, 95, .	2.7	40
1715	Comparative genomics for non-O1/O139 <i>Vibrio cholerae</i> isolates recovered from the Yangtze River Estuary versus <i>V. cholerae</i> representative isolates from serogroup O1. <i>Molecular Genetics and Genomics</i> , 2019, 294, 417-430.	2.1	8
1716	Genetic basis for the establishment of endosymbiosis in <i>Paramecium</i> . <i>ISME Journal</i> , 2019, 13, 1360-1369.	9.8	30
1717	Characterization and complete genome analysis of the surfactin-producing, plant-protecting bacterium <i>Bacillus velezensis</i> 9D-6. <i>BMC Microbiology</i> , 2019, 19, 5.	3.3	62
1718	Comparative mitochondrial genome analysis of the firefly, <i>Inflata indica</i> (Coleoptera: Lampyridae) and the first evidence of heteroplasmy in fireflies. <i>International Journal of Biological Macromolecules</i> , 2019, 121, 671-676.	7.5	13
1719	Comparative Genomics of <i>Lactobacillus brevis</i> Reveals a Significant Plasmidome Overlap of Brewery and Insect Isolates. <i>Current Microbiology</i> , 2019, 76, 37-47.	2.2	13
1720	Long-range PCR and high-throughput sequencing of Ostreid herpesvirus 1 indicate high genetic diversity and complex evolution process. <i>Virology</i> , 2019, 526, 81-90.	2.4	29
1721	In vitro and in vivo evaluation of <i>Lactobacillus</i> strains and comparative genomic analysis of <i>Lactobacillus plantarum</i> CGMCC12436 reveal candidates of colonise-related genes. <i>Food Research International</i> , 2019, 119, 813-821.	6.2	11
1722	Whole-Genome Alignment and Comparative Annotation. <i>Annual Review of Animal Biosciences</i> , 2019, 7, 41-64.	7.4	62
1723	Characterization and comparison of the mitochondrial genomes from two <i>Lyophyllum</i> fungal species and insights into phylogeny of Agaricomycetes. <i>International Journal of Biological Macromolecules</i> , 2019, 121, 364-372.	7.5	42

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1724	Molecular phylogenetics supports a clade of red algal parasites retaining native plastids: taxonomy and terminology revised. <i>Journal of Phycology</i> , 2019, 55, 279-288.	2.3	8
1725	The complete chloroplast and mitochondrial genomes of the diatom <i>Nitzschia palea</i> (Bacillariophyceae) demonstrate high sequence similarity to the endosymbiont organelles of the dinotom <i>Durinskia baltica</i> . <i>Journal of Phycology</i> , 2019, 55, 352-364.	2.3	20
1726	Conservation of mitochondrial genome arrangements in brittle stars (Echinodermata, Ophiuroidea). <i>Molecular Phylogenetics and Evolution</i> , 2019, 130, 115-120.	2.7	18
1727	Genetic, evolutionary and phylogenetic aspects of the plastome of annatto (<i>Bixa orellana</i> L.), the Amazonian commercial species of natural dyes. <i>Planta</i> , 2019, 249, 563-582.	3.2	15
1728	Characterization and comparative analysis of six complete mitochondrial genomes from ectomycorrhizal fungi of the <i>Lactarius</i> genus and phylogenetic analysis of the Agaricomycetes. <i>International Journal of Biological Macromolecules</i> , 2019, 121, 249-260.	7.5	56
1729	“Tupanvirus”, a new genus in the family Mimiviridae. <i>Archives of Virology</i> , 2019, 164, 325-331.	2.1	23
1730	Impact of probiotic <i>Lactobacillus</i> sp. on autochthonous lactobacilli in weaned piglets. <i>Journal of Applied Microbiology</i> , 2019, 126, 242-254.	3.1	16
1731	Comparative genomic analysis of <i>Lactobacillus mucosae</i> LM1 identifies potential niche-specific genes and pathways for gastrointestinal adaptation. <i>Genomics</i> , 2019, 111, 24-33.	2.9	47
1732	Reconstruction and in silico analysis of new <i>Marinobacter adhaerens</i> t76_800 with potential for long-chain hydrocarbon bioremediation associated with marine environmental lipases. <i>Marine Genomics</i> , 2020, 49, 100685.	1.1	5
1733	Phylogenetic determinants of toxin gene distribution in genomes of <i>Brevibacillus laterosporus</i> . <i>Genomics</i> , 2020, 112, 1042-1053.	2.9	19
1734	Complete plastome sequencing of <i>Allium paradoxum</i> reveals unusual rearrangements and the loss of the <i>ndh</i> genes as compared to <i>Allium ursinum</i> and other onions. <i>Gene</i> , 2020, 726, 144154.	2.2	11
1735	A case of “blown pack” spoilage of vacuum-packaged pork likely associated with <i>Clostridium estertheticum</i> in Canada. <i>Letters in Applied Microbiology</i> , 2020, 70, 13-20.	2.2	15
1736	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.	2.8	13
1737	<i>Vampirovibrio chlorellavorus</i> draft genome sequence, annotation, and preliminary characterization of pathogenicity determinants. <i>Phycological Research</i> , 2020, 68, 23-29.	1.6	3
1738	Comparative plastid genomics of <i>Pinus</i> species: Insights into sequence variations and phylogenetic relationships. <i>Journal of Systematics and Evolution</i> , 2020, 58, 118-132.	3.1	30
1739	Plastid phylogenomics improve phylogenetic resolution in the Lauraceae. <i>Journal of Systematics and Evolution</i> , 2020, 58, 423-439.	3.1	56
1740	The complete genome sequence of <i>Rahnella aquatilis</i> ZF7 reveals potential beneficial properties and stress tolerance capabilities. <i>Archives of Microbiology</i> , 2020, 202, 483-499.	2.2	16
1741	Informatic tools and platforms for enhancing plant R-gene discovery process. , 2020, , 121-135.		1

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1742	Comparative genomic analysis reveals a high prevalence of inter-species inÂvivo transfer of carbapenem-resistance plasmids in patients with haematological malignancies. <i>Clinical Microbiology and Infection</i> , 2020, 26, 780.e1-780.e8.	6.0	21
1743	Complete genome and bimodal genomic structure of the amoebal symbiont <i>Neochlamydia</i> strain S13 revealed by ultra-long reads obtained from MinION. <i>Journal of Human Genetics</i> , 2020, 65, 41-48.	2.3	1
1744	A Comparative Characterization of the Mitochondrial Genomes of <i>Paramoeba</i> <i>aparasomata</i> and <i>Neoparamoeba</i> <i>pemaquidensis</i> (Amoebozoa, Paramoebidae). <i>Journal of Eukaryotic Microbiology</i> , 2020, 67, 167-175.	1.7	2
1745	Transposons played a major role in the diversification between the closely related almond and peach genomes: results from the almond genome sequence. <i>Plant Journal</i> , 2020, 101, 455-472.	5.7	94
1746	The complete mitochondrial genomes of two model ectomycorrhizal fungi (<i>Laccaria</i>): features, intron dynamics and phylogenetic implications. <i>International Journal of Biological Macromolecules</i> , 2020, 145, 974-984.	7.5	52
1747	An Improved Melon Reference Genome With Single-Molecule Sequencing Uncovers a Recent Burst of Transposable Elements With Potential Impact on Genes. <i>Frontiers in Plant Science</i> , 2019, 10, 1815.	3.6	48
1748	Chloroplast genome of an extremely endangered conifer <i>Thuja sutchuenensis</i> Franch.: gene organization, comparative and phylogenetic analysis. <i>Physiology and Molecular Biology of Plants</i> , 2020, 26, 409-418.	3.1	10
1749	The complete chloroplast genome sequence of yellow mustard (<i>Sinapis alba</i> L.) and its phylogenetic relationship to other Brassicaceae species. <i>Gene</i> , 2020, 731, 144340.	2.2	43
1750	PaSiT: a novel approach based on short-oligonucleotide frequencies for efficient bacterial identification and typing. <i>Bioinformatics</i> , 2020, 36, 2337-2344.	4.1	5
1751	Genome sequence of <i>Pseudomonas aeruginosa</i> PAO1161, a PAO1 derivative with the ICEPae1161 integrative and conjugative element. <i>BMC Genomics</i> , 2020, 21, 14.	2.8	17
1752	Detection and phylogeny of <i>Staphylococcus aureus</i> sequence type 398 in Taiwan. <i>Journal of Biomedical Science</i> , 2020, 27, 15.	7.0	14
1753	Distinct Catalytic Behaviors between Two 1,4-Dioxane-Degrading Monooxygenases: Kinetics, Inhibition, and Substrate Range. <i>Environmental Science & Technology</i> , 2020, 54, 1898-1908.	10.0	29
1754	Isolation and subunit compositions of the xylanosome complexes produced by <i>Cellulosimicrobium</i> species. <i>Enzyme and Microbial Technology</i> , 2020, 133, 109445.	3.2	4
1755	Genomic sequence data and single nucleotide polymorphism genotyping of <i>Bacillus anthracis</i> strains isolated from animal anthrax outbreaks in Northern Cape Province, South Africa. <i>Data in Brief</i> , 2020, 28, 105040.	1.0	3
1756	Characterization of the ferret TRB locus guided by V, D, J, and C gene expression analysis. <i>Immunogenetics</i> , 2020, 72, 101-108.	2.4	14
1757	Organelomic data sets confirm a cryptic consensus on (unrooted) landâ€plant relationships and provide new insights into bryophyte molecular evolution. <i>American Journal of Botany</i> , 2020, 107, 91-115.	1.7	38
1758	Complete genome sequence and comparative analysis of <i>Streptomyces seoulensis</i> , a pioneer strain of nickel superoxide dismutase. <i>Genes and Genomics</i> , 2020, 42, 273-281.	1.4	4
1759	Plant growth-promoting activities and genomic analysis of the stress-resistant <i>Bacillus megaterium</i> STB1, a bacterium of agricultural and biotechnological interest. <i>Biotechnology Reports (Amsterdam, Tj ETQq1 1 0.784314 rgsBT /Overlo</i>	1.4	4

#	ARTICLE	IF	CITATIONS
1760	The mitochondrial genome of <i>Morchella importuna</i> (272.2Âkb) is the largest among fungi and contains numerous introns, mitochondrial non-conserved open reading frames and repetitive sequences. <i>International Journal of Biological Macromolecules</i> , 2020, 143, 373-381.	7.5	63
1761	Evolution of an <i>Eleusine</i> -Specific Subgroup of <i>Pyricularia oryzae</i> Through a Gain of an Avirulence Gene. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 153-165.	2.6	16
1762	Evolutionary changes of an intestinal <i>Lactobacillus reuteri</i> during probiotic manufacture. <i>MicrobiologyOpen</i> , 2020, 9, e972.	3.0	3
1764	An angular dioxygenase gene cluster responsible for the initial phenazine-1-carboxylic acid degradation step in <i>Rhodococcus</i> sp. WH99 can protect sensitive organisms from toxicity. <i>Science of the Total Environment</i> , 2020, 706, 135726.	8.0	7
1765	“Parasite turnover zone” at secondary contact: A new pattern in host–parasite population genetics. <i>Molecular Ecology</i> , 2020, 29, 4653-4664.	3.9	7
1766	Transposon Insertion in the <i>purL</i> Gene Induces Biofilm Depletion in <i>Escherichia coli</i> ATCC 25922. <i>Pathogens</i> , 2020, 9, 774.	2.8	9
1767	Transit From Autotrophism to Heterotrophism: Sequence Variation and Evolution of Chloroplast Genomes in <i>Orobanchaceae</i> Species. <i>Frontiers in Genetics</i> , 2020, 11, 542017.	2.3	6
1768	Development of PCR-based markers and whole-genome selection model for anthracnose resistance in white lupin (<i>Lupinus albus</i> L.). <i>Journal of Applied Genetics</i> , 2020, 61, 531-545.	1.9	8
1769	The algal selenoproteomes. <i>BMC Genomics</i> , 2020, 21, 699.	2.8	7
1770	Characteristics of Organellar Genomes and Nuclear Internal Transcribed Spacers in the Tertiary Relict Genus <i>Dipelta</i> and Their Phylogenomic Implications. <i>Frontiers in Genetics</i> , 2020, 11, 573226.	2.3	3
1771	p-Aminophenylalanine Involved in the Biosynthesis of Antitumor Dnacin B1 for Quinone Moiety Formation. <i>Molecules</i> , 2020, 25, 4186.	3.8	2
1772	Signs of a phyllospheric lifestyle in the genome of the stress-tolerant strain <i>Azospirillum brasilense</i> Az19. <i>Systematic and Applied Microbiology</i> , 2020, 43, 126130.	2.8	5
1773	Translocation of Viable Gut Microbiota to Mesenteric Adipose Drives Formation of Creeping Fat in Humans. <i>Cell</i> , 2020, 183, 666-683.e17.	28.9	211
1774	The Genome and Transcriptome Analysis of the <i>Vigna mungo</i> Chloroplast. <i>Plants</i> , 2020, 9, 1247.	3.5	6
1775	Concordance of disk diffusion, broth microdilution, and whole-genome sequencing for determination of in vitro antimicrobial susceptibility of <i>Mannheimia haemolytica</i> . <i>Journal of Veterinary Internal Medicine</i> , 2020, 34, 2158-2168.	1.6	4
1776	Genome Complexity Browser: Visualization and quantification of genome variability. <i>PLoS Computational Biology</i> , 2020, 16, e1008222.	3.2	1
1777	The complete mitochondrial genome of medicinal fungus <i>Taiwanofungus camphoratus</i> reveals gene rearrangements and intron dynamics of Polyporales. <i>Scientific Reports</i> , 2020, 10, 16500.	3.3	18
1778	Characterization of Mobile Genetic Elements Using Long-Read Sequencing for Tracking <i>Listeria monocytogenes</i> from Food Processing Environments. <i>Pathogens</i> , 2020, 9, 822.	2.8	11

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1779	Whitefly genomes contain ribotoxin coding genes acquired from plants. <i>Scientific Reports</i> , 2020, 10, 15503.	3.3	24
1780	The complete chloroplast genome of <i>Gleditsia sinensis</i> and <i>Gleditsia japonica</i> : genome organization, comparative analysis, and development of taxon specific DNA mini-barcodes. <i>Scientific Reports</i> , 2020, 10, 16309.	3.3	11
1781	Evolution of a Record-Setting AT-Rich Genome: Indel Mutation, Recombination, and Substitution Bias. <i>Genome Biology and Evolution</i> , 2020, 12, 2344-2354.	2.5	16
1782	Antimicrobial Resistance in Wildlife in Guadeloupe (French West Indies): Distribution of a Single blaCTXâ€“1/IncI1/ST3 Plasmid Among Humans and Wild Animals. <i>Frontiers in Microbiology</i> , 2020, 11, 1524.	3.5	25
1783	Comparative Genomic and Metabolomic Analyses of Two <i>Pseudomonas aeruginosa</i> Strains With Different Antifungal Activities. <i>Frontiers in Microbiology</i> , 2020, 11, 1841.	3.5	15
1784	Beyond Cholera: Characterization of zot-Encoding Filamentous Phages in the Marine Fish Pathogen <i>Vibrio anguillarum</i> . <i>Viruses</i> , 2020, 12, 730.	3.3	16
1785	Draft-genome sequence data and phylogenomic comparison of two marine-sourced bacterial strains <i>Pseudoalteromonas</i> sp. MIP2626 and <i>Psychrobacter</i> sp. BI730. <i>Data in Brief</i> , 2020, 31, 105898.	1.0	2
1786	New insights into the variability of lactic acid production in <i>Lachancea thermotolerans</i> at the phenotypic and genomic level. <i>Microbiological Research</i> , 2020, 238, 126525.	5.3	18
1787	Phylogenetic and evolutionary features of the plastome of <i>Tropaeolum pentaphyllum</i> Lam. (<i>Tropaeolaceae</i>). <i>Planta</i> , 2020, 252, 17.	3.2	9
1788	Intraspecific variation within Castor bean (<i>Ricinus communis</i> L.) based on chloroplast genomes. <i>Industrial Crops and Products</i> , 2020, 155, 112779.	5.2	29
1789	Adaptive divergence across Southern Ocean gradients in the pelagic diatom <i>Fragilariopsis kerguelensis</i> . <i>Molecular Ecology</i> , 2020, 29, 4913-4924.	3.9	15
1790	<i>Klenkia terrae</i> resistant to DNA extraction in germ-free mice stools illustrates the extraction pitfall faced by metagenomics. <i>Scientific Reports</i> , 2020, 10, 10228.	3.3	1
1791	An xa5 Resistance Gene-Breaking Indian Strain of the Rice Bacterial Blight Pathogen <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> Is Nearly Identical to a Thai Strain. <i>Frontiers in Microbiology</i> , 2020, 11, 579504.	3.5	8
1792	Persistence of extendedâ€“spectrum β -lactamase plasmids among Enterobacteriaceae in commercial broiler farms. <i>Microbiology and Immunology</i> , 2020, 64, 712-718.	1.4	5
1793	The complete chloroplast genome sequences of five pinnate-leaved <i>Primula</i> species and phylogenetic analyses. <i>Scientific Reports</i> , 2020, 10, 20782.	3.3	13
1794	Draft genome sequences of concurrent <i>Escherichia coli</i> blood and fecal isolates from a patient with bacteremia and diarrhea belie BioFire-based detection of fecal enteropathogenic <i>E. coli</i> . <i>Pathogens and Disease</i> , 2020, 78, .	2.0	1
1795	Whole-Genome Analysis of Clinical <i>Vibrio cholerae</i> O1 in Kolkata, India, and Dhaka, Bangladesh, Reveals Two Lineages of Circulating Strains, Indicating Variation in Genomic Attributes. <i>MBio</i> , 2020, 11, .	4.1	17
1796	Repeated gain and loss of a single gene modulates the evolution of vascular plant pathogen lifestyles. <i>Science Advances</i> , 2020, 6, .	10.3	58

#	ARTICLE	IF	CITATIONS
1797	Bacteriophages vB_Sen-TO17 and vB_Sen-E22, Newly Isolated Viruses from Chicken Feces, Specific for Several Salmonella enterica Strains. International Journal of Molecular Sciences, 2020, 21, 8821.	4.1	13
1798	Distribution and Evolution of the Bacteriophage WO and Its Antagonism With Wolbachia. Frontiers in Microbiology, 2020, 11, 595629.	3.5	12
1799	Chloroplast genomes elucidate diversity, phylogeny, and taxonomy of Pulsatilla (Ranunculaceae). Scientific Reports, 2020, 10, 19781.	3.3	20
1800	Genome-based characterization of two Colombian clinical Providencia rettgeri isolates co-harboring NDM-1, VIM-2, and other β -lactamases. BMC Microbiology, 2020, 20, 345.	3.3	12
1801	Infection Kinetics and Phylogenetic Analysis of vB_EcoD_SU57, a Virulent T1-Like Drexelviriidae Coliphage. Frontiers in Microbiology, 2020, 11, 565556.	3.5	9
1802	The complete chloroplast genome of Isochrysis galbana and comparison with related haptophyte species. Algal Research, 2020, 50, 101989.	4.6	14
1803	Chloroplast Genome Variation and Evolutionary Analysis of Olea europaea L.. Genes, 2020, 11, 879.	2.4	14
1804	Host Adaptation Predisposes Pseudomonas aeruginosa to Type VI Secretion System-Mediated Predation by the Burkholderia cepacia Complex. Cell Host and Microbe, 2020, 28, 534-547.e3.	11.0	34
1805	Evolutionary dynamics of the chloroplast genome sequences of six Colobanthus species. Scientific Reports, 2020, 10, 11522.	3.3	19
1806	A performant bridge between fixed-size and variable-size seeding. BMC Bioinformatics, 2020, 21, 328.	2.6	3
1807	Analysis of the Antifungal Properties of Bacillus velezensis B-4 Through a Bioassay and Complete-Genome Sequencing. Frontiers in Genetics, 2020, 11, 703.	2.3	11
1808	The Isolation and Genome Sequencing of Five Novel Bacteriophages From the Rumen Active Against Butyrivibrio fibrisolvens. Frontiers in Microbiology, 2020, 11, 1588.	3.5	5
1809	How Tupanvirus Degrades the Ribosomal RNA of Its Amoebal Host? The Ribonuclease T2 Track. Frontiers in Microbiology, 2020, 11, 1691.	3.5	6
1810	Characterization and Comparative Analysis of Two Rheum Complete Chloroplast Genomes. BioMed Research International, 2020, 2020, 1-11.	1.9	5
1811	Complete Chloroplast Genome of Rhipsalis baccifera, the only Cactus with Natural Distribution in the Old World: Genome Rearrangement, Intron Gain and Loss, and Implications for Phylogenetic Studies. Plants, 2020, 9, 979.	3.5	9
1812	Scalable Pairwise Whole-Genome Homology Mapping of Long Genomes with BubbZ. IScience, 2020, 23, 101224.	4.1	11
1813	Whole-genome sequencing and genomic-based acid tolerance mechanisms of Lactobacillus delbrueckii subsp. bulgaricus LJJ. Applied Microbiology and Biotechnology, 2020, 104, 7631-7642.	3.6	12
1814	Evol2Circos: A Web-Based Tool for Genome Synteny and Collinearity Analysis and its Visualization in Fishes. Journal of Heredity, 2020, 111, 486-490.	2.4	4

#	ARTICLE	IF	CITATIONS
1815	Influence of the polar light cycle on seasonal dynamics of an Antarctic lake microbial community. <i>Microbiome</i> , 2020, 8, 116.	11.1	32
1816	Genome reconstruction of white spot syndrome virus (WSSV) from archival Davidson's-fixed paraffin embedded shrimp (<i>Penaeus vannamei</i>) tissue. <i>Scientific Reports</i> , 2020, 10, 13425.	3.3	14
1817	Characterization and expression pattern analysis of pheromone receptor-like genes in Winter Mushroom <i>Flammulina filiformis</i> . <i>Archives of Microbiology</i> , 2020, 202, 2671-2678.	2.2	2
1818	The complete plastome of <i>Passiflora cirrhiflora</i> A. Juss.: structural features, RNA editing sites, hotspots of nucleotide diversity and molecular markers within the subgenus <i>Deildamioides</i> . <i>Revista Brasileira De Botanica</i> , 2020, 43, 839-853.	1.3	5
1819	A novel <i>Thermotoga</i> strain TFO isolated from a Californian petroleum reservoir phylogenetically related to <i>Thermotoga petrophila</i> and <i>T. naphthophila</i> , two thermophilic anaerobic isolates from a Japanese reservoir: Taxonomic and genomic considerations. <i>Systematic and Applied Microbiology</i> , 2020, 43, 126132.	2.8	6
1820	Complete Mitochondrial Genomes Reveal Population-Level Patterns in the Widespread Red Alga <i>Gelidiella fanii</i> (Gelidiales, Rhodophyta). <i>Frontiers in Marine Science</i> , 2020, 7, .	2.5	8
1821	The complete chloroplast genome of an endangered orchid <i>Paphiopedilum spicerianum</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3594-3595.	0.4	3
1822	Origins of cultivars of <i>Chrysanthemum</i> – Evidence from the chloroplast genome and nuclear LFY gene. <i>Journal of Systematics and Evolution</i> , 2020, 58, 925-944.	3.1	30
1823	Mitogenomes of Two <i>Phallus</i> Mushroom Species Reveal Gene Rearrangement, Intron Dynamics, and Basidiomycete Phylogeny. <i>Frontiers in Microbiology</i> , 2020, 11, 573064.	3.5	3
1824	Colonization of a hand washing sink in a veterinary hospital by an <i>Enterobacter hormaechei</i> strain carrying multiple resistances to high importance antimicrobials. <i>Antimicrobial Resistance and Infection Control</i> , 2020, 9, 163.	4.1	13
1825	Mitochondrial evolution in the entomopathogenic fungal genus <i>Beauveria</i> . <i>Archives of Insect Biochemistry and Physiology</i> , 2020, 105, e21754.	1.5	5
1826	Lost and Found: Re-searching and Re-scoring Proteomics Data Aids Genome Annotation and Improves Proteome Coverage. <i>MSystems</i> , 2020, 5, .	3.8	13
1827	Spirochetes isolated from arthropods constitute a novel genus <i>Entomospira</i> genus novum within the order Spirochaetales. <i>Scientific Reports</i> , 2020, 10, 17053.	3.3	5
1828	A Review on Sequence Alignment Algorithms for Short Reads Based on Next-Generation Sequencing. <i>IEEE Access</i> , 2020, 8, 189811-189822.	4.2	7
1829	Chronological set of <i>E. coli</i> O157:H7 bovine strains establishes a role for repeat sequences and mobile genetic elements in genome diversification. <i>BMC Genomics</i> , 2020, 21, 562.	2.8	3
1830	Comparative genomics of <i>Xanthomonas fragariae</i> and <i>Xanthomonas arboricola</i> pv. <i>fragariae</i> reveals intra- and interspecies variations. <i>Phytopathology Research</i> , 2020, 2, .	2.4	8
1831	The Chloroplast Genome of <i>Salvia</i> : Genomic Characterization and Phylogenetic Analysis. <i>International Journal of Plant Sciences</i> , 2020, 181, 812-830.	1.3	15
1832	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, .	0.6	6

#	ARTICLE	IF	CITATIONS
1833	Complete Genome and Comparative Genome Analysis of <i>Lactobacillus reuteri</i> YSJL-12, a Potential Probiotics Strain Isolated From Healthy Sow Fresh Feces. <i>Evolutionary Bioinformatics</i> , 2020, 16, 117693432094219.	1.2	4
1834	Review on the Computational Genome Annotation of Sequences Obtained by Next-Generation Sequencing. <i>Biology</i> , 2020, 9, 295.	2.8	45
1835	Global reprogramming of virulence and antibiotic resistance in <i>Pseudomonas aeruginosa</i> by a single nucleotide polymorphism in elongation factor, <i>fusA1</i> . <i>Journal of Biological Chemistry</i> , 2020, 295, 16411-16426.	3.4	17
1836	A novel therapeutic antibody screening method using bacterial high-content imaging reveals functional antibody binding phenotypes of <i>Escherichia coli</i> ST131. <i>Scientific Reports</i> , 2020, 10, 12414.	3.3	9
1837	Nucleotide substitution rates of diatom plastid encoded protein genes are positively correlated with genome architecture. <i>Scientific Reports</i> , 2020, 10, 14358.	3.3	7
1838	A survey of non-coding RNAs in the social and predatory myxobacterium <i>Myxococcus xanthus</i> DK1622. <i>Molecular Omics</i> , 2020, 16, 492-502.	2.8	4
1839	Sequencing and assembly of the Egyptian buffalo genome. <i>PLoS ONE</i> , 2020, 15, e0237087.	2.5	11
1840	Genomic Surveillance of Ceftriaxone-Resistant <i>Escherichia coli</i> in Western New York Suggests the Extended-Spectrum β -Lactamase blaCTX-M-27 Is Emerging on Distinct Plasmids in ST38. <i>Frontiers in Microbiology</i> , 2020, 11, 1747.	3.5	16
1841	Near-Complete Genome Sequences of a <i>Wolbachia</i> Strain Isolated from <i>Diaphorina citri</i> Kuwayama (<i>Hemiptera</i> : <i>Liviidae</i>). <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	5
1842	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.	1.2	2
1843	Genomic Signatures of Honey Bee Association in an Acetic Acid Symbiont. <i>Genome Biology and Evolution</i> , 2020, 12, 1882-1894.	2.5	18
1844	Genomic Surveillance for One Health Antimicrobial Resistance: Understanding Human, Animal, and Environmental Reservoirs and Transmission. <i>Handbook of Environmental Chemistry</i> , 2020, , 71-100.	0.4	2
1845	Characterization of a Protease Hyper-Productive Mutant of <i>Bacillus pumilus</i> by Comparative Genomic and Transcriptomic Analysis. <i>Current Microbiology</i> , 2020, 77, 3612-3622.	2.2	4
1846	Gammaproteobacteria mediating utilization of methyl-, sulfur- and petroleum organic compounds in deep ocean hydrothermal plumes. <i>ISME Journal</i> , 2020, 14, 3136-3148.	9.8	36
1847	Characterization of the Complete Mitochondrial Genomes of Two Sibling Species of Parasitic Roundworms, <i>Haemonchus contortus</i> and <i>Teladorsagia circumcincta</i> . <i>Frontiers in Genetics</i> , 2020, 11, 573395.	2.3	13
1848	Scalable multiple whole-genome alignment and locally collinear block construction with SibeliaZ. <i>Nature Communications</i> , 2020, 11, 6327.	12.8	39
1849	Mutation of <i>hilD</i> in a <i>Salmonella</i> Derby lineage linked to swine adaptation and reduced risk to human health. <i>Scientific Reports</i> , 2020, 10, 21539.	3.3	7
1850	Comparative Genome Analyses of 18 <i>Verticillium dahliae</i> Tomato Isolates Reveals Phylogenetic and Race Specific Signatures. <i>Frontiers in Microbiology</i> , 2020, 11, 573755.	3.5	13

#	ARTICLE	IF	CITATIONS
1851	Reverse Engineering Targets for Recombinant Protein Production in <i>Corynebacterium glutamicum</i> Inspired by a Fast-Growing Evolved Descendant. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 588070.	4.1	2
1852	Comparative and Functional Analyses of Two Sequenced <i>Paenibacillus polymyxa</i> Genomes Provides Insights Into Their Potential Genes Related to Plant Growth-Promoting Features and Biocontrol Mechanisms. <i>Frontiers in Genetics</i> , 2020, 11, 564939.	2.3	9
1853	Rapid Transmission of a Hyper-Virulent Meningococcal Clone Due to High Effective Contact Numbers and Super Spreaders. <i>Frontiers in Genetics</i> , 2020, 11, 579411.	2.3	3
1854	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.	2.4	4
1855	Nitrate Respiration in <i>Thermus thermophilus</i> NAR1: from Horizontal Gene Transfer to Internal Evolution. <i>Genes</i> , 2020, 11, 1308.	2.4	5
1856	Lysogenization of a Lactococcal Host with Three Distinct Temperate Phages Provides Homologous and Heterologous Phage Resistance. <i>Microorganisms</i> , 2020, 8, 1685.	3.6	13
1857	Chromosome-scale genome assembly for the duckweed <i>Spirodela intermedia</i> , integrating cytogenetic maps, PacBio and Oxford Nanopore libraries. <i>Scientific Reports</i> , 2020, 10, 19230.	3.3	23
1858	Comparative Genomics Analysis of <i>Vibrio anguillarum</i> Isolated from Lumpfish (<i>Cyclopterus lumpus</i>) in Newfoundland Reveal Novel Chromosomal Organizations. <i>Microorganisms</i> , 2020, 8, 1666.	3.6	11
1859	Biotic exchange leaves detectable genomic patterns in the Australian rain forest flora. <i>Biotropica</i> , 2020, 52, 627-635.	1.6	6
1860	Draft Genome Sequence of <i>Adlercreutzia equolifaciens</i> IPLA 37004, a Human Intestinal Strain That Does Not Produce Equol from Daidzein. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	2
1861	Closed Genome Sequences of 28 Foodborne Pathogens from the CFSAN Verification Set, Determined by a Combination of Long and Short Reads. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	3
1862	Whole-Genome Sequencing of Mexican Strains of <i>Anaplasma marginale</i> : An Approach to the Causal Agent of Bovine Anaplasmosis. <i>International Journal of Genomics</i> , 2020, 2020, 1-7.	1.6	6
1863	Implications of plastome evolution in the true lilies (monocot order Liliales). <i>Molecular Phylogenetics and Evolution</i> , 2020, 148, 106818.	2.7	23
1864	Intrinsically disordered regions are abundant in simplexvirus proteomes and display signatures of positive selection. <i>Virus Evolution</i> , 2020, 6, veaa028.	4.9	10
1865	Discovery and Characterization of <i>Thermoproteus</i> Spherical Piliferous Virus 1: a Spherical Archaeal Virus Decorated with Unusual Filaments. <i>Journal of Virology</i> , 2020, 94, .	3.4	2
1866	Comparative genomics of whole-cell pertussis vaccine strains from India. <i>BMC Genomics</i> , 2020, 21, 345.	2.8	6
1867	Genome-wide Analysis of Four <i>Enterobacter cloacae</i> complex type strains: Insights into Virulence and Niche Adaptation. <i>Scientific Reports</i> , 2020, 10, 8150.	3.3	18
1868	Telomeric and sub-telomeric regions undergo rapid turnover within a <i>Streptomyces</i> population. <i>Scientific Reports</i> , 2020, 10, 7720.	3.3	15

#	ARTICLE	IF	CITATIONS
1869	Past and ongoing adaptation of human cytomegalovirus to its host. <i>PLoS Pathogens</i> , 2020, 16, e1008476.	4.7	19
1870	Assessment of a Potential Role of <i>Dickeya dadantii</i> DSM 18020 as a Pectinase Producer for Utilization in Poultry Diets Based on in silico Analyses. <i>Frontiers in Microbiology</i> , 2020, 11, 751.	3.5	4
1871	Bacterial riboproteogenomics: the era of N-terminal proteoform existence revealed. <i>FEMS Microbiology Reviews</i> , 2020, 44, 418-431.	8.6	12
1872	Comprehensive dissection of dispensable genomic regions in <i>Streptomyces</i> based on comparative analysis approach. <i>Microbial Cell Factories</i> , 2020, 19, 99.	4.0	14
1873	Genome Report—A Genome Sequence Analysis of the RB51 Strain of <i>Brucella abortus</i> in the Context of Its Vaccine Properties. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1175-1181.	1.8	4
1874	Genetic variants and source of introduction of SARS-CoV-2 in South America. <i>Journal of Medical Virology</i> , 2020, 92, 2139-2145.	5.0	33
1875	Whole genome sequence analysis of <i>Cupriavidus campinensis</i> S14E4C, a heavy metal resistant bacterium. <i>Molecular Biology Reports</i> , 2020, 47, 3973-3985.	2.3	16
1876	Prospects of Indole derivatives as methyl transfer inhibitors: antimicrobial resistance managers. <i>BMC Pharmacology & Toxicology</i> , 2020, 21, 33.	2.4	4
1877	Emerging Threat of Antimicrobial Resistance in β -Hemolytic <i>Streptococci</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 797.	3.5	15
1878	Responses of mature symbiotic nodules to the whole-plant systemic nitrogen signaling. <i>Journal of Experimental Botany</i> , 2020, 71, 5039-5052.	4.8	22
1879	Discovery of thermophilic <i>Bacillales</i> using reduced-representation genotyping for identification. <i>BMC Microbiology</i> , 2020, 20, 114.	3.3	4
1880	Leveraging plastomes for comparative analysis and phylogenomic inference within <i>Scutellarioideae</i> (<i>Lamiaceae</i>). <i>PLoS ONE</i> , 2020, 15, e0232602.	2.5	21
1881	Comparative Analyses of Mitochondrial Genomes Provide Evolutionary Insights Into Nematode-Trapping Fungi. <i>Frontiers in Microbiology</i> , 2020, 11, 617.	3.5	38
1882	High Synteny and Sequence Identity between Genomes of <i>Nitrosococcus oceanus</i> Strains Isolated from Different Oceanic Gyres Reveals Genome Economization and Autochthonous Clonal Evolution. <i>Microorganisms</i> , 2020, 8, 693.	3.6	4
1883	Comparative analysis of plastid genomes within the <i>Campanulaceae</i> and phylogenetic implications. <i>PLoS ONE</i> , 2020, 15, e0233167.	2.5	11
1884	First isolation and characterization of <i>Brucella suis</i> from yak. <i>Genome</i> , 2020, 63, 397-405.	2.0	1
1885	Tracking the evolution of the two successful CC59 methicillin-resistant <i>Staphylococcus aureus</i> clones in Taiwan: the divergence time of the two clades is estimated to be the 1980s. <i>International Journal of Antimicrobial Agents</i> , 2020, 56, 106047.	2.5	4
1886	Dual-Seq reveals genome and transcriptome of <i>Caedibacter taeniospiralis</i> , obligate endosymbiont of <i>Paramecium</i> . <i>Scientific Reports</i> , 2020, 10, 9727.	3.3	8

#	ARTICLE	IF	CITATIONS
1887	Pan-GWAS of <i>Streptococcus agalactiae</i> Highlights Lineage-Specific Genes Associated with Virulence and Niche Adaptation. <i>MBio</i> , 2020, 11, .	4.1	47
1888	Microevolution and Gain or Loss of Mobile Genetic Elements of Outbreak-Related <i>Listeria monocytogenes</i> in Food Processing Environments Identified by Whole Genome Sequencing Analysis. <i>Frontiers in Microbiology</i> , 2020, 11, 866.	3.5	13
1889	A genomic perspective of metal-resistant bacteria from gold particles: Possible survival mechanisms during gold biogeochemical cycling. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	2.7	11
1890	The nuclear and mitochondrial genomes of <i>Frieseomelitta varia</i> – a highly eusocial stingless bee (Meliponini) with a permanently sterile worker caste. <i>BMC Genomics</i> , 2020, 21, 386.	2.8	15
1891	Diversity of cyclic antimicrobial lipopeptides from <i>Bacillus</i> P34 revealed by functional annotation and comparative genome analysis. <i>Microbiological Research</i> , 2020, 238, 126515.	5.3	17
1892	In vivo dual RNA-seq reveals that neutrophil recruitment underlies differential tissue tropism of <i>Streptococcus pneumoniae</i> . <i>Communications Biology</i> , 2020, 3, 293.	4.4	22
1893	Comparative Genomics of <i>Acinetobacter baumannii</i> Clinical Strains From Brazil Reveals Polyclonal Dissemination and Selective Exchange of Mobile Genetic Elements Associated With Resistance Genes. <i>Frontiers in Microbiology</i> , 2020, 11, 1176.	3.5	24
1894	Comparative Genomic Analysis Reveals the Metabolism and Evolution of the Thermophilic Archaeal Genus <i>Metallosphaera</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 1192.	3.5	8
1895	Complete genome analysis of <i>Pantoea agglomerans</i> -infecting bacteriophage vB_PagM_AAM22. <i>Archives of Virology</i> , 2020, 165, 2111-2114.	2.1	3
1896	Insights Into Chloroplast Genome Evolution Across <i>Opuntioideae</i> (Cactaceae) Reveals Robust Yet Sometimes Conflicting Phylogenetic Topologies. <i>Frontiers in Plant Science</i> , 2020, 11, 729.	3.6	38
1897	Isolation of <i>Mycoplasma anseris</i> alpingitidis from swan goose (<i>Anser cygnoides</i>) in China. <i>BMC Veterinary Research</i> , 2020, 16, 178.	1.9	16
1898	Beta-Lactam Sensitive Bacteria Can Acquire ESBL-Resistance via Conjugation after Long-Term Exposure to Lethal Antibiotic Concentration. <i>Antibiotics</i> , 2020, 9, 296.	3.7	6
1899	The complete chloroplast genome and characteristics analysis of <i>Callistemon rigidus</i> R.Br.. <i>Molecular Biology Reports</i> , 2020, 47, 5013-5024.	2.3	10
1900	Genetic and Functional Analyses of Virulence Potential of an <i>Escherichia coli</i> O157:H7 Strain Isolated From Super-Shedder Cattle. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 271.	3.9	14
1901	Plastome sequences of the subgenus <i>Passiflora</i> reveal highly divergent genes and specific evolutionary features. <i>Plant Molecular Biology</i> , 2020, 104, 21-37.	3.9	13
1902	A multiple drug-resistant <i>Streptococcus pneumoniae</i> of serotype 15A occurring from serotype 19A by capsular switching. <i>Vaccine</i> , 2020, 38, 5114-5118.	3.8	5
1903	Comparative Mitogenome Analysis Reveals Mitochondrial Genome Differentiation in Ectomycorrhizal and Asymbiotic <i>Amanita</i> Species. <i>Frontiers in Microbiology</i> , 2020, 11, 1382.	3.5	42
1904	Comparison of Chloroplast Genomes among Species of Unisexual and Bisexual Clades of the Monocot Family <i>Araceae</i> . <i>Plants</i> , 2020, 9, 737.	3.5	23

#	ARTICLE	IF	CITATIONS
1905	Genome relationships and LTR-retrotransposon diversity in three cultivated Capsicum L. (Solanaceae) species. BMC Genomics, 2020, 21, 237.	2.8	20
1906	The Biotherapeutic Potential of Lactobacillus reuteri Characterized Using a Target-Specific Selection Process. Frontiers in Microbiology, 2020, 11, 532.	3.5	15
1907	Toward a chimeric vaccine against multiple isolates of Mycobacteroides - An integrative approach. Life Sciences, 2020, 250, 117541.	4.3	11
1908	Comparative Genomics of Actinobacillus pleuropneumoniae Serotype 8 Reveals the Importance of Prophages in the Genetic Variability of the Species. International Journal of Genomics, 2020, 2020, 1-12.	1.6	7
1909	Closing Clostridium botulinum Group I Genomes Using a Combination of Short- and Long-Reads. Frontiers in Microbiology, 2020, 11, 239.	3.5	10
1910	Comparative Genomic Analysis Confirms Five Genetic Populations of the Select Agent, Rathayibacter toxicus. Microorganisms, 2020, 8, 366.	3.6	3
1911	Combining short and long read sequencing to characterize antimicrobial resistance genes on plasmids applied to an unauthorized genetically modified Bacillus. Scientific Reports, 2020, 10, 4310.	3.3	57
1912	Ancestral Reconstruction of Karyotypes Reveals an Exceptional Rate of Nonrandom Chromosomal Evolution in Sunflower. Genetics, 2020, 214, 1031-1045.	2.9	31
1913	Parallel Sequencing of Wolbachia wCer2 from Donor and Novel Hosts Reveals Multiple Incompatibility Factors and Genome Stability after Host Transfers. Genome Biology and Evolution, 2020, 12, 720-735.	2.5	14
1914	The draft genome of a new Verminephrobacter eiseniae strain: a nephridial symbiont of earthworms. Annals of Microbiology, 2020, 70, .	2.6	3
1915	Emergence of vancomycin-resistant Enterococcus faecium ST1421 lacking the pstS gene in Korea. European Journal of Clinical Microbiology and Infectious Diseases, 2020, 39, 1349-1356.	2.9	10
1916	Crucial Role of the Accessory Genome in the Evolutionary Trajectory of Acinetobacter baumannii Global Clone 1. Frontiers in Microbiology, 2020, 11, 342.	3.5	16
1917	New Insights Into the Plastome Evolution of the Millettoid/Phaseoloid Clade (Papilionoideae,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 262	3.6	21
1918	Rhizosphere assisted biodegradation of benzo(a)pyrene by cadmium resistant plant-probiotic Serratia marcescens S217, and its genomic traits. Scientific Reports, 2020, 10, 5279.	3.3	19
1919	Bacteriophage-Insensitive Mutants of Antimicrobial-Resistant Salmonella Enterica are Altered in their Tetracycline Resistance and Virulence in Caco-2 Intestinal Cells. International Journal of Molecular Sciences, 2020, 21, 1883.	4.1	13
1920	Genomic Stability of Composite SCCmec ACME and COMER-Like Genetic Elements in Staphylococcus epidermidis Correlates With Rate of Excision. Frontiers in Microbiology, 2020, 11, 166.	3.5	12
1921	Novel Bacteriophages Capable of Disrupting Biofilms From Clinical Strains of Aeromonas hydrophila. Frontiers in Microbiology, 2020, 11, 194.	3.5	22
1922	Complete Chloroplast Genomes of Chlorophytum comosum and Chlorophytum gallabatense: Genome Structures, Comparative and Phylogenetic Analysis. Plants, 2020, 9, 296.	3.5	33

#	ARTICLE	IF	CITATIONS
1923	Genomic Analysis of <i>Bacillus megaterium</i> NCT-2 Reveals Its Genetic Basis for the Bioremediation of Secondary Salinization Soil. International Journal of Genomics, 2020, 2020, 1-11.	1.6	11
1924	Horizontal gene transfer and silver nanoparticles production in a new <i>Marinomonas</i> strain isolated from the Antarctic psychrophilic ciliate <i>Euplotes focardii</i> . Scientific Reports, 2020, 10, 10218.	3.3	22
1925	The Basis for Natural Multiresistance to Phage in <i>Pseudomonas aeruginosa</i> . Antibiotics, 2020, 9, 339.	3.7	12
1926	Characterisation of the <i>Pseudomonas savastanoi</i> pv. <i>phaseolicola</i> population found in Eastern Australia associated with halo blight disease in <i>Vigna radiata</i> . Australasian Plant Pathology, 2020, 49, 515-524.	1.0	3
1927	Adaptation and Survival of <i>Burkholderia cepacia</i> and <i>B. contaminans</i> During Long-Term Incubation in Saline Solutions Containing Benzalkonium Chloride. Frontiers in Bioengineering and Biotechnology, 2020, 8, 630.	4.1	14
1928	The complete chloroplast genome sequence of <i>Rubus lambertianus</i> var. <i>glaber</i> : sequence divergence and phylogenetic application. Mitochondrial DNA Part B: Resources, 2020, 5, 1261-1262.	0.4	3
1929	Draft genome sequence of antimicrobial producing <i>Paenibacillus alvei</i> strain MP1 reveals putative novel antimicrobials. BMC Research Notes, 2020, 13, 280.	1.4	7
1930	Diversity of Pectobacteriaceae Species in Potato Growing Regions in Northern Morocco. Microorganisms, 2020, 8, 895.	3.6	14
1931	A novel <i>Borrelia</i> species, intermediate between Lyme disease and relapsing fever groups, in neotropical passerine-associated ticks. Scientific Reports, 2020, 10, 10596.	3.3	32
1932	<i>tepR</i> encoding a bacterial enhancer-binding protein orchestrates the virulence and interspecies competition of <i>Burkholderia glumae</i> through <i>qsmR</i> and a type VI secretion system. Molecular Plant Pathology, 2020, 21, 1042-1054.	4.2	4
1933	Comparative Plastid Genomics of Neotropical <i>Bulbophyllum</i> (Orchidaceae; Epidendroideae). Frontiers in Plant Science, 2020, 11, 799.	3.6	24
1934	<i>Clostridium massiliamazoniense</i> sp. nov., New Bacterial Species Isolated from Stool Sample of a Volunteer Brazilian. Current Microbiology, 2020, 77, 2008-2015.	2.2	10
1935	Comparison of the transcriptomes of different life history stages of the freshwater Rhodophyte <i>Thorea hispida</i> . Genomics, 2020, 112, 3978-3990.	2.9	3
1936	<i>Staphylococcus</i> Agr virulence is critical for epidermal colonization and associates with atopic dermatitis development. Science Translational Medicine, 2020, 12, .	12.4	62
1937	Complete Chloroplast Genomes of <i>Anthurium huixtlense</i> and <i>Pothos scandens</i> (Pothoideae, Araceae): Unique Inverted Repeat Expansion and Contraction Affect Rate of Evolution. Journal of Molecular Evolution, 2020, 88, 562-574.	1.8	33
1938	Molecular evolutionary and 3D protein structural analyses of <i>Lactobacillus fermentum</i> elongation factor Tu, a novel brain health promoting factor. Genomics, 2020, 112, 3915-3924.	2.9	1
1939	Metabolism of Soy Isoflavones by Intestinal Bacteria: Genome Analysis of an <i>Adlercreutzia equolifaciens</i> Strain That Does Not Produce Equol. Biomolecules, 2020, 10, 950.	4.0	11
1941	A Unique Isolation of a Lytic Bacteriophage Infected <i>Bacillus anthracis</i> Isolate from Pafuri, South Africa. Microorganisms, 2020, 8, 932.	3.6	5

#	ARTICLE	IF	CITATIONS
1942	De Novo Genome Assemblies for Three North American Bumble Bee Species: <i>Bombus bifarius</i> , <i>Bombus vancouverensis</i> , and <i>Bombus vosnesenskii</i> . <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2585-2592.	1.8	18
1943	Comparative genome analysis provides shreds of molecular evidence for reclassification of <i>Leuconostoc mesenteroides</i> MTCC 10508 as a strain of <i>Leu. suionicum</i> . <i>Genomics</i> , 2020, 112, 4023-4031.	2.9	13
1944	Comparative genomics of <i>Streptococcus parauberis</i> : new target for molecular identification of serotype III. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 6211-6222.	3.6	9
1945	Comparative Genomic Analysis of 19 Clinical Isolates of Tigecycline-Resistant <i>Acinetobacter baumannii</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 1321.	3.5	10
1946	A Novel Cyanobacterium <i>Synechococcus elongatus</i> PCC 11802 has Distinct Genomic and Metabolomic Characteristics Compared to its Neighbor PCC 11801. <i>Scientific Reports</i> , 2020, 10, 191.	3.3	54
1947	<p><p><p>Consequences Of Long-Term Bacteria&TM's Exposure To Silver Nanoformulations With Different PhysicoChemical Properties</p></p>. <i>International Journal of Nanomedicine</i> , 2020, Volume 15, 199-213.	6.7	14
1948	Chloroplast and nuclear ribosomal cistron phylogenomics in a group of closely related sections in <i>Salvia</i> subg. <i>Calosphace</i> . <i>Revista Brasileira De Botanica</i> , 2020, 43, 177-191.	1.3	5
1949	First isolation of foot and mouth disease virus from wild boars in the Middle East. <i>Transboundary and Emerging Diseases</i> , 2020, 67, 1725-1729.	3.0	3
1950	Analysis of two Mexican <i>Pectobacterium brasiliense</i> strains reveals an inverted relationship between c-di-GMP levels with exopolysaccharide production and swarming motility. <i>Microbiological Research</i> , 2020, 235, 126427.	5.3	7
1951	Molecular evolution of chloroplast genomes in <i>Monsteroideae</i> (Araceae). <i>Planta</i> , 2020, 251, 72.	3.2	59
1952	Abundance of mobile genetic elements in an <i>Acinetobacter lwoffii</i> strain isolated from Transylvanian honey sample. <i>Scientific Reports</i> , 2020, 10, 2969.	3.3	26
1953	Statistical Mitogenome Assembly with RepeaTs. <i>Journal of Computational Biology</i> , 2020, 27, 1407-1421.	1.6	8
1954	Hybridization and introgression drive genome evolution of Dutch elm disease pathogens. <i>Nature Ecology and Evolution</i> , 2020, 4, 626-638.	7.8	44
1955	The complete mitochondrial genome of the chiltepin pepper (<i>Capsicum annuum</i> var.) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf Resources, 2020, 5, 683-684.	0.4	12
1956	Differential evolution in 3²UTRs leads to specific gene expression in <i>Staphylococcus</i> . <i>Nucleic Acids Research</i> , 2020, 48, 2544-2563.	14.5	19
1957	Functional Genomics Insights Into the Pathogenicity, Habitat Fitness, and Mechanisms Modifying Plant Development of <i>Rhodococcus</i> sp. PBTS1 and PBTS2. <i>Frontiers in Microbiology</i> , 2020, 11, 14.	3.5	20
1958	Thirty complete <i>Streptomyces</i> genome sequences for mining novel secondary metabolite biosynthetic gene clusters. <i>Scientific Data</i> , 2020, 7, 55.	5.3	67
1959	Comparative genomic analysis of Chinese human leptospirosis vaccine strain and circulating isolate. <i>Human Vaccines and Immunotherapeutics</i> , 2020, 16, 1345-1353.	3.3	0

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1960	<i>Escherichia coli</i> ST302: Genomic Analysis of Virulence Potential and Antimicrobial Resistance Mediated by Mobile Genetic Elements. <i>Frontiers in Microbiology</i> , 2020, 10, 3098.	3.5	14
1961	Complete chloroplast genome of <i>Sophora alopecuroides</i> (Papilionoideae): molecular structures, comparative genome analysis and phylogenetic analysis. <i>Journal of Genetics</i> , 2020, 99, 1.	0.7	17
1962	Initial Characterization of the Chloroplast Genome of <i>Vicia sepium</i> , an Important Wild Resource Plant, and Related Inferences About Its Evolution. <i>Frontiers in Genetics</i> , 2020, 11, 73.	2.3	26
1963	Antibiotic resistance, genome analysis and further safe traits of <i>Clostridium perfringens</i> ICVB082; a strain capable of producing an inhibitory compound directed only against a closely related pathogenic strain. <i>Anaerobe</i> , 2020, 62, 102177.	2.1	5
1964	The extreme plantâ€growthâ€promoting properties of <i>Pantoea phytobeneficialis</i> MSR2 revealed by functional and genomic analysis. <i>Environmental Microbiology</i> , 2020, 22, 1341-1355.	3.8	29
1965	Insights Obtained by Culturing <i>Saccharibacteria</i> With Their Bacterial Hosts. <i>Journal of Dental Research</i> , 2020, 99, 685-694.	5.2	62
1966	Whole genome sequencing of carbapenem-resistant <i>Klebsiella pneumoniae</i> : evolutionary analysis for outbreak investigation. <i>Future Microbiology</i> , 2020, 15, 203-212.	2.0	7
1967	Complete genome and methylome analysis of <i>Neisseria meningitidis</i> associated with increased serogroup Y disease. <i>Scientific Reports</i> , 2020, 10, 3644.	3.3	2
1968	Identifying the drivers of computationally detected correlated evolution among sites under antibiotic selection. <i>Evolutionary Applications</i> , 2020, 13, 781-793.	3.1	3
1969	Whole-Genome Sequencing of <i>Lactobacillus helveticus</i> D75 and D76 Confirms Safety and Probiotic Potential. <i>Microorganisms</i> , 2020, 8, 329.	3.6	20
1970	Complete genome sequence analysis of the <i>Vibrio owensii</i> strain SH-14 isolated from shrimp with acute hepatopancreatic necrosis disease. <i>Archives of Microbiology</i> , 2020, 202, 1097-1106.	2.2	4
1971	Extensive Genomic Rearrangements along with Distinct Mobilome and TALome are Associated with Extreme Pathotypes of a Rice Pathogen. <i>Genome Biology and Evolution</i> , 2020, 12, 3951-3956.	2.5	2
1972	Nextâ€Generation Microbial Workhorses: Comparative Genomic Analysis of Fastâ€Growing <i>Vibrio</i> Strains Reveals Their Biotechnological Potential. <i>Biotechnology Journal</i> , 2020, 15, e1900499.	3.5	9
1973	Isolation, Substrate Specificity, and Subunit Characterization of the Xylanosomes Produced by <i>Oerskovia turbata</i> JCM 3160. <i>Current Microbiology</i> , 2020, 77, 924-930.	2.2	1
1974	Bacteriophages Isolated from Stunted Children Can Regulate Gut Bacterial Communities in an Age-Specific Manner. <i>Cell Host and Microbe</i> , 2020, 27, 199-212.e5.	11.0	85
1975	Clades of huge phages from across Earthâ€™s ecosystems. <i>Nature</i> , 2020, 578, 425-431.	27.8	331
1976	Isolation and genomic characterization of a new mimivirus of lineage B from a Brazilian river. <i>Archives of Virology</i> , 2020, 165, 853-863.	2.1	3
1977	Genomic Acquisitions in Emerging Populations of <i>Xanthomonas vasicola</i> pv. <i>vasculorum</i> Infecting Corn in the United States and Argentina. <i>Phytopathology</i> , 2020, 110, 1161-1173.	2.2	16

#	ARTICLE	IF	CITATIONS
1978	Evolutionary dynamics of chloroplast genomes in subfamily Aroideae (Araceae). <i>Genomics</i> , 2020, 112, 2349-2360.	2.9	79
1979	Comparative Plastid Genomics of <i>Cryptomonas</i> Species Reveals Fine-Scale Genomic Responses to Loss of Photosynthesis. <i>Genome Biology and Evolution</i> , 2020, 12, 3926-3937.	2.5	27
1980	Isolation of Four Lytic Phages Infecting <i>Klebsiella pneumoniae</i> K22 Clinical Isolates from Spain. <i>International Journal of Molecular Sciences</i> , 2020, 21, 425.	4.1	19
1981	Subchromosome-Scale Nuclear and Complete Mitochondrial Genome Characteristics of <i>Morchella crassipes</i> . <i>International Journal of Molecular Sciences</i> , 2020, 21, 483.	4.1	27
1982	Resistance Sniffer: An online tool for prediction of drug resistance patterns of <i>Mycobacterium tuberculosis</i> isolates using next generation sequencing data. <i>International Journal of Medical Microbiology</i> , 2020, 310, 151399.	3.6	17
1983	High quality 3C de novo assembly and annotation of a multidrug resistant ST-111 <i>Pseudomonas aeruginosa</i> genome: Benchmark of hybrid and non-hybrid assemblers. <i>Scientific Reports</i> , 2020, 10, 1392.	3.3	32
1984	Complete Chloroplast Genome Sequence of Chinese Lacquer Tree (<i>Toxicodendron vernicifluum</i>), Tj ETQq0 0.0rgBT /Overlock 10 Tj S	1.9	15
1985	Stepwise evolution and convergent recombination underlie the global dissemination of carbapenemase-producing <i>Escherichia coli</i> . <i>Genome Medicine</i> , 2020, 12, 10.	8.2	40
1986	Species-specific recruitment of transcription factors dictates toxin expression. <i>Nucleic Acids Research</i> , 2020, 48, 2388-2400.	14.5	28
1987	Characterization of sequence variability hotspots in <i>Cranichideae</i> plastomes (Orchidaceae,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tj S	2.5	25
1988	Vanillin Production in <i>Pseudomonas</i> : Whole-Genome Sequencing of <i>Pseudomonas</i> sp. Strain 9.1 and Reannotation of <i>Pseudomonas putida</i> CalA as a Vanillin Reductase. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	17
1989	Comprehensive analysis of the mechanisms underlying enhanced growth and root N acquisition in rice by the endophytic diazotroph, <i>Burkholderia vietnamiensis</i> RS1. <i>Plant and Soil</i> , 2020, 450, 537-555.	3.7	8
1990	Complete Genome Sequences for Two <i>Myoviridae</i> Strains Infecting Cyanobacteria in a Subarctic Lake. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	3
1991	Evolution and Genetic Diversity of Primate Cytomegaloviruses. <i>Microorganisms</i> , 2020, 8, 624.	3.6	11
1992	<i>Pantoea agglomerans</i> -Infecting Bacteriophage vB_PagS_AAS21: A Cold-Adapted Virus Representing a Novel Genus within the Family Siphoviridae. <i>Viruses</i> , 2020, 12, 479.	3.3	5
1993	The complete chloroplast genome of <i>Myriophyllum spicatum</i> reveals a 4â€b inversion and new insights regarding plastome evolution in Haloragaceae. <i>Ecology and Evolution</i> , 2020, 10, 3090-3102.	1.9	7
1994	Complete genome analysis of <i>Glutamicibacter creatinolyticus</i> from mare abscess and comparative genomics provide insight of diversity and adaptation for <i>Glutamicibacter</i> . <i>Gene</i> , 2020, 741, 144566.	2.2	14
1995	Taxogenomic assessment and genomic characterisation of <i>Weissella cibaria</i> strain 92 able to metabolise oligosaccharides derived from dietary fibres. <i>Scientific Reports</i> , 2020, 10, 5853.	3.3	15

#	ARTICLE	IF	CITATIONS
1996	Complete Genome Sequence of <i>Chlamydia avium</i> PV 4360/2, Isolated from a Feral Pigeon in Italy. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	4
1997	2SigFinder: the combined use of small-scale and large-scale statistical testing for genomic island detection from a single genome. <i>BMC Bioinformatics</i> , 2020, 21, 159.	2.6	29
1998	Genomic characterization of <i>Lactobacillus fermentum</i> DSM 20052. <i>BMC Genomics</i> , 2020, 21, 328.	2.8	15
1999	Description of Three Novel Members in the Family Geobacteraceae, <i>Oryzomonas japonicum</i> gen. nov., sp. nov., <i>Oryzomonas sagensis</i> sp. nov., and <i>Oryzomonas ruber</i> sp. nov.. <i>Microorganisms</i> , 2020, 8, 634.	3.6	29
2000	Comparative Genomic and Transcriptomic Analyses of <i>Mycobacterium kansasii</i> Subtypes Provide New Insights Into Their Pathogenicity and Taxonomy. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 122.	3.9	10
2001	The complete genome of lytic <i>Salmonella</i> phage vB_SenM-PA13076 and therapeutic potency in the treatment of lethal <i>Salmonella</i> Enteritidis infections in mice. <i>Microbiological Research</i> , 2020, 237, 126471.	5.3	41
2002	The Organelle Genomes in the Photosynthetic Red Algal Parasite <i>Pterocladia</i> <i>hemisphaerica</i> (Florideophyceae, Rhodophyta) Have Elevated Substitution Rates and Extreme Gene Loss in the Plastid Genome. <i>Journal of Phycology</i> , 2020, 56, 1006-1018.	2.3	7
2003	Comparative genomic analysis and mosquito larvicidal activity of four <i>Bacillus thuringiensis</i> serovar israelensis strains. <i>Scientific Reports</i> , 2020, 10, 5518.	3.3	6
2004	Development of a workflow for identification of nuclear genotyping markers for <i>Cyclospora cayentanensis</i> . <i>Parasite</i> , 2020, 27, 24.	2.0	13
2005	Global clonal spread of mcr-3-carrying MDR ST34 <i>Salmonella enterica</i> serotype Typhimurium and monophasic 1,4,[5],12:i:~ variants from clinical isolates. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 1756-1765.	3.0	37
2006	Mild Stress Conditions during Laboratory Culture Promote the Proliferation of Mutations That Negatively Affect Sigma B Activity in <i>Listeria monocytogenes</i> . <i>Journal of Bacteriology</i> , 2020, 202, .	2.2	22
2007	Draft Genome Sequence of <i>Candidatus Arthromitus</i> UMNCA01, a Suspected Commensal Isolated from the Gut Microbiome of Commercial Turkey. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	1
2008	Draft Genome Sequence of a <i>Serratia marcescens</i> Strain Isolated from the Pitcher Fluids of a <i>Sarracenia</i> Pitcher Plant. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	2
2009	Draft Genome Sequences of 12 <i>Leuconostoc carnosum</i> Strains Isolated from Cooked Ham Packaged in a Modified Atmosphere and from Fresh Sausages. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	6
2010	The Complete Chloroplast Genome of Two Important Annual Clover Species, <i>Trifolium alexandrinum</i> and <i>T. resupinatum</i> : Genome Structure, Comparative Analyses and Phylogenetic Relationships with Relatives in Leguminosae. <i>Plants</i> , 2020, 9, 478.	3.5	26
2011	Complete Genome Sequence of a <i>Legionella longbeachae</i> Serogroup 2 Isolate Derived from a Patient with Legionnaires' Disease. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	1
2012	Draft Genome Sequences of <i>Bifidobacterium animalis</i> Consecutively Isolated from Healthy Japanese Individuals. <i>Journal of Genomics</i> , 2020, 8, 37-42.	0.9	0
2013	The Remarkable Dual-Level Diversity of Prokaryotic Flagellins. <i>MSystems</i> , 2020, 5, .	3.8	11

#	ARTICLE	IF	CITATIONS
2014	Plastome Evolution in Saxifragaceae and Multiple Plastid Capture Events Involving Heuchera and Tiarella. <i>Frontiers in Plant Science</i> , 2020, 11, 361.	3.6	34
2015	Whole-Genome-Sequence-Based Characterization of Extensively Drug-Resistant <i>Acinetobacter baumannii</i> Hospital Outbreak. <i>MSphere</i> , 2020, 5, .	2.9	36
2016	Exploring the success of Brazilian endemic clone <i>Pseudomonas aeruginosa</i> ST277 and its association with the CRISPR-Cas system type I-C. <i>BMC Genomics</i> , 2020, 21, 255.	2.8	15
2017	Tetracycline degradation by <i>Klebsiella</i> sp. strain TR5: Proposed degradation pathway and possible genes involved. <i>Chemosphere</i> , 2020, 253, 126729.	8.2	48
2018	Persistent contamination of raw milk by <i>Campylobacter jejuni</i> ST-883. <i>PLoS ONE</i> , 2020, 15, e0231810.	2.5	25
2019	Whole genome analysis of multidrug-resistant <i>Citrobacter freundii</i> B9-C2 isolated from preterm neonate's stool in the first week. <i>Journal of Global Antimicrobial Resistance</i> , 2020, 21, 246-251.	2.2	8
2020	<i>Lentibacillus cibarius</i> sp. nov., isolated from kimchi, a Korean fermented food. <i>Journal of Microbiology</i> , 2020, 58, 387-394.	2.8	16
2021	First detection of a plasmid located carbapenem resistant bla _{VIM} -1 gene in <i>E. coli</i> isolated from meat products at retail in Belgium in 2015. <i>International Journal of Food Microbiology</i> , 2020, 324, 108624.	4.7	16
2022	The complete plastome sequences of five <i>Aponogeton</i> species (<i>Aponogetonaceae</i>): Insights into the structural organization and mutational hotspots. <i>Plant Diversity</i> , 2020, 42, 334-342.	3.7	10
2023	Gcluster: a simple-to-use tool for visualizing and comparing genome contexts for numerous genomes. <i>Bioinformatics</i> , 2020, 36, 3871-3873.	4.1	11
2024	Isolation and characterization of Hena1 – a novel <i>Erwinia amylovora</i> bacteriophage. <i>FEMS Microbiology Letters</i> , 2020, 367, .	1.8	11
2025	SARS-CoV-2, an evolutionary perspective of interaction with human ACE2 reveals undiscovered amino acids necessary for complex stability. <i>Evolutionary Applications</i> , 2020, 13, 2168-2178.	3.1	38
2026	Molecular and Clinical Characterization of Multidrug-Resistant and Hypervirulent <i>Klebsiella pneumoniae</i> Strains from Liver Abscess in Taiwan. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	3.2	21
2027	Emergence of a Novel <i>Salmonella enterica</i> Serotype Reading Clonal Group Is Linked to Its Expansion in Commercial Turkey Production, Resulting in Unanticipated Human Illness in North America. <i>MSphere</i> , 2020, 5, .	2.9	22
2028	Complete genome sequence and annotation of the laboratory reference strain <i>Shigella flexneri</i> serotype 5a M90T and genome-wide transcriptional start site determination. <i>BMC Genomics</i> , 2020, 21, 285.	2.8	7
2029	Temporal Dynamics of <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Agona Isolates From a Recurrent Multistate Outbreak. <i>Frontiers in Microbiology</i> , 2020, 11, 478.	3.5	14
2030	Correlations among oligonucleotide repeats, nucleotide substitutions, and insertion-deletion mutations in chloroplast genomes of plant family <i>Malvaceae</i> . <i>Journal of Systematics and Evolution</i> , 2021, 59, 388-402.	3.1	43
2031	Incorporating the plasmidome into antibiotic resistance surveillance in animal agriculture. <i>Plasmid</i> , 2021, 113, 102529.	1.4	2

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2032	Acquisition of a genomic resistance island (AbGRI5) from global clone 2 through homologous recombination in a clinical <i>Acinetobacter baumannii</i> isolate. <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 65-69.	3.0	13
2033	Genetics and regulation of nitrogen fixation in <i>Paenibacillus brasiliensis</i> PB24. <i>Microbiological Research</i> , 2021, 243, 126647.	5.3	6
2034	Complete genome reconstruction and genetic analysis of Taura syndrome virus of shrimp from archival Davidson's-fixed paraffin embedded tissue. <i>Virology</i> , 2021, 553, 117-121.	2.4	7
2035	Deciphering the origin of <i>Aspergillus flavus</i> NRRL21882, the active biocontrol agent of <i>Afla-Guard</i> [®] . <i>Letters in Applied Microbiology</i> , 2021, 72, 509-516.	2.2	11
2036	Whole genome sequencing and genome annotation of <i>Dermacoccus abyssi</i> strain HZAU 226 isolated from spoiled eggs. <i>Genomics</i> , 2021, 113, 1199-1206.	2.9	5
2037	Genotyping <i>Dickeya dianthicola</i> Causing Potato Blackleg and Soft Rot Outbreak Associated With Inoculum Geography in the United States. <i>Plant Disease</i> , 2021, 105, PDIS-10-20-2138.	1.4	5
2038	High Sequence Divergence but Limited Architectural Rearrangements in Organelle Genomes of <i>Cyanophora</i> (Glaucomphyta) Species. <i>Journal of Eukaryotic Microbiology</i> , 2021, 68, e12831.	1.7	0
2039	Whole-genome Sequencing and Mining of Protease Coding Genes in <i>Bacillus paralicheniformis</i> MKU3, and its Degradomics in Feather Meal Medium. <i>Current Microbiology</i> , 2021, 78, 206-217.	2.2	3
2040	SNP-based genotyping and whole-genome sequencing reveal previously unknown genetic diversity in <i>Xanthomonas vasicola</i> pv. <i>musacearum</i> , causal agent of banana xanthomonas wilt, in its presumed Ethiopian origin. <i>Plant Pathology</i> , 2021, 70, 534-543.	2.4	3
2041	Development of a real-time PCR assay for detection and quantification of <i>Streptococcus iniae</i> using the lactate permease gene. <i>Journal of Fish Diseases</i> , 2021, 44, 53-61.	1.9	14
2042	A single nucleotide polymorphism in an IgA1 protease gene determines <i>Streptococcus pneumoniae</i> adaptation to the middle ear during otitis media. <i>Pathogens and Disease</i> , 2021, 79, .	2.0	5
2043	Phylogeny of <i>Orthotrichum</i> s.l. and <i>Ulota</i> s.l. (Orthotrichaceae, Bryophyta): Insights into stomatal evolution. <i>Journal of Systematics and Evolution</i> , 2022, 60, 876-900.	3.1	3
2044	CRISPR-Cas systems restrict horizontal gene transfer in <i>Pseudomonas aeruginosa</i> . <i>ISME Journal</i> , 2021, 15, 1420-1433.	9.8	59
2045	Development of genomic resources for the genus <i>Celtis</i> (Cannabaceae) based on genome skimming data. <i>Plant Diversity</i> , 2021, 43, 43-53.	3.7	13
2046	Chloroplast genome evolution in the <i>Dracunculus</i> clade (Aroideae, Araceae). <i>Genomics</i> , 2021, 113, 183-192.	2.9	27
2047	Mosaic genome evolution and phylogenetics of <i>Chrysodeixis includens</i> nucleopolyhedrovirus (ChinNPV) and virulence of seven new isolates from the Brazilian states of Minas Gerais and Mato Grosso. <i>Archives of Virology</i> , 2021, 166, 125-138.	2.1	1
2048	Phylogeny of Veneridae (Bivalvia) based on mitochondrial genomes. <i>Zoologica Scripta</i> , 2021, 50, 58-70.	1.7	13
2049	Life and Death of Selfish Genes: Comparative Genomics Reveals the Dynamic Evolution of Cytoplasmic Incompatibility. <i>Molecular Biology and Evolution</i> , 2021, 38, 2-15.	8.9	72

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2050	Comparative genome analysis of 12 <i>Shigella sonnei</i> strains: virulence, resistance, and their interactions. <i>International Microbiology</i> , 2021, 24, 83-91.	2.4	1
2051	<i>Myxosporea</i> (Myxozoa, Cnidaria) Lack DNA Cytosine Methylation. <i>Molecular Biology and Evolution</i> , 2021, 38, 393-404.	8.9	12
2052	Draft Genome of <i>Fusarium oxysporum</i> f. sp. <i>cubense</i> Strain Tropical Race-4 Infecting Cavendish (AAA) Group of Banana in India. <i>Plant Disease</i> , 2021, 105, 481-483.	1.4	17
2053	Phageome Analysis of <i>Bifidobacteria</i> -Rich Samples. <i>Methods in Molecular Biology</i> , 2021, 2278, 71-85.	0.9	0
2054	Complete Genome Sequence of <i>Francisella</i> sp. Strain LA11-2445 (FDC406), a Novel Species Isolated from a Human Skin Lesion. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	0
2055	New insights into the evolutionary characteristic between the New World and Old World <i>Lupinus</i> species using complete chloroplast genomes. <i>International Journal of Transgender Health</i> , 2021, 14, 414-427.	2.3	2
2056	Genome Sequences of 104 <i>Escherichia coli</i> O157:H7 Isolates from Pigs, Cattle, and Pork Production Environments in Alberta, Canada. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	1
2057	Phylogenomic and evolutionary dynamics of inverted repeats across <i>Angelica</i> plastomes. <i>BMC Plant Biology</i> , 2021, 21, 26.	3.6	32
2058	Mechanisms of aerobic dechlorination of hexachlorobenzene and pentachlorophenol by <i>Nocardioide</i> sp. PD653. <i>Journal of Pesticide Sciences</i> , 2021, 46, 373-381.	1.4	3
2059	Proof of the triple prerequisite conditions which are essential for carbapenem resistance development in <i>Klebsiella pneumoniae</i> by using radiation-mediated mutagenesis. <i>FEMS Microbiology Letters</i> , 2021, 368, .	1.8	0
2060	Comparative genomic analysis of <i>Polypodiaceae</i> chloroplasts reveals fine structural features and dynamic insertion sequences. <i>BMC Plant Biology</i> , 2021, 21, 31.	3.6	14
2061	Genetic Sequence Alignment Computing for Ensuring Cyber Security of the IoT Systems. <i>Advances in Sustainability Science and Technology</i> , 2021, , 235-252.	0.6	2
2062	Genome analysis of the metabolically versatile <i>Pseudomonas umsongensis</i> GO16: the genetic basis for PET monomer upcycling into polyhydroxyalkanoates. <i>Microbial Biotechnology</i> , 2021, 14, 2463-2480.	4.2	35
2063	<i>Bifidobacterium dentium</i> N8 with potential probiotic characteristics prevents LPS-induced intestinal barrier injury by alleviating the inflammatory response and regulating the tight junction in Caco-2 cell monolayers. <i>Food and Function</i> , 2021, 12, 7171-7184.	4.6	31
2064	The mitogenomes of two saprophytic <i>Boletales</i> species (<i>Coniophora</i>) reveals intron dynamics and accumulation of plasmid-derived and non-conserved genes. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 401-414.	4.1	23
2065	<i>Culex quinquefasciatus</i> carrying <i>Wolbachia</i> is less susceptible to entomopathogenic bacteria. <i>Scientific Reports</i> , 2021, 11, 1094.	3.3	9
2066	Geno-informatics for Prediction of Virulence and Drug Resistance in Bacterial Pathogens. , 2021, , 3-18.		0
2067	Comparative Chloroplast Genomics of <i>Corydalis</i> Species (<i>Papaveraceae</i>): Evolutionary Perspectives on Their Unusual Large Scale Rearrangements. <i>Frontiers in Plant Science</i> , 2020, 11, 600354.	3.6	30

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2068	Genomic Analysis of Antimicrobial Resistance and Resistance Plasmids in Salmonella Serovars from Poultry in Nigeria. <i>Antibiotics</i> , 2021, 10, 99.	3.7	29
2069	The Effect of Alignment on Peoples Ability to Judge Event Sequence Similarity. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2021, PP, 1-1.	4.4	0
2070	Uncovering dynamic evolution in the plastid genome of seven <i>Ligusticum</i> species provides insights into species discrimination and phylogenetic implications. <i>Scientific Reports</i> , 2021, 11, 988.	3.3	10
2071	Draft Genome Sequence of <i>Pseudomonas</i> sp. Strain T2.31D-1, Isolated from a Drilling Core Sample Obtained 414 Meters below Surface in the Iberian Pyrite Belt. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	3
2072	Whole plastomes are not enough: phylogenomic and morphometric exploration at multiple demographic levels of the bee orchid clade <i>Ophrys</i> sect. <i>Sphegodes</i> . <i>Journal of Experimental Botany</i> , 2021, 72, 654-681.	4.8	15
2073	Genetic and evolutionary analyses of plastomes of the subfamily Cactoideae (Cactaceae) indicate relaxed protein biosynthesis and tRNA import from cytosol. <i>Revista Brasileira De Botanica</i> , 2021, 44, 97-116.	1.3	7
2074	Assembly, Annotation, and Comparative Analysis of Bifidobacterial Genomes. <i>Methods in Molecular Biology</i> , 2021, 2278, 31-44.	0.9	0
2075	Comparative Genomics, from the Annotated Genome to Valuable Biological Information: A Case Study. <i>Methods in Molecular Biology</i> , 2021, 2242, 91-112.	0.9	0
2076	Potential Whole-Cell Biosensors for Detection of Metal Using MerR Family Proteins from <i>Enterobacter</i> sp. YSU and <i>Stenotrophomonas maltophilia</i> OR02. <i>Micromachines</i> , 2021, 12, 142.	2.9	2
2077	Morphological and genomic evidence for a new species of <i>Corallorhiza</i> (Orchidaceae Epidendroideae) from SW China. <i>Plant Diversity</i> , 2021, 43, 409-419.	3.7	1
2078	Genomic sequencing of different sequevars of <i>Ralstonia solanacearum</i> belonging to the Moko ecotype. <i>Genetics and Molecular Biology</i> , 2021, 44, e20200172.	1.3	5
2080	A biological and genomic comparison of a drug-resistant and a drug-susceptible strain of <i>Candida auris</i> isolated from Beijing, China. <i>Virulence</i> , 2021, 12, 1388-1399.	4.4	11
2081	Comprehensive genomic analysis reveals virulence factors and antibiotic resistance genes in <i>Pantoea agglomerans</i> KM1, a potential opportunistic pathogen. <i>PLoS ONE</i> , 2021, 16, e0239792.	2.5	21
2082	Comparative mitochondrial genome analysis reveals intron dynamics and gene rearrangements in two <i>Trametes</i> species. <i>Scientific Reports</i> , 2021, 11, 2569.	3.3	13
2083	Genomic Characterization of Multidrug-Resistant <i>Escherichia coli</i> BH100 Sub-strains. <i>Frontiers in Microbiology</i> , 2020, 11, 549254.	3.5	5
2084	Genome-wide genetic marker analysis and genotyping of <i>Escherichia fergusonii</i> strain OTSVEF-60. <i>Brazilian Journal of Microbiology</i> , 2021, 52, 989-1004.	2.0	14
2085	Rapid divergence of the male reproductive proteins in the <i>Drosophila dunni</i> group and implications for postmating incompatibilities between species. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	4
2086	Complete Genome Sequence of <i>Campylobacter hepaticus</i> USA52, Associated with Chicken Spotty Liver Disease. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	2

#	ARTICLE	IF	CITATIONS
2087	A comparison of fourteen fully characterized mammalian-associated <i>Campylobacter fetus</i> isolates suggests that loss of defense mechanisms contribute to high genomic plasticity and subspecies evolution. <i>PeerJ</i> , 2021, 9, e10586.	2.0	5
2088	Comparative Genomic Analysis of Three <i>Pseudomonas</i> Species Isolated from the Eastern Oyster (<i>Crassostrea virginica</i>) Tissues, Mantle Fluid, and the Overlying Estuarine Water Column. <i>Microorganisms</i> , 2021, 9, 490.	3.6	7
2089	Comprehensive genomics depict accessory genes encoding pathogenicity and biofilm determinants in <i>Enterococcus faecalis</i> . <i>Future Microbiology</i> , 2021, 16, 143-157.	2.0	2
2091	Comparative Genomics of <i>Mycobacterium avium</i> Subspecies <i>Paratuberculosis</i> Sheep Strains. <i>Frontiers in Veterinary Science</i> , 2021, 8, 637637.	2.2	7
2093	Portable CRISPR-Cas9 ^N System for Flexible Genome Engineering in <i>Lactobacillus acidophilus</i> , <i>Lactobacillus gasseri</i> , and <i>Lactobacillus paracasei</i> . <i>Applied and Environmental Microbiology</i> , 2021, 87, .	3.1	18
2094	Co-Bridges: Pair-wise Visual Connection and Comparison for Multi-item Data Streams. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2021, 27, 1612-1622.	4.4	11
2095	Zinc limitation in <i>Klebsiella pneumoniae</i> profiled by quantitative proteomics influences transcriptional regulation and cation transporter-associated capsule production. <i>BMC Microbiology</i> , 2021, 21, 43.	3.3	5
2096	Detection and identification of <i>Xanthomonas campestris</i> pv. <i>campestris</i> and pv. <i>raphani</i> by multiplex polymerase chain reaction using specific primers. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 1991-2002.	3.6	3
2097	Whole Genome Sequencing and Antimicrobial Resistance of <i>Staphylococcus aureus</i> from Surgical Site Infections in Ghana. <i>Pathogens</i> , 2021, 10, 196.	2.8	4
2098	Multiple Displacement Amplification as a Solution for Low Copy Number Plasmid Sequencing. <i>Frontiers in Microbiology</i> , 2021, 12, 617487.	3.5	2
2100	Comparative Analyses of <i>Euonymus</i> Chloroplast Genomes: Genetic Structure, Screening for Loci With Suitable Polymorphism, Positive Selection Genes, and Phylogenetic Relationships Within <i>Celastrineae</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 593984.	3.6	25
2101	Dissemination of Extended-Spectrum-β-Lactamase-Producing <i>Enterobacter cloacae</i> Complex from a Hospital to the Nearby Environment in Guadeloupe (French West Indies): ST114 Lineage Coding for a Successful IncHI2/ST1 Plasmid. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, .	3.2	9
2102	Harnessing CRISPR-Cas9 for Genome Editing in <i>Streptococcus pneumoniae</i> D39V. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	3.1	6
2103	Characterization of a pericentric inversion in plateau fence lizards (<i>Sceloporus tristichus</i>): evidence from chromosome-scale genomes. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	8
2104	A novel DNA chromatography method to discriminate <i>Mycobacterium abscessus</i> subspecies and macrolide susceptibility. <i>EBioMedicine</i> , 2021, 64, 103187.	6.1	16
2105	Genomic Characterization Provides an Insight into the Pathogenicity of the Poplar Canker Bacterium <i>Lonsdalea populi</i> . <i>Genes</i> , 2021, 12, 246.	2.4	0
2106	Identification and characterization of a spreadable IncI1 plasmid harbouring a blaCTX-M-15 gene in an Italian human isolate of <i>Salmonella</i> serovar Napoli. <i>Plasmid</i> , 2021, 114, 102566.	1.4	3
2107	In-Silico Pangenomics of SARS-CoV-2 Isolates Reveal Evidence for Subtle Adaptive Expression Strategies, Continued Clonal Evolution, and Sub-Clonal Emergences, Despite Genome Stability. <i>Microbiology Research</i> , 2021, 12, 204-233.	1.9	4

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2108	Characterization of multidrug-resistant <i>Acinetobacter baumannii</i> strain ATCC BAA1605 using whole-genome sequencing. <i>BMC Research Notes</i> , 2021, 14, 83.	1.4	8
2109	Whole-Genome Sequencing and Comparative Genomics of Three <i>Helicobacter pylori</i> Strains Isolated from the Stomach of a Patient with Adenocarcinoma. <i>Pathogens</i> , 2021, 10, 331.	2.8	5
2111	The plastome of <i>Phaius hainanensis</i> (Orchidaceae): an endangered species endemic to Hainan province, China. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1253-1255.	0.4	0
2112	The first eleven mitochondrial genomes from the ectomycorrhizal fungal genus (<i>Boletus</i>) reveal intron loss and gene rearrangement. <i>International Journal of Biological Macromolecules</i> , 2021, 172, 560-572.	7.5	38
2114	Analysis of Secreted Proteins and Potential Virulence via the ICEs-Mediated Pathway of the Foodborne Pathogen <i>Vibrio parahaemolyticus</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 612166.	3.5	3
2115	A bifunctional enzyme belonging to cytochrome P450 family involved in the O-dealkylation and N-dealkoxymethylation toward chloroacetanilide herbicides in <i>Rhodococcus</i> sp. B2. <i>Microbial Cell Factories</i> , 2021, 20, 61.	4.0	8
2116	Complete Annotated Genome Sequence of the <i>Salmonella enterica</i> Serovar Typhimurium LT7 Strain STK003, Historically Used in Gene Transfer Studies. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	1
2117	Chloroplast genome sequence of Chongming lima bean (<i>Phaseolus lunatus</i> L.) and comparative analyses with other legume chloroplast genomes. <i>BMC Genomics</i> , 2021, 22, 194.	2.8	26
2119	The complete chloroplast genome of <i>Stauntonia chinensis</i> and compared analysis revealed adaptive evolution of subfamily Lardizabaloideae species in China. <i>BMC Genomics</i> , 2021, 22, 161.	2.8	26
2120	Field evaluation of PGP <i>Bacillus</i> sp. strain D5 native to <i>Crocus sativus</i> , in traditional and non traditional areas, and mining of PGP genes from its genome. <i>Scientific Reports</i> , 2021, 11, 5454.	3.3	24
2121	Francisellosis of Yesso scallops <i>Mizuhopecten yessoensis</i> in Japan is caused by a novel type of <i>Francisella haliotidica</i> . <i>Diseases of Aquatic Organisms</i> , 2021, 144, 9-19.	1.0	2
2122	Complete chloroplast genome sequence of <i>Adenophora racemosa</i> (Campanulaceae): Comparative analysis with congeneric species. <i>PLoS ONE</i> , 2021, 16, e0248788.	2.5	9
2123	Draft Genome Sequence of <i>Saccharomyces cerevisiae</i> LW2591Y, a Laboratory Strain for <i>In Vivo</i> Multigene Assemblies. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	1
2124	Comparative genome analysis of three Group A <i>Streptococcus dysgalactiae</i> subsp. <i>equisimilis</i> strains isolated in Japan. <i>Journal of Medical Microbiology</i> , 2021, 70, .	1.8	1
2125	Draft Genome of <i>Proteus mirabilis</i> Serogroup O18 Elaborating Phosphocholine-Decorated O Antigen. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 620010.	3.9	3
2126	Draft Genome Resource of a Novel Virulent <i>Fusarium oxysporum</i> f. sp. <i>cubense</i> Race 1 Strain (VCG 0124) Infecting Cavendish (AAA) Group of Banana in India. <i>Plant Disease</i> , 2021, 105, 2708-2710.	1.4	5
2127	Expression of fungal biosynthetic gene clusters in <i>S. cerevisiae</i> for natural product discovery. <i>Synthetic and Systems Biotechnology</i> , 2021, 6, 20-22.	3.7	6
2128	Comparative analysis of the complete chloroplast genome of seven <i>Nymphaea</i> species. <i>Aquatic Botany</i> , 2021, 170, 103353.	1.6	13

#	ARTICLE	IF	CITATIONS
2129	Authentication of <i>Aspergillus parasiticus</i> strains in the genome database of the National Center for Biotechnology Information. BMC Research Notes, 2021, 14, 111.	1.4	5
2130	The Distribution of Onion Virulence Gene Clusters Among <i>Pantoea</i> spp.. Frontiers in Plant Science, 2021, 12, 643787.	3.6	12
2131	Insights into <i>Acinetobacter baumannii</i> fatty acid synthesis 3-oxoacyl-ACP reductases. Scientific Reports, 2021, 11, 7050.	3.3	9
2132	Analysis of a Methanogen and an Actinobacterium Dominating the Thermophilic Microbial Community of an Electromethanogenic Biocathode. Archaea, 2021, 2021, 1-13.	2.3	4
2133	Alvis: a tool for contig and read Alignment VISualisation and chimera detection. BMC Bioinformatics, 2021, 22, 124.	2.6	14
2134	Nitric oxide (NO) elicits aminoglycoside tolerance in <i>Escherichia coli</i> but antibiotic resistance gene carriage and NO sensitivity have not co-evolved. Archives of Microbiology, 2021, 203, 2541-2550.	2.2	7
2135	New Genotype of <i>Yersinia pestis</i> Found in Live Rodents in Yunnan Province, China. Frontiers in Microbiology, 2021, 12, 628335.	3.5	5
2136	High Rates of Genome Rearrangements and Pathogenicity of <i>Shigella</i> spp.. Frontiers in Microbiology, 2021, 12, 628622.	3.5	13
2137	Complete Genome Sequence of <i>Bifidobacterium longum</i> subsp. <i>longum</i> JCM7052. Microbiology Resource Announcements, 2021, 10, .	0.6	1
2138	Molecular characterization of <i>Neisseria gonorrhoeae</i> isolates collected through a national surveillance programme in Japan, 2013: evidence of the emergence of a ceftriaxone-resistant strain from a ceftriaxone-susceptible lineage. Journal of Antimicrobial Chemotherapy, 2021, 76, 1769-1775.	3.0	8
2139	Antiviral Resistance and Phage Counter Adaptation to Antibiotic-Resistant Extraintestinal Pathogenic <i>Escherichia coli</i> . MBio, 2021, 12, .	4.1	23
2140	Genomic diversity and molecular epidemiology of <i>Pasteurella multocida</i> . PLoS ONE, 2021, 16, e0249138.	2.5	36
2142	Isolation and Characterization of a Virulent Bacteriophage for Controlling <i>Salmonella Enteritidis</i> Growth in Ready-to-Eat Mixed-Ingredient Salads. Journal of Food Protection, 2021, 84, 1629-1639.	1.7	8
2144	Third-generation sequencing revises the molecular karyotype for <i>Toxoplasma gondii</i> and identifies emerging copy number variants in sexual recombinants. Genome Research, 2021, 31, 834-851.	5.5	19
2145	Genomic features underlying the evolutionary transitions of <i>Apibacter</i> to honey bee gut symbionts. Insect Science, 2022, 29, 259-275.	3.0	13
2146	Identification and Characterization of a Novel Genomic Island Harboring Cadmium and Arsenic Resistance Genes in <i>Listeria welshimeri</i> . Biomolecules, 2021, 11, 560.	4.0	7
2147	Draft Genome Sequence of <i>Bacillus</i> sp. Strain IGA-FME-2, Isolated from the Bulk Soil of Soybean (<i>Glycine max</i> L.) in Northeast China. Microbiology Resource Announcements, 2021, 10, .	0.6	0
2148	A Novel Structure Harboring blaCTX-M-27 on IncF Plasmids in <i>Escherichia coli</i> Isolated from Swine in China. Antibiotics, 2021, 10, 387.	3.7	8

#	ARTICLE	IF	CITATIONS
2149	Insights into genomic evolution from the chromosomal and mitochondrial genomes of <i>Ustilaginoidea virens</i> . <i>Phytopathology Research</i> , 2021, 3, .	2.4	9
2150	Microbial community characterization of shrimp survivors to AHPND challenge test treated with an effective shrimp probiotic (<i>Vibrio diabolis</i>). <i>Microbiome</i> , 2021, 9, 88.	11.1	36
2151	Combination Therapy of Phage vB_KpnM_P-KP2 and Gentamicin Combats Acute Pneumonia Caused by K47 Serotype <i>Klebsiella pneumoniae</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 674068.	3.5	24
2152	Population genomics and antimicrobial resistance dynamics of <i>Escherichia coli</i> in wastewater and river environments. <i>Communications Biology</i> , 2021, 4, 457.	4.4	20
2153	Association between the blaCTX-M-14-harboring <i>Escherichia coli</i> Isolated from Weasels and Domestic Animals Reared on a University Campus. <i>Antibiotics</i> , 2021, 10, 432.	3.7	6
2154	The Development of Bacteriophage Resistance in <i>Vibrio alginolyticus</i> Depends on a Complex Metabolic Adaptation Strategy. <i>Viruses</i> , 2021, 13, 656.	3.3	6
2155	Quantitative Control of Early Flowering in White Lupin (<i>Lupinus albus</i> L.). <i>International Journal of Molecular Sciences</i> , 2021, 22, 3856.	4.1	4
2156	Whole genome sequencing of a clinical drug resistant <i>Candida albicans</i> isolate reveals known and novel mutations in genes involved in resistance acquisition mechanisms. <i>Journal of Medical Microbiology</i> , 2021, 70, .	1.8	7
2157	Phylogenetic origin of two Japanese <i>Torreya</i> taxa found in two regions with strongly contrasting snow depth. <i>Journal of Plant Research</i> , 2021, 134, 907-919.	2.4	3
2158	Complete genome sequence of the <i>Pseudomonas oleovorans</i> strain ODT-83 isolated from oyster. <i>Archives of Microbiology</i> , 2021, 203, 3117-3124.	2.2	2
2159	Occurrence and Transmission of <i>bla</i> -NDM-Carrying <i>Enterobacteriaceae</i> from Geese and the Surrounding Environment on a Commercial Goose Farm. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	3.1	13
2160	Genomic Insight of <i>Alicyclobacillus mali</i> FL18 Isolated From an Arsenic-Rich Hot Spring. <i>Frontiers in Microbiology</i> , 2021, 12, 639697.	3.5	17
2161	Plastid and nuclear phylogenomic incongruences and biogeographic implications of <i>Magnolia</i> s.l. (<i>Magnoliaceae</i>). <i>Journal of Systematics and Evolution</i> , 2022, 60, 1-15.	3.1	29
2162	Prevalence and Genetic Analysis of Chromosomal mcr-3/7 in <i>Aeromonas</i> From U.S. Animal-Derived Samples. <i>Frontiers in Microbiology</i> , 2021, 12, 667406.	3.5	12
2163	Complete chloroplast genome of <i>Myracrodruon urundeuva</i> and its phylogenetics relationships in <i>Anacardiaceae</i> family. <i>Physiology and Molecular Biology of Plants</i> , 2021, 27, 801-814.	3.1	7
2164	Microbiome assembly for sulfonamide subsistence and the transfer of genetic determinants. <i>ISME Journal</i> , 2021, 15, 2817-2829.	9.8	10
2165	Genomic-Led Discovery of a Novel Glycopeptide Antibiotic by <i>Nonomuraea coxensis</i> DSM 45129. <i>ACS Chemical Biology</i> , 2021, 16, 915-928.	3.4	16
2167	Trends in Molecular Diagnosis and Diversity Studies for Phytosanitary Regulated <i>Xanthomonas</i> . <i>Microorganisms</i> , 2021, 9, 862.	3.6	22

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2168	Complete Chloroplast Genome of <i>Clethra fargesii</i> Franch., an Original Sympetalous Plant from Central China: Comparative Analysis, Adaptive Evolution, and Phylogenetic Relationships. <i>Forests</i> , 2021, 12, 441.	2.1	22
2169	Divergence times and plastid phylogenomics within the intron-rich order Erythropeltales (Compsopogonophyceae, Rhodophyta). <i>Journal of Phycology</i> , 2021, 57, 1035-1044.	2.3	3
2171	SSG-LUGIA: Single Sequence based Genome Level Unsupervised Genomic Island Prediction Algorithm. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	3
2172	Complete Genome Sequence of <i>Chlamydia abortus</i> MRI-10/19, Isolated from a Sheep Vaccinated with the Commercial Live <i>C. abortus</i> 1B Vaccine Strain. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	2
2173	Closed Genome Sequence of a <i>Salmonella enterica</i> Serotype Senftenberg Strain Carrying the <i>mcr-9</i> Gene Isolated from Broken Chicken Eggshells in Trinidad and Tobago. <i>Microbiology Resource Announcements</i> , 2021, 10, e0146520.	0.6	7
2174	Re-examination of two diatom reference genomes using long-read sequencing. <i>BMC Genomics</i> , 2021, 22, 379.	2.8	22
2175	Extensive Comparative Genomic Analysis of <i>Enterococcus faecalis</i> and <i>Enterococcus faecium</i> Reveals a Direct Association between the Absence of CRISPR-Cas Systems, the Presence of Anti-Endonuclease (<i>ardA</i>) and the Acquisition of Vancomycin Resistance in <i>E. faecium</i> . <i>Microorganisms</i> , 2021, 9, 1118.	3.6	6
2177	Genome-informed approach to identify genetic determinants of <i>Flavobacterium psychrophilum</i> phage susceptibility. <i>Environmental Microbiology</i> , 2021, 23, 4185-4199.	3.8	8
2178	Adaptive laboratory evolution accelerated glutarate production by <i>Corynebacterium glutamicum</i> . <i>Microbial Cell Factories</i> , 2021, 20, 97.	4.0	19
2179	The pESI mega-plasmid conferring virulence and multiple-drug resistance is detected in <i>Salmonella</i> <i>Infantis</i> genome from Brazil. <i>Infection, Genetics and Evolution</i> , 2021, 95, 104934.	2.3	10
2180	Whole-Genome Analysis of <i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> IS900 Insertions Reveals Strain Type-Specific Modalities. <i>Frontiers in Microbiology</i> , 2021, 12, 660002.	3.5	7
2181	Comparative Analysis of Mitochondrial Genome Features among Four <i>Clonostachys</i> Species and Insight into Their Systematic Positions in the Order Hypocreales. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5530.	4.1	7
2183	Novel chromosomal insertions of ISEcp1-blaCTX-M-15 and diverse antimicrobial resistance genes in Zambian clinical isolates of <i>Enterobacter cloacae</i> and <i>Escherichia coli</i> . <i>Antimicrobial Resistance and Infection Control</i> , 2021, 10, 79.	4.1	24
2184	A chromosome-level genome of a Kordofan melon illuminates the origin of domesticated watermelons. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	37
2185	Phylogenomics and biogeography of <i>Wisteria</i> : Implications on plastome evolution among inverted repeat-lacking clade (IRLC) legumes. <i>Journal of Systematics and Evolution</i> , 2022, 60, 253-265.	3.1	10
2186	Characterization of the Complete Mitochondrial Genome of Basidiomycete Yeast <i>Hannaella oryzae</i> : Intron Evolution, Gene Rearrangement, and Its Phylogeny. <i>Frontiers in Microbiology</i> , 2021, 12, 646567.	3.5	25
2187	Identification of Three Type II Toxin-Antitoxin Systems in Model Bacterial Plant Pathogen <i>Dickeya dadantii</i> 3937. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5932.	4.1	4
2188	Genomic Island Prediction via Chi-Square Test and Random Forest Algorithm. <i>Computational and Mathematical Methods in Medicine</i> , 2021, 2021, 1-9.	1.3	32

#	ARTICLE	IF	CITATIONS
2189	Complete genome sequence of the newly discovered temperate Clostridioides difficile bacteriophage phiCDKH01 of the family Siphoviridae. Archives of Virology, 2021, 166, 2305-2310.	2.1	8
2190	Comparative plastome analysis of <i>Blumea</i> , with implications for genome evolution and phylogeny of Asteroideae. Ecology and Evolution, 2021, 11, 7810-7826.	1.9	29
2191	Genomic sequencing of a frog virus 3 strain from cultured American bullfrogs (Lithobates) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 662 Td	2.1	4
2193	Relationship of the Pine Growth Promoting Pantoea eucalypti FBS135 with Type Strains P. eucalypti LMG 24197T and P. vagans 24199T. Life, 2021, 11, 608.	2.4	3
2194	Chitosan flocculation associated with biofilms of C. saccharolyticus and C. owensensis enhances biomass retention in a CSTR. International Journal of Hydrogen Energy, 2021, 46, 21338-21347.	7.1	2
2195	The global emergence of a novel <i>Streptococcus suis</i> clade associated with human infections. EMBO Molecular Medicine, 2021, 13, e13810.	6.9	33
2196	How Bacteria Change after Exposure to Silver Nanoformulations: Analysis of the Genome and Outer Membrane Proteome. Pathogens, 2021, 10, 817.	2.8	1
2197	Genomic Analysis of Prophages Recovered from Listeria monocytogenes Lysogens Found in Seafood and Seafood-Related Environment. Microorganisms, 2021, 9, 1354.	3.6	5
2198	Whole genome data from Curtobacterium flaccumfaciens pv. flaccumfaciens strains associated with tan spot of mungbean and soybean reveal diverse plasmid profiles. Molecular Plant-Microbe Interactions, 2021, 34, 1216-1222.	2.6	7
2199	Comparative Genomics of Closely Related Tetragenococcus halophilus Strains Elucidate the Diversity and Microevolution of CRISPR Elements. Frontiers in Microbiology, 2021, 12, 687985.	3.5	5
2200	Molecular characterization of antimicrobial resistance in Klebsiella pneumoniae isolated from Brazilian dairy herds. Journal of Dairy Science, 2021, 104, 7210-7224.	3.4	8
2201	The proximity of Hydrocotyle umbellata L. with araliaceae as evident from plastome and phylotranscriptomic analyses. Journal of King Saud University - Science, 2021, 33, 101412.	3.5	0
2202	Horizontal Gene Transfer of Genes Encoding Copper-Containing Membrane-Bound Monooxygenase (CuMMO) and Soluble Di-iron Monooxygenase (SDIMO) in Ethane- and Propane-Oxidizing <i>Rhodococcus</i> Bacteria. Applied and Environmental Microbiology, 2021, 87, e0022721.	3.1	5
2203	Functional and genomic characterization of Komagataeibacter uvaceti FXV3, a multiple stress resistant bacterium producing increased levels of cellulose. Biotechnology Reports (Amsterdam,) Tj ETQq1 1 0.784314 rgBT /Overlock 1	3.1	1
2204	Phylogenomic Analyses of Hepatica Species and Comparative Analyses Within Tribe Anemoneae (Ranunculaceae). Frontiers in Plant Science, 2021, 12, 638580.	3.6	2
2205	Investigation of Plasmids Among Clinical Staphylococcus aureus and Staphylococcus haemolyticus Isolates From Egypt. Frontiers in Microbiology, 2021, 12, 659116.	3.5	11
2206	Variability of the response of human vaginal Lactobacillus crispatus to 17 β -estradiol. Scientific Reports, 2021, 11, 11533.	3.3	5
2207	Genome Scale Analysis Reveals IscR Directly and Indirectly Regulates Virulence Factor Genes in Pathogenic Yersinia. MBio, 2021, 12, e0063321.	4.1	4

#	ARTICLE	IF	CITATIONS
2208	Mitogenomics and Evolutionary History of Rodent Whipworms (<i>Trichuris</i> spp.) Originating from Three Biogeographic Regions. <i>Life</i> , 2021, 11, 540.	2.4	2
2209	Genomic Rearrangements and Sequence Evolution across Brown Algal Organelles. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	12
2210	Evolution of Interbacterial Antagonism in Bee Gut Microbiota Reflects Host and Symbiont Diversification. <i>MSystems</i> , 2021, 6, .	3.8	13
2211	Molecular Clocks and Archeogenomics of a Late Period Egyptian Date Palm Leaf Reveal Introgression from Wild Relatives and Add Timestamps on the Domestication. <i>Molecular Biology and Evolution</i> , 2021, 38, 4475-4492.	8.9	14
2212	Genomic and Phenotypic Characterization of <i>Chloracidobacterium</i> Isolates Provides Evidence for Multiple Species. <i>Frontiers in Microbiology</i> , 2021, 12, 704168.	3.5	3
2213	High-Quality Genome Reconstruction of <i>Candida albicans</i> CHN1 Using Nanopore and Illumina Sequencing and Hybrid Assembly. <i>Microbiology Resource Announcements</i> , 2021, 10, e0029921.	0.6	3
2214	Comparative Chloroplast Genomics of <i>Litsea</i> Lam. (Lauraceae) and Its Phylogenetic Implications. <i>Forests</i> , 2021, 12, 744.	2.1	13
2216	Phenotypic and genomic hallmarks of a novel, potentially pathogenic rapidly growing <i>Mycobacterium</i> species related to the <i>Mycobacterium fortuitum</i> complex. <i>Scientific Reports</i> , 2021, 11, 13011.	3.3	6
2217	<i>Staphylococcus saprophyticus</i> From Clinical and Environmental Origins Have Distinct Biofilm Composition. <i>Frontiers in Microbiology</i> , 2021, 12, 663768.	3.5	12
2219	Genome Analysis of a Verrucomicrobial Endosymbiont With a Tiny Genome Discovered in an Antarctic Lake. <i>Frontiers in Microbiology</i> , 2021, 12, 674758.	3.5	18
2220	Molecular Evolution and Adaptation of Livestock-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> (LA-MRSA) Sequence Type 9. <i>MSystems</i> , 2021, 6, e0049221.	3.8	36
2222	The Virulence of <i>S. marcescens</i> Strains Isolated From Contaminated Blood Products Is Divergent in the <i>C. elegans</i> Infection Model. <i>Frontiers in Genetics</i> , 2021, 12, 667062.	2.3	1
2223	Detection of CTX-M-27 β -Lactamase Genes on Two Distinct Plasmid Types in ST38 <i>Escherichia coli</i> from Three U.S. States. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, e0082521.	3.2	11
2224	Forward genetics in <i>Wolbachia</i> : Regulation of <i>Wolbachia</i> proliferation by the amplification and deletion of an additive genomic island. <i>PLoS Genetics</i> , 2021, 17, e1009612.	3.5	24
2225	Grand Challenges in Bioinformatics Data Visualization. <i>Frontiers in Bioinformatics</i> , 2021, 1, .	2.1	18
2226	Stable high-density and maternally inherited <i>Wolbachia</i> infections in <i>Anopheles moucheti</i> and <i>Anopheles demeilloni</i> mosquitoes. <i>Current Biology</i> , 2021, 31, 2310-2320.e5.	3.9	49
2227	Full-Genome Sequences of Alphacoronaviruses and Astroviruses from <i>Myotis</i> and <i>Pipistrelle</i> Bats in Denmark. <i>Viruses</i> , 2021, 13, 1073.	3.3	15
2228	Genome reduction and relaxed selection is associated with the transition to symbiosis in the basidiomycete genus <i>Podaxis</i> . <i>IScience</i> , 2021, 24, 102680.	4.1	9

#	ARTICLE	IF	CITATIONS
2230	Rubrolone production by <i>Dactylosporangium vinaceum</i> : biosynthesis, modulation and possible biological function. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 5541-5551.	3.6	5
2231	A Novel Polyvalent Bacteriophage vB_EcoM_swi3 Infects Pathogenic <i>Escherichia coli</i> and <i>Salmonella enteritidis</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 649673.	3.5	14
2233	Comparative and phylogenetic analyses of the chloroplast genomes of species of <i>Paeoniaceae</i> . <i>Scientific Reports</i> , 2021, 11, 14643.	3.3	19
2234	A chimeric nuclease substitutes a phage CRISPR-Cas system to provide sequence-specific immunity against subviral parasites. <i>ELife</i> , 2021, 10, .	6.0	31
2235	Pangenomic Analysis of <i>Dickeya dianthicola</i> Strains Related to the Outbreak of Blackleg and Soft Rot of Potato in USA. <i>Plant Disease</i> , 2021, , PDIS03210587RE.	1.4	5
2236	Chloroplast Genome Sequencing, Comparative Analysis, and Discovery of Unique Cytoplasmic Variants in Pomegranate (<i>Punica granatum</i> L.). <i>Frontiers in Genetics</i> , 2021, 12, 704075.	2.3	10
2237	C-protein $\hat{\pm}$ -antigen modulates the lantibiotic thusin resistance in <i>Streptococcus agalactiae</i> . <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 1595-1607.	1.7	1
2239	<i>Mycobacterium tuberculosis</i> complex lineage 5 exhibits high levels of within-lineage genomic diversity and differing gene content compared to the type strain H37Rv. <i>Microbial Genomics</i> , 2021, 7, .	2.0	9
2240	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.	3.6	16
2241	Experimental and Genomic Evaluation of the Oestrogen Degrading Bacterium <i>Rhodococcus equi</i> ATCC13557. <i>Frontiers in Microbiology</i> , 2021, 12, 670928.	3.5	2
2243	Structures of the alkanesulfonate monooxygenase MsuD provide insight into C–S bond cleavage, substrate scope, and an unexpected role for the tetramer. <i>Journal of Biological Chemistry</i> , 2021, 297, 100823.	3.4	5
2244	A two-component monooxygenase for continuous denitration and dechlorination of chlorinated 4-nitrophenol in <i>Ensifer</i> sp. strain 22-1. <i>Environmental Research</i> , 2021, 198, 111216.	7.5	9
2246	Evolutionary Insights Into Two Widespread Ectomycorrhizal Fungi (<i>Pisolithus</i>) From Comparative Analysis of Mitochondrial Genomes. <i>Frontiers in Microbiology</i> , 2021, 12, 583129.	3.5	2
2247	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, .	7.1	15
2249	Current status of structural variation studies in plants. <i>Plant Biotechnology Journal</i> , 2021, 19, 2153-2163.	8.3	65
2250	<i>Clostridium culturomicum</i> sp. nov. and <i>Clostridium jeddahitimonense</i> sp. nov., novel members of the <i>Clostridium</i> genus isolated from the stool of an obese Saudi Arabian. <i>Current Microbiology</i> , 2021, 78, 3586-3595.	2.2	3
2251	The <i>Pseudoalteromonas</i> multipartite genome: distribution and expression of pangene categories, and a hypothesis for the origin and evolution of the chromid. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	6
2252	Complete Genome Sequence of vB_EcoP_SU7, a Podoviridae Coliphage with the Rare C3 Morphotype. <i>Microorganisms</i> , 2021, 9, 1576.	3.6	6

#	ARTICLE	IF	CITATIONS
2253	Comparative chloroplast genome analysis of Impatiens species (Balsaminaceae) in the karst area of China: insights into genome evolution and phylogenomic implications. BMC Genomics, 2021, 22, 571.	2.8	27
2254	The Emergence and Molecular Characteristics of New Delhi Metallo β -Lactamase-Producing Escherichia coli From Ducks in Guangdong, China. Frontiers in Microbiology, 2021, 12, 677633.	3.5	7
2255	Draft Genome Sequence of Enterococcus mundtii SCPM-O-B-8398 (E28), Isolated from Fermented Milk in the Moscow Region, Russian Federation. Microbiology Resource Announcements, 2021, 10, e0027721.	0.6	0
2256	Repeated exposure of nosocomial pathogens to silver does not select for silver resistance but does impact ciprofloxacin susceptibility. Acta Biomaterialia, 2021, 134, 760-773.	8.3	1
2257	Rapid strain-specific identification of two Lactobacillus rhamnosus strains using PCR based on gene family analysis. LWT - Food Science and Technology, 2021, 146, 111395.	5.2	10
2258	Novel genomic islands and a new vanD-subtype in the first sporadic VanD-type vancomycin resistant enterococci in Norway. PLoS ONE, 2021, 16, e0255187.	2.5	6
2259	Genome Characterization, Comparison and Phylogenetic Analysis of Complete Mitochondrial Genome of Evolvulus alsinoides Reveals Highly Rearranged Gene Order in Solanales. Life, 2021, 11, 769.	2.4	10
2260	Complete Genome Sequence of Pseudomonas amygdali pv. tabaci Strain 6605, a Causal Agent of Tobacco Wildfire Disease. Microbiology Resource Announcements, 2021, 10, e0040521.	0.6	2
2261	Plastid phylogenomics and biogeography of the genus <i>Monochoria</i> (Pontederiaceae). Journal of Systematics and Evolution, 2021, 59, 1027-1039.	3.1	6
2262	The first complete genome sequence of species Shewanella decolorationis, from a bioremediation competent strain Nii-3. G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	2
2263	The mitochondrial genome of <i>Ophiostoma himal-ulmi</i> and comparison with other fungi causing Dutch elm disease. Canadian Journal of Microbiology, 2021, 67, 584-598.	1.7	5
2264	Plastid genomes and phylogenomics of liverworts (Marchantiophyta): Conserved genome structure but highest relative plastid substitution rate in land plants. Molecular Phylogenetics and Evolution, 2021, 161, 107171.	2.7	12
2265	The Sisal Virome: Uncovering the Viral Diversity of Agave Varieties Reveals New and Organ-Specific Viruses. Microorganisms, 2021, 9, 1704.	3.6	5
2266	Genomic-Assisted Marker Development Suitable for CsCvy-1 Selection in Cucumber Breeding. Frontiers in Plant Science, 2021, 12, 691576.	3.6	4
2267	The plastome sequence of Bactris gasipaes and evolutionary analysis in tribe Cocoseae (Arecaceae). PLoS ONE, 2021, 16, e0256373.	2.5	7
2268	Genome-Wide Analysis of Four Pathotypes of Wheat Rust Pathogen (Puccinia graminis) Reveals Structural Variations and Diversifying Selection. Journal of Fungi (Basel, Switzerland), 2021, 7, 701.	3.5	2
2269	A widely diverged locus involved in locomotor adaptation in <i>Heliconius</i> butterflies. Science Advances, 2021, 7, .	10.3	9
2270	Comparative Genome Analysis Provides Molecular Evidence for Reclassification of the Photosynthetic Bacterium Rhodobacter sphaeroides EBL0706 as a Strain of Luteovulum azotoformans. Microorganisms, 2021, 9, 1754.	3.6	3

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2271	The Insights into Mitochondrial Genomes of Sunflowers. <i>Plants</i> , 2021, 10, 1774.	3.5	7
2272	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.	3.6	16
2273	The complete chloroplast genome of <i>Rhodobryum laxelimbatum</i> (Hampe ex Ochi) Z. Iwatsuki and T. J. Koponen. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2632-2634.	0.4	0
2274	Genomic Characterization of Multidrug-Resistant <i>Salmonella</i> Serovars Derby and Rissen From the Pig Value Chain in Vietnam. <i>Frontiers in Veterinary Science</i> , 2021, 8, 705044.	2.2	7
2275	Comparative analysis of plastomes in Oxalidaceae: Phylogenetic relationships and potential molecular markers. <i>Plant Diversity</i> , 2021, 43, 281-291.	3.7	12
2276	Genome-Resolved Metagenomic Analyses Reveal the Presence of a Putative Bacterial Endosymbiont in an Avian Nasal Mite (Rhinonyssidae; Mesostigmata). <i>Microorganisms</i> , 2021, 9, 1734.	3.6	1
2277	Identification of a Family of <i>Vibrio</i> Type III Secretion System Effectors That Contain a Conserved Serine/Threonine Kinase Domain. <i>MSphere</i> , 2021, 6, e0059921.	2.9	6
2278	Comparative Genomic Analyses of <i>Flavobacterium psychrophilum</i> Isolates Reveals New Putative Genetic Determinants of Virulence Traits. <i>Microorganisms</i> , 2021, 9, 1658.	3.6	5
2279	Virulent Drexelviral Bacteriophage MSK, Morphological and Genome Resemblance With Rtp Bacteriophage Inhibits the Multidrug-Resistant Bacteria. <i>Frontiers in Microbiology</i> , 2021, 12, 706700.	3.5	5
2280	The chloroplast genome of <i>Prunus zhengheensis</i> : Genome comparative and phylogenetic relationships analysis. <i>Gene</i> , 2021, 793, 145751.	2.2	6
2281	Pathogenicity and genomic features of vapN-harboring <i>Rhodococcus equi</i> isolated from human patients. <i>International Journal of Medical Microbiology</i> , 2021, 311, 151519.	3.6	15
2282	Comparative Chloroplast Genomics in Phyllanthaceae Species. <i>Diversity</i> , 2021, 13, 403.	1.7	6
2283	Comparison between genome sequences of Chilean <i>Tenacibaculum dicentrarchi</i> isolated from red conger eel (<i>Genypterus chilensis</i>) and Atlantic salmon (<i>Salmo salar</i>) focusing on bacterial virulence determinants. <i>Journal of Fish Diseases</i> , 2021, 44, 1843-1860.	1.9	11
2284	Reduction trend of mcr-1 circulation in Emilia-Romagna Region, Italy. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2021, 40, 2585-2592.	2.9	7
2285	Genome analyses of four <i>Wolbachia</i> strains and associated mitochondria of <i>Rhagoletis cerasi</i> expose cumulative modularity of cytoplasmic incompatibility factors and cytoplasmic hitchhiking across host populations. <i>BMC Genomics</i> , 2021, 22, 616.	2.8	4
2286	Characterization and Dynamics of Intracellular Gene Transfer in Plastid Genomes of <i>Viola</i> (Violaceae) and Order Malpighiales. <i>Frontiers in Plant Science</i> , 2021, 12, 678580.	3.6	5
2287	Plastid phylogenomics of Pleurothallidinae (Orchidaceae): Conservative plastomes, new variable markers, and comparative analyses of plastid, nuclear, and mitochondrial data. <i>PLoS ONE</i> , 2021, 16, e0256126.	2.5	1
2289	Multiple-Drug Resistant Nasopharyngeal <i>Streptococcus pneumoniae</i> Isolated in Russia: Serotypes, Antimicrobial Susceptibility, and Molecular Characterization of the Emergent Serotype 13/ST2754 Lineage. <i>Microbial Drug Resistance</i> , 2022, 28, 39-47.	2.0	4

#	ARTICLE	IF	CITATIONS
2290	Carboxylicivirga marinus sp. nov., Isolated From Marine Sediment, and Genome Insight of the Genus Carboxylicivirga. <i>Frontiers in Marine Science</i> , 2021, 8, .	2.5	9
2291	Isolation, characterization and comparison of lytic Epseptomavirus phages targeting Salmonella. <i>Food Research International</i> , 2021, 147, 110480.	6.2	12
2293	Genetic Variation in Host-Specific Competitiveness of the Symbiont Rhizobium leguminosarum Symbiovar viciae. <i>Frontiers in Plant Science</i> , 2021, 12, 719987.	3.6	4
2294	Whole-genome sequencing reveals forgotten lineages and recurrent hybridizations within the kelp genus <i>Alaria</i> (Phaeophyceae). <i>Journal of Phycology</i> , 2021, 57, 1721-1738.	2.3	10
2295	The complete genome of 2,6-dichlorobenzamide (BAM) degrader Aminobacter sp. MSH1 suggests a polyploid chromosome, phylogenetic reassignment, and functions of plasmids. <i>Scientific Reports</i> , 2021, 11, 18943.	3.3	5
2296	Molecular Confirmation of Ranavirus Infection in Amphibians From Chad, Africa. <i>Frontiers in Veterinary Science</i> , 2021, 8, 733939.	2.2	2
2297	Lineage-Specific Variation in IR Boundary Shift Events, Inversions, and Substitution Rates among Caprifoliaceae s.l. (Dipsacales) Plastomes. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10485.	4.1	4
2298	Whole-genome sequence data of the proteolytic and bacteriocin producing strain <i>Enterococcus faecalis</i> PK23 isolated from the traditional Halitzia cheese produced in Cyprus. <i>Data in Brief</i> , 2021, 38, 107437.	1.0	4
2299	Genomic Analysis of the 1-Aminocyclopropane-1-Carboxylate Deaminase-Producing <i>Pseudomonas thivervalensis</i> SC5 Reveals Its Multifaceted Roles in Soil and in Beneficial Interactions With Plants. <i>Frontiers in Microbiology</i> , 2021, 12, 752288.	3.5	12
2300	Antimicrobial plant secondary metabolites, MDR transporters and antimicrobial resistance in cereal-associated lactobacilli: is there a connection?. <i>Food Microbiology</i> , 2022, 102, 103917.	4.2	12
2301	Draft Genome Sequence of <i>Salegentibacter</i> sp. Strain BDJ18, a Plankton-Associated Bacterium in the Northeast Atlantic Ocean. <i>Microbiology Resource Announcements</i> , 2021, 10, e0062821.	0.6	0
2302	Genomic analysis revealed conserved acid tolerance mechanisms from native microorganisms in fermented feed. <i>Journal of Applied Microbiology</i> , 2022, 132, 1152-1165.	3.1	2
2303	Phylogenomics, CAZyme and core secondary metabolome of <i>Streptomyces albus</i> species. <i>Molecular Genetics and Genomics</i> , 2021, 296, 1299-1311.	2.1	5
2304	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.	3.8	11
2305	Complete Genome Sequencing of <i>Leptospira interrogans</i> Isolates from Malaysia Reveals Massive Genome Rearrangement but High Conservation of Virulence-Associated Genes. <i>Pathogens</i> , 2021, 10, 1198.	2.8	4
2306	Genomic characterization of <i>Enterobacter xiangfangensis</i> STP-3: Application to real time petroleum oil sludge bioremediation. <i>Microbiological Research</i> , 2021, 253, 126882.	5.3	8
2307	Engineering of a robust <i>Escherichia coli</i> chassis and exploitation for large-scale production processes. <i>Metabolic Engineering</i> , 2021, 67, 75-87.	7.0	15
2308	The chloroplast genome of <i>Amygdalus</i> L. (Rosaceae) reveals the phylogenetic relationship and divergence time. <i>BMC Genomics</i> , 2021, 22, 645.	2.8	14

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2309	A Unifying Framework for Analysis of Spatial-Temporal Event Sequence Similarity and Its Applications. <i>ISPRS International Journal of Geo-Information</i> , 2021, 10, 594.	2.9	1
2310	Complete Genome Sequence of <i>Weissella confusa</i> LM1 and Comparative Genomic Analysis. <i>Frontiers in Microbiology</i> , 2021, 12, 749218.	3.5	6
2311	Genome sequencing of the neotype strain CBS 554.65 reveals the MAT1 α 2 locus of <i>Aspergillus niger</i> . <i>BMC Genomics</i> , 2021, 22, 679.	2.8	5
2312	Morphological and Genomic Features of the New Klosneuvirinae Isolate Fadolivirus IHUMI-VV54. <i>Frontiers in Microbiology</i> , 2021, 12, 719703.	3.5	9
2313	Comprehensive genomic analysis of <i>Bacillus velezensis</i> AL7 reveals its biocontrol potential against <i>Verticillium</i> wilt of cotton. <i>Molecular Genetics and Genomics</i> , 2021, 296, 1287-1298.	2.1	13
2315	Complete Plastome of Three Korean <i>Asarum</i> (Aristolochiaceae): Confirmation Tripartite Structure within Korean <i>Asarum</i> and Comparative Analyses. <i>Plants</i> , 2021, 10, 2056.	3.5	2
2317	<i>Escherichia coli</i> Nissle 1917 secondary metabolism: aryl polyene biosynthesis and phosphopantetheinyl transferase crosstalk. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 7785-7799.	3.6	3
2318	Genetic Characterization of <i>Clostridium botulinum</i> Isolated from the First Case of Infant Botulism in Korea. <i>Annals of Laboratory Medicine</i> , 2021, 41, 489-492.	2.5	2
2319	Description of <i>Stenotrophomonas seipia</i> sp. nov., isolated from blood culture of a hospitalized patient as a new member of <i>Stenotrophomonas maltophilia</i> complex. <i>New Microbes and New Infections</i> , 2021, 43, 100920.	1.6	6
2320	Inactivation of SARS-CoV-2 by Simulated Sunlight on Contaminated Surfaces. <i>Microbiology Spectrum</i> , 2021, 9, e0033321.	3.0	18
2321	Genome collinearity analysis illuminates the evolution of donkey chromosome 1 and horse chromosome 5 in perissodactyls: A comparative study. <i>BMC Genomics</i> , 2021, 22, 665.	2.8	3
2322	Comparative Genomic Understanding of Gram-Positive Plant Growth-Promoting <i>Leifsonia</i> . <i>Phytobiomes Journal</i> , 2021, 5, 263-274.	2.7	2
2323	The complete chloroplast genome and characteristics analysis of <i>Musa basjoo</i> Siebold. <i>Molecular Biology Reports</i> , 2021, 48, 7113-7125.	2.3	3
2324	Whole genome sequencing of <i>Enterobacter mori</i> , an emerging pathogen of kiwifruit and the potential genetic adaptation to pathogenic lifestyle. <i>AMB Express</i> , 2021, 11, 129.	3.0	4
2325	Comparative genetic analyses provide clues about capsule switching in <i>Streptococcus suis</i> 2 strains with different virulence levels and genetic backgrounds. <i>Microbiological Research</i> , 2021, 250, 126814.	5.3	8
2326	Global Expansion of Linezolid-Resistant Coagulase-Negative Staphylococci. <i>Frontiers in Microbiology</i> , 2021, 12, 661798.	3.5	14
2327	The Characterization of a Novel Phage, pPa_SNUABM_DT01, Infecting <i>Pseudomonas aeruginosa</i> . <i>Microorganisms</i> , 2021, 9, 2040.	3.6	7
2328	<i>Aspergillus fumigatus</i> versus Genus <i>Aspergillus</i> : Conservation, Adaptive Evolution and Specific Virulence Genes. <i>Microorganisms</i> , 2021, 9, 2014.	3.6	4

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2329	Plastomes from tribe Plantagineae (Plantaginaceae) reveal infrageneric structural synapomorphies and localized hypermutation for <i>Plantago</i> and functional loss of <i>ndh</i> genes from <i>Littorella</i> . <i>Molecular Phylogenetics and Evolution</i> , 2021, 162, 107217.	2.7	23
2330	Genomic and Phenotypic Analysis of Heat and Sanitizer Resistance in <i>Escherichia coli</i> from Beef in Relation to the Locus of Heat Resistance. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0157421.	3.1	8
2331	<i>Limosilactobacillus caccae</i> sp. nov., a new bacterial species isolated from the human gut microbiota. <i>FEMS Microbiology Letters</i> , 2021, 368, .	1.8	1
2332	Bacterial Long-Range Warfare: Aerial Killing of <i>Legionella pneumophila</i> by <i>Pseudomonas fluorescens</i> . <i>Microbiology Spectrum</i> , 2021, 9, e0040421.	3.0	6
2333	Genetic Analysis of <i>mcr-1</i> -Carrying Plasmids From Gram-Negative Bacteria in a Dutch Tertiary Care Hospital: Evidence for Inpatient and Interspecies Transmission Events. <i>Frontiers in Microbiology</i> , 2021, 12, 727435.	3.5	7
2334	Mitochondrial genes are involved in the fertility transformation of the thermosensitive male-sterile line YS3038 in wheat. <i>Molecular Breeding</i> , 2021, 41, 1.	2.1	3
2335	Whole-Genome Assessment of Clinical <i>Acinetobacter baumannii</i> Isolates Uncovers Potentially Novel Factors Influencing Carbapenem Resistance. <i>Frontiers in Microbiology</i> , 2021, 12, 714284.	3.5	3
2336	Potentiating effects of leaderless enterocin DD14 in combination with methicillin on clinical methicillin-resistant <i>Staphylococcus aureus</i> S1 strain. <i>Microbiological Research</i> , 2021, 252, 126864.	5.3	12
2337	Characterization of a <i>Streptococcus</i> species isolated from <i>Siganus guttatus</i> in South China. <i>Aquaculture</i> , 2021, 545, 737163.	3.5	0
2338	Metabolism analysis of 17 β -ethynylestradiol by <i>Pseudomonas citronellolis</i> SJTE-3 and identification of the functional genes. <i>Journal of Hazardous Materials</i> , 2022, 423, 127045.	12.4	8
2339	Biofilm formation by Non-O157 Shiga toxin-producing <i>Escherichia coli</i> in monocultures and co-cultures with meat processing surface bacteria. <i>Food Microbiology</i> , 2022, 102, 103902.	4.2	10
2340	Mitochondrial genome of <i>Bulinus truncatus</i> (Gastropoda: Lymnaeoidea): Implications for snail systematics and schistosome epidemiology. <i>Current Research in Parasitology and Vector-borne Diseases</i> , 2021, 1, 100017.	1.9	6
2341	Phylogenomics of the <i>Maverick</i> Virus-Like Mobile Genetic Elements of Vertebrates. <i>Molecular Biology and Evolution</i> , 2021, 38, 1731-1743.	8.9	22
2342	Factors enforcing the species boundary between the human pathogens <i>Cryptococcus neoformans</i> and <i>Cryptococcus deneoformans</i> . <i>PLoS Genetics</i> , 2021, 17, e1008871.	3.5	13
2343	Genome-Based Analyses of Fitness Effects and Compensatory Changes Associated with Acquisition of <i>bla</i> CMY-, <i>bla</i> CTX-M-, and <i>bla</i> OXA-48/VIM-1-Containing Plasmids in <i>Escherichia coli</i> . <i>Antibiotics</i> , 2021, 10, 90.	3.7	9
2344	A Bioinformatic Pipeline for Improved Genome Analysis and Clustering of Isolates during Outbreaks of Legionnaires' Disease. <i>Journal of Clinical Microbiology</i> , 2021, 59, .	3.9	3
2345	Core and Accessory Genome Analysis of <i>Vibrio mimicus</i> . <i>Microorganisms</i> , 2021, 9, 191.	3.6	6
2346	Precision long-read metagenomics sequencing for food safety by detection and assembly of Shiga toxin-producing <i>Escherichia coli</i> in irrigation water. <i>PLoS ONE</i> , 2021, 16, e0245172.	2.5	28

#	ARTICLE	IF	CITATIONS
2348	A New Asset for Pathogen Informatics – the Enteropathogen Resource Integration Center (ERIC), an NIAID Bioinformatics Resource Center for Biodefense and Emerging/Re-emerging Infectious Disease. <i>Advances in Experimental Medicine and Biology</i> , 2007, 603, 28-42.	1.6	9
2349	Sequence Comparison Without Alignment: The SpaM Approaches. <i>Methods in Molecular Biology</i> , 2021, 2231, 121-134.	0.9	10
2350	Informatics for Infectious Disease Research and Control. , 2010, , 1-26.		1
2351	Large-Scale Multiple Sequence Alignment and Phylogeny Estimation. <i>Computational Biology</i> , 2013, , 85-146.	0.2	14
2352	Comparative Analyses of Extrachromosomal Bacterial Replicons, Identification of Chromids, and Experimental Evaluation of Their Indispensability. <i>Methods in Molecular Biology</i> , 2015, 1231, 15-29.	0.9	7
2353	Analysis of Genome Rearrangement by Block-Interchanges. <i>Methods in Molecular Biology</i> , 2007, 396, 121-134.	0.9	1
2354	Genome Rearrangement by the Double Cut and Join Operation. <i>Methods in Molecular Biology</i> , 2008, 452, 385-416.	0.9	13
2355	In Sffamily Identification of Genes in Bacteriophage DNA. <i>Methods in Molecular Biology</i> , 2009, 502, 57-89.	0.9	25
2356	Bioinformatics for Analysis of Poxvirus Genomes. <i>Methods in Molecular Biology</i> , 2012, 890, 233-258.	0.9	8
2357	Heuristic Alignment Methods. <i>Methods in Molecular Biology</i> , 2014, 1079, 29-43.	0.9	4
2358	Horizontal Gene Transfer in Fungi. <i>Grand Challenges in Biology and Biotechnology</i> , 2020, , 317-332.	2.4	3
2359	The Bacterial Guide to Designing a Diversified Gene Portfolio. , 2020, , 51-87.		15
2360	Sibelia: A Scalable and Comprehensive Synteny Block Generation Tool for Closely Related Microbial Genomes. <i>Lecture Notes in Computer Science</i> , 2013, , 215-229.	1.3	74
2361	The characteristics and genome analysis of vB_ApiP_XC38, a novel phage infecting <i>Acinetobacter pittii</i> . <i>Virus Genes</i> , 2020, 56, 498-507.	1.6	7
2362	Metal resistant bacteria on gold particles: Implications of how anthropogenic contaminants could affect natural gold biogeochemical cycling. <i>Science of the Total Environment</i> , 2020, 727, 138698.	8.0	9
2363	Identification, characterization, and phylogenetic analysis of eight new inducible prophages in <i>Lactobacillus</i> . <i>Virus Research</i> , 2020, 286, 198003.	2.2	11
2364	Verrucomicrobia use hundreds of enzymes to digest the algal polysaccharide fucoidan. <i>Nature Microbiology</i> , 2020, 5, 1026-1039.	13.3	182
2365	Detection of mcr-1-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.	0.9	20

#	ARTICLE	IF	CITATIONS
2366	Characterization of the Î†CTX-like <i>Pseudomonas aeruginosa</i> phage Dobby isolated from the kidney stone microbiota. <i>Access Microbiology</i> , 2019, 1, .	0.5	11
2367	Isolation and characterization of <i>Kingella negevensis</i> sp. nov., a novel <i>Kingella</i> species detected in a healthy paediatric population. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 2370-2376.	1.7	34
2368	<i>Pectobacterium polaris</i> sp. nov., isolated from potato (<i>Solanum tuberosum</i>). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 5222-5229.	1.7	100
2369	Whole-genome sequence analysis of the <i>Mycobacterium avium</i> complex and proposal of the transfer of <i>Mycobacterium yongonense</i> to <i>Mycobacterium intracellulare</i> subsp. <i>yongonense</i> subsp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 1998-2005.	1.7	25
2370	<i>Marinobacter maroccanus</i> sp. nov., a moderately halophilic bacterium isolated from a saline soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 227-234.	1.7	12
2371	<i>Borrelia maritima</i> sp. nov., a novel species of the <i>Borrelia burgdorferi</i> sensu lato complex, occupying a basal position to North American species. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 849-856.	1.7	27
2372	<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.	1.7	16
2373	Reclassification of <i>Francisella noatunensis</i> subsp. <i>orientalis</i> Ottem et al. 2009 as <i>Francisella orientalis</i> sp. nov., <i>Francisella noatunensis</i> subsp. <i>chilensis</i> subsp. nov. and emended description of <i>Francisella noatunensis</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 2034-2048.	1.7	38
2374	Elucidating the genetic diversity of <i>Phthorimaea operculella</i> granulovirus (PhopGV). <i>Journal of General Virology</i> , 2019, 100, 679-690.	2.9	7
2375	Genetic environment of the KPC gene in <i>Acinetobacter baumannii</i> ST2 clone from Puerto Rico and genomic insights into its drug resistance. <i>Journal of Medical Microbiology</i> , 2016, 65, 784-792.	1.8	38
2376	Defining the role of pneumococcal neuraminidases and O-glycosidase in pneumococcal haemolytic uraemic syndrome. <i>Journal of Medical Microbiology</i> , 2016, 65, 975-984.	1.8	14
2377	Molecular characteristics of <i>Streptococcus agalactiae</i> strains deficient in alpha-like protein encoding genes. <i>Journal of Medical Microbiology</i> , 2017, 66, 26-33.	1.8	8
2378	Manual curation and reannotation of the genomes of <i>Clostridium difficile</i> 630Î”erm and <i>C. difficile</i> 630. <i>Journal of Medical Microbiology</i> , 2017, 66, 286-293.	1.8	117
2379	Repeated local emergence of carbapenem-resistant <i>Acinetobacter baumannii</i> in a single hospital ward. <i>Microbial Genomics</i> , 2016, 2, e000050.	2.0	65
2380	Whole-genome sequencing of a quarter-century melioidosis outbreak in temperate Australia uncovers a region of low-prevalence endemicity. <i>Microbial Genomics</i> , 2016, 2, e000067.	2.0	23
2381	Phase variable DNA repeats in <i>Neisseria gonorrhoeae</i> influence transcription, translation, and protein sequence variation. <i>Microbial Genomics</i> , 2016, 2, e000078.	2.0	11
2382	Taxonogenomics reveal multiple novel genomospecies associated with clinical isolates of <i>Stenotrophomonas maltophilia</i> . <i>Microbial Genomics</i> , 2018, 4, .	2.0	24
2383	A genomic view of experimental intraspecies and interspecies transformation of a rifampicin-resistance allele into <i>Neisseria meningitidis</i> . <i>Microbial Genomics</i> , 2018, 4, .	2.0	10

#	ARTICLE	IF	CITATIONS
2384	The characterization of mobile colistin resistance (<i>mcr</i>) genes among 33â€™000 <i>Salmonella enterica</i> genomes from routine public health surveillance in England. <i>Microbial Genomics</i> , 2020, 6, .	2.0	16
2385	Transposable elements contribute to the genome plasticity of <i>Ralstonia solanacearum</i> species complex. <i>Microbial Genomics</i> , 2020, 6, .	2.0	13
2386	Analysis of complete <i>Campylobacter concisus</i> genomes identifies genomospecies features, secretion systems and novel plasmids and their association with severe ulcerative colitis. <i>Microbial Genomics</i> , 2020, 6, .	2.0	13
2387	Epigenomics, genomics, resistome, mobilome, virulome and evolutionary phylogenomics of carbapenem-resistant <i>Klebsiella pneumoniae</i> clinical strains. <i>Microbial Genomics</i> , 2020, 6, .	2.0	24
2388	Novel genomic rearrangements mediated by multiple genetic elements in <i>Streptococcus pyogenes</i> M23ND confer potential for evolutionary persistence. <i>Microbiology (United Kingdom)</i> , 2016, 162, 1346-1359.	1.8	6
2389	Evolution of bacteria seen through their essential genes: the case of <i>Pseudomonas aeruginosa</i> and <i>Azotobacter vinelandii</i> . <i>Microbiology (United Kingdom)</i> , 2019, 165, 976-984.	1.8	6
2390	Genome sequence comparison and superinfection between two related <i>Pseudomonas aeruginosa</i> phages, D3112 and MP22. <i>Microbiology (United Kingdom)</i> , 2007, 153, 2885-2895.	1.8	56
2444	<i>Bacillus anthracis</i> . , 0, , 165-183.		1
2445	<i>Clostridium perfringens</i> . , 0, , 213-221.		1
2446	Identification of Genes Required for Glucan Exopolysaccharide Production in <i>Lactobacillus johnsonii</i> Suggests a Novel Biosynthesis Mechanism. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	13
2447	Draft Genome Sequence of <i>Xenophilus</i> sp., a Novel Bacterium Isolated from the Skin of a Southern Leopard Frog (<i>Rana sphenoccephala</i>) in Florida, USA. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
2448	Genome Sequence of â€™ <i>Candidatus</i> Nitrosocosmicus franklandusâ€™C13, a Terrestrial Ammonia-Oxidizing Archaeon. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	11
2449	High-Quality Draft Genome Sequence and Annotation of the Basidiomycete Yeast <i>Sporisorium graminicola</i> CBS10092, a Producer of Mannosylerythritol Lipids. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	6
2450	Complete Genome Sequence of Subcluster 5.2 <i>Synechococcus</i> sp. Strain CB0101, Isolated from the Chesapeake Bay. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	5
2451	Draft Genome Sequence of <i>Agrobacterium fabrum</i> ARqua1. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	4
2452	Complete Genome Sequences of Four <i>Salmonella enterica</i> Strains Associated with Pistachios Assembled Using a Combination of Short- and Long-Read Sequencing. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	4
2453	Complete Genome Sequences of Three <i>Mycoplasma anserisalpingitis</i> (<i>Mycoplasma</i> sp. 1220) Strains. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	6
2454	Phylogenomic characterization of ranaviruses isolated from cultured fish and amphibians in Thailand. <i>Facets</i> , 2020, 5, 963-979.	2.4	5

#	ARTICLE	IF	CITATIONS
2455	Comparative analyses of <i>Legionella</i> species identifies genetic features of strains causing Legionnaires' disease. <i>Genome Biology</i> , 2014, 15, 505.	9.6	62
2456	Comparative chloroplast genomics of the genus <i>Taxodium</i> . <i>BMC Genomics</i> , 2020, 21, 114.	2.8	23
2457	Proteins involved in the biosynthesis of lipophosphoglycan in <i>Leishmania</i> : a comparative genomic and evolutionary analysis. <i>Parasites and Vectors</i> , 2020, 13, 44.	2.5	9
2458	NovoGraph: Human genome graph construction from multiple long-read de novo assemblies. <i>F1000Research</i> , 2018, 7, 1391.	1.6	5
2459	Chloroplast Genome Sequence Annotation of <i>Dendrobium nobile</i> (Asparagales: Orchidaceae), an Endangered Medicinal Orchid from Northeast India. <i>PLOS Currents</i> , 2017, 9, .	1.4	2
2460	A Methodological Framework for the Reconstruction of Contiguous Regions of Ancestral Genomes and Its Application to Mammalian Genomes. <i>PLoS Computational Biology</i> , 2008, 4, e1000234.	3.2	108
2461	Diversity and distribution of nuclease bacteriocins in bacterial genomes revealed using Hidden Markov Models. <i>PLoS Computational Biology</i> , 2017, 13, e1005652.	3.2	52
2462	MUMmer4: A fast and versatile genome alignment system. <i>PLoS Computational Biology</i> , 2018, 14, e1005944.	3.2	1,412
2463	Localized Plasticity in the Streamlined Genomes of Vinyl Chloride Respiring <i>Dehalococcoides</i> . <i>PLoS Genetics</i> , 2009, 5, e1000714.	3.5	162
2464	Virus Satellites Drive Viral Evolution and Ecology. <i>PLoS Genetics</i> , 2015, 11, e1005609.	3.5	49
2465	Genetic diversity of the <i>Plasmodium falciparum</i> GTP-cyclohydrolase 1, dihydrofolate reductase and dihydropteroate synthetase genes reveals new insights into sulfadoxine-pyrimethamine antimalarial drug resistance. <i>PLoS Genetics</i> , 2020, 16, e1009268.	3.5	15
2466	<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.	3.0	26
2467	Complete Genomic Characterization of a Pathogenic A.II Strain of <i>Francisella tularensis</i> Subspecies <i>tularensis</i> . <i>PLoS ONE</i> , 2007, 2, e947.	2.5	46
2468	An Anomalous Type IV Secretion System in <i>Rickettsia</i> Is Evolutionarily Conserved. <i>PLoS ONE</i> , 2009, 4, e4833.	2.5	89
2469	Metagenomic Sequencing of an In Vitro-Simulated Microbial Community. <i>PLoS ONE</i> , 2010, 5, e10209.	2.5	200
2470	The Genome of a <i>Bacillus</i> Isolate Causing Anthrax in Chimpanzees Combines Chromosomal Properties of <i>B. cereus</i> with <i>B. anthracis</i> Virulence Plasmids. <i>PLoS ONE</i> , 2010, 5, e10986.	2.5	157
2471	progressiveMauve: Multiple Genome Alignment with Gene Gain, Loss and Rearrangement. <i>PLoS ONE</i> , 2010, 5, e11147.	2.5	3,652
2472	Anchor-Based Whole Genome Phylogeny (ABWGP): A Tool for Inferring Evolutionary Relationship among Closely Related Microorganisms. <i>PLoS ONE</i> , 2010, 5, e14159.	2.5	10

#	ARTICLE	IF	CITATIONS
2473	New Implications on Genomic Adaptation Derived from the <i>Helicobacter pylori</i> Genome Comparison. PLoS ONE, 2011, 6, e17300.	2.5	15
2474	Phage Encoded H-NS: A Potential Achilles Heel in the Bacterial Defence System. PLoS ONE, 2011, 6, e20095.	2.5	59
2475	Metabolic Versatility and Antibacterial Metabolite Biosynthesis Are Distinguishing Genomic Features of the Fire Blight Antagonist <i>Pantoea vagans</i> C9-1. PLoS ONE, 2011, 6, e22247.	2.5	56
2476	The Genome Sequence of the North-European Cucumber (<i>Cucumis sativus</i> L.) Unravels Evolutionary Adaptation Mechanisms in Plants. PLoS ONE, 2011, 6, e22728.	2.5	112
2477	<i>Pseudomonas syringae</i> pv. <i>actinidiae</i> Draft Genomes Comparison Reveal Strain-Specific Features Involved in Adaptation and Virulence to <i>Actinidia</i> Species. PLoS ONE, 2011, 6, e27297.	2.5	137
2478	Genome-Wide Analysis of the Emerging Infection with <i>Mycobacterium avium</i> Subspecies <i>paratuberculosis</i> in the Arabian Camels (<i>Camelus dromedarius</i>). PLoS ONE, 2012, 7, e31947.	2.5	69
2479	Isolation and Characterization of Cytotoxic, Aggregative <i>Citrobacter freundii</i> . PLoS ONE, 2012, 7, e33054.	2.5	63
2480	Comparative Genome Analysis of the High Pathogenicity <i>Salmonella</i> Typhimurium Strain UK-1. PLoS ONE, 2012, 7, e40645.	2.5	23
2481	Characterization and Differential Gene Expression between Two Phenotypic Phase Variants in <i>Salmonella enterica</i> Serovar Typhimurium. PLoS ONE, 2012, 7, e43592.	2.5	19
2482	In Vivo Capsular Switch in <i>Streptococcus pneumoniae</i> – Analysis by Whole Genome Sequencing. PLoS ONE, 2012, 7, e47983.	2.5	22
2483	Identification of <i>Wolbachia</i> Strains in Mosquito Disease Vectors. PLoS ONE, 2012, 7, e49922.	2.5	33
2484	Capturing the Biofuel Wellhead and Powerhouse: The Chloroplast and Mitochondrial Genomes of the Leguminous Feedstock Tree <i>Pongamia pinnata</i> . PLoS ONE, 2012, 7, e51687.	2.5	73
2485	Genome Analysis and Phylogenetic Relatedness of <i>Gallibacterium anatis</i> Strains from Poultry. PLoS ONE, 2013, 8, e54844.	2.5	32
2486	Phylogenetics and Differentiation of <i>Salmonella</i> Newport Lineages by Whole Genome Sequencing. PLoS ONE, 2013, 8, e55687.	2.5	63
2487	<i>Pseudomonas syringae</i> pv. <i>actinidiae</i> from Recent Outbreaks of Kiwifruit Bacterial Canker Belong to Different Clones That Originated in China. PLoS ONE, 2013, 8, e57464.	2.5	143
2488	The Complete Genome and Phenome of a Community-Acquired <i>Acinetobacter baumannii</i> . PLoS ONE, 2013, 8, e58628.	2.5	93
2489	Multiple Single-Cell Genomes Provide Insight into Functions of Uncultured Deltaproteobacteria in the Human Oral Cavity. PLoS ONE, 2013, 8, e59361.	2.5	44
2490	Complete Sequence and Analysis of Plastid Genomes of Two Economically Important Red Algae: <i>Pyropia haitanensis</i> and <i>Pyropia yezoensis</i> . PLoS ONE, 2013, 8, e65902.	2.5	68

#	ARTICLE	IF	CITATIONS
2491	Comparative Genome Analysis of <i>Enterobacter cloacae</i> . PLoS ONE, 2013, 8, e74487.	2.5	72
2492	Detection of Homologous Recombination Events in Bacterial Genomes. PLoS ONE, 2013, 8, e75230.	2.5	3
2493	A Genomic Redefinition of <i>Pseudomonas avellanae</i> species. PLoS ONE, 2013, 8, e75794.	2.5	40
2494	GenomeFingerprinter: The Genome Fingerprint and the Universal Genome Fingerprint Analysis for Systematic Comparative Genomics. PLoS ONE, 2013, 8, e77912.	2.5	1
2495	Architecture and Gene Repertoire of the Flexible Genome of the Extreme Acidophile <i>Acidithiobacillus caldus</i> . PLoS ONE, 2013, 8, e78237.	2.5	68
2496	The Genome Sequence of the Fungal Pathogen <i>Fusarium virguliforme</i> That Causes Sudden Death Syndrome in Soybean. PLoS ONE, 2014, 9, e81832.	2.5	50
2497	Unusual Large-Scale Chromosomal Rearrangements in <i>Mycobacterium tuberculosis</i> Beijing B0/W148 Cluster Isolates. PLoS ONE, 2014, 9, e84971.	2.5	23
2498	Genomic Evolution of 11 Type Strains within Family Planctomycetaceae. PLoS ONE, 2014, 9, e86752.	2.5	18
2499	Whole Genome Analysis of a Community-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> ST59 Isolate from a Case of Human Sepsis and Severe Pneumonia in China. PLoS ONE, 2014, 9, e89235.	2.5	19
2500	Direct Amplification, Sequencing and Profiling of <i>Chlamydia trachomatis</i> Strains in Single and Mixed Infection Clinical Samples. PLoS ONE, 2014, 9, e99290.	2.5	24
2501	Genome Sequence of <i>Candidatus Nitrososphaera evergladensis</i> from Group I.1b Enriched from Everglades Soil Reveals Novel Genomic Features of the Ammonia-Oxidizing Archaea. PLoS ONE, 2014, 9, e101648.	2.5	87
2502	Virulence and Draft Genome Sequence Overview of Multiple Strains of the Swine Pathogen <i>Haemophilus parasuis</i> . PLoS ONE, 2014, 9, e103787.	2.5	37
2503	Large-Scale Phylogenetic Classification of Fungal Chitin Synthases and Identification of a Putative Cell-Wall Metabolism Gene Cluster in <i>Aspergillus</i> Genomes. PLoS ONE, 2014, 9, e104920.	2.5	18
2504	Complete Chloroplast Genome Sequence of Omani Lime (<i>Citrus aurantiifolia</i>) and Comparative Analysis within the Rosids. PLoS ONE, 2014, 9, e113049.	2.5	60
2505	A Role for Tn6029 in the Evolution of the Complex Antibiotic Resistance Gene Loci in Genomic Island 3 in Enterohemorrhagic <i>Escherichia coli</i> O104:H4. PLoS ONE, 2015, 10, e0115781.	2.5	43
2506	Interrogation of the <i>Burkholderia pseudomallei</i> Genome to Address Differential Virulence among Isolates. PLoS ONE, 2014, 9, e115951.	2.5	29
2507	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.	2.5	36
2508	Discovery of Putative Small Non-Coding RNAs from the Obligate Intracellular Bacterium <i>Wolbachia pipientis</i> . PLoS ONE, 2015, 10, e0118595.	2.5	13

#	ARTICLE	IF	CITATIONS
2509	The Complete Chloroplast and Mitochondrial Genomes of the Green Macroalga <i>Ulva</i> sp. UNA00071828 (Ulvophyceae, Chlorophyta). PLoS ONE, 2015, 10, e0121020.	2.5	66
2510	Initial Evidence for Adaptive Selection on the NADH Subunit Two of Freshwater Dolphins by Analyses of Mitochondrial Genomes. PLoS ONE, 2015, 10, e0123543.	2.5	28
2511	Genetically and Phenotypically Distinct <i>Pseudomonas aeruginosa</i> Cystic Fibrosis Isolates Share a Core Proteomic Signature. PLoS ONE, 2015, 10, e0138527.	2.5	37
2512	Analysis of the Complete Chloroplast Genome of a Medicinal Plant, <i>Dianthus superbus</i> var. <i>longicalycinus</i> , from a Comparative Genomics Perspective. PLoS ONE, 2015, 10, e0141329.	2.5	58
2513	Genomic and Gene-Expression Comparisons among Phage-Resistant Type-IV Pilus Mutants of <i>Pseudomonas syringae</i> pathovar <i>phaseolicola</i> . PLoS ONE, 2015, 10, e0144514.	2.5	11
2514	Identifying Likely Transmission Pathways within a 10-Year Community Outbreak of Tuberculosis by High-Depth Whole Genome Sequencing. PLoS ONE, 2016, 11, e0150550.	2.5	24
2515	<i>Bacillus pumilus</i> SAFR-032 Genome Revisited: Sequence Update and Re-Annotation. PLoS ONE, 2016, 11, e0157331.	2.5	21
2516	Comparative Genomics and Metabolic Analysis Reveals Peculiar Characteristics of <i>Rhodococcus opacus</i> Strain M213 Particularly for Naphthalene Degradation. PLoS ONE, 2016, 11, e0161032.	2.5	21
2517	Comparative Genomics of <i>Acetobacter pasteurianus</i> Ab3, an Acetic Acid Producing Strain Isolated from Chinese Traditional Rice Vinegar Meiguichu. PLoS ONE, 2016, 11, e0162172.	2.5	12
2518	Experimental Evolution of <i>Mycobacterium tuberculosis</i> in Human Macrophages Results in Low-Frequency Mutations Not Associated with Selective Advantage. PLoS ONE, 2016, 11, e0167989.	2.5	6
2519	Genomic sequence of 'Candidatus <i>Liberibacter solanacearum</i> ' haplotype C and its comparison with haplotype A and B genomes. PLoS ONE, 2017, 12, e0171531.	2.5	39
2520	The quantitative impact of read mapping to non-native reference genomes in comparative RNA-Seq studies. PLoS ONE, 2017, 12, e0180904.	2.5	9
2521	Comparative pathogenomics of <i>Clostridium tetani</i> . PLoS ONE, 2017, 12, e0182909.	2.5	36
2522	Identification and genomic comparison of temperate bacteriophages derived from emetic <i>Bacillus cereus</i> . PLoS ONE, 2017, 12, e0184572.	2.5	20
2523	Treatment with high-dose antidepressants severely exacerbates the pathological outcome of experimental <i>Escherichia coli</i> infections in poultry. PLoS ONE, 2017, 12, e0185914.	2.5	7
2524	Genomic diversity of <i>Taylorella equigenitalis</i> introduced into the United States from 1978 to 2012. PLoS ONE, 2018, 13, e0194253.	2.5	2
2525	Ancestry of the AUTS2 family—A novel group of polycomb-complex proteins involved in human neurological disease. PLoS ONE, 2020, 15, e0232101.	2.5	4
2526	Dissemination and Mechanism for the MCR-1 Colistin Resistance. PLoS Pathogens, 2016, 12, e1005957.	4.7	205

#	ARTICLE	IF	CITATIONS
2527	Automated transcription start site prediction for comparative Transcriptomics using the SuperGenome. EMBnet Journal, 2013, 19, 19.	0.6	4
2528	Fusaricidins in <i>Paenibacillus polymyxa</i> A21 and their antagonistic activity against <i>Botrytis cinerea</i> on tomato. Frontiers of Agricultural Science and Engineering, 2018, .	1.4	2
2529	The complete chloroplast genome of <i>Papaver setigerum</i> and comparative analyses in Papaveraceae. Genetics and Molecular Biology, 2020, 43, e20190272.	1.3	12
2530	Molecular Detection of <i>Salmonella enterica</i> subsp. <i>arizonae</i> by Quantitative PCR. Avian Diseases, 2020, 64, 305-309.	1.0	3
2531	Chromatiblock: scalable whole-genome visualization of structural differences in prokaryotes. Journal of Open Source Software, 2020, 5, 2451.	4.6	1
2532	Low Coverage Whole Genome Sequencing Yields the Complete Mitogenome of <i>Hypselodoris bullocki</i> and <i>Hypselodoris apolegma</i> (Mollusca: Chromodorididae). Journal of Coastal Research, 2019, 97, 23.	0.3	3
2533	Characterization of the Chloroplast Genome Facilitated the Transformation of <i>Parachlorella kessleri</i> -I, A Potential Marine Alga for Biofuel Production. Current Genomics, 2020, 21, 610-623.	1.6	4
2534	Constraints of Drug Resistance in <i>Mycobacterium tuberculosis</i> - Prospects for Pharmacological Reversion of Susceptibility to Antibiotics. The Open Conference Proceedings Journal, 2017, 8, 33-43.	0.6	3
2535	Two multi-fragment recombination events resulted in the β -lactam-resistant serotype 11A-ST6521 related to Spain9V-ST156 pneumococcal clone spreading in south-western Europe, 2008 to 2016. Eurosurveillance, 2020, 25, .	7.0	12
2536	mcr-Colistin Resistance Genes Mobilized by IncX4, IncHI2, and IncI2 Plasmids in <i>Escherichia coli</i> of Pigs and White Stork in Spain. Frontiers in Microbiology, 2019, 10, 3072.	3.5	57
2537	Genome-Wide Association Studies for the Detection of Genetic Variants Associated With Daptomycin and Ceftaroline Resistance in <i>Staphylococcus aureus</i> . Frontiers in Microbiology, 2021, 12, 639660.	3.5	11
2538	Genomic Insight into <i>Pediococcus acidilactici</i> HN9, a Potential Probiotic Strain Isolated from the Traditional Thai-Style Fermented Beef Nhang. Microorganisms, 2021, 9, 50.	3.6	18
2539	Complete Genome Sequence of <i>Ovine Mycobacterium avium</i> subsp. <i>paratuberculosis</i> Strain JIII-386 (MAP-S/type III) and Its Comparison to MAP-S/type I, MAP-C, and <i>M. avium</i> Complex Genomes. Microorganisms, 2021, 9, 70.	3.6	13
2540	Isolation and Characterization of <i>Salmonella</i> Jumbo-Phage pSal-SNUABM-04. Viruses, 2021, 13, 27.	3.3	20
2541	The complete mitochondrial genome sequence of <i>Scolopendra mutilans</i> L. Koch, 1878 (<i>Scolopendromorpha</i> , <i>Scolopendridae</i>), with a comparative analysis of other centipede genomes. ZooKeys, 2020, 925, 73-88.	1.1	7
2542	In silico Analysis of <i>Chlorobium</i> Genomes Divulge Insights into the Lifestyle of the Bacteria. Research Journal of Microbiology, 2008, 3, 600-613.	0.2	4
2543	Comparative genome analysis of 15 clinical <i>Shigella flexneri</i> strains regarding virulence and antibiotic resistance. AIMS Microbiology, 2019, 5, 205-222.	2.2	9
2544	Isolation and characterization of the <i>Staphylococcus aureus</i> bacteriophage vB_SauS_SA2. AIMS Microbiology, 2019, 5, 285-307.	2.2	14

#	ARTICLE	IF	CITATIONS
2545	Non-contiguous finished genome sequence and description of <i>Paenibacillus senegalensis</i> sp. nov.. Standards in Genomic Sciences, 2012, 7, 70-81.	1.5	47
2546	Diversified lineages and drug-resistance profiles of clinical isolates of <i>Mycobacterium tuberculosis</i> complex in Malaysia. International Journal of Mycobacteriology, 2019, 8, 320.	0.6	3
2547	GI₂FeGSH</sub>: A New Genomic Island Might Explain the Differences in <i>Brucella</i> Virulence. Open Journal of Animal Sciences, 2017, 07, 141-148.	0.6	4
2548	Decoding the Genomic Architecture of Mammalian and Plant Genomes: Synteny Blocks and Large-scale Duplications. Communications in Information and Systems, 2010, 10, 1-22.	0.5	2
2549	A novice's guide to analyzing NGS-derived organelle and metagenome data. Algae, 2016, 31, 137-154.	2.3	17
2550	Comparative Genome Analysis of <i>Rathayibacter tritici</i> NCPB 1953 with <i>Rathayibacter toxicus</i> Strains Can Facilitate Studies on Mechanisms of Nematode Association and Host Infection. Plant Pathology Journal, 2017, 33, 370-381.	1.7	6
2551	Functional annotations in bacterial genomes based on small RNA signatures. Bioinformatics, 2008, 2, 284-295.	0.5	4
2553	Expansion of the fatty acyl reductase gene family shaped pheromone communication in Hymenoptera. ELife, 2019, 8, .	6.0	26
2554	Panton's "Valentine leucocidin is the key determinant of <i>Staphylococcus aureus</i> pyomyositis in a bacterial GWAS. ELife, 2019, 8, .	6.0	56
2555	Phage integration alters the respiratory strategy of its host. ELife, 2019, 8, .	6.0	24
2556	Post-acute COVID-19 associated with evidence of bystander T-cell activation and a recurring antibiotic-resistant bacterial pneumonia. ELife, 2020, 9, .	6.0	26
2557	AliTV's interactive visualization of whole genome comparisons. PeerJ Computer Science, 0, 3, e116.	4.5	80
2558	Plastome structure and adaptive evolution of <i>Calanthe</i> s.l. species. PeerJ, 2020, 8, e10051.	2.0	15
2559	Isolation and evolutionary analyses of porcine epidemic diarrhea virus in Asia. PeerJ, 2020, 8, e10114.	2.0	11
2560	Biases in genome reconstruction from metagenomic data. PeerJ, 2020, 8, e10119.	2.0	32
2561	Phylogenetic relationships and taxonomic position of genus <i>Hyperacrius</i> (Rodentia: Arvicolinae) from Kashmir based on evidences from analysis of mitochondrial genome and study of skull morphology. PeerJ, 2020, 8, e10364.	2.0	3
2562	Augmenting transcriptome assembly by combining <i>de novo</i> and genome-guided tools. PeerJ, 2013, 1, e133.	2.0	19
2563	Gall-ID: tools for genotyping gall-causing phytopathogenic bacteria. PeerJ, 2016, 4, e2222.	2.0	37

#	ARTICLE	IF	CITATIONS
2564	Chromosomal rearrangements and protein globularity changes in <i>Mycobacterium tuberculosis</i> isolates from cerebrospinal fluid. PeerJ, 2016, 4, e2484.	2.0	5
2565	<i>Legionella</i> shows a diverse secondary metabolism dependent on a broad spectrum Sfp-type phosphopantetheinyl transferase. PeerJ, 2016, 4, e2720.	2.0	5
2566	The complete chloroplast genome sequence of <i>Helwingia himalaica</i> (Helwingiaceae, Aquifoliales) and a chloroplast phylogenomic analysis of the Campanulidae. PeerJ, 2016, 4, e2734.	2.0	10
2567	Evolutionary origins of the emergent ST796 clone of vancomycin resistant <i>Enterococcus faecium</i> . PeerJ, 2017, 5, e2916.	2.0	46
2568	Plastomes of the green algae <i>Hydrodictyon reticulatum</i> and <i>Pediastrum duplex</i> (Sphaeropleales, Chlorophyceae). PeerJ, 2017, 5, e3325.	2.0	8
2569	Chloroplast genome expansion by intron multiplication in the basal psychrophilic euglenoid <i>Eutreptiella pomquetensis</i> . PeerJ, 2017, 5, e3725.	2.0	11
2570	Complete genome sequence and comparative genomics of the golden pompano (<i>Trachinotus</i>) Tj ETQq0 0 0 rgBTJ/Overlock 10 Tf 50	2.0	33
2571	Strain-level genetic diversity of <i>Methylophaga nitrareducens</i> confers plasticity to denitrification capacity in a methylophilic marine denitrifying biofilm. PeerJ, 2018, 6, e4679.	2.0	9
2572	TarSynFlow, a workflow for bacterial genome comparisons that revealed genes putatively involved in the probiotic character of <i>Shewanella putrefaciens</i> strain Pdp11. PeerJ, 2019, 7, e6526.	2.0	3
2573	The complete chloroplast genome of <i>Fagus crenata</i> (subgenus <i>Fagus</i>) and comparison with <i>F. engleriana</i> (subgenus <i>Engleriana</i>). PeerJ, 2019, 7, e7026.	2.0	16
2574	Mitochondrial genomics of human pathogenic parasite <i>Leishmania</i> (<i>Viannia</i>) <i>panamensis</i> . PeerJ, 2019, 7, e7235.	2.0	13
2575	The sugarcane mitochondrial genome: assembly, phylogenetics and transcriptomics. PeerJ, 2019, 7, e7558.	2.0	15
2576	Detection and identification of <i>Xanthomonas</i> pathotypes associated with citrus diseases using comparative genomics and multiplex PCR. PeerJ, 2019, 7, e7676.	2.0	10
2577	Plastome of mycoheterotrophic <i>Burmannia itoana</i> Mak. (Burmanniaceae) exhibits extensive degradation and distinct rearrangements. PeerJ, 2019, 7, e7787.	2.0	5
2578	<scp>L</scp>-cysteine transporter-PCR to detect hydrogen sulfide-producing <i>Campylobacter fetus</i> . PeerJ, 2019, 7, e7820.	2.0	9
2579	Development of molecular markers for invasive alien plants in Korea: a case study of a toxic weed, <i>Cenchrus longispinus</i> L., based on next generation sequencing data. PeerJ, 2019, 7, e7965.	2.0	2
2580	Characteristics of the complete mitochondrial genome of the monotypic genus <i>Arctictis</i> (Family:) Tj ETQq0 0 0 rgBTJ/Overlock 10 Tf 50	2.0	3
2581	Complete plastid genome sequences of two species of the Neotropical genus <i>Brunellia</i> (Brunelliaceae). PeerJ, 2020, 8, e8392.	2.0	3

#	ARTICLE	IF	CITATIONS
2582	Pan-Genome Analysis of Effectors in Korean Strains of the Soybean Pathogen <i>Xanthomonas citri</i> pv. <i>glycines</i> . <i>Microorganisms</i> , 2021, 9, 2065.	3.6	4
2583	Characterization of chloroplast genome of the marine diatom <i>Chaetoceros gracilis</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 3159-3161.	0.4	0
2584	Third generation cephalosporin resistance in clinical non-typhoidal <i>Salmonella enterica</i> in Germany and emergence of bla CTX-M-harboursing pESI plasmids. <i>Microbial Genomics</i> , 2021, 7, .	2.0	11
2585	Complete Genome Sequence of the Marine-Derived Bacterium <i>Streptomyces</i> sp. Strain GMY02. <i>Microbiology Resource Announcements</i> , 2021, 10, e0068121.	0.6	1
2586	Emergence of 16S rRNA methyltransferases among carbapenemase-producing Enterobacterales in Spain studied by whole-genome sequencing. <i>International Journal of Antimicrobial Agents</i> , 2022, 59, 106456.	2.5	11
2587	The complete mitochondrial genome of <i>Ophiocordyceps gracilis</i> and its comparison with related species. <i>IMA Fungus</i> , 2021, 12, 31.	3.8	7
2588	Transition of Serotype 35B Pneumococci From Commensal to Prevalent Virulent Strain in Children. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 744742.	3.9	3
2589	Establishment of a near-contiguous genome sequence of the citric acid producing yeast <i>Yarrowia lipolytica</i> DSM 3286 with resolution of rDNA clusters and telomeres. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab085.	3.2	4
2590	Genomic Changes and Genetic Divergence of <i>Vibrio alginolyticus</i> Under Phage Infection Stress Revealed by Whole-Genome Sequencing and Resequencing. <i>Frontiers in Microbiology</i> , 2021, 12, 710262.	3.5	3
2591	Fish genomics and its impact on fundamental and applied research of vertebrate biology. <i>Reviews in Fish Biology and Fisheries</i> , 2022, 32, 357-385.	4.9	7
2592	Phage Therapy Related Microbial Succession Associated with Successful Clinical Outcome for a Recurrent Urinary Tract Infection. <i>Viruses</i> , 2021, 13, 2049.	3.3	33
2593	Whole-Genome Sequencing Analysis of a stx-Negative <i>Escherichia</i> O63:H6 Isolate Associated with Hemolytic Uremic Syndrome. <i>Diagnostics</i> , 2021, 11, 1823.	2.6	2
2594	Minimalistic mycoplasmas harbor different functional toxin-antitoxin systems. <i>PLoS Genetics</i> , 2021, 17, e1009365.	3.5	7
2595	Identification and genomic analysis of <i>Mycobacterium ulcerans</i> ecovar <i>Liflandii</i> from the farmed Chinese tongue sole, <i>Cynoglossus semilaevis</i> . <i>Aquaculture</i> , 2022, 548, 737614.	3.5	4
2596	Dynamic impact of virome on colitis and colorectal cancer: Immunity, inflammation, prevention and treatment. <i>Seminars in Cancer Biology</i> , 2022, 86, 943-954.	9.6	17
2597	Complete genomes of the eukaryotic poultry parasite <i>Histomonas meleagridis</i> : linking sequence analysis with virulence / attenuation. <i>BMC Genomics</i> , 2021, 22, 753.	2.8	17
2599	Genomic sequence data of bacterial isolates from pistachio trees and other woody plants in California are inconsistent with a role of <i>Rhodococcus</i> as the causative agent of Pistachio Bushy Top Syndrome. <i>PhytoFrontiers</i> , 0, .	1.6	0
2600	Probiotic effects of the <i>Bacillus velezensis</i> GY65 strain in the mandarin fish, <i>Siniperca chuatsi</i> . <i>Aquaculture Reports</i> , 2021, 21, 100902.	1.7	10

#	ARTICLE	IF	CITATIONS
2601	Genome analysis of an OXA-48-producing carbapenem- and colistin-resistant <i>Klebsiella pneumoniae</i> sequence type 11 clone isolated from an inpatient. <i>Gene Reports</i> , 2021, 25, 101394.	0.8	1
2602	First report of two foodborne <i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Bovismorbificans</i> isolates carrying a novel mega-plasmid harboring <i>blaDHA-1</i> and <i>qnrB4</i> genes. <i>International Journal of Food Microbiology</i> , 2021, 360, 109439.	4.7	5
2603	MEDITE: A Unilingual Textual Aligner. <i>Lecture Notes in Computer Science</i> , 2006, , 458-469.	1.3	2
2604	Rough Computational Annotation and Hierarchical Conserved Area Viewing Tool for Genomes Using Multiple Relation Graph.. <i>Journal of Life Science</i> , 2008, 18, 565-571.	0.2	0
2605	Alignment and Analysis of Closely Related Genomes. <i>Lecture Notes in Computer Science</i> , 2009, , 343-352.	1.3	0
2606	Pangenomic Reverse Vaccinology. , 2010, , 203-221.		1
2607	Practical Multiple Sequence Alignment. , 2010, , 21-43.		0
2608	Overview: The Impact of Microbial Genomics on Food Safety. , 2011, , 1-27.		0
2609	Functional Inference in Microbial Genomics Based on Large-Scale Comparative Analysis. , 2011, , 55-92.		0
2610	Hidden Breakpoints in Genome Alignments. <i>Lecture Notes in Computer Science</i> , 2012, , 391-403.	1.3	0
2611	Identification of Genomic Islands by Pattern Discovery. , 2012, , 166-181.		0
2612	Organization, expression and evolution of flagellar genes in <i>Rhodobacter sphaeroides</i> </i>2.4.1. <i>Open Journal of Genetics</i> , 2012, 02, 5-10.	0.1	0
2613	Contribution of Transcription Factor Binding Site Motif Variants to Condition-Specific Gene Expression Patterns in Budding Yeast. <i>PLoS ONE</i> , 2012, 7, e32274.	2.5	0
2614	Sequence Homology Handling. <i>Computational Biology</i> , 2013, , 301-334.	0.2	1
2615	Visualization in Biology and Medicine. <i>Mathematics and Visualization</i> , 2014, , 247-263.	0.6	0
2616	<i>Alternaria</i> Comparative Genomics: The Secret Life of Rots. , 2014, , 45-63.		3
2617	Application of Genome Studies of Coffee Rust. <i>Advances in Intelligent Systems and Computing</i> , 2014, , 133-139.	0.6	1
2618	Aggregation of Similarity Measures for Ortholog Detection: Validation with Measures Based on Rough Set Theory. <i>Computacion Y Sistemas</i> , 2014, 18, .	0.3	1

#	ARTICLE	IF	CITATIONS
2623	In Silico Signature Prediction Modeling in Cytolethal Distending Toxin-Producing <i>Escherichia coli</i> Strains. <i>Genomics and Informatics</i> , 2017, 15, 69.	0.8	1
2642	NovoGraph: Genome graph construction from multiple long-read de novo assemblies. <i>F1000Research</i> , 2018, 7, 1391.	1.6	8
2644	Analysis of the genome of the bacteria <i>Bacillus amyloliquefaciens</i> BIM B-439D. , 2018, 62, 592-600.	0.1	1
2648	Multiple Chromosomes in Bacteria: Low Level of Evolutionary Constraint Drives the Rapid Genetic Divergence of Chromosome II. <i>Advances in Microbiology</i> , 2019, 09, 656-677.	0.6	0
2653	Adaptation of metal and antibiotic resistant traits in novel \hat{I}^2 -Proteobacterium <i>Achromobacter xylosoxidans</i> BHW-15. <i>PeerJ</i> , 2019, 7, e6537.	2.0	5
2655	An orthogonal amber initiator tRNA functions similarly across diverse <i>Escherichia coli</i> laboratory strains. <i>Matters</i> , 0, , .	1.0	0
2657	The completely assembled genome of a strain from the New Zealand <i>Pseudomonas syringae</i> pv. <i>actinidiae</i> (PSA) outbreak. <i>Acta Horticulturae</i> , 2019, , 23-28.	0.2	1
2659	Draft Genome Sequence of <i>Brevundimonas</i> sp. Strain T2.26MG-97, Isolated from a Rock Core Sample from 492.6 Meters Deep on the Subsurface of the Iberian Pyrite Belt. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	1
2660	Complete Genome Sequence of a <i>Pseudomonas aeruginosa</i> Isolate from a Kidney Stone. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	3
2661	Genomic differences among carriage and invasive nontypeable pneumococci circulating in South Africa. <i>Microbial Genomics</i> , 2019, 5, .	2.0	0
2664	Draft Genome Sequence of <i>Bacillus safensis</i> RP10, Isolated from Soil in the Atacama Desert, Chile. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	2
2673	Lumen and mucosa-associated <i>Lactobacillus rhamnosus</i> from the intestinal tract of organ donors. <i>Gut Microbiome</i> , 2020, 1, .	3.2	1
2683	Complete Genome Sequences of Diverse Uropathogenic <i>Staphylococcus saprophyticus</i> Isolates from a College Health Center. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	0
2684	An Explorative Tool for Mutation Tracking in the Spike Glycoprotein of SARS-CoV-2. , 2021, , .		0
2686	Whole genome global insight of antibiotic resistance gene repertoire and virulome of high - risk multidrug-resistant Uropathogenic <i>Escherichia coli</i> . <i>Microbial Pathogenesis</i> , 2021, 161, 105256.	2.9	12
2687	Complete Genome Analysis of Undecylprodigiosin Pigment Biosynthesizing Marine <i>Streptomyces</i> Species Displaying Potential Bioactive Applications. <i>Microorganisms</i> , 2021, 9, 2249.	3.6	5
2688	Mitochondrial genomes do not appear to regulate flowering pattern / reproductive strategy in <i>Cannabis sativa</i> . <i>AoB PLANTS</i> , 2022, 14, plab068.	2.3	1
2689	Characterization and adaptation of <i>Caldicellulosiruptor</i> strains to higher sugar concentrations, targeting enhanced hydrogen production from lignocellulosic hydrolysates. <i>Biotechnology for Biofuels</i> , 2021, 14, 210.	6.2	4

#	ARTICLE	IF	CITATIONS
2691	Comparative genome analyses of <i>Mycobacteroides immunogenum</i> reveals two potential novel subspecies. <i>Microbial Genomics</i> , 2020, 6, .	2.0	5
2692	Swine Conjunctivitis Associated with a Novel <i>Mycoplasma</i> Species Closely Related to <i>Mycoplasma hyorhinis</i> . <i>Pathogens</i> , 2021, 10, 13.	2.8	5
2693	Complete chloroplast genome comparisons for <i>Pityopsis</i> (Asteraceae). <i>PLoS ONE</i> , 2020, 15, e0241391.	2.5	7
2696	Genomic and Phenotypic Diversity of Carbapenemase-Producing Enterobacteriaceae Isolates from Bacteremia in China: A Multicenter Epidemiological, Microbiological, and Genetic Study. <i>Engineering</i> , 2022, 12, 90-100.	6.7	15
2697	<i>Culicoidibacter</i> larvae gen. nov., sp. nov., from the gastrointestinal tract of the biting midge (<i>Culicoides sonorensis</i>) larva, belongs to a novel lineage Culicoidibacteraceae fam. nov., Culicoidibacterales ord. nov. and Culicoidibacteria classis nov. of the phylum Firmicutes. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 6482-6490.	1.7	14
2698	<i>Helicobacter pylori</i> diversification during chronic infection within a single host generates sub-populations with distinct phenotypes. <i>PLoS Pathogens</i> , 2020, 16, e1008686.	4.7	7
2699	Sequencing of Complete Chloroplast Genomes. <i>Methods in Molecular Biology</i> , 2021, 2222, 89-105.	0.9	0
2700	Bioinspired Intrusion Detection in ITC Infrastructures. <i>Lecture Notes in Networks and Systems</i> , 2021, , 10-22.	0.7	5
2701	Sequence Alignment Algorithms for Intrusion Detection in the Internet of Things. <i>Nonlinear Phenomena in Complex Systems</i> , 2020, 23, 397-404.	0.3	8
2702	Bovine abortion by a vaccine strain of <i>Bacillus anthracis</i> . <i>Ciencia Rural</i> , 2020, 50, .	0.5	0
2703	Phenotypic and Genotypic Characterisation of Clinical Isolates of Nosocomial Infections. <i>Eurasian Journal of Applied Biotechnology</i> , 2020, , .	0.1	1
2704	Comparative Analyses and Phylogenetic Relationships between <i>Cryptomeria fortunei</i> and Related Species Based on Complete Chloroplast Genomes. <i>Phyton</i> , 2020, 89, 957-986.	0.7	1
2705	Draft genome sequences of <i>Enterococcus durans</i> EDD2 strain associated with honeybees. <i>AIMS Agriculture and Food</i> , 2020, 5, 288-291.	1.6	1
2706	Complete genome sequence of a methicillin-resistant <i>Staphylococcus schleiferi</i> strain from canine otitis externa in Korea. <i>Journal of Veterinary Science</i> , 2020, 21, e11.	1.3	3
2707	Comparative Genome Analysis of <i>Psychrobacillus</i> Strain PB01, Isolated from an Iceberg. <i>Journal of Microbiology and Biotechnology</i> , 2020, 30, 237-243.	2.1	6
2709	Whole-Genome Sequence of Drug-Resistant <i>Mycobacterium tuberculosis</i> Strain S7, Isolated from a Patient with Pulmonary Tuberculosis. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	1
2711	Bactericidal Effect of <i>Pseudomonas oryziphila</i> sp. nov., a Novel <i>Pseudomonas</i> Species Against <i>Xanthomonas oryzae</i> Reduces Disease Severity of Bacterial Leaf Streak of Rice. <i>Frontiers in Microbiology</i> , 2021, 12, 759536.	3.5	12
2712	Complete Genome Sequence of <i>Bacillus velezensis</i> GMEKP1, Isolated from a Natural Bamboo Hive of Stingless Bees. <i>Microbiology Resource Announcements</i> , 2021, 10, e0065921.	0.6	0

#	ARTICLE	IF	CITATIONS
2714	Different gene rearrangements of the genus <i>Dardanus</i> (Anomura: Diogenidae) and insights into the phylogeny of Paguroidea. <i>Scientific Reports</i> , 2021, 11, 21833.	3.3	7
2716	Re-classification of <i>Streptomyces venezuelae</i> strains and mining secondary metabolite biosynthetic gene clusters. <i>IScience</i> , 2021, 24, 103410.	4.1	2
2717	Complete Genome Sequence of <i>Rickettsia parkeri</i> Strain Black Gap. <i>Microbiology Resource Announcements</i> , 2021, 10, e0062321.	0.6	1
2718	Comprehensive analysis of complete mitochondrial genome of <i>Sapindus mukorossi</i> Gaertn.: an important industrial oil tree species in China. <i>Industrial Crops and Products</i> , 2021, 174, 114210.	5.2	16
2721	Identification of Genomic Islands by Pattern Discovery. , 0, , 742-758.		0
2722	Merging Multi-Version Texts: a Generic Solution to the Overlap Problem. <i>Balisage Series on Markup Technologies</i> , 0, , .	0.0	4
2723	Omics-based comparative analysis of putative mobile genetic elements in <i>Lactococcus lactis</i> . <i>FEMS Microbiology Letters</i> , 2019, 366, i105-i113.	1.8	1
2724	Draft Genome Sequence of <i>Shewanella</i> sp. Strain T2.3D-1.1, Isolated from 121.8 Meters Deep in the Subsurface of the Iberian Pyrite Belt. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	2
2725	Draft Genome Sequence of <i>Escherichia coli</i> Strain Tj, Isolated from the Varzob River in Tajikistan. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	1
2729	Symbiosis islands of Loteae-nodulating <i>Mesorhizobium</i> comprise three radiating lineages with concordant nod gene complements and nodulation host-range groupings. <i>Microbial Genomics</i> , 2020, 6, .	2.0	7
2733	Development of PCR-Based Molecular Marker for Detection of <i>Xanthomonas campestris</i> pv. <i>campestris</i> Race 6, the Causative Agent of Black Rot of Brassicas. <i>Plant Pathology Journal</i> , 2020, 36, 418-427.	1.7	7
2736	Complete Plastome of <i>Carlina acaulis</i> and Implications on Systematics of the Tribe Cardueae (Asteraceae). <i>Annales Botanici Fennici</i> , 2021, 58, .	0.1	0
2737	Genomic evidence for stability of the <i>Bacillus Calmette-Guérin</i> (BCG) vaccine strain (Pasteur 1173P2) from different batches in Iran. <i>Journal of Applied Microbiology</i> , 2021, , .	3.1	0
2738	Accurate long-read de novo assembly evaluation with Inspector. <i>Genome Biology</i> , 2021, 22, 312.	8.8	46
2739	Extensive Genome Exploration of <i>Clostridium botulinum</i> Group III Field Strains. <i>Microorganisms</i> , 2021, 9, 2347.	3.6	9
2740	Phylogeny of Maleae (Rosaceae) Based on Complete Chloroplast Genomes Supports the Distinction of <i>Aria</i> , <i>Chamaemespilus</i> and <i>Torminalis</i> as Separate Genera, Different from <i>Sorbus</i> sp.. <i>Plants</i> , 2021, 10, 2534.	3.5	8
2741	Deciphering the Molecular Basis for Attenuation of <i>Flavobacterium columnare</i> Strain Fc1723 Used as Modified Live Vaccine against Columnaris Disease. <i>Vaccines</i> , 2021, 9, 1370.	4.4	3
2742	Genomic characterization and production of antimicrobial lipopeptides by <i>Bacillus velezensis</i> P45 growing on feather by-products. <i>Journal of Applied Microbiology</i> , 2022, 132, 2067-2079.	3.1	4

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2743	Comparative Chloroplast Genome Analyses of the Winter-Blooming Eastern Asian Endemic Genus <i>Chimonanthus</i> (Calycanthaceae) With Implications For Its Phylogeny and Diversification. <i>Frontiers in Genetics</i> , 2021, 12, 709996.	2.3	1
2744	Prediction and Analysis in silico of Genomic Islands in <i>Aeromonas hydrophila</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 769380.	3.5	2
2745	<i>Paralysiella testudinis</i> gen. nov., sp. nov., isolated from the cloaca of a toad-headed turtle (<i>Mesoclemmys nasuta</i>). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	1.7	9
2748	Remarkably coherent population structure for a dominant Antarctic <i>Chlorobium</i> species. <i>Microbiome</i> , 2021, 9, 231.	11.1	5
2749	Mitochondrial genomes of two parasitic <i>Cuscuta</i> species lack clear evidence of horizontal gene transfer and retain unusually fragmented ccmFC genes. <i>BMC Genomics</i> , 2021, 22, 816.	2.8	11
2750	The Gene Rearrangement, Loss, Transfer, and Deep Intronic Variation in Mitochondrial Genomes of <i>Conidiobolus</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 765733.	3.5	5
2751	Comparative Genomics Analyses Support the Reclassification of Bisgaard Taxon 40 as <i>Mergibacter</i> gen. nov., With <i>Mergibacter septicus</i> sp. nov. as Type Species: Novel Insights Into the Phylogeny and Virulence Factors of a Pasteurellaceae Family Member Associated With Mortality Events in Seabirds. <i>Frontiers in Microbiology</i> , 2021, 12, 667356.	3.5	4
2754	Comparative genomics and phylogenetic relationships of two endemic and endangered species (<i>Handeliendron bodinieri</i> and <i>Eurycorymbus cavaleriei</i>) of two monotypic genera within Sapindales. <i>BMC Genomics</i> , 2022, 23, 27.	2.8	12
2755	Characterization, genome analysis and in vitro activity of a novel phage vB_EcoA_RDN8.1 active against multi-drug resistant and extensively drug-resistant biofilm-forming uropathogenic <i>Escherichia coli</i> isolates, India. <i>Journal of Applied Microbiology</i> , 2022, 132, 3387-3404.	3.1	5
2756	Mobile Genetic Elements Drive Antimicrobial Resistance Gene Spread in Pasteurellaceae Species. <i>Frontiers in Microbiology</i> , 2021, 12, 773284.	3.5	11
2757	Regulation of Heterogenous LexA Expression in <i>Staphylococcus aureus</i> by an Antisense RNA Originating from Transcriptional Read-Through upon Natural Mispairings in the <i>sbrB</i> Intrinsic Terminator. <i>International Journal of Molecular Sciences</i> , 2022, 23, 576.	4.1	1
2758	Plasmids Bring Additional Capabilities to <i>Caulobacter</i> Isolates. <i>Current Microbiology</i> , 2022, 79, 45.	2.2	0
2759	Plastome structure, evolution, and phylogeny of <i>Selaginella</i> . <i>Molecular Phylogenetics and Evolution</i> , 2022, 169, 107410.	2.7	11
2760	Comparative Genomic and Phylogenetic Analysis of Spike and Nucleocapsid Proteins of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) and 9 Other Taxonomically Related Coronaviruses using in-Silico Tools. <i>Vantage: Journal of Thematic Analysis</i> , 2020, 1, 46-81.	0.0	0
2762	Genome analysis of <i>Lysinibacillus sphaericus</i> isolate 6.2 pathogenic to <i>Culex quinquefasciatus</i> Say, 1823 (Diptera: Culicidae). <i>Biodiversitas</i> , 2021, 22, .	0.6	0
2763	Genetic characteristics of an amikacin-resistant <i>Brucella abortus</i> strain first isolated from <i>Marmota himalayana</i> . <i>Microbial Pathogenesis</i> , 2022, 164, 105402.	2.9	3
2764	Genomic insights into the plant-associated lifestyle of <i>Kosakonia radicincitans</i> MUSA4, a diazotrophic plant-growth-promoting bacterium. <i>Systematic and Applied Microbiology</i> , 2022, 45, 126303.	2.8	6
2765	Phage JS02, a putative temperate phage, a novel biofilm-degrading agent for <i>Staphylococcus aureus</i> . <i>Letters in Applied Microbiology</i> , 2022, 75, 643-654.	2.2	9

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2766	Complete sequence of classic F-type plasmid pRK100 shows unique conservation over time and geographic location. <i>Plasmid</i> , 2022, 119-120, 102618.	1.4	0
2767	A Novel Method to Create Efficient Phage Cocktails via Use of Phage-Resistant Bacteria. <i>Applied and Environmental Microbiology</i> , 2022, 88, aem0232321.	3.1	16
2768	Identification of candidate type 3 effectors that determine host specificity associated with emerging <i>Ralstonia pseudosolanacearum</i> strains. <i>European Journal of Plant Pathology</i> , 2022, 163, 35-50.	1.7	9
2770	Genome diversity of domesticated <i>Acinetobacter baumannii</i> ATCC 19606T strains. <i>Microbial Genomics</i> , 2022, 8, .	2.0	7
2771	Complete de novo assembly of <i>Wolbachia</i> endosymbiont of <i>Diaphorina citri</i> Kuwayama (Hemiptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	3.3	14
2772	Novel insights into <i>Pinus</i> species plastids genome through phylogenetic relationships and repeat sequence analysis. <i>PLoS ONE</i> , 2022, 17, e0262040.	2.5	3
2773	A PARTHENOGENESIS allele from apomictic dandelion can induce egg cell division without fertilization in lettuce. <i>Nature Genetics</i> , 2022, 54, 84-93.	21.4	56
2774	Complete Chloroplast Genome Sequence of <i>Fagus longipetiolata</i> Seemen (Fagaceae): Genome Structure, Adaptive Evolution, and Phylogenetic Relationships. <i>Life</i> , 2022, 12, 92.	2.4	15
2775	Systematics of <i>Mukdenia</i> and <i>Oresitrophe</i> (Saxifragaceae): Insights from genome skimming data. <i>Journal of Systematics and Evolution</i> , 2023, 61, 99-114.	3.1	3
2776	Structural and evolutive features of the <i>Plinia phitrantha</i> and <i>P. cauliflora</i> plastid genomes and evolutionary relationships within tribe Myrteae (Myrtaceae). <i>Genetics and Molecular Biology</i> , 2022, 45, e20210193.	1.3	0
2777	Characterization and validation of an alternative reference bacterium Korean Pharmacopoeia <i>Staphylococcus aureus</i> strain. <i>Journal of Microbiology</i> , 2022, 60, 187-191.	2.8	1
2778	Modular evolution of secretion systems and virulence plasmids in a bacterial species complex. <i>BMC Biology</i> , 2022, 20, 16.	3.8	16
2780	Chloroplast Genome Evolution in Four Montane Zingiberaceae Taxa in China. <i>Frontiers in Plant Science</i> , 2021, 12, 774482.	3.6	16
2781	Selective Isolation of <i>Eggerthella lenta</i> from Human Faeces and Characterisation of the Species Prophage Diversity. <i>Microorganisms</i> , 2022, 10, 195.	3.6	9
2783	Complete chloroplast genomes of <i>Rubus</i> species (Rosaceae) and comparative analysis within the genus. <i>BMC Genomics</i> , 2022, 23, 32.	2.8	17
2784	The first complete plastome of <i>Mimusops coriacea</i> (A. DC.) Miq. (Sapotaceae). <i>Genetics and Molecular Biology</i> , 2022, 45, e20210174.	1.3	0
2785	Complete Genome Sequences of <i>Mycobacterium chimaera</i> Strains 850 and 852, Isolated from Heater-Cooler Unit Water. <i>Microbiology Resource Announcements</i> , 2022, 11, e0102121.	0.6	2
2786	Plastome phylogenomics of <i>Allaeanthus</i> , <i>Broussonetia</i> and <i>Malaisia</i> (Dorstenieae, Moraceae) and the origin of <i>B. kazinoki</i> . <i>Journal of Plant Research</i> , 2022, 135, 203-220.	2.4	4

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2787	The Complete Mitogenome of <i>Elymus sibiricus</i> and Insights Into Its Evolutionary Pattern Based on Simple Repeat Sequences of Seed Plant Mitogenomes. <i>Frontiers in Plant Science</i> , 2021, 12, 802321.	3.6	21
2788	Genomic Features and Pervasive Negative Selection in <i>Rhodanobacter</i> Strains Isolated from Nitrate and Heavy Metal Contaminated Aquifer. <i>Microbiology Spectrum</i> , 2022, 10, e0259121.	3.0	8
2789	The complete chloroplast genome sequencing analysis revealed an unusual IRs reduction in three species of subfamily Zygothelloideae. <i>PLoS ONE</i> , 2022, 17, e0263253.	2.5	11
2790	Comparative Genomic Analysis of Pathogenic Factors of <i>Pectobacterium</i> Species Isolated in South Korea Using Whole-Genome Sequencing. <i>Plant Pathology Journal</i> , 2022, 38, 12-24.	1.7	1
2791	Persistence and Dissemination Capacities of a blaNDM-5-Harboring IncX-3 Plasmid in <i>Escherichia coli</i> Isolated from an Urban River in Montpellier, France. <i>Antibiotics</i> , 2022, 11, 196.	3.7	4
2792	The plastome of <i>Melocactus glaucescens</i> Buining & Brederoo reveals unique evolutionary features and loss of essential tRNA genes. <i>Planta</i> , 2022, 255, 57.	3.2	5
2793	Dissemination Routes of Carbapenem and Pan-Aminoglycoside Resistance Mechanisms in Hospital and Urban Wastewater Canalizations of Ghana. <i>MSystems</i> , 2022, 7, e0101921.	3.8	7
2794	Complete genome assembly of the levano-positive strain <i>PVF11</i> of <i>Pseudomonas savastanoi</i> pv. <i>savastanoi</i> isolated from olive knots in Central Italy. <i>Environmental Microbiology Reports</i> , 2022, 14, 274-285.	2.4	7
2795	The complete chloroplast genome sequence of <i>Cicer echinospermum</i> , genome organization and comparison with related species. <i>Scientia Horticulturae</i> , 2022, 296, 110912.	3.6	7
2796	Evolutionary classification of tumor- and root-inducing plasmids based on T-DNAs and virulence regions. <i>Molecular Phylogenetics and Evolution</i> , 2022, 169, 107388.	2.7	5
2798	The Complete Chloroplast Genome Sequence of <i>Cicer bijugum</i> , Genome Organization, and Comparison with Related Species. <i>Current Genomics</i> , 2022, 23, 50-65.	1.6	3
2799	Endogenous CRISPR-Cas Systems in Group I <i>Clostridium botulinum</i> and <i>Clostridium sporogenes</i> Do Not Directly Target the Botulinum Neurotoxin Gene Cluster. <i>Frontiers in Microbiology</i> , 2021, 12, 787726.	3.5	8
2800	Comparison of Magnoliaceae Plastomes: Adding Neotropical Magnolia to the Discussion. <i>Plants</i> , 2022, 11, 448.	3.5	7
2801	The First Mitochondrial Genome of <i>Ciborinia camelliae</i> and Its Position in the Sclerotiniaceae Family. <i>Frontiers in Fungal Biology</i> , 2022, 2, .	2.0	4
2802	Long-Read Sequencing Reveals Genetic Adaptation of <i>Bartonella Adhesin A</i> Among Different <i>Bartonella henselae</i> Isolates. <i>Frontiers in Microbiology</i> , 2022, 13, 838267.	3.5	9
2803	Dual RNA sequencing reveals dendritic cell reprogramming in response to typhoidal <i>Salmonella</i> invasion. <i>Communications Biology</i> , 2022, 5, 111.	4.4	11
2804	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.	3.6	12
2805	Defining the mutation sites in chickpea nodulation mutants PM233 and PM405. <i>BMC Plant Biology</i> , 2022, 22, 66.	3.6	3

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2806	Identification of Type VI Secretion Systems Effector Proteins That Contribute to Interbacterial Competition in Salmonella Dublin. <i>Frontiers in Microbiology</i> , 2022, 13, 811932.	3.5	9
2807	<i>Aspergillus flavus</i> La3279, a component strain of the Aflasafe [®] biocontrol product, contains a partial aflatoxin biosynthesis gene cluster followed by a genomic region highly variable among <i>A. flavus</i> isolates. <i>International Journal of Food Microbiology</i> , 2022, 366, 109559.	4.7	7
2808	GEnView: a gene-centric, phylogeny-based comparative genomics pipeline for bacterial genomes and plasmids. <i>Bioinformatics</i> , 2022, 38, 1727-1728.	4.1	6
2809	Complete plastid genome of <i>L. (Surianaceae)</i> and its implications in phylogenetic reconstruction of Fabales. <i>Journal of Genetics</i> , 2019, 98, .	0.7	0
2810	Complete chloroplast genome of (<i>Papilionoideae</i>): molecular structures, comparative genome analysis and phylogenetic analysis. <i>Journal of Genetics</i> , 2020, 99, .	0.7	7
2811	Complete Genome Sequence of Four Strains of <i>Leptospira borgpetersenii</i> serovar Hardjo isolated from Cattle in the Central United States. <i>Journal of Genomics</i> , 2022, 10, 45-48.	0.9	4
2812	Trans-Regional and Cross-Host Spread of ϕ -Carrying Plasmids Revealed by Complete Plasmid Sequences â€” 44 Countries, 1998â”2020. <i>China CDC Weekly</i> , 2022, 4, 242-248.	2.3	6
2813	Comparative mitochondrial genome analyses reveal conserved gene arrangement but massive expansion/contraction in two closely related <i>Exserohilum</i> pathogens. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 1456-1469.	4.1	4
2814	The first de novo genome assembly and sex marker identification of Pluang Chomphu fish (<i>Tor tambra</i>) from Southern Thailand. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 1470-1480.	4.1	2
2815	Phenotypic and Genomic Diversification in Complex Carbohydrate-Degrading Human Gut Bacteria. <i>MSystems</i> , 2022, 7, e0094721.	3.8	40
2816	Genome Mining and Analysis of PKS Genes in <i>Eurotium cristatum</i> E1 Isolated from Fuzhuan Brick Tea. <i>Journal of Fungi</i> (Basel, Switzerland), 2022, 8, 193.	3.5	3
2817	Isolation and Characterization of Levoglucosan-Metabolizing Bacteria. <i>Applied and Environmental Microbiology</i> , 2022, 88, AEM0186821.	3.1	6
2818	Comparative Genome Analysis of Two <i>Bacillus pumilus</i> Strains Producing High Level of Extracellular Hydrolases. <i>Genes</i> , 2022, 13, 409.	2.4	8
2819	Characterization and genomic analysis of a <i>Demerecviridae</i> phage SP76 with lytic multiple-serotypes of <i>Salmonella</i> . <i>Archives of Microbiology</i> , 2022, 204, 175.	2.2	1
2821	Experimental evaluation of ecological principles to understand and modulate the outcome of bacterial strain competition in gut microbiomes. <i>ISME Journal</i> , 2022, 16, 1594-1604.	9.8	24
2822	Population Dynamics of a Two Phagesâ”One Host Infection System Using <i>Escherichia coli</i> Strain ECOR57 and Phages vB_EcoP_SUI0 and vB_EcoD_SU57. <i>Pharmaceuticals</i> , 2022, 15, 268.	3.8	2
2823	Oxytetracycline and Streptomycin Resistance Genes in <i>Xanthomonas arboricola</i> pv. <i>pruni</i> , the Causal Agent of Bacterial Spot in Peach. <i>Frontiers in Microbiology</i> , 2022, 13, 821808.	3.5	13
2824	Decoding the Gene Variants of Two Native Probiotic <i>Lactiplantibacillus plantarum</i> Strains through Whole-Genome Resequencing: Insights into Bacterial Adaptability to Stressors and Antimicrobial Strength. <i>Genes</i> , 2022, 13, 443.	2.4	6

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2825	The Use of Long-Read Sequencing Technologies in Infection Control: Horizontal Transfer of a blaCTX-M-27 Containing IncFII Plasmid in a Patient Screening Sample. <i>Microorganisms</i> , 2022, 10, 491.	3.6	5
2826	Phylogenomic and comparative analyses of Coffeae alliance (Rubiaceae): deep insights into phylogenetic relationships and plastome evolution. <i>BMC Plant Biology</i> , 2022, 22, 88.	3.6	17
2827	Genomic and Phenotypic Characterization of the Nontoxigenic <i>Clostridioides difficile</i> Strain CCUG37785 and Demonstration of Its Therapeutic Potential for the Prevention of <i>C. difficile</i> Infection. <i>Microbiology Spectrum</i> , 2022, 10, e0178821.	3.0	7
2828	The <i>Bacillus</i> phage ϕ SP1 ² and its relatives: a temperate phage model system reveals new strains, species, prophage integration loci, conserved proteins and lysogeny management components. <i>Environmental Microbiology</i> , 2022, 24, 2098-2118.	3.8	19
2829	The Importance of Shiga Toxin-Producing <i>Escherichia coli</i> O145:NM[H28]/H28 Infections in Argentina, 1998–2020. <i>Microorganisms</i> , 2022, 10, 582.	3.6	6
2830	Use of Nanopore Sequencing to Characterise the Genomic Architecture of Mobile Genetic Elements Encoding blaCTX-M-15 in <i>Escherichia coli</i> Causing Travellers' Diarrhoea. <i>Frontiers in Microbiology</i> , 2022, 13, 862234.	3.5	4
2831	A mobile restriction–modification system provides phage defence and resolves an epigenetic conflict with an antagonistic endonuclease. <i>Nucleic Acids Research</i> , 2022, 50, 3348-3361.	14.5	17
2834	Complete Chloroplast Genomes and Comparative Analyses of Three Ornamental <i>Impatiens</i> Species. <i>Frontiers in Genetics</i> , 2022, 13, 816123.	2.3	4
2835	Complete Genome Assemblies of All <i>Xanthomonas translucens</i> Pathotype Strains Reveal Three Genetically Distinct Clades. <i>Frontiers in Microbiology</i> , 2021, 12, 817815.	3.5	19
2836	Ensifer meliloti L6-AK89, an Effective Inoculant of <i>Medicago lupulina</i> Varieties: Phenotypic and Deep-Genome Screening. <i>Agronomy</i> , 2022, 12, 766.	3.0	8
2837	The Space-Exposed Kombucha Microbial Community Member <i>Komagataeibacter oboediens</i> Showed Only Minor Changes in Its Genome After Reactivation on Earth. <i>Frontiers in Microbiology</i> , 2022, 13, 782175.	3.5	5
2838	CovDif, a Tool to Visualize the Conservation between SARS-CoV-2 Genomes and Variants. <i>Viruses</i> , 2022, 14, 561.	3.3	1
2840	Environmental Potential for Microbial 1,4-Dioxane Degradation Is Sparse despite Mobile Elements Playing a Role in Trait Distribution. <i>Applied and Environmental Microbiology</i> , 2022, 88, e0209121.	3.1	8
2841	Successful Intra- but Not Inter-species Recombination of msr(D) in <i>Neisseria subflava</i> . <i>Frontiers in Microbiology</i> , 2022, 13, 855482.	3.5	1
2842	In Vitro Evolution of Specific Phages Infecting the Fish Pathogen <i>Flavobacterium psychrophilum</i> . <i>Phage</i> , 2022, 3, 28-37.	1.7	1
2843	Comparative Genomic Analysis Reveals Intestinal Habitat Adaptation of <i>Ligilactobacillus</i> Rich in Prophage and Degrading Cellulase. <i>Molecules</i> , 2022, 27, 1867.	3.8	1
2844	Identification of the Genes of the Plant Pathogen <i>Pseudomonas syringae</i> MB03 Required for the Nematicidal Activity Against <i>Caenorhabditis elegans</i> Through an Integrated Approach. <i>Frontiers in Microbiology</i> , 2022, 13, 826962.	3.5	3
2845	Characterization of strain-specific <i>Bacillus cereus</i> swimming motility and flagella by means of specific antibodies. <i>PLoS ONE</i> , 2022, 17, e0265425.	2.5	3

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2846	Independent Size Expansions and Intron Proliferation in Red Algal Plastid and Mitochondrial Genomes. <i>Genome Biology and Evolution</i> , 2022, 14, .	2.5	5
2847	Comparative genomic analysis of vertebrate mitochondrial reveals a differential of rearrangements rate between taxonomic class. <i>Scientific Reports</i> , 2022, 12, 5479.	3.3	13
2848	Complex mitogenomic rearrangements within the Pectinidae (Mollusca: Bivalvia). <i>Bmc Ecology and Evolution</i> , 2022, 22, 29.	1.6	6
2849	A comparative study on the genomes, transcriptomes, and metabolic properties of <i>Escherichia coli</i> strains Nissle 1917, BL21(DE3), and MG1655. <i>Engineering Microbiology</i> , 2022, 2, 100012.	4.7	9
2850	A high-quality reference genome for the fish pathogen <i>Streptococcus iniae</i> . <i>Microbial Genomics</i> , 2022, 8, .	2.0	0
2851	Screening of Potential <i>Vibrio cholerae</i> Bacteriophages for Cholera Therapy: A Comparative Genomic Approach. <i>Frontiers in Microbiology</i> , 2022, 13, 803933.	3.5	4
2852	Isolation of a Colistin-Susceptible MDR <i>Pantoea calida</i> Harboring the <i>mcr-9</i> Gene Suggests the Silent Spread of the Resistance Factor. <i>Microbial Drug Resistance</i> , 2022, 28, 408-412.	2.0	2
2853	Tracking habitat or testing its suitability? Similar distributional patterns can hide very different histories of persistence versus nonequilibrium dynamics. <i>Evolution; International Journal of Organic Evolution</i> , 2022, 76, 1209-1228.	2.3	3
2854	Genomic evolution and adaptation of arthropod-associated <i>Rickettsia</i> . <i>Scientific Reports</i> , 2022, 12, 3807.	3.3	25
2855	Genomic, biochemical, and phylogenetic evaluation of bacteria isolated from deep-sea sediment harboring methane hydrates. <i>Archives of Microbiology</i> , 2022, 204, 205.	2.2	0
2856	The complete plastomes of seven <i>Peucedanum</i> plants: comparative and phylogenetic analyses for the <i>Peucedanum</i> genus. <i>BMC Plant Biology</i> , 2022, 22, 101.	3.6	25
2857	Comparative analysis of complete <i>Ilex</i> (Aquifoliaceae) chloroplast genomes: insights into evolutionary dynamics and phylogenetic relationships. <i>BMC Genomics</i> , 2022, 23, 203.	2.8	11
2858	Lytic Phages against ST11 K47 Carbapenem-Resistant <i>Klebsiella pneumoniae</i> and the Corresponding Phage Resistance Mechanisms. <i>MSphere</i> , 2022, 7, e0008022.	2.9	7
2859	Comparative Draft Genomes of <i>Leishmania orientalis</i> Isolate PCM2 (Formerly Named <i>Leishmania</i>) Tj ETQq1 1 0.784314 rgBT /Overlock Biology, 2022, 11, 515.	2.8	6
2861	Black pepper and tarragon essential oils suppress the lipolytic potential and the type II secretion system of <i>P. psychrophila</i> KM02. <i>Scientific Reports</i> , 2022, 12, 5487.	3.3	2
2862	Detection and characterisation of 16S rRNA methyltransferase-producing <i>Pseudomonas aeruginosa</i> from the UK and Republic of Ireland from 2003–2015. <i>International Journal of Antimicrobial Agents</i> , 2022, 59, 106550.	2.5	8
2863	Whole genome sequence analysis of <i>Salmonella</i> Typhi in Papua New Guinea reveals an established population of genotype 2.1.7 sensitive to antimicrobials. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010306.	3.0	6
2864	Isolation and Characterization of Lytic Bacteriophages Targeting Diverse <i>Enterobacter</i> spp. Clinical Isolates. <i>Phage</i> , 2022, 3, 50-58.	1.7	1

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2865	Genetic Diversity of Antimicrobial Resistance and Key Virulence Features in Two Extensively Drug-Resistant <i>Acinetobacter baumannii</i> Isolates. <i>International Journal of Environmental Research and Public Health</i> , 2022, 19, 2870.	2.6	4
2867	Population genomics of the grapevine pathogen <i>Eutypa lata</i> reveals evidence for population expansion and intraspecific differences in secondary metabolite gene clusters. <i>PLoS Genetics</i> , 2022, 18, e1010153.	3.5	10
2868	Comparative and phylogenetic analyses of six Kenya <i>Polystachya</i> (Orchidaceae) species based on the complete chloroplast genome sequences. <i>BMC Plant Biology</i> , 2022, 22, 177.	3.6	37
2869	Rates of evolutionary change of resident <i>Escherichia coli</i> O157:H7 differ within the same ecological niche. <i>BMC Genomics</i> , 2022, 23, 275.	2.8	3
2870	Comparative Genomic Analysis of a Pantone®-Valentine Leukocidin-Positive ST22 Community-Acquired Methicillin-Resistant <i>Staphylococcus aureus</i> from Pakistan. <i>Antibiotics</i> , 2022, 11, 496.	3.7	6
2871	Genome Wide Analysis of the Potato Soft Rot Pathogen <i>Pectobacterium carotovorum</i> Strain ICMP 5702 to Predict Novel Insights into Its Genetic Features. <i>Plant Pathology Journal</i> , 2022, 38, 102-114.	1.7	1
2872	Safety Assessment of <i>Lactiplantibacillus plantarum</i> TWK10 Based on Whole-Genome Sequencing, Phenotypic, and Oral Toxicity Analysis. <i>Microorganisms</i> , 2022, 10, 784.	3.6	9
2873	<i>Bifidobacterium longum</i> subsp. <i>longum</i> K5 alleviates inflammatory response and prevents intestinal barrier injury induced by LPS in vitro based on comparative genomics. <i>Journal of Functional Foods</i> , 2022, 92, 105030.	3.4	10
2874	Comparative mitochondrial genomes of the <i>Rhus</i> gall aphid <i>Kaburagia rhusicola</i> subspecies with variable gall shapes. <i>Gene</i> , 2022, 824, 146379.	2.2	0
2875	Genetic characterization and comparative genomics of a multi drug resistant (MDR) <i>Escherichia coli</i> SCM-21 isolated from a subclinical case of bovine mastitis. <i>Comparative Immunology, Microbiology and Infectious Diseases</i> , 2022, 85, 101799.	1.6	6
2876	Isolation and genomic analysis of temperate phage 5W targeting multidrug-resistant <i>Acinetobacter baumannii</i> . <i>Archives of Microbiology</i> , 2022, 204, 58.	2.2	9
2877	A dual endosymbiosis supports nutritional adaptation to hematophagy in the invasive tick <i>Hyalomma marginatum</i> . <i>ELife</i> , 2021, 10, .	6.0	32
2878	Genomic diversity of antimicrobial resistance in non-typhoidal <i>Salmonella</i> in Victoria, Australia. <i>Microbial Genomics</i> , 2021, 7, .	2.0	2
2879	Analyses of Chloroplast Genome of <i>Eutrema japonicum</i> Provide New Insights into the Evolution of <i>Eutrema</i> Species. <i>Agronomy</i> , 2021, 11, 2546.	3.0	5
2880	Increased Pathogenicity of the Nematophagous Fungus <i>Drechmeria coniospora</i> Following Long-Term Laboratory Culture. <i>Frontiers in Fungal Biology</i> , 2021, 2, .	2.0	0
2881	Comparative Chloroplast Genomics of <i>Sophora</i> Species: Evolution and Phylogenetic Relationships in the Early-Diverging Legume Subfamily Papilionoideae (Fabaceae). <i>Frontiers in Plant Science</i> , 2021, 12, 778933.	3.6	7
2882	Genomic comparison and phenotypic profiling of small colony variants of <i>Burkholderia pseudomallei</i> . <i>PLoS ONE</i> , 2021, 16, e0261382.	2.5	1
2883	Proteome and secretome profiling of zinc availability in <i>Cryptococcus neoformans</i> identifies Wos2 as a subtle influencer of fungal virulence determinants. <i>BMC Microbiology</i> , 2021, 21, 341.	3.3	6

#	ARTICLE	IF	CITATIONS
2884	Prochlorococcus have low global mutation rate and small effective population size. <i>Nature Ecology and Evolution</i> , 2022, 6, 183-194.	7.8	16
2885	Signatures of Adaptation in Mitochondrial Genomes of Palearctic Subterranean Voles (Arvicolinae.) <i>Tj ETQq1 1 0.784314 rgBT /Overlock</i>	2.4	5
2886	Assembling the puzzle: Complete chloroplast genome sequences of <i>Discocactus bahiensis</i> Britton & Rose and <i>Melocactus ernestii</i> Vaupel (Cactaceae) and their evolutionary significance. <i>Revista Brasileira De Botanica</i> , 2021, 44, 877-888.	1.3	3
2887	Plastome Diversity and Phylogenomic Relationships in Asteraceae. <i>Plants</i> , 2021, 10, 2699.	3.5	13
2888	Mobilization of vitamin B12 transporters alters competitive dynamics in a human gut microbe. <i>Cell Reports</i> , 2021, 37, 110164.	6.4	8
2889	Prevalence of an Insect-Associated Genomic Region in Environmentally Acquired <i>Burkholderiaceae</i> Symbionts. <i>Applied and Environmental Microbiology</i> , 2022, 88, e0250221.	3.1	2
2890	Comparative Genomic Analysis Reveals Potential Pathogenicity and Slow-Growth Characteristics of Genus <i>Brevundimonas</i> and Description of <i>Brevundimonas pishanensis</i> sp. nov.. <i>Microbiology Spectrum</i> , 2022, 10, e0246821.	3.0	5
2891	GenomeSyn: a bioinformatics tool for visualizing genome synteny and structural variations. <i>Journal of Genetics and Genomics</i> , 2022, 49, 1174-1176.	3.9	16
2892	Antimicrobial resistance and genetic background of non-typhoidal <i>Salmonella enterica</i> strains isolated from human infections in São Paulo, Brazil (2000–2019). <i>Brazilian Journal of Microbiology</i> , 2022, 53, 1249-1262.	2.0	5
2894	Comparative Genomic Analysis of <i>Vibrio cincinnatiensis</i> Provides Insights into Genetic Diversity, Evolutionary Dynamics, and Pathogenic Traits of the Species. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4520.	4.1	3
2895	Genomic Insights into Omega-3 Polyunsaturated Fatty Acid Producing <i>Shewanella</i> sp. N2AIL from Fish Gut. <i>Biology</i> , 2022, 11, 632.	2.8	4
2896	Diversity of genomic clusters and <i>CfiA/cfiA</i> alleles in <i>Bacteroides fragilis</i> isolates from human and animals. <i>Anaerobe</i> , 2022, 75, 102567.	2.1	5
3322	Integrative Genomics Sheds Light on Evolutionary Forces Shaping the Acidithiobacillia Class Acidophilic Lifestyle. <i>Frontiers in Microbiology</i> , 2021, 12, 822229.	3.5	10
3323	<i>Wolbachia</i> endosymbionts in two <i>Anopheles</i> species indicates independent acquisitions and lack of prophage elements. <i>Microbial Genomics</i> , 2022, 8, .	2.0	3
3324	Construction and Analysis of the Complete Genome Sequence of Leprosy Agent <i>Mycobacterium lepromatosis</i> . <i>Microbiology Spectrum</i> , 2022, 10, e0169221.	3.0	7
3325	Whole genome sequencing and taxonomic profiling of two <i>Pantoea</i> sp. isolated from environmental samples in Israel. <i>BMC Genomic Data</i> , 2022, 23, 31.	1.7	1
3326	Gene loss, genome rearrangement, and accelerated substitution rates in plastid genome of <i>Hypericum ascyron</i> (Hypericaceae). <i>BMC Plant Biology</i> , 2022, 22, 135.	3.6	16
3327	Comparative analysis of the complete mitochondrial genomes of four cordyceps fungi. <i>Ecology and Evolution</i> , 2022, 12, e8818.	1.9	3

#	ARTICLE	IF	CITATIONS
3328	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.	1.7	3
3329	Genome Resource of <i>Colletotrichum spaethianum</i> , the Causal Agent of Leaf Anthracnose in <i>Polygonatum falcatum</i> . <i>PhytoFrontiers</i> , 2022, 2, 152-155.	1.6	6
3330	Genomic Analysis of Two Representative Strains of <i>Shewanella putrefaciens</i> Isolated from Bigeye Tuna: Biofilm and Spoilage-Associated Behavior. <i>Foods</i> , 2022, 11, 1261.	4.3	8
3332	Complete Genome Sequences of Four Strains of <i>Erwinia tracheiphila</i> : A Resource for Studying a Bacterial Plant Pathogen with a Highly Complex Genome. <i>Molecular Plant-Microbe Interactions</i> , 2022, 35, 500-504.	2.6	4
3333	Genomic Comparison of Eight Closed Genomes of Multidrug-Resistant <i>Salmonella enterica</i> Strains Isolated From Broiler Farms and Processing Plants in Trinidad and Tobago. <i>Frontiers in Microbiology</i> , 2022, 13, .	3.5	2
3334	Genomic analysis of two Chinese isolates of <i>hyphantria cunea</i> nucleopolyhedrovirus reveals a novel species of alphabaculovirus that infects <i>hyphantria cunea</i> drury (lepidoptera: arctiidae). <i>BMC Genomics</i> , 2022, 23, 367.	2.8	2
3335	Sequence Analysis of the Complete Mitochondrial Genome of a Medicinal Plant, <i>Vitex rotundifolia</i> Linnaeus f. (Lamiales: Lamiaceae). <i>Genes</i> , 2022, 13, 839.	2.4	11
3336	Comparative Genomics of <i>Synechococcus elongatus</i> Explains the Phenotypic Diversity of the Strains. <i>MBio</i> , 2022, 13, e0086222.	4.1	13
3337	Genomic and Phenotypic Characterization of <i>Clostridium botulinum</i> Isolates from an Infant Botulism Case Suggests Adaptation Signatures to the Gut. <i>MBio</i> , 2022, 13, e0238421.	4.1	5
3338	Description of a novel IncP plasmid harboring blaKPC-2 recovered from a SPM-1-producing <i>Pseudomonas aeruginosa</i> from ST277. <i>Infection, Genetics and Evolution</i> , 2022, , 105302.	2.3	4
3339	The genetic basis of natural variation in the timing of vegetative phase change in <i>Arabidopsis thaliana</i> . <i>Development (Cambridge)</i> , 2022, 149, .	2.5	8
3340	B-assembler: a circular bacterial genome assembler. <i>BMC Genomics</i> , 2022, 23, 361.	2.8	3
3341	Genomic insights into the diversity of non-coding RNAs in <i>Bacillus cereus</i> sensu lato. <i>Current Genetics</i> , 2022, , .	1.7	0
3342	Structural Variation of Plastomes Provides Key Insight Into the Deep Phylogeny of Ferns. <i>Frontiers in Plant Science</i> , 2022, 13, .	3.6	11
3343	Distribution of pBS72-like conjugative plasmids among natural bacteria of the genus <i>Bacillus</i> . <i>Vestsi Natsyianal'nai Akademii Navuk Belarusi Seryia Biilahichnykh Navuk</i> , 2022, 67, 219-228.	0.1	0
3344	Biochemical and molecular characterization of three serologically different <i>Vibrio harveyi</i> strains isolated from farmed <i>Dicentrarchus labrax</i> from the Adriatic Sea. <i>Scientific Reports</i> , 2022, 12, 7309.	3.3	4
3345	Dressing like a pathogen: Comparative analysis of different <i>Pseudomonas</i> genomospecies wearing different features to infect <i>Corylus avellana</i> . <i>Journal of Phytopathology</i> , 2022, 170, 504-516.	1.0	4
3346	Whole Genome Sequencing and Biological Characteristics of Two Strains of Porcine <i>Escherichia coli</i> Isolated from Saba Pigs. <i>Current Microbiology</i> , 2022, 79, 182.	2.2	3

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3347	Genomic characterization of lytic bacteriophages targeting genetically diverse <i>Pseudomonas aeruginosa</i> clinical isolates. <i>IScience</i> , 2022, 25, 104372.	4.1	16
3348	Comparative genomics among cyst nematodes reveals distinct evolutionary histories among effector families and an irregular distribution of effector-associated promoter motifs. <i>Molecular Ecology</i> , 2023, 32, 1515-1529.	3.9	7
3349	Draft genome sequence of <i>Bacillus</i> sp. strain FSQ1, a biological control agent against white mold in common bean (<i>Phaseolus vulgaris</i> L.). <i>Current Research in Microbial Sciences</i> , 2022, 3, 100138.	2.3	3
3350	Sequence-based pangenomic core detection. <i>IScience</i> , 2022, 25, 104413.	4.1	5
3351	High Prevalence of blaCTXM-1/IncI1-Î³/ST3 Plasmids in Extended-Spectrum Î²-Lactamase-Producing <i>Escherichia coli</i> Isolates Collected From Domestic Animals in Guadeloupe (French West Indies). <i>Frontiers in Microbiology</i> , 2022, 13, .	3.5	3
3352	<i>Streptomyces benahoarensis</i> sp. nov. Isolated From a Lava Tube of La Palma, Canary Islands, Spain. <i>Frontiers in Microbiology</i> , 2022, 13, .	3.5	3
3353	Genome mining of <i>Burkholderia ambifaria</i> strain T16, a rhizobacterium able to produce antimicrobial compounds and degrade the mycotoxin fusaric acid. <i>World Journal of Microbiology and Biotechnology</i> , 2022, 38, 114.	3.6	8
3354	Full Issue PDF. <i>Molecular Plant-Microbe Interactions</i> , 2022, 35, 439-508.	2.6	0
3356	Chromosome organization affects genome evolution in <i>Sulfolobus</i> archaea. <i>Nature Microbiology</i> , 2022, 7, 820-830.	13.3	12
3357	Widespread stop-codon recoding in bacteriophages may regulate translation of lytic genes. <i>Nature Microbiology</i> , 2022, 7, 918-927.	13.3	25
3358	Multi-omics analysis reveals the mechanism of seed coat color formation in <i>Brassica rapa</i> L.. <i>Theoretical and Applied Genetics</i> , 2022, 135, 2083-2099.	3.6	7
3359	Evolutionary Dynamics and Lateral Gene Transfer in Raphidophyceae Plastid Genomes. <i>Frontiers in Plant Science</i> , 2022, 13, .	3.6	3
3360	Genomic structural plasticity of rodent-associated <i>Bartonella</i> in nature. <i>Molecular Ecology</i> , 0, .	3.9	1
3363	Complete Genome Sequence of <i>Streptomyces albus</i> Strain G153. <i>Microbiology Resource Announcements</i> , 0, .	0.6	1
3364	Genome of <i>Malassezia arunalokei</i> and Its Distribution on Facial Skin. <i>Microbiology Spectrum</i> , 2022, 10, .	3.0	7
3365	Natural Products Produced in Culture by Biosynthetically Talented <i>Salinispora arenicola</i> Strains Isolated from Northeastern and South Pacific Marine Sediments. <i>Molecules</i> , 2022, 27, 3569.	3.8	1
3366	The Maternal Donor of Chrysanthemum Cultivars Revealed by Comparative Analysis of the Chloroplast Genome. <i>Frontiers in Plant Science</i> , 2022, 13, .	3.6	8
3367	Phenotypic characterization and analysis of complete genomes of two distinct strains of the proposed species <i>œL. swaminathanii</i> . <i>Scientific Reports</i> , 2022, 12, .	3.3	6

#	ARTICLE	IF	CITATIONS
3368	Physiological and biochemical characterization and genome analysis of <i>Rhodococcus qingshengii</i> strain 7B capable of crude oil degradation and plant stimulation. <i>Biotechnology Reports</i> (Amsterdam,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.4	0
3373	Experimental Pathogenicity and Comparative Genome Analysis of High- and Low-Virulence Strains of Rabbit-Origin <i>Pasteurella Multocida</i> . <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
3374	Rediscovering "Baculovirus-A" (Johnson, 1976): The Complete Genome of "Callinectes Sapidus Nudivirus" (Nudiviridae: Gammanudivirus). <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
3375	Whole-genome analysis of <i>Bacillus subtilis</i> G8 isolated from natto. <i>Biodiversitas</i> , 2022, 23, .	0.6	0
3376	Characterization of the Complete Chloroplast Genome Sequence of the Socotra Dragon's Blood Tree (<i>Dracaena cinnabari</i> Balf.). <i>Forests</i> , 2022, 13, 932.	2.1	3
3377	Suggestion for a new bacteriophage genus for the <i>Klebsiella pneumoniae</i> phage "B_KpnS-Carvaje". <i>Current Genetics</i> , 2022, 68, 393-406.	1.7	3
3378	Plastome characteristics and species identification of Chinese medicinal wintergreens (<i>Gaultheria</i>), Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	3.7	4
3379	Complete genome sequences and genomic characterization of five plasmids harbored by environmentally persistent <i>Cronobacter sakazakii</i> strains ST83 H322 and ST64 CK1025B obtained from powdered infant formula manufacturing facilities. <i>Gut Pathogens</i> , 2022, 14, .	3.4	4
3380	The compact mitogenome of <i>Ceratocystopsis pallidobrunnea</i> . <i>Canadian Journal of Microbiology</i> , 2022, 68, 569-575.	1.7	1
3381	Characterization and Complete Genomic Analysis of <i>Vibrio Parahaemolyticus</i> -Infecting Phage KIT05. <i>Current Microbiology</i> , 2022, 79, .	2.2	3
3382	Complete Genome Sequences of <i>Rhizobium gallicum</i> M101 and Two Potential New <i>Rhizobium</i> Species Isolated from Soils in Central Canada. <i>Microbiology Resource Announcements</i> , 2022, 11, .	0.6	1
3383	New insights into intergeneric relationships of <i>Hickeliinae</i> (Poaceae: Bambusoideae) revealed by complete plastid genomes. <i>Plant Diversity</i> , 2023, 45, 125-132.	3.7	1
3385	Discovery of the First Lytic <i>Staphylococcus pseudintermedius</i> / <i>Staphylococcus aureus</i> Polyvalent Bacteriophages. <i>Phage</i> , 2022, 3, 116-124.	1.7	1
3386	Accumulation of endosymbiont genomes in an insect autosome followed by endosymbiont replacement. <i>Current Biology</i> , 2022, 32, 2786-2795.e5.	3.9	8
3387	Simplexviruses Successfully Adapt to Their Host by Fine-Tuning Immune Responses. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	3
3388	Taxonomic Re-Evaluation and Genomic Comparison of Novel Extracellular Electron Uptake-Capable <i>Rhodovulum visakhapatnamense</i> and <i>Rhodovulum sulfidophilum</i> Isolates. <i>Microorganisms</i> , 2022, 10, 1235.	3.6	0
3389	Annotation-free delineation of prokaryotic homology groups. <i>PLoS Computational Biology</i> , 2022, 18, e1010216.	3.2	0
3390	The organellar genomes of <i>Silvetia siliquosa</i> (Fucales, Phaeophyceae) and comparative analyses of the brown algae. <i>PLoS ONE</i> , 2022, 17, e0269631.	2.5	0

#	ARTICLE	IF	CITATIONS
3391	Genome Sequences of Two New Pandoravirus Strains Isolated from Brazil and France. Microbiology Resource Announcements, 2022, 11, .	0.6	1
3392	Chromosome-scale assembly with a phased sex-determining region resolves features of early Z and W chromosome differentiation in a wild octoploid strawberry. G3: Genes, Genomes, Genetics, 2022, 12, .	1.8	11
3393	Draft genome sequence and functional analysis of Lysinibacillus xylanilyticus t26, a plant growth-promoting bacterium isolated from Capsicum chinense rhizosphere. Journal of Biosciences, 2022, 47, .	1.1	2
3394	Phylogenomic and functional characterization of an evolutionary conserved cytochrome P450-based insecticide detoxification mechanism in bees. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	31
3395	Reclassification of Streptococcus ilei as a later heterotypic synonym of Streptococcus koreensis based on whole-genome sequence analysis. Archives of Microbiology, 2022, 204, .	2.2	1
3396	Widespread phages of endosymbionts: Phage WO genomics and the proposed taxonomic classification of Symbioviridae. PLoS Genetics, 2022, 18, e1010227.	3.5	22
3397	PRODUCTION OF MANNOSYLERYTHRITOL LIPIDS: BIOSYNTHESIS, MULTI-OMICS APPROACHES AND COMMERCIAL EXPLOITATION. Molecular Omics, 0, , .	2.8	0
3398	Chromosome-level assembly and annotation of the blue catfish <i> Ictalurus furcatus</i> , an aquaculture species for hybrid catfish reproduction, epigenetics, and heterosis studies. GigaScience, 2022, 11, .	6.4	8
3399	Virulence plasmid pINV as a genetic signature for Shigella flexneri phylogeny. Microbial Genomics, 2022, 8, .	2.0	3
3400	Plastid Phylogenomics and Plastome Evolution of Nandinoideae (Berberidaceae). Frontiers in Plant Science, 0, 13, .	3.6	2
3401	The complete chloroplast genome of the Egyptian henbane (<i>Hyoscyamus muticus</i> L., Solanaceae). Mitochondrial DNA Part B: Resources, 2022, 7, 1109-1111.	0.4	1
3402	Comparative Genome Analysis of Two Heterotrophic Nitrifying Pseudomonas putida Strains Isolated from Freshwater Shrimp Ponds in Soc Trang Province. Fermentation, 2022, 8, 336.	3.0	1
3403	Revised Species Delimitation in the Giant Water Lily Genus Victoria (Nymphaeaceae) Confirms a New Species and Has Implications for Its Conservation. Frontiers in Plant Science, 0, 13, .	3.6	9
3404	Identification of Peptoniphilus vaginalis-Like Bacteria, Peptoniphilus septimus sp. nov., From Blood Cultures in a Cervical Cancer Patient Receiving Chemotherapy: Case and Implications. Frontiers in Cellular and Infection Microbiology, 0, 12, .	3.9	3
3405	Characterization of Bordetella pertussis Strains Isolated from India. Pathogens, 2022, 11, 794.	2.8	1
3406	Comparative genomics of Nocardia seriolae reveals recent importation and subsequent widespread dissemination in mariculture farms in the South Central Coast region, Vietnam. Microbial Genomics, 2022, 8, .	2.0	1
3407	Within-host evolution of a gut pathobiont facilitates liver translocation. Nature, 2022, 607, 563-570.	27.8	65
3408	Characterization and phylogenetic analysis of the complete mitochondrial genome sequence of Diospyros oleifera, the first representative from the family Ebenaceae. Heliyon, 2022, 8, e09870.	3.2	5

#	ARTICLE	IF	CITATIONS
3409	Structural Characterization of the <i>Acer ukurunduense</i> Chloroplast Genome Relative to Related Species in the <i>Acer</i> Genus. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	0
3410	The C-Terminal Repeat Units of SpaA Mediate Adhesion of <i>Erysipelothrix rhusiopathiae</i> to Host Cells and Regulate Its Virulence. <i>Biology</i> , 2022, 11, 1010.	2.8	1
3412	A Chromosome Level Genome Assembly of a Winter Turnip Rape (<i>Brassica rapa</i> L.) to Explore the Genetic Basis of Cold Tolerance. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	4
3413	Genetic Characteristics and Enzymatic Activities of <i>Bacillus velezensis</i> KS04AU as a Stable Biocontrol Agent against Phytopathogens. <i>International Journal of Plant Biology</i> , 2022, 13, 201-222.	2.6	10
3414	Sympatric Recombination in Zoonotic <i>Cryptosporidium</i> Leads to Emergence of Populations with Modified Host Preference. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	10
3416	Analysis of 90 <i>Listeria monocytogenes</i> contaminated in poultry and livestock meat through whole-genome sequencing. <i>Food Research International</i> , 2022, 159, 111641.	6.2	8
3417	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.	3.5	2
3418	Comparative Analysis of the Complete Chloroplast Genomes in <i>Allium</i> Section <i>Bromatorrhiza</i> Species (<i>Amaryllidaceae</i>): Phylogenetic Relationship and Adaptive Evolution. <i>Genes</i> , 2022, 13, 1279.	2.4	5
3419	Time Series Genomics of <i>Pseudomonas aeruginosa</i> Reveals the Emergence of a Hypermutator Phenotype and Within-Host Evolution in Clinical Inpatients. <i>Microbiology Spectrum</i> , 2022, 10, .	3.0	2
3420	Characterization and Fitness Cost of Tn7100, a Novel Integrative and Conjugative Element Conferring Multidrug Resistance in <i>Haemophilus influenzae</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	3
3421	Molecular Characterization of pBOq-IncQ and pBOq-95LK Plasmids of <i>Escherichia coli</i> BOq 01, a New Isolated Strain from Poultry Farming, Involved in Antibiotic Resistance. <i>Microorganisms</i> , 2022, 10, 1509.	3.6	2
3422	Phylogenomic analysis of <i>Salmonella</i> Indiana ST17, an emerging MDR clonal group in China. <i>Journal of Antimicrobial Chemotherapy</i> , 2022, 77, 2937-2945.	3.0	7
3424	Genomic evaluation of novel Kenyan virulent phage isolates infecting carbapenemase-producing <i>Klebsiella pneumoniae</i> and safety determination of their lysates in Balb/c mice. <i>Archives of Microbiology</i> , 2022, 204, .	2.2	4
3425	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.	3.5	3
3426	Complete chloroplast genomes and phylogeny in three <i>Euterpe</i> palms (<i>E. edulis</i> , <i>E. oleracea</i> and <i>E.</i>) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	2.5	2
3427	New <i>Microviridae</i> isolated from <i>Sulfitobacter</i> reveals two cosmopolitan subfamilies of single-stranded DNA phages infecting marine and terrestrial Alphaproteobacteria. <i>Virus Evolution</i> , 2022, 8, .	4.9	5
3428	Genomic and Functional Characterization of Vancomycin-Resistant Enterococci-Specific Bacteriophages in the <i>Galleria mellonella</i> Wax Moth Larvae Model. <i>Pharmaceutics</i> , 2022, 14, 1591.	4.5	7
3430	Comparative Genomics of <i>Escherichia coli</i> Serotype O55:H7 Using Complete Closed Genomes. <i>Microorganisms</i> , 2022, 10, 1545.	3.6	0

#	ARTICLE	IF	CITATIONS
3431	Hidden dissemination of carbapenem-susceptible OXA-48-producing <i>Proteus mirabilis</i> . Journal of Antimicrobial Chemotherapy, 2022, 77, 3009-3015.	3.0	4
3432	Phylogenetic and Multiple-Locus Variable number tandem repeat analysis of <i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> isolates from Argentina. Veterinary Research Communications, 2022, 46, 1121-1129.	1.6	2
3433	Two New <i>Rhizobiales</i> Species Isolated from Root Nodules of Common Sainfoin (<i>Onobrychis</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	3.0	6
3434	Intrinsic tet(L) sub-class in <i>Bacillus velezensis</i> and <i>Bacillus amyloliquefaciens</i> is associated with a reduced susceptibility toward tetracycline. Frontiers in Microbiology, 0, 13, .	3.5	1
3436	<i>FLOWERING LOCUS T</i> indel variants confer vernalization-independent and photoperiod-insensitive flowering of yellow lupin (<i>Lupinus luteus</i> L.). Horticulture Research, 0, , .	6.3	0
3437	Genomic insights into symbiosis and host adaptation of an ascidian-associated bacterium <i>Bacillus aryabhattai</i> MCCB 387. Symbiosis, 0, , .	2.3	0
3438	PanExplorer: a web-based tool for exploratory analysis and visualization of bacterial pan-genomes. Bioinformatics, 2022, 38, 4412-4414.	4.1	3
3439	Genomic features of <i>Mycoplasma bovis</i> subtypes currently circulating in France. BMC Genomics, 2022, 23, .	2.8	2
3440	The transcriptional regulator CtrA controls gene expression in Alphaproteobacteria phages: Evidence for a lytic deferment pathway. Frontiers in Microbiology, 0, 13, .	3.5	4
3441	Comparative genomic analysis of five freshwater cyanophages and reference-guided metagenomic data mining. Microbiome, 2022, 10, .	11.1	8
3442	Bioinformatics and its role in the study of the evolution and probiotic potential of lactic acid bacteria. Food Science and Biotechnology, 2023, 32, 389-412.	2.6	4
3443	Genomic analysis reveals the role of integrative and conjugative elements in plant pathogenic bacteria. Mobile DNA, 2022, 13, .	3.6	6
3444	Isolation and Characterization of the Lytic <i>Pseudoxanthomonas kaohsiungensi</i> Phage PW916. Viruses, 2022, 14, 1709.	3.3	4
3446	Insights into Evolutionary, Genomic, and Biogeographic Characterizations of <i>Chryseobacterium nepalense</i> Represented by a Polyvinyl Alcohol-Degrading Bacterium, AC3. Microbiology Spectrum, 2022, 10, .	3.0	1
3447	Genomic comparison of <i>Planktothrix agardhii</i> isolates from a Lake Erie embayment. PLoS ONE, 2022, 17, e0273454.	2.5	6
3448	A large chromosomal inversion affects antimicrobial sensitivity of <i>Escherichia coli</i> to sodium deoxycholate. Microbiology (United Kingdom), 2022, 168, .	1.8	2
3450	Complete genome sequence of a multiple-stress-tolerant bacterium <i>Halomonas piezotolerans</i> NBT06E8T isolated from a deep-sea sediment sample of the New Britain Trench. 3 Biotech, 2022, 12, .	2.2	1
3451	In silico analysis reveals the co-existence of CRISPR-Cas type I-F1 and type I-F2 systems and its association with restricted phage invasion in <i>Acinetobacter baumannii</i> . Frontiers in Microbiology, 0, 13, .	3.5	5

#	ARTICLE	IF	CITATIONS
3452	Genome Sequence of a Potent Biosurfactant-Producing Bacterium, <i>Franconibacter</i> sp. Strain IITDAS19. Microbiology Resource Announcements, 2022, 11, .	0.6	0
3453	Microbiota of the Pregnant Mouse: Characterization of the Bacterial Communities in the Oral Cavity, Lung, Intestine, and Vagina through Culture and DNA Sequencing. Microbiology Spectrum, 2022, 10, .	3.0	6
3454	Genomic and Phenotypic Characterization of Cutibacterium acnes Bacteriophages Isolated from Acne Patients. Antibiotics, 2022, 11, 1041.	3.7	5
3455	First report and whole-genome sequencing of Pseudochrobactrum saccharolyticum in Latin America. Microbes and Infection, 2023, 25, 105018.	1.9	0
3456	The Sixth Element: a 102-kb RepABC Plasmid of Xenologous Origin Modulates Chromosomal Gene Expression in Dinoroseobacter shibae. MSystems, 0, , .	3.8	0
3457	Sequencing and comparative analysis of chloroplast genomes of three medicinal plants: Gentiana manshurica, G. scabra and G. triflora. Physiology and Molecular Biology of Plants, 0, , .	3.1	3
3458	The microbiome of a bacterivorous marine choanoflagellate contains a resource-demanding obligate bacterial associate. Nature Microbiology, 2022, 7, 1466-1479.	13.3	5
3459	New Insights Into the Backbone Phylogeny and Character Evolution of Corydalis (Papaveraceae) Based on Plastome Data. Frontiers in Plant Science, 0, 13, .	3.6	4
3460	Comprehensive investigation of antibiotic resistance gene content in cfiA-harboring Bacteroides fragilis isolates of human and animal origins by whole genome sequencing. International Journal of Medical Microbiology, 2022, 312, 151559.	3.6	8
3461	Histological characterization of anther structure in Tetep-cytoplasmic male sterility and fine mapping of restorer-of-fertility gene in rice. PLoS ONE, 2022, 17, e0268174.	2.5	0
3462	Development and evaluation of temperature-sensitive <i>Mycoplasma anseris</i> clones as vaccine candidates. Avian Pathology, 2022, 51, 535-549.	2.0	2
3463	CulebrONT: a streamlined long reads multi-assembler pipeline for prokaryotic and eukaryotic genomes. , 0, 2, .		5
3464	Structural mutations of small single copy (SSC) region in the plastid genomes of five Cistanche species and inter-species identification. BMC Plant Biology, 2022, 22, .	3.6	5
3465	Phylogenetic analysis based on single-copy orthologous proteins in highly variable chloroplast genomes of Corydalis. Scientific Reports, 2022, 12, .	3.3	1
3467	The chloroplast genome of Salix floderusii and characterization of chloroplast regulatory elements. Frontiers in Plant Science, 0, 13, .	3.6	2
3469	Genomic characteristics of two most widely used BCG vaccine strains: Danish 1331 and Pasteur 1173P2. BMC Genomics, 2022, 23, .	2.8	1
3470	Phage Resistance Accompanies Reduced Fitness of Uropathogenic Escherichia coli in the Urinary Environment. MSphere, 2022, 7, .	2.9	12
3471	Molecular Factors and Mechanisms Driving Multidrug Resistance in Uropathogenic Escherichia coli—An Update. Genes, 2022, 13, 1397.	2.4	19

#	ARTICLE	IF	CITATIONS
3472	Tracking the Transmission of Antimicrobial-Resistant Non-O157 <i>Escherichia coli</i> and <i>Salmonella</i> Isolates at the Interface of Food Animals and Fresh Produce from Agriculture Operations Using Whole-Genome Sequencing. <i>Foodborne Pathogens and Disease</i> , 0, .	1.8	0
3473	Rediscovering “Baculovirus” (Johnson, 1976): The complete genome of “ <i>Callinectes sapidus nudivirus</i> ” TM . <i>Journal of Invertebrate Pathology</i> , 2022, 194, 107822.	3.2	3
3474	Plastome structure, phylogenomics, and divergence times of tribe Cinnamomeae (Lauraceae). <i>BMC Genomics</i> , 2022, 23, .	2.8	7
3475	Clonal Dissemination of Extended-Spectrum Cephalosporin-Resistant Enterobacterales between Dogs and Humans in Households and Animal Shelters of Romania. <i>Antibiotics</i> , 2022, 11, 1242.	3.7	8
3476	Analysis of complete chloroplast genome sequences and insight into the phylogenetic relationships of <i>Ferula</i> L.. <i>BMC Genomics</i> , 2022, 23, .	2.8	11
3477	Characterization, comparative phylogenetic, and gene transfer analyses of organelle genomes of <i>Rhododendron A— pulchrum</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	2
3478	<i>Pseudomonas putida</i> mediates bacterial killing, biofilm invasion and biocontrol with a type IVB secretion system. <i>Nature Microbiology</i> , 2022, 7, 1547-1557.	13.3	23
3479	Effects of a <i>Carnobacterium maltaromaticum</i> strain at natural contamination levels on the microbiota of vacuum-packaged beef steaks during chilled storage. <i>LWT - Food Science and Technology</i> , 2022, 168, 113944.	5.2	2
3480	Genome-scale prediction of bacterial promoters. <i>BioSystems</i> , 2022, 221, 104771.	2.0	3
3481	The complete plastome of <i>Blidingia marginata</i> and comparative analysis with the relative species in Ulvales. <i>Aquatic Botany</i> , 2022, 183, 103568.	1.6	1
3482	The entire chloroplast genome sequence of <i>Asparagus cochinchinensis</i> and genetic comparison to <i>Asparagus</i> species. <i>Open Life Sciences</i> , 2022, 17, 893-906.	1.4	3
3483	Multiple genome alignment in the telomere-to-telomere assembly era. <i>Genome Biology</i> , 2022, 23, .	8.8	17
3484	Comparative chloroplast genome analyses of 23 species in <i>Swertia</i> L. (Gentianaceae) with implications for its phylogeny. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	10
3485	Complete Chloroplast Genomes of 14 Subspecies of <i>D. glomerata</i> : Phylogenetic and Comparative Genomic Analyses. <i>Genes</i> , 2022, 13, 1621.	2.4	6
3486	Telomere-to-telomere genome sequence of the model mould pathogen <i>Aspergillus fumigatus</i> . <i>Nature Communications</i> , 2022, 13, .	12.8	8
3487	Plastome structure, phylogenomic analyses and molecular dating of Arecaceae. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	2
3488	Convergent structure with divergent adaptations in combinatorial microbiome communities. <i>FEMS Microbiology Ecology</i> , 2022, 98, .	2.7	0
3489	A functional selection reveals previously undetected anti-phage defence systems in the <i>E. coli</i> pangenome. <i>Nature Microbiology</i> , 2022, 7, 1568-1579.	13.3	108

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3490	Genomic Profiling of Non-O157 Shiga Toxigenic <i>Escherichia coli</i> -Infecting Bacteriophages from South Africa. <i>Phage</i> , 2022, 3, 221-230.	1.7	1
3491	Genome-guided prediction of acid resistance mechanisms in acidophilic methanotrophs of phylogenetically deep-rooted Verrucomicrobia isolated from geothermal environments. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	1
3492	Weizmannia faecalis sp. nov., isolated from a human stool sample. <i>Archives of Microbiology</i> , 2022, 204, .	2.2	4
3493	A turn in species conservation for hairpin banksias: demonstration of oversplitting leads to better management of diversity. <i>American Journal of Botany</i> , 2022, 109, 1652-1671.	1.7	5
3494	Intraspecific comparison of mitochondrial genomes reveals the evolution in medicinal fungus <i>Ganoderma lingzhi</i> . <i>Journal of Bioscience and Bioengineering</i> , 2022, 134, 374-383.	2.2	1
3495	Pangenomes-identified singletons for designing specific primers to identify bacterial strains in a plant growth-promoting consortium. <i>Molecular Biology Reports</i> , 2022, 49, 10489-10498.	2.3	3
3496	The complete mitochondrial genome of <i>Isochrysis galbana</i> harbors a unique repeat structure and a specific trans-spliced cox1 gene. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	1
3497	Comparative chloroplast genome and phylogenetic analyses of Chinese <i>Polyspora</i> . <i>Scientific Reports</i> , 2022, 12, .	3.3	5
3498	Complete Chloroplast Genome of <i>Gladiolus gandavensis</i> (<i>Gladiolus</i>) and Genetic Evolutionary Analysis. <i>Genes</i> , 2022, 13, 1599.	2.4	2
3499	A Plasmid Carrying bla _{IMP-56} in <i>Pseudomonas aeruginosa</i> Belonging to a Novel Resistance Plasmid Family. <i>Microorganisms</i> , 2022, 10, 1863.	3.6	3
3501	Breaking the ICE: an easy workflow for identifying and analyzing integrative and conjugative elements in bacterial genomes. <i>Functional and Integrative Genomics</i> , 0, , .	3.5	5
3502	Complete chloroplast genome sequence of <i>Lens ervoides</i> and comparison to <i>Lens culinaris</i> . <i>Scientific Reports</i> , 2022, 12, .	3.3	5
3503	Isolation and characterization of a <i>Vibrio owensii</i> phage phi50-12. <i>Scientific Reports</i> , 2022, 12, .	3.3	2
3504	The complete chloroplast genome of <i>Campsis grandiflora</i> (Bignoniaceae). <i>Korean Journal of Plant Taxonomy</i> , 2022, 52, 156-172.	0.7	2
3506	Characterization of Phage Resistance and Their Impacts on Bacterial Fitness in <i>Pseudomonas aeruginosa</i> . <i>Microbiology Spectrum</i> , 2022, 10, .	3.0	6
3507	Integrating diverse layers of omic data to identify novel drug targets in <i>Listeria monocytogenes</i> . <i>Frontiers in Drug Discovery</i> , 0, 2, .	2.8	4
3508	Comparative mitogenome analysis reveals mitochondrial genome characteristics in eight strains of <i>Beauveria</i> . <i>PeerJ</i> , 0, 10, e14067.	2.0	2
3509	Evolutionary Comparison of the Complete Chloroplast Genomes in <i>Convallaria</i> Species and Phylogenetic Study of Asparagaceae. <i>Genes</i> , 2022, 13, 1724.	2.4	5

#	ARTICLE	IF	CITATIONS
3511	Prevalence and mobility of integrative and conjugative elements within a <i>Streptomyces</i> natural population. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	3
3512	Comparative genomic and functional analyses of <i>Paenibacillus peoriae</i> ZBSF16 with biocontrol potential against grapevine diseases, provide insights into its genes related to plant growth-promoting and biocontrol mechanisms. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	1
3513	Identification of Male-Specific Molecular Marker and Development of PCR-Based Genetic Sex Identification Technique in Spotted Knifejaw (<i>Oplegnathus punctatus</i>). <i>Marine Biotechnology</i> , 0, , .	2.4	0
3515	Whole genome sequence analysis of two subspecies of <i>Companilactobacillus Futsaii</i> and experimental verification of drug resistance and effect on the exploratory behavior of mice based on unique gene. <i>PLoS ONE</i> , 2022, 17, e0274244.	2.5	1
3516	Role of <i>Bifidobacterium pseudocatenulatum</i> in Degradation and Consumption of Xylan-Derived Carbohydrates. <i>Applied and Environmental Microbiology</i> , 2022, 88, .	3.1	6
3517	Spontaneous Prophage Induction Contributes to the Production of Membrane Vesicles by the Gram-Positive Bacterium <i>Lactocaseibacillus casei</i> BL23. <i>MBio</i> , 2022, 13, .	4.1	9
3518	Whole genome population structure of North Atlantic kelp confirms high-latitude glacial refugia. <i>Molecular Ecology</i> , 2022, 31, 6473-6488.	3.9	5
3519	Monkeypox virus: The changing facets of a zoonotic pathogen. <i>Infection, Genetics and Evolution</i> , 2022, 105, 105372.	2.3	16
3520	Designing Tobacco Genomes for Resistance to Biotic Stresses. , 2022, , 441-581.		1
3521	Abiotic Stress Resistance in Tobacco: Advances and Strategies. , 2022, , 329-427.		0
3522	The Effect of Mutation in Lipopolysaccharide Biosynthesis on Bacterial Fitness. <i>Cells</i> , 2022, 11, 3249.	4.1	1
3523	Whole genome sequence data of <i>Stenotrophomonas maltophilia</i> SCAID WND1-2022 (370). <i>Data in Brief</i> , 2022, , 108694.	1.0	0
3524	Borgs are giant genetic elements with potential to expand metabolic capacity. <i>Nature</i> , 2022, 610, 731-736.	27.8	29
3525	Folding Features and Dynamics of 3D Genome Architecture in Plant Fungal Pathogens. <i>Microbiology Spectrum</i> , 2022, 10, .	3.0	5
3526	The acquisition of transferable extrachromosomal <i>fec</i> operon is associated with a cefiderocol MIC increase in Enterobacterales. <i>Journal of Antimicrobial Chemotherapy</i> , 0, , .	3.0	3
3528	Emergence of a Novel Lineage and Wide Spread of a blaCTX-M-15/IncHI2/ST1 Plasmid among Nosocomial Enterobacter in Guadeloupe. <i>Antibiotics</i> , 2022, 11, 1443.	3.7	1
3529	Comparison of clinical severity, genotype and toxin gene expression of binary toxin-producing <i>Clostridioides difficile</i> clinical isolates in Japan. <i>Access Microbiology</i> , 2022, 4, .	0.5	1
3530	Ancient homomorphy of molluscan sex chromosomes sustained by reversible sex-biased genes and sex determiner translocation. <i>Nature Ecology and Evolution</i> , 2022, 6, 1891-1906.	7.8	23

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3531	Complete Genome Sequences of Two <i>Rhizobium</i> Strains Producing Azol(in)e-Modified Antibiotics. <i>Microbiology Resource Announcements</i> , 2022, 11, .	0.6	1
3532	Comparative Genomic Analysis of Phytopathogenic <i>Xanthomonas</i> Species Suggests High Level of Genome Plasticity Related to Virulence and Host Adaptation. , 2022, 1, 218-241.		4
3534	Development of Genome-Driven, Lifestyle-Informed Markers for Identification of the Cereal-Infecting Pathogens <i>Xanthomonas translucens</i> Pathovars <i>undulosa</i> and <i>translucens</i> . <i>Phytopathology</i> , 2023, 113, 2110-2118.	2.2	6
3535	Detection of an IMI-2 carbapenemase-producing <i>Enterobacter asburiae</i> at a Swedish feed mill. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	5
3536	Characterization and Comparative Analysis of Chloroplast Genomes in Five <i>Uncaria</i> Species Endemic to China. <i>International Journal of Molecular Sciences</i> , 2022, 23, 11617.	4.1	10
3537	Endogenous giant viruses contribute to intraspecies genomic variability in the model green alga <i>Chlamydomonas reinhardtii</i> . <i>Virus Evolution</i> , 2022, 8, .	4.9	12
3538	An update to the database for <i>Acinetobacter baumannii</i> capsular polysaccharide locus typing extends the extensive and diverse repertoire of genes found at and outside the K locus. <i>Microbial Genomics</i> , 2022, 8, .	2.0	13
3539	Genomic Features of <i>Pseudomonas putida</i> PCL1760: A Biocontrol Agent Acting via Competition for Nutrient and Niche. <i>Applied Microbiology</i> , 2022, 2, 749-765.	1.6	1
3540	Draft Genome Sequences of <i>Bacillus pumilus</i> 36R ATNSAL and <i>B. safensis</i> 13L LOBSAL, Two Potential Candidate Probiotic Strains for Shrimp Aquaculture. <i>Journal of Global Antimicrobial Resistance</i> , 2022, , .	2.2	1
3541	Genome sequence of the entomopathogenic <i>Serratia entomophila</i> isolate 626 and characterisation of the species specific itaconate degradation pathway. <i>BMC Genomics</i> , 2022, 23, .	2.8	4
3542	Sequencing and de novo assembly of the Koshihikari genome and identification of the genomic region related to the eating quality of cooked rice. <i>Molecular Breeding</i> , 2022, 42, .	2.1	1
3543	Comparative analysis of the complete chloroplast genomes of six threatened subgenus <i>Gynopodium</i> (<i>Magnolia</i>) species. <i>BMC Genomics</i> , 2022, 23, .	2.8	1
3544	New <i>Saccharomyces cerevisiae</i> - <i>Kluyveromyces marxianus</i> fusant shows enhanced alcoholic fermentation performance. <i>World Journal of Microbiology and Biotechnology</i> , 2022, 38, .	3.6	1
3545	A High-Quality Genome Assembly of the Mitochondrial Genome of the Oil-Tea Tree <i>Camellia gigantocarpa</i> (<i>Theaceae</i>). <i>Diversity</i> , 2022, 14, 850.	1.7	6
3546	Draft Genome Sequence of <i>Candidatus</i> <i>Nardonella dryophthoridicola</i> Strain NARMHE1, Endosymbiont of <i>Metamasius hemipterus</i> (Coleoptera, Curculionidae, Dryophthorinae). <i>Microbiology Resource Announcements</i> , 2022, 11, .	0.6	1
3547	Phylogenomics and plastome evolution of a Brazilian mycoheterotrophic orchid, <i>Pogoniopsis schenckii</i> . <i>American Journal of Botany</i> , 2022, 109, 2030-2050.	1.7	8
3549	In silico genomic analysis of the potential probiotic <i>Lactiplantibacillus pentosus</i> CF2-10N reveals promising beneficial effects with health promoting properties. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	6
3550	Hybrid assembly using long reads resolves repeats and completes the genome sequence of a laboratory strain of <i>Staphylococcus aureus</i> subsp. <i>Aureus</i> RN4220. <i>Heliyon</i> , 2022, , e11376.	3.2	0

#	ARTICLE	IF	CITATIONS
3551	Deciphering the potential of a plant growth promoting endophyte <i>Rhizobium</i> sp. WYJ-E13, and functional annotation of the genes involved in the metabolic pathway. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	1
3552	Experimental pathogenicity and comparative genome analysis of high- and low-virulence strains of rabbit-origin <i>Pasteurella multocida</i> . <i>Comparative Immunology, Microbiology and Infectious Diseases</i> , 2022, 90-91, 101889.	1.6	0
3553	A specific reverse complement sequence for distinguishing <i>Brucella canis</i> from other <i>Brucella</i> species. <i>Frontiers in Veterinary Science</i> , 0, 9, .	2.2	0
3554	In silico genomic analysis of <i>Rhodopseudomonas palustris</i> strains revealed potential biocontrol agents and crop yield enhancers. <i>Biological Control</i> , 2022, 176, 105085.	3.0	9
3555	Evolution of the orthopoxvirus core genome. <i>Virus Research</i> , 2023, 323, 198975.	2.2	3
3556	Comparative genomic analyses of <i>Lutimaribacter degradans</i> sp. nov. With the ability to PAHs-biodegradation and transformation. <i>International Biodeterioration and Biodegradation</i> , 2023, 176, 105505.	3.9	8
3557	The complete plastid genome of <i>Bactris riparia</i> (Arecaceae) and a comparative analysis in Bactridinae (Cocoseae, Arecaceae). <i>Genetics and Molecular Biology</i> , 2022, 45, .	1.3	0
3558	Full-length whole-genome sequencing analysis of emerged meropenem-resistant mutants during long-term <i>in vitro</i> exposure to meropenem for borderline meropenem-susceptible carbapenemase-producing and non-carbapenemase-producing <i>Enterobacterales</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2023, 78, 209-215.	3.0	2
3559	Comparative Analyses of Plastomes of Four <i>Anubias</i> (Araceae) Taxa, Tropical Aquatic Plants Endemic to Africa. <i>Genes</i> , 2022, 13, 2043.	2.4	1
3560	<scp>NGSEP</scp> 4: Efficient and accurate identification of orthogroups and whole-genome alignment. <i>Molecular Ecology Resources</i> , 2023, 23, 712-724.	4.8	7
3561	Evaluation of tangential flow filtration coupled to long-read sequencing for ostreid herpesvirus type 1 genome assembly. <i>Microbial Genomics</i> , 2022, 8, .	2.0	2
3562	Shared properties of gene transfer agent and core genes revealed by comparative genomics of Alphaproteobacteria. <i>Microbial Genomics</i> , 2022, 8, .	2.0	0
3563	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, .	1.8	3
3564	Complete Genome and Partial Megaplasmid Sequences of <i>Mycobacterium pseudoshottsii</i> Strain NJB1907-Z4, Isolated from an Aquarium-Reared Japanese Sardine (<i>Sardinops melanostictus</i>) in Japan. <i>Microbiology Resource Announcements</i> , 2022, 11, .	0.6	1
3565	The complete chloroplast genome sequences of eight <i>Orostachys</i> species: Comparative analysis and assessment of phylogenetic relationships. <i>PLoS ONE</i> , 2022, 17, e0277486.	2.5	5
3566	Comparative genomic analyses reveal genetic characteristics and pathogenic factors of <i>Bacillus pumilus</i> HM-7. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	0
3567	Molecular Structure and Phylogenetic Analyses of the Plastomes of Eight <i>Sorbus</i> Sensu Stricto Species. <i>Biomolecules</i> , 2022, 12, 1648.	4.0	2
3568	Whole-genome sequence of the filamentous diazotrophic cyanobacterium <i>Tolypothrix</i> sp. PCC 7712 and its comparison with non-diazotrophic <i>Tolypothrix</i> sp. PCC 7601. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	2

#	ARTICLE	IF	CITATIONS
3569	Next-generation sequencing data show rapid radiation and several long-distance dispersal events in early Costaceae. <i>Molecular Phylogenetics and Evolution</i> , 2023, 179, 107664.	2.7	3
3570	The phylogeny of <i>Seseli</i> (Apiaceae, Apioideae): insights from molecular and morphological data. <i>BMC Plant Biology</i> , 2022, 22, .	3.6	4
3571	Phage Cocktail in Combination with Kasugamycin as a Potential Treatment for Fire Blight Caused by <i>Erwinia amylovora</i> . <i>Antibiotics</i> , 2022, 11, 1566.	3.7	6
3572	Comparative genomics to examine the endophytic potential of <i>Pantoea agglomerans</i> DAPP-PG 734. <i>BMC Genomics</i> , 2022, 23, .	2.8	6
3573	Characterization of the Evolutionary Pressure on <i>Anisodus tanguticus</i> Maxim. with Complete Chloroplast Genome Sequence. <i>Genes</i> , 2022, 13, 2125.	2.4	3
3574	Genomic analysis of <i>Paenibacillus</i> sp. MDMC362 from the Merzouga desert leads to the identification of a potentially thermostable catalase. <i>Antonie Van Leeuwenhoek</i> , 2023, 116, 21-38.	1.7	1
3575	Metagenome-assembled genome extraction and analysis from microbiomes using KBase. <i>Nature Protocols</i> , 2023, 18, 208-238.	12.0	7
3576	Type IV Pili Are a Critical Virulence Factor in Clinical Isolates of <i>Paenibacillus thiaminolyticus</i> . <i>MBio</i> , 2022, 13, .	4.1	2
3577	Whole genome analysis for plant growth promotion profiling of <i>Pantoea agglomerans</i> CPHN2, a non-rhizobial nodule endophyte. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	3
3578	Introducing the Bacterial and Viral Bioinformatics Resource Center (BV-BRC): a resource combining PATRIC, IRD and ViPR. <i>Nucleic Acids Research</i> , 2023, 51, D678-D689.	14.5	229
3580	The first complete genome of the simian malaria parasite <i>Plasmodium brasilianum</i> . <i>Scientific Reports</i> , 2022, 12, .	3.3	5
3581	Genomic Analysis to Elucidate the Lignocellulose Degrading Capability of a New Halophile <i>Robertkochia solimangrovi</i> . <i>Genes</i> , 2022, 13, 2135.	2.4	0
3582	Twisting development, the birth of a potential new gene. <i>IScience</i> , 2022, 25, 105627.	4.1	4
3583	Analysis of the Features of the Genomic Organization of Plague Microbe Strains Suitable for the Creation of a New Attenuated Vaccine. <i>Epidemiologiya I Vaktsinoprofilaktika</i> , 2022, 21, 49-57.	0.8	0
3585	Genomic Analysis of 13 Putative Active Prophages Located in the Genomes of Walnut Blight Pathogen <i>Xanthomonas arboricola</i> pv. <i>juglandis</i> . <i>Microbiology and Biotechnology Letters</i> , 2022, 50, 563-573.	0.4	0
3586	HELIOS: High-speed sequence alignment in optics. <i>PLoS Computational Biology</i> , 2022, 18, e1010665.	3.2	1
3587	<i>Proteiniphilum propionicum</i> sp. nov., a novel member of the phylum Bacteroidota isolated from pit clay used to produce Chinese liquor. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	1.7	1
3588	Throughput screening of <i>Bacillus subtilis</i> strains that abundantly secrete surfactin in vitro identifies effective probiotic candidates. <i>PLoS ONE</i> , 2022, 17, e0277412.	2.5	5

#	ARTICLE	IF	CITATIONS
3589	Evidence from Phylogenomics and Morphology Provide Insights into the Phylogeny, Plastome Evolution, and Taxonomy of Kitagawia. <i>Plants</i> , 2022, 11, 3275.	3.5	4
3590	Recombination Events in Putative Tail Fibre Gene in Litunavirus Phages Infecting <i>Pseudomonas aeruginosa</i> and Their Phylogenetic Consequences. <i>Viruses</i> , 2022, 14, 2669.	3.3	1
3592	Complete Chloroplast Genome Sequence of a New Variety of <i>Brasenia schreberi</i> : Genome Characteristics, Comparative Analysis, and Phylogenetic Relationships. <i>Agronomy</i> , 2022, 12, 2972.	3.0	1
3594	Untargeted metabolomics screening reveals unique secondary metabolite production from <i>Alternaria</i> section <i>Alternaria</i> . <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	3.5	0
3595	Genome Analysis and Antibiofilm Activity of Phage 590B against Multidrug-Resistant and Extensively Drug-Resistant Uropathogenic <i>Escherichia coli</i> Isolates, India. <i>Pathogens</i> , 2022, 11, 1448.	2.8	4
3596	Species-Specific Duplication of Surface Antigen Genes in <i>Paramecium</i> . <i>Microorganisms</i> , 2022, 10, 2378.	3.6	1
3597	Untying the Gordian knot of plastid phylogenomic conflict: A case from ferns. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	0
3598	Complete genome sequencing and comparative genomic analyses of a new spotted-fever <i>Rickettsia heilongjiangensis</i> strain B8. <i>Emerging Microbes and Infections</i> , 2023, 12, .	6.5	4
3599	Identifying magnetosome-associated genes in the extended CtrA regulon in <i>Magnetospirillum magneticum</i> AMB-1 using a combinational approach. <i>Briefings in Functional Genomics</i> , 0, , .	2.7	0
3600	Biocomputational Identification of sRNAs in <i>Leptospira interrogans</i> Serovar Lai. <i>Indian Journal of Microbiology</i> , 0, , .	2.7	0
3601	Comparative chloroplast genomics provides insights into the genealogical relationships of endangered <i>Tetraena mongolica</i> and the chloroplast genome evolution of related <i>Zygophyllaceae</i> species. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	3
3604	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, .	3.0	6
3605	Genomic diversity and comprehensive taxonomical classification of 61 <i>Bacillus subtilis</i> group member infecting bacteriophages, and the identification of ortholog taxonomic signature genes. <i>BMC Genomics</i> , 2022, 23, .	2.8	0
3606	Genomics, Transcriptomics, and Metabolomics Reveal That Minimal Modifications in the Host Are Crucial for the Compensatory Evolution of ColE1-Like Plasmids. <i>MSphere</i> , 2022, 7, .	2.9	5
3607	Horizontal Transfer of Bacteriocin Biosynthesis Genes Requires Metabolic Adaptation To Improve Compound Production and Cellular Fitness. <i>Microbiology Spectrum</i> , 2023, 11, .	3.0	4
3608	High-Quality Genome and Annotation Resource of Orange Pink Rot Pathogen <i>Trichothecium roseum</i> strain YXFP-22015 Isolated from Hubei, China. <i>Plant Disease</i> , 0, , .	1.4	0
3609	Diverse infective and lytic machineries identified in genome analysis of tailed coliphages against broad spectrum multidrug-resistant <i>Escherichia coli</i> . <i>International Microbiology</i> , 0, , .	2.4	1
3610	Characterization of the complete mitochondrial genome of the striped soldier shrimp, <i>Plesionika edwardsii</i> (Brandt, 1851) (Crustacea: Decapoda: Pandalidae), and comparison with other species of Caridea. <i>Journal of Crustacean Biology</i> , 2022, 42, .	0.8	1

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3611	<i>Fervidobacterium pennivorans</i> subsp. <i>keratinolyticus</i> subsp. nov., a Novel Feather-Degrading Anaerobic Thermophile. <i>Microorganisms</i> , 2023, 11, 22.	3.6	0
3613	Genomic diversity of <i>Helicobacter pylori</i> populations from different regions of the human stomach. <i>Gut Microbes</i> , 2022, 14, .	9.8	4
3614	Genetic Adaptation and Acquisition of Macrolide Resistance in <i>Haemophilus</i> spp. during Persistent Respiratory Tract Colonization in Chronic Obstructive Pulmonary Disease (COPD) Patients Receiving Long-Term Azithromycin Treatment. <i>Microbiology Spectrum</i> , 2023, 11, .	3.0	6
3615	New Insights into Lymphocystis Disease Virus Genome Diversity. <i>Viruses</i> , 2022, 14, 2741.	3.3	3
3617	Genomic Characterization of Livestock-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> ST7 Isolates from a Case of Human Bacteremia in China. <i>Infection and Drug Resistance</i> , 0, Volume 15, 7449-7457.	2.7	3
3618	Jack of all trades: Genome assembly of Wild Jack and comparative genomics of <i>Artocarpus</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	1
3619	Disinfectant Susceptibility of Third-Generation-Cephalosporin/Carbapenem-Resistant Gram-Negative Bacteria Isolated from the Oral Cavity of Residents of Long-Term-Care Facilities. <i>Applied and Environmental Microbiology</i> , 2023, 89, .	3.1	1
3620	Morphological Characteristics and Comparative Chloroplast Genome Analyses between Red and White Flower Phenotypes of <i>Pyracantha fortuneana</i> (Maxim.) Li (Rosaceae), with Implications for Taxonomy and Phylogeny. <i>Genes</i> , 2022, 13, 2404.	2.4	3
3621	Type IV pili trigger episyntrophic association of <i>Saccharibacteria</i> with its bacterial host. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	18
3622	Phylogenomic analyses based on the plastid genome and concatenated nrDNA sequence data reveal cytonuclear discordance in genus <i>Atractylodes</i> (Asteraceae: Carduoideae). <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	5
3624	Comparative Genomic Analysis of the Hydrocarbon-Oxidizing Dibenzothiophene-Desulfurizing <i>Gordonia</i> Strains. <i>Microorganisms</i> , 2023, 11, 4.	3.6	5
3625	An Emerging Lineage of Uropathogenic Extended Spectrum β -Lactamase <i>Escherichia coli</i> ST127. <i>Microbiology Spectrum</i> , 2022, 10, .	3.0	1
3626	Comparative genomics of trimethoprim-sulfamethoxazole-resistant <i>Achromobacter xylosoxidans</i> clinical isolates from Serbia reveals shortened variant of class 1 integron integrase gene. <i>Folia Microbiologica</i> , 2023, 68, 431-440.	2.3	2
3627	At the threshold of symbiosis: the genome of obligately endosymbiotic <i>Candidatus</i> <i>Nebulobacter yamunensis</i> is almost indistinguishable from that of a cultivable strain. <i>Microbial Genomics</i> , 2022, 8, .	2.0	1
3628	Identification of a conserved maxicircle and unique minicircles as part of the mitochondrial genome of <i>Leishmania martiniquensis</i> strain PCM3 in Thailand. <i>Parasites and Vectors</i> , 2022, 15, .	2.5	0
3629	The chloroplast genome of black pepper (<i>Piper nigrum</i> L.) and its comparative analysis with related <i>Piper</i> species. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	3
3630	Complete chloroplast genome and phylogenetic relationship of <i>Nymphaea nouchali</i> (Nymphaeaceae), a rare species of water lily in China. <i>Gene</i> , 2023, 858, 147139.	2.2	1
3631	Insights into chloroplast genome structure, intraspecific variation, and phylogeny of <i>Cyclamen</i> species (Myrsinoideae). <i>Scientific Reports</i> , 2023, 13, .	3.3	2

#	ARTICLE	IF	CITATIONS
3632	Pan-genome association study of <i>Mycobacterium tuberculosis</i> lineage-4 revealed specific genes related to the high and low prevalence of the disease in patients from the North-Eastern area of Medellín, Colombia. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	2
3633	Comparative Genomics Revealed a Potential Threat of <i>Aeromonas</i> <i>Ä</i> <i>r</i> <i>i</i> <i>p</i> <i>o</i> <i>l</i> <i>l</i> <i>e</i> <i>n</i> <i>s</i> <i>i</i> <i>s</i> G87 Strain and Its Antibiotic Resistance. <i>Antibiotics</i> , 2023, 12, 131.	3.7	1
3634	Towards the isolation of more robust next generation probiotics: The first aerotolerant <i>Bifidobacterium bifidum</i> strain. <i>Food Research International</i> , 2023, 165, 112481.	6.2	2
3635	A comparison of 25 complete chloroplast genomes between sister mangrove species <i>Kandelia obovata</i> and <i>Kandelia candel</i> geographically separated by the South China Sea. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	2
3636	Complete sequence and comparative analysis of the mitochondrial genome of the rare and endangered <i>Clematis acerifolia</i> , the first clematis mitogenome to provide new insights into the phylogenetic evolutionary status of the genus. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	6
3637	Whole-â€“genome sequencing, annotation, and biological characterization of a novel Siphoviridae phage against multi-â€“drug resistant <i>Propionibacterium acne</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	1
3638	Phylogenetic Analysis of Wild Pomegranate (<i>Punica granatum</i> L.) Based on Its Complete Chloroplast Genome from Tibet, China. <i>Agronomy</i> , 2023, 13, 126.	3.0	4
3639	The Complete Chloroplast Genomes of Two <i>Physalis</i> Species, <i>Physalis macrophysa</i> and <i>P. ixocarpa</i> : Comparative Genomics, Evolutionary Dynamics and Phylogenetic Relationships. <i>Agronomy</i> , 2023, 13, 135.	3.0	4
3640	Phylogenomics, divergence time estimation, and adaptive evolution in the Polygonoideae (Polygonaceae). <i>Journal of Systematics and Evolution</i> , 2023, 61, 1004-1019.	3.1	0
3641	PRAWNS: compact pan-genomic features for whole-genome population genomics. <i>Bioinformatics</i> , 2023, 39, .	4.1	0
3642	Two <i>Xylella fastidiosa</i> subsp. <i>Ä</i> <i>m</i> <i>u</i> <i>l</i> <i>t</i> <i>i</i> <i>p</i> <i>l</i> <i>e</i> <i>x</i> strains isolated from almond in Spain differ in plasmid content and virulence traits. <i>Phytopathology</i> , 0, , .	2.2	1
3643	Plastid Phylogenomics Provide Evidence to Accept Two New Members of <i>Ligusticopsis</i> (Apiaceae), Tj ETQq1 1 0.784314 rgBT ₀ /Overlook	4.1	0
3644	Plastid Phylogenomic Analyses Reveal the Taxonomic Position of <i>Peucedanum franchetii</i> . <i>Plants</i> , 2023, 12, 97.	3.5	1
3645	Seeds of <i>Stevia rebaudiana</i> Bertoni as a Source of Plant Growth-Promoting Endophytic Bacteria with the Potential to Synthesize Rebaudioside A. <i>International Journal of Molecular Sciences</i> , 2023, 24, 2174.	4.1	5
3646	Chloroplast genomes of four <i>Carex</i> species: Long repetitive sequences trigger dramatic changes in chloroplast genome structure. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	8
3647	Using a combination of short- and long-read sequencing to investigate the diversity in plasmid- and chromosomally encoded extended-spectrum beta-lactamases (ESBLs) in clinical <i>Shigella</i> and <i>Salmonella</i> isolates in Belgium. <i>Microbial Genomics</i> , 2023, 9, .	2.0	1
3648	The effect of in vitro consecutive passages and culture medium on the genetic variations in BCG Pasteur 1173P2 vaccine. <i>PLoS ONE</i> , 2023, 18, e0280294.	2.5	0
3649	Pathological Features and Genomic Characterization of an <i>Actinobacillus equuli</i> subsp. <i>Ä</i> <i>e</i> <i>q</i> <i>u</i> <i>l</i> <i>i</i> Bearing Unique Virulence-Associated Genes from an Adult Horse with Pleuropneumonia. <i>Pathogens</i> , 2023, 12, 224.	2.8	0

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3650	<i>Klebsiella pneumoniae</i> carrying multiple alleles of antigen 43-encoding gene of <i>Escherichia coli</i> associated with biofilm formation. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2023, 42, 371-377.	2.9	0
3651	Genomic Diversity among <i>Actinomyces naeslundii</i> Strains and Closely Related Species. <i>Microorganisms</i> , 2023, 11, 254.	3.6	1
3652	Characterization of <i>Escherichia coli</i> and Other Enterobacterales Resistant to Extended-Spectrum Cephalosporins Isolated from Dairy Manure in Ontario, Canada. <i>Applied and Environmental Microbiology</i> , 2023, 89, .	3.1	2
3653	In Silico Genomic Characterization of <i>Bacillus velezensis</i> Strain AAK_S6 for Secondary Metabolite and Biocontrol Potential. <i>Current Microbiology</i> , 2023, 80, .	2.2	3
3654	<i>Wolbachia</i> in natural <i>Drosophila simulans</i> (Diptera: Drosophilidae) populations in Ukraine. <i>Symbiosis</i> , 0, , .	2.3	0
3655	Leveraging comparative genomics to uncover alien genes in bacterial genomes. <i>Microbial Genomics</i> , 2023, 9, .	2.0	4
3656	Description and Genomic Analysis of the First Facultatively Lithoautotrophic, Thermophilic Bacteria of the Genus <i>Thermaerobacter</i> Isolated from Low-temperature Sediments of Lake Baikal. <i>Microbial Ecology</i> , 0, , .	2.8	0
3657	Chloroplast genome sequence of triploid <i>Toxicodendron vernicifluum</i> and comparative analyses with other lacquer chloroplast genomes. <i>BMC Genomics</i> , 2023, 24, .	2.8	3
3658	Plastid phylogenomics and molecular evolution of <i>Thismiaceae</i> (Dioscoreales). <i>American Journal of Botany</i> , 2023, 110, .	1.7	3
3659	Complete chloroplast genome sequences of the medicinal plant <i>Aconitum transsectum</i> (Ranunculaceae): comparative analysis and phylogenetic relationships. <i>BMC Genomics</i> , 2023, 24, .	2.8	6
3660	Genome sequences of BCG Pasteur ATCC 35734 and its derivative, the vaccine candidate BCG ⁺ BCG1419c. <i>BMC Genomics</i> , 2023, 24, .	2.8	2
3661	Phylogenomics and phylogeography of <i>Menispermum</i> (Menispermaceae). <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	0
3662	Structural Diversity among <i>Edwardsiellaceae</i> Core Oligosaccharides. <i>International Journal of Molecular Sciences</i> , 2023, 24, 4768.	4.1	0
3663	Revised classification of the Cyanidiophyceae based on plastid genome data with descriptions of the Cavernicolales ord. nov. and Galdieriales ord. nov. (Rhodophyta). <i>Journal of Phycology</i> , 2023, 59, 444-466.	2.3	11
3665	Characterization and phylogenetic analyses of ten complete plastomes of <i>Spiraea</i> species. <i>BMC Genomics</i> , 2023, 24, .	2.8	2
3666	The Evolution of Mitochondrial Genomes between Two <i>Cymbidium</i> Sister Species: Dozens of Circular Chromosomes and the Maintenance and Deterioration of Genome Synteny. <i>Genes</i> , 2023, 14, 864.	2.4	7
3667	Polluted wetlands contain multidrug-resistance plasmids encoding CTX-M-type extended-spectrum β -lactamases. <i>Plasmid</i> , 2023, 126, 102682.	1.4	0
3668	A K-17 serotype specific <i>Klebsiella</i> phage JKP2 with biofilm reduction potential. <i>Virus Research</i> , 2023, 329, 199107.	2.2	1

#	ARTICLE	IF	CITATIONS
3669	Genomic insights into a <i>Pseudomonas amygdali</i> isolate from <i>Hibiscus rosa-sinensis</i> . <i>Genomics</i> , 2023, 115, 110600.	2.9	2
3670	Phylogenomics and taxon-rich phylogenies of new and historical specimens shed light on the systematics of <i>Hypnea</i> (Cystocloniaceae, Rhodophyta). <i>Molecular Phylogenetics and Evolution</i> , 2023, 183, 107752.	2.7	1
3673	<i>Stutzerimonas decontaminans</i> sp. nov. isolated from marine polluted sediments. <i>Systematic and Applied Microbiology</i> , 2023, 46, 126400.	2.8	4
3674	Plastome evolution and phylogenomics of <i>Impatiens</i> (Balsaminaceae). <i>Planta</i> , 2023, 257, .	3.2	3
3677	Plastid Phylogenomic Insights into the Inter-Tribal Relationships of Plantaginaceae. <i>Biology</i> , 2023, 12, 263.	2.8	2
3678	Interplay between transcriptional regulators and <scp>VapBC toxinâ€“antitoxin</scp> loci during thermal stress response in extremely thermoacidophilic archaea. <i>Environmental Microbiology</i> , 2023, 25, 1200-1215.	3.8	4
3679	Investigating the origin of subtelomeric and centromeric AT-rich elements in <i>Aspergillus flavus</i> . <i>PLoS ONE</i> , 2023, 18, e0279148.	2.5	1
3680	Comparative Genomics of <i>Legionella pneumophila</i> Isolates from the West Bank and Germany Support Molecular Epidemiology of Legionnairesâ€™ Disease. <i>Microorganisms</i> , 2023, 11, 449.	3.6	2
3681	Comparative Genomic Analysis of a Thermophilic Protease-Producing Strain <i>Geobacillus stearothermophilus</i> H6. <i>Genes</i> , 2023, 14, 466.	2.4	1
3682	Complete Chloroplast Genome Sequence of the Long Blooming Cultivar <i>Camellia</i> â€“Xiari Qixinâ€™™: Genome Features, Comparative and Phylogenetic Analysis. <i>Genes</i> , 2023, 14, 460.	2.4	0
3683	Biotechnologically potential genes in a polysaccharide-degrading epibiont of the Indonesian brown algae <i>Hydroclathrus</i> sp.. <i>Journal of Genetic Engineering and Biotechnology</i> , 2023, 21, 18.	3.3	1
3684	Kojic Acid Gene Clusters and the Transcriptional Activation Mechanism of <i>Aspergillus flavus</i> KojR on Expression of Clustered Genes. <i>Journal of Fungi</i> (Basel, Switzerland), 2023, 9, 259.	3.5	4
3685	Staying below the Radar: Unraveling a New Family of Ubiquitous â€œCrypticâ€•Non-Tailed Temperate Vibriophages and Implications for Their Bacterial Hosts. <i>International Journal of Molecular Sciences</i> , 2023, 24, 3937.	4.1	1
3686	Insight into the Organization of the B10v3 Cucumber Genome by Integration of Biological and Bioinformatic Data. <i>International Journal of Molecular Sciences</i> , 2023, 24, 4011.	4.1	4
3687	Resistance to the Bacteriocin Lcn972 Deciphered by Genome Sequencing. <i>Microorganisms</i> , 2023, 11, 501.	3.6	2
3689	Horizontal Gene Transfer and Fusion Spread Carotenogenesis Among Diverse Heterotrophic Protists. <i>Genome Biology and Evolution</i> , 2023, 15, .	2.5	4
3690	Strainâ€™specific quorumâ€™sensing responses determine virulence properties in <scp><i>Vibrio anguillarum</i></scp>. <i>Environmental Microbiology</i> , 2023, 25, 1344-1362.	3.8	4
3691	Profiling of Antimicrobial Metabolites Synthesized by the Endophytic and Genetically Amenable Biocontrol Strain <i>Bacillus velezensis</i> DMW1. <i>Microbiology Spectrum</i> , 2023, 11, .	3.0	5

#	ARTICLE	IF	CITATIONS
3692	Genomic Epidemiological Analysis of Antimicrobial-Resistant Bacteria with Nanopore Sequencing. <i>Methods in Molecular Biology</i> , 2023, , 227-246.	0.9	0
3693	Characterization of a novel <i>Bacillus methylotrophicus</i> phage BM-P1. <i>Food Quality and Safety</i> , 2023, 7, .	1.8	3
3694	Genomic Characteristics and Molecular Epidemiology of Multidrug-Resistant <i>Klebsiella pneumoniae</i> Strains Carried by Wild Birds. <i>Microbiology Spectrum</i> , 2023, 11, .	3.0	0
3697	Genomic characterization and molecular dating of the novel bacterium <i>Permianibacter aggregans</i> HW001T, which originated from Permian ground water. <i>Marine Life Science and Technology</i> , 2023, 5, 12-27.	4.6	0
3698	Isolation, characterization, therapeutic potency, and genomic analysis of a novel bacteriophage vB_KshKPC-M against carbapenemase-producing <i>Klebsiella pneumoniae</i> strains (CRKP) isolated from Ventilator-associated pneumoniae (VAP) infection of COVID-19 patients. <i>Annals of Clinical Microbiology and Antimicrobials</i> , 2023, 22, .	3.8	4
3699	Adaptations of <i>Pseudoxylaria</i> towards a comb-associated lifestyle in fungus-farming termite colonies. <i>ISME Journal</i> , 2023, 17, 733-747.	9.8	4
3700	A new and accurate qPCR protocol to detect plant pathogenic bacteria of the genus <i>Candidatus Liberibacter</i> ™ in plants and insects. <i>Scientific Reports</i> , 2023, 13, .	3.3	1
3701	Prevalence and molecular characteristics of mcr-1-positive <i>Escherichia coli</i> isolated from duck farms and the surrounding environments in coastal China. <i>Microbiological Research</i> , 2023, 270, 127348.	5.3	2
3702	Pan-Chromosome and Comparative Analysis of <i>Agrobacterium fabrum</i> Reveal Important Traits Concerning the Genetic Diversity, Evolutionary Dynamics, and Niche Adaptation of the Species. <i>Microbiology Spectrum</i> , 2023, 11, .	3.0	0
3703	Emergence of Carbapenemase-Producing Hypervirulent <i>Klebsiella pneumoniae</i> in Switzerland. <i>Antimicrobial Agents and Chemotherapy</i> , 0, , .	3.2	4
3704	A caste differentiation mutant elucidates the evolution of socially parasitic ants. <i>Current Biology</i> , 2023, 33, 1047-1058.e4.	3.9	4
3705	Complete Genome Sequence of <i>Oceanotoga</i> sp. Strain T3B (DSM 15011). <i>Microbiology Resource Announcements</i> , 2023, 12, .	0.6	0
3706	The Complete Mitochondrial Genome of <i>Dendrogale murina</i> (Tupaiaidae) and Phylogeny of Scandentia. <i>Genes</i> , 2023, 14, 624.	2.4	1
3707	Genomic Comparisons Reveal Selection Pressure and Functional Variation Between Nutritional Endosymbionts of Cave-Adapted and Epigeal Hawaiian Planthoppers. <i>Genome Biology and Evolution</i> , 2023, 15, .	2.5	5
3708	Whole-Genome Sequencing-Based Resistome Analysis of Nosocomial Multidrug-Resistant Non-Fermenting Gram-Negative Pathogens from the Balkans. <i>Microorganisms</i> , 2023, 11, 651.	3.6	4
3709	Genomic Investigation of <i>Salmonella Typhi</i> in Hong Kong Revealing the Predominance of Genotype 3.2.2 and the First Case of an Extensively Drug-Resistant H58 Genotype. <i>Microorganisms</i> , 2023, 11, 667.	3.6	1
3710	The terrestrial isopod symbiont <i>Candidatus Hepatincola porcellionum</i> ™ is a potential nutrient scavenger related to <i>Holosporales</i> symbionts of protists. <i>ISME Communications</i> , 2023, 3, .	4.2	2
3711	Complete chloroplast genome sequence and phylogenetic analysis of <i>Rhododendron molle</i> G. Don, an endangered Ericaceae species located on Dabie Mountains (central China). <i>Plant Biotechnology Reports</i> , 0, , .	1.5	0

#	ARTICLE	IF	CITATIONS
3712	Investigation of monacolin K, yellow pigments, and citrinin production capabilities of <i>Monascus purpureus</i> and <i>Monascus ruber</i> (<i>Monascus pilosus</i>). <i>Journal of Food and Drug Analysis</i> , 2023, 31, 85-94.	1.9	2
3713	The complete mitochondrial genome of a wild-collected <i>Kappaphycus malesianus</i> (Solieriaceae.) <i>Tj ETQq1 1 0.7843141rgBT /Over</i>	0.4	1
3715	Mitogenomic and Phylogenetic Analysis of the Entomopathogenic Fungus <i>Ophiocordyceps lanpingensis</i> and Comparative Analysis with Other <i>Ophiocordyceps</i> Species. <i>Genes</i> , 2023, 14, 710.	2.4	3
3716	Characterization of <i>Shigella flexneri</i> Serotype 6 Strains Isolated from Bangladesh and Identification of a New Phylogenetic Cluster. <i>Journal of Bacteriology</i> , 2023, 205, .	2.2	1
3717	Adaptation Strategies to High Hydrostatic Pressures in <i>Pseudothermotoga</i> species Revealed by Transcriptional Analyses. <i>Microorganisms</i> , 2023, 11, 773.	3.6	1
3718	Complete sequences of six major histocompatibility complex haplotypes, including all the major <scp>MHC</scp> class <scp>II</scp> structures. <i>Hla</i> , 2023, 102, 28-43.	0.6	5
3719	Integrative omics identifies conserved and pathogen-specific responses of sepsis-causing bacteria. <i>Nature Communications</i> , 2023, 14, .	12.8	10
3720	Plastid Genome Assembly Using Long-read data. <i>Molecular Ecology Resources</i> , 2023, 23, 1442-1457.	4.8	4
3721	Examination of Large Chromosomal Inversions in the Genome of <i>Erwinia amylovora</i> Strains Reveals Worldwide Distribution and North America-Specific Types. <i>Phytopathology</i> , 2023, 113, 2174-2186.	2.2	3
3723	A Complete Genome of the Alphaproteobacterial Methanotroph <i>Methylocystis parvus</i> OBBP. <i>Microbiology Resource Announcements</i> , 2023, 12, .	0.6	0
3724	The evolution of white-tailed jackrabbit camouflage in response to past and future seasonal climates. <i>Science</i> , 2023, 379, 1238-1242.	12.6	5
3725	Global scenario of the RmtE pan-aminoglycoside-resistance mechanism: emergence of the rmtE4 gene in South America associated with a hospital-related IncL plasmid. <i>Microbial Genomics</i> , 2023, 9, .	2.0	0
3726	Comparative analysis of complete <i>Artemisia</i> subgenus <i>Seriphidium</i> (Asteraceae: Anthemideae) chloroplast genomes: insights into structural divergence and phylogenetic relationships. <i>BMC Plant Biology</i> , 2023, 23, .	3.6	5
3727	Comparative genome and phylogenetic analysis revealed the complex mitochondrial genome and phylogenetic position of <i>Conopomorpha sinensis</i> Bradley. <i>Scientific Reports</i> , 2023, 13, .	3.3	0
3728	Assembling highly repetitive <i>Xanthomonas</i> TALomes using Oxford Nanopore sequencing. <i>BMC Genomics</i> , 2023, 24, .	2.8	3
3729	Highly contiguous genomes of human clinical isolates of <i>Giardia duodenalis</i> reveal assemblage- and sub-assemblage-specific presence-absence variation in protein-coding genes. <i>Microbial Genomics</i> , 2023, 9, .	2.0	1
3730	NGS Reads Dataset of Sunflower Interspecific Hybrids. <i>Data</i> , 2023, 8, 67.	2.3	1
3731	Genome Alignments. , 2023, , .		0

#	ARTICLE	IF	CITATIONS
3732	Vibrio type III secretion system 2 is not restricted to the Vibrionaceae and encodes differentially distributed repertoires of effector proteins. Microbial Genomics, 2023, 9, .	2.0	0
3733	Genomic Islands in Helicobacter Species. , 2023, , 197-206.		0
3734	Computation Tools for Prediction and Analysis of Genomic Islands. , 2023, , 17-31.		0
3735	Parapatric speciation of Meiothermus in serpentinite-hosted aquifers in Oman. Frontiers in Microbiology, 0, 14, .	3.5	1
3736	A conserved hymenopteran-specific family of cytochrome P450s protects bee pollinators from toxic nectar alkaloids. Science Advances, 2023, 9, .	10.3	4
3737	Genome Organization of Four Brazilian Xanthomonas albilineans Strains Does Not Correlate with Aggressiveness. Microbiology Spectrum, 0, , .	3.0	1
3738	Exploration of the diversity of multi-drug resistant Mycobacterium tuberculosis complex in Lagos, Nigeria using WGS: Distribution of lineages, drug resistance patterns and genetic mutations. Tuberculosis, 2023, 140, 102343.	1.9	0
3739	Draft Genome Sequences and Genome Characterization of Three Toxigenic and Two Nontoxigenic Clostridioides difficile Clinical Isolates from Florida, USA. Microbiology Resource Announcements, 0, , .	0.6	0
3741	Genomic determination of breeding systems and trans-specific evolution of <i>HD MAT</i> genes in suilloid fungi. Genetics, 2023, 224, .	2.9	1
3742	Plastid Phylogenomic Analyses Reveal a Cryptic Species of Ligusticopsis (Apiaceae, Angiosperms). International Journal of Molecular Sciences, 2023, 24, 7419.	4.1	1
3743	A pathogenicity locus of Streptococcus gallolyticus subspecies gallolyticus. Scientific Reports, 2023, 13, .	3.3	4
3744	Comparative genomic insights into habitat adaptation of coral-associated Prosthecochloris. Frontiers in Microbiology, 0, 14, .	3.5	1
3745	Integrated computational approaches to aid precision medicine for cancer therapy: Present scenario and future prospects. , 2023, , 403-424.		0
3746	Asfarviruses and Closely Related Giant Viruses. Viruses, 2023, 15, 1015.	3.3	1
3747	Complete Mitogenome and Phylogenetic Analysis of the Carthamus tinctorius L.. Genes, 2023, 14, 979.	2.4	3
3748	Near-Complete Genome Sequence of White Spot Syndrome Virus Infecting Cultivated Shrimp (Penaeus) Tj ETQq1 1,0.784314 rgBT /Ove	0.6	0
3749	The complete chloroplast genome sequence of Eugenia klotzschiana O. Berg unveils the evolutionary dynamics in plastomes of Myrteae DC. Tribe (Myrtaceae). Gene, 2023, 876, 147488.	2.2	2
3750	Whole Genome Analysis and Assessment of the Metabolic Potential of Gordonia rubripertincta Strain 112, a Degradar of Aromatic and Aliphatic Compounds. Biology, 2023, 12, 721.	2.8	1

#	ARTICLE	IF	CITATIONS
3751	First report of whole genome sequence of septicemic <i>Pasteurella multocida</i> serovar B:2 â€”Sorona™ strain isolated from swine. <i>Brazilian Journal of Microbiology</i> , 0, , .	2.0	0
3752	ï¿½The identity of <i>Sasa oblongula</i> C.H.Hu (Poaceae, Bambusoideae, Arundinarieae): evidence from morphology and molecular data. <i>PhytoKeys</i> , 0, 226, 17-32.	1.0	0
3753	Complete Chloroplast Genome of Bamboo Species <i>Pleioblastus ovatoauritus</i> and Comparative Analysis of <i>Pleioblastus</i> from China and Japan. <i>Forests</i> , 2023, 14, 1051.	2.1	0
3754	Discovery of the Azaserine Biosynthetic Pathway Uncovers a Biological Route for Î±â€”Diazooester Production. <i>Angewandte Chemie</i> , 2023, 135, .	2.0	0
3756	<i>Bacillus cabrialesii</i> subsp. <i>cabrialesii</i> subsp. nov. and <i>Bacillus cabrialesii</i> subsp. <i>tritici</i> subsp. nov., plant growth-promoting bacteria and biological control agents isolated from wheat (<i>Triticum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 582 Evolutionary Microbiology, 2023, 73, .	1.7	2
3757	Isolation and Characterization of a Novel Phage Collection against Avian-Pathogenic <i>Escherichia coli</i>. <i>Microbiology Spectrum</i> , 2023, 11, .	3.0	5
3758	Assembly of the Complete Mitochondrial Genome of <i>Pereskia aculeata</i> Revealed That Two Pairs of Repetitive Elements Mediated the Recombination of the Genome. <i>International Journal of Molecular Sciences</i> , 2023, 24, 8366.	4.1	8
3759	Discovery of the Azaserine Biosynthetic Pathway Uncovers a Biological Route for Î±â€”Diazooester Production. <i>Angewandte Chemie - International Edition</i> , 2023, 62, .	13.8	10
3760	<i>Bulbophyllum wolongense</i> , a New Orchidaceae Species from Sichuan Province in China, and Its Plastome Comparative Analysis. <i>Ecosystem Health and Sustainability</i> , 2023, 9, .	0.0	0
3761	The plastome reveals new insights into the evolutionary and domestication history of peonies in East Asia. <i>BMC Plant Biology</i> , 2023, 23, .	3.6	2
3762	Characterization of a Nonagglutinating Toxigenic <i>Vibrio cholerae</i> Isolate. <i>Microbiology Spectrum</i> , 2023, 11, .	3.0	0
3763	Emerging Pathogens in Planetary Health and Lessons from Comparative Genome Analyses of Three <i>Clostridia</i> Species. <i>OMICS A Journal of Integrative Biology</i> , 2023, 27, 247-259.	2.0	0
3764	De novo mitochondrial genome sequencing of <i>Cladonia subulata</i> and phylogenetic analysis with other dissimilar species. <i>PLoS ONE</i> , 2023, 18, e0285818.	2.5	1
3765	Extracellular Polysaccharide Receptor and Receptor-Binding Proteins of the <i>Rhodobacter capsulatus</i> Bacteriophage-like Gene Transfer Agent RcGTA. <i>Genes</i> , 2023, 14, 1124.	2.4	0
3766	Genomes comparison of two <i>Proteus mirabilis</i> clones showing varied swarming ability. <i>Molecular Biology Reports</i> , 2023, 50, 5817-5826.	2.3	1
3767	<i>Schizosaccharomyces lindneri</i> sp. nov., a fission yeast occurring in honey. <i>Yeast</i> , 2023, 40, 237-253.	1.7	7
3768	Comprehensive analysis of the complete mitochondrial genomes of three <i>Coptis</i> species (<i>C. chinensis</i> ,) Tj ETQq0 0 0 rgBT /Overlock 10 T 14, .	3.6	3
3769	Comparative Genomic Analysis of Multi-Drug Resistant <i>Pseudomonas aeruginosa</i> Sequence Type 235 Isolated from Sudan. <i>Microorganisms</i> , 2023, 11, 1432.	3.6	0

#	ARTICLE	IF	CITATIONS
3770	Chloroplast genome characteristics and phylogeny of the sinodielsia clade (apiaceae: apioideae). BMC Plant Biology, 2023, 23, .	3.6	1
3772	The Influence of Heteroresistance on Minimum Inhibitory Concentration, Investigated Using Weak-Acid Stress in Food Spoilage Yeasts. Applied and Environmental Microbiology, 2023, 89, .	3.1	0
3773	Antagonistic transcriptome profile reveals potential mechanisms of action on Xanthomonas oryzae pv. oryzae by the cell-free supernatants of Bacillus velezensis 504, a versatile plant probiotic bacterium. Frontiers in Cellular and Infection Microbiology, 0, 13, .	3.9	2
3774	Genomic and phenotypic features of Acinetobacter baumannii isolated from oil reservoirs reveal a novel subspecies specialized in degrading hazardous hydrocarbons. Microbiological Research, 2023, 273, 127420.	5.3	1
3775	Whole Genome Sequencing of Levilactobacillus brevis HQ1-1 for Understanding the Characteristics of Its Antibiotic Resistance Genes. Microbiology, 2023, 92, 358-369.	1.2	0
3776	The complete plastid genome and characteristics analysis of Achillea millefolium. Functional and Integrative Genomics, 2023, 23, .	3.5	1
3777	Complete genome sequence of biocontrol strain Bacillus velezensis YC89 and its biocontrol potential against sugarcane red rot. Frontiers in Microbiology, 0, 14, .	3.5	3
3780	Epidemiology and zoonotic transmission of mcr-positive and carbapenemase-producing Enterobacterales on German turkey farms. Frontiers in Microbiology, 0, 14, .	3.5	1
3781	Mitogenomic Research of Silverleaf Sunflower (HelianthusÂargophyllus) and Its Interspecific Hybrids. Current Issues in Molecular Biology, 2023, 45, 4841-4849.	2.4	1
3782	Detecting gene breakpoints in noisy genome sequences using position-annotated colored de-Bruijn graphs. BMC Bioinformatics, 2023, 24, .	2.6	0
3783	Genomic and Evolutionary Features of Nine AHPND Positive Vibrio parahaemolyticus Strains Isolated from South American Shrimp Farms. Microbiology Spectrum, 0, , .	3.0	0
3784	IdentificaciÃ³n y secuenciaciÃ³n de SARS-CoV-2 en una leona africana (Panthera leo), bajo el cuidado tÃ©cnico profesional, en Colombia. Revista De Salud Publica, 2022, 24, 1-9.	0.1	0
3785	A novel variant of the Listeria monocytogenes type VII secretion system EssC component is associated with an Rhs toxin. Microbial Genomics, 2023, 9, .	2.0	2
3786	Real-time on-site detection of the three â€Candidatus Liberibacterâ€™ species associated with HLB disease: a rapid and validated method. Frontiers in Plant Science, 0, 14, .	3.6	1
3787	Isolation and Characterization of Jumbo Coliphage vB_EcoM_Lh1B as a Promising Therapeutic Agent against Chicken Colibacillosis. Microorganisms, 2023, 11, 1524.	3.6	2
3788	Complete chloroplast genomes of five Cuscuta species and their evolutionary significance in the Cuscuta genus. BMC Genomics, 2023, 24, .	2.8	0
3789	Characterisation of key genotypic and phenotypic traits of clinical cystic fibrosis Staphylococcus aureus isolates. Journal of Medical Microbiology, 2023, 72, .	1.8	0
3790	Are Current <i>Aspergillus sojae</i> Strains Originated from a Native Aflatoxigenic <i>Aspergillus</i> Species Population Also Present in California?. Mycobiology, 2023, 51, 139-147.	1.7	3

#	ARTICLE	IF	CITATIONS
3791	Characterization and Comparative Analysis of Chloroplast Genomes of Medicinal Herb <i>Scrophularia ningpoensis</i> and Its Common Adulterants (<i>Scrophulariaceae</i>). <i>International Journal of Molecular Sciences</i> , 2023, 24, 10034.	4.1	3
3792	Homologous genes shared between probiotics and pathogens affect the adhesion of probiotics and exclusion of pathogens in the gut mucus of shrimp. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	1
3793	A global genomic analysis of <i>Salmonella</i> Concord reveals lineages with high antimicrobial resistance in Ethiopia. <i>Nature Communications</i> , 2023, 14, .	12.8	3
3795	<i>Vibrio</i> Phage VMJ710 Can Prevent and Treat Disease Caused by Pathogenic MDR <i>V. cholerae</i> O1 in an Infant Mouse Model. <i>Antibiotics</i> , 2023, 12, 1046.	3.7	1
3796	Host shift promotes divergent evolution between closely related holoparasitic species. <i>Molecular Phylogenetics and Evolution</i> , 2023, 186, 107842.	2.7	1
3797	Comparison of Attenuated and Virulent Strains of African Swine Fever Virus Genotype I and Serogroup 2. <i>Viruses</i> , 2023, 15, 1373.	3.3	0
3798	Comparative chloroplast genome analysis of <i>Sambucus</i> L. (<i>Viburnaceae</i>): inference for phylogenetic relationships among the closely related <i>Sambucus adnata</i> Wall. ex DC <i>Sambucus javanica</i> Blume. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	1
3800	Characterization of bacteriophage vB_KleM_KB2 possessing high control ability to pathogenic <i>Klebsiella pneumoniae</i> . <i>Scientific Reports</i> , 2023, 13, .	3.3	1
3801	The analysis of the function, diversity, and evolution of the <i>Bacillus</i> phage genome. <i>BMC Microbiology</i> , 2023, 23, .	3.3	1
3802	Suboptimal environmental conditions prolong phage epidemics in bacterial populations. <i>Molecular Ecology</i> , 0, , .	3.9	2
3803	Russian collection of <i>Brucella abortus</i> vaccine strains: annotation, implementation and genomic analysis. <i>Frontiers in Veterinary Science</i> , 0, 10, .	2.2	0
3804	Comparative genomics and phenotypic studies to determine site-specificity of <i>Escherichia coli</i> in the lower gastrointestinal tract of humans. <i>Gut Microbes</i> , 2023, 15, .	9.8	0
3805	Insights into phylogenetic relationships in <i>Pinus</i> inferred from a comparative analysis of complete chloroplast genomes. <i>BMC Genomics</i> , 2023, 24, .	2.8	0
3806	Comparative analysis of 17 complete chloroplast genomes reveals intraspecific variation and relationships among <i>Pseudostellaria heterophylla</i> (Miq.) Pax populations. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	1
3807	Empirically derived sequence similarity thresholds to study the genomic epidemiology of plasmids shared among healthcare-associated bacterial pathogens. <i>EBioMedicine</i> , 2023, 93, 104681.	6.1	3
3808	Molecular evaluation of the metabolism of estrogenic di(2-ethylhexyl) phthalate in <i>Mycobacterium</i> sp.. <i>Microbial Cell Factories</i> , 2023, 22, .	4.0	3
3809	<i>Cryptomonas pyrenoidifera</i> organellar genomes and estimation of its ITS2 sequence diversity using lineage directed barcode primers. <i>Phycologia</i> , 2023, 62, 280-291.	1.4	1
3810	Unravelling the Evolutionary Dynamics of High-Risk <i>Klebsiella pneumoniae</i> ST147 Clones: Insights from Comparative Pangenome Analysis. <i>Genes</i> , 2023, 14, 1037.	2.4	2

#	ARTICLE	IF	CITATIONS
3811	Comprehensive Characterization of a Streptococcus agalactiae Phage Isolated from a Tilapia Farm in Selangor, Malaysia, and Its Potential for Phage Therapy. Pharmaceuticals, 2023, 16, 698.	3.8	0
3812	Combined actions of bacteriophage-encoded genes in Wolbachia-induced male lethality. IScience, 2023, 26, 106842.	4.1	6
3813	Complete genome resource unravels the close relation of an Indian Xanthomonas oryzae pv. oryzae strain IXOBB0003 with Philippines strain causing bacterial blight of rice. 3 Biotech, 2023, 13, .	2.2	0
3814	Comparative Genomic Analyses of Escherichia coli from a Meat Processing Environment in Relation to Their Biofilm Formation and Persistence. Microbiology Spectrum, 2023, 11, .	3.0	3
3815	Two complete mitogenomes of Ocypodoidea (Decapoda: Brachyura), Cleistostoma dilatatum (Camptandriidae) and Euplax sp. (Macrophthalmidae) and its phylogenetic implications. Acta Oceanologica Sinica, 2023, 42, 81-92.	1.0	0
3816	Genomic variability correlates with biofilm phenotypes in multidrug resistant clinical isolates of Pseudomonas aeruginosa. Scientific Reports, 2023, 13, .	3.3	2
3817	Characterization of <i>Bifidobacterium kashiwanohense</i> that utilizes both milk- and plant-derived oligosaccharides. Gut Microbes, 2023, 15, .	9.8	1
3818	Isolation and in vitro characterization of novel S. epidermidis phages for therapeutic applications. Frontiers in Cellular and Infection Microbiology, 0, 13, .	3.9	2
3821	Transmission Dynamics of a Mycobacterium tuberculosis Complex Outbreak in an Indigenous Population in the Colombian Amazon Region. Microbiology Spectrum, 2023, 11, .	3.0	0
3822	Insights into chloroplast genome structure and phylogenetic relationships within the Sesamum species complex (Pedaliaceae). Frontiers in Genetics, 0, 14, .	2.3	1
3823	Comparative genomics of <i>Xanthomonas translucens</i> pv. <i>undulosa</i> strains isolated from weedy grasses and cultivated wild rice. Phytopathology, 0, , .	2.2	1
3824	Multiscale analysis of pangenomes enables improved representation of genomic diversity for repetitive and clinically relevant genes. Nature Methods, 2023, 20, 1213-1221.	19.0	7
3825	Comparative genomics of the Liberibacter genus reveals widespread diversity in genomic content and positive selection history. Frontiers in Microbiology, 0, 14, .	3.5	1
3826	Factors contributing to mitogenome size variation and a recurrent intracellular DNA transfer in Melastoma. BMC Genomics, 2023, 24, .	2.8	2
3828	Exopolysaccharide is the potential effector of Lactobacillus fermentum PS150, a hypnotic psychobiotic strain. Frontiers in Microbiology, 0, 14, .	3.5	0
3829	Analysis of Thaumatotibia leucotreta (Lepidoptera: Tortricidae: Olethreutinae) mitochondrial genomes in the context of a recent host range expansion. BMC Ecology and Evolution, 2023, 23, .	1.6	0
3830	High subtelomeric GC content in the genome of a zoonotic Cryptosporidium species. Microbial Genomics, 2023, 9, .	2.0	0
3831	Comparative Genomic Analysis of a Novel Vibrio sp. Isolated from an Ulcer Disease Event in Atlantic Salmon (Salmo salar). Microorganisms, 2023, 11, 1736.	3.6	1

#	ARTICLE	IF	CITATIONS
3833	Influence of mobile genetic elements and insertion sequences in long- and short-term adaptive processes of <i>Acidithiobacillus ferrooxidans</i> strains. <i>Scientific Reports</i> , 2023, 13, .	3.3	2
3834	Race-specific genotypes of <i>Pseudomonas syringae</i> pv. tomato are defined by the presence of mobile DNA elements within the genome. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	0
3835	<i>Salmonella gallinarum</i> strains from outbreaks of fowl typhoid fever in Southern Africa closely related to SG9R vaccines. <i>Frontiers in Veterinary Science</i> , 0, 10, .	2.2	1
3836	<i>In Silico</i> Evaluation of Variant Calling Methods for Bacterial Whole-Genome Sequencing Assays. <i>Journal of Clinical Microbiology</i> , 0, , .	3.9	1
3837	Horizontal Gene Transfer and CRISPR Targeting Drive Phage-Bacterial Host Interactions and Coevolution in <i>Pink Berry</i> Marine Microbial Aggregates. <i>Applied and Environmental Microbiology</i> , 2023, 89, .	3.1	3
3838	Whole-genome sequence analysis of carbapenem-resistant <i>Enterobacteriaceae</i> recovered from hospitalized patients. <i>Journal of Global Antimicrobial Resistance</i> , 2023, 34, 150-160.	2.2	3
3839	Phenotypic and genetic insights into efflux pump mechanism in <i>Mycoplasma anseris</i> alpingitidis. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	0
3840	Characterization of a novel and active temperate phage vB_AbaM_ABMM1 with antibacterial activity against <i>Acinetobacter baumannii</i> infection. <i>Scientific Reports</i> , 2023, 13, .	3.3	2
3841	Comparative analysis of <i>Diospyros</i> (Ebenaceae) plastomes: Insights into genomic features, mutational hotspots, and adaptive evolution. <i>Ecology and Evolution</i> , 2023, 13, .	1.9	1
3842	Plastome evolution and phylogenomic insights into the evolution of <i>Lysimachia</i> (Primulaceae): Tj ETQq1 1 0.784314 rgBT /Overlock 107	3.6	1
3843	Characteristics and Whole-Genome Analysis of <i>Limosilactobacillus fermentum</i> Phage LFP02. <i>Foods</i> , 2023, 12, 2716.	4.3	0
3844	Metabolic engineering of <i>Corynebacterium glutamicum</i> for fatty alcohol production from glucose and wheat straw hydrolysate. , 2023, 16, .		2
3845	Founding of the culture collection of antibiotic-resistant strains of zoonotic bacteria in the Russian Federation. <i>Veterinary World</i> , 2023, , 1451-1460.	1.7	0
3846	Complete chloroplast genomes of three wild perennial <i>Hordeum</i> species from Central Asia: genome structure, mutation hotspot, phylogenetic relationships, and comparative analysis. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	0
3848	Recently evolved combination of unique sulfatase and amidase genes enables bacterial degradation of the wastewater micropollutant acesulfame worldwide. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	6
3850	Development and application of a qPCR-based genotyping assay for <i>Ophidiomyces ophidiicola</i> to investigate the epidemiology of ophidiomycosis. <i>PLoS ONE</i> , 2023, 18, e0289159.	2.5	1
3851	Historical biogeography and evolutionary diversification of <i>Lilium</i> (Liliaceae): New insights from plastome phylogenomics. <i>Plant Diversity</i> , 2024, 46, 219-228.	3.7	0
3852	Integrative analysis of chloroplast genome, chemicals, and illustrations in Bencao literature provides insights into the medicinal value of <i>Peucedanum huangshanense</i> . <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	0

#	ARTICLE	IF	CITATIONS
3853	Phage tailspike modularity and horizontal gene transfer reveals specificity towards E. coli O-antigen serogroups. <i>Virology Journal</i> , 2023, 20, .	3.4	3
3855	The First Complete Chloroplast Genome of <i>Campanula carpatica</i> : Genome Characterization and Phylogenetic Diversity. <i>Genes</i> , 2023, 14, 1597.	2.4	0
3856	Data mining and molecular dynamics analysis to detect HIV-1 reverse transcriptase RNase H activity inhibitor. <i>Molecular Diversity</i> , 0, , .	3.9	0
3859	Geneâ€rich plastid genomes of two parasitic red algal species, <i>Laurencia australis</i> and <i>L. verruciformis</i> (Rhodomelaceae, Ceramiales), and a taxonomic revision of <i>Janczewskia</i> . <i>Journal of Phycology</i> , 2023, 59, 950-962.	2.3	1
3860	The characterization and genome analysis of a novel phage phiA034 targeting multiple species of <i>Aeromonas</i> . <i>Virus Research</i> , 2023, 336, 199193.	2.2	1
3861	A novel culture-enriched metagenomic sequencing strategy effectively guarantee the microbial safety of drinking water by uncovering the low abundance pathogens. <i>Journal of Environmental Management</i> , 2023, 345, 118737.	7.8	0
3862	Whole genome analysis and cold adaptation strategies of <i>Pseudomonas sivasensis</i> W-6 isolated from the Napahai plateau wetland. <i>Scientific Reports</i> , 2023, 13, .	3.3	0
3863	Precision metagenomics sequencing for food safety: hybrid assembly of Shiga toxin-producing <i>Escherichia coli</i> in enriched agricultural water. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	0
3865	Functional annotation and comparative genomics analysis of <i>Balamuthia mandrillaris</i> reveals potential virulence-related genes. <i>Scientific Reports</i> , 2023, 13, .	3.3	0
3866	Novel ribotype/sequence type associations and diverse CRISPR-Cas systems in environmental <i>Clostridioides difficile</i> strains from northern Iraq. <i>FEMS Microbiology Letters</i> , 2023, 370, .	1.8	0
3867	Draft genome sequences of 14 <i>Lactiseibacillus</i> spp. strains, representatives of a collection of 200 strains. <i>Microbiology Resource Announcements</i> , 2023, 12, .	0.6	0
3868	Comparative genomic analysis of <i>Periweissella</i> and the characterization of novel motile species. <i>Applied and Environmental Microbiology</i> , 0, , .	3.1	2
3869	Characterization of Complete Mitochondrial Genomes of the Five <i>Peltigera</i> and Comparative Analysis with Relative Species. <i>Journal of Fungi (Basel, Switzerland)</i> , 2023, 9, 969.	3.5	0
3870	Long-read assembled metagenomic approaches improve our understanding on metabolic potentials of microbial community in mangrove sediments. <i>Microbiome</i> , 2023, 11, .	11.1	2
3871	De novo genome assembly resolving repetitive structures enables genomic analysis of 35 European <i>Mycoplasma bovis</i> strains. <i>BMC Genomics</i> , 2023, 24, .	2.8	0
3872	Plastoquinone synthesis inhibition by tetrabromo biphenyldiol as a widespread algicidal mechanism of marine bacteria. <i>ISME Journal</i> , 2023, 17, 1979-1992.	9.8	5
3873	Maast: genotyping thousands of microbial strains efficiently. <i>Genome Biology</i> , 2023, 24, .	8.8	1
3874	A fungal sesquiterpene biosynthesis gene cluster critical for mutualist-pathogen transition in <i>Colletotrichum tofieldiae</i> . <i>Nature Communications</i> , 2023, 14, .	12.8	4

#	ARTICLE	IF	CITATIONS
3875	Identification and distribution of new candidate T6SS effectors encoded in Salmonella Pathogenicity Island 6. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	1
3876	Probiotic potential of Bacillus Isolates from Polish Bee Pollen and Bee Bread. <i>Probiotics and Antimicrobial Proteins</i> , 0, , .	3.9	0
3877	Genomic evidence of genetic diversity and functional evolution in <i>Flavobacterium columnare</i> . <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	0
3878	Comparative chloroplast genomics and insights into the molecular evolution of <i>Tanaecium</i> (Bignoniaceae, Bignoniaceae). <i>Scientific Reports</i> , 2023, 13, .	3.3	0
3879	Analysis of the Complete Mitochondrial Genome of <i>Pteronura brasiliensis</i> and <i>Lontra canadensis</i> . <i>Animals</i> , 2023, 13, 3165.	2.3	0
3880	Genome diversity of <i>Borrelia garinii</i> in marine transmission cycles does not match host associations but reflects the strains evolutionary history. <i>Infection, Genetics and Evolution</i> , 2023, 115, 105502.	2.3	0
3881	Can Genome Sequencing Coupled to Flux Balance Analyses Offer Precision Guidance for Industrial Strain Development? The Lessons from Carbon Trafficking in <i>Corynebacterium glutamicum</i> ATCC 21573. <i>OMICS A Journal of Integrative Biology</i> , 2023, 27, 434-443.	2.0	0
3882	Complete chloroplast genome of <i>Lens lamottei</i> reveals intraspecies variation among with <i>Lens culinaris</i> . <i>Scientific Reports</i> , 2023, 13, .	3.3	0
3883	Assembly and phylogeographical analysis of novel <i>Taenia solium</i> mitochondrial genomes suggest stratification within the African-American genotype. <i>Parasites and Vectors</i> , 2023, 16, .	2.5	0
3884	Comparative genomic analysis of two Arctic <i>Pseudomonas</i> strains reveals insights into the aerobic denitrification in cold environments. <i>BMC Genomics</i> , 2023, 24, .	2.8	1
3885	Pangenome-level analysis of nucleoid-associated proteins in the Acidithiobacillia class: insights into their functional roles in mobile genetic elements biology. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	0
3886	Whole-genome sequencing and antimicrobial potential of bacteria isolated from Polish honey. <i>Applied Microbiology and Biotechnology</i> , 2023, 107, 6389-6406.	3.6	1
3887	Chromosome-level genome assemblies of <i>Cutaneotrichosporon</i> spp. (Trichosporonales,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 267 Td (BMC Genomics, 2023, 24, .	2.8	1
3888	Evolutionary conservation of <i>Trichomonas</i> -mycoplasma symbiosis across the host species barrier. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	0
3889	Comparison and phylogeny on mitochondrial genome of marine and freshwater taxa of genus <i>Hildenbrandia</i> (Florideophyceae, Rhodophyta). <i>Journal of Oceanology and Limnology</i> , 0, , .	1.3	0
3890	Sequence Alignment/Map format: a comprehensive review of approaches and applications. <i>Briefings in Bioinformatics</i> , 2023, 24, .	6.5	2
3891	More than a spiny morphology: plastome variation in the prickly pear cacti (Opuntieae). <i>Annals of Botany</i> , 0, , .	2.9	1
3892	Complete Chloroplast Genomes and Phylogenetic Relationships of <i>Bougainvillea spectabilis</i> and <i>Bougainvillea glabra</i> (Nyctaginaceae). <i>International Journal of Molecular Sciences</i> , 2023, 24, 13044.	4.1	2

#	ARTICLE	IF	CITATIONS
3893	Genetic rearrangements in <i>Pseudomonas amygdali</i> pathovar <i>aesculi</i> shape coronatine plasmids. <i>Infection, Genetics and Evolution</i> , 2023, 113, 105486.	2.3	0
3894	Pangenome graphs in infectious disease: a comprehensive genetic variation analysis of <i>Neisseria meningitidis</i> leveraging Oxford Nanopore long reads. <i>Frontiers in Genetics</i> , 0, 14, .	2.3	0
3896	Complete chloroplast genome sequence of <i>Rhododendron mariesii</i> and comparative genomics of related species in the family Ericaceae. <i>Comparative Cytogenetics</i> , 0, 17, 163-180.	0.8	0
3897	Efficient precision editing of endogenous <i>Chlamydomonas reinhardtii</i> genes with CRISPR-Cas. <i>Cell Reports Methods</i> , 2023, 3, 100562.	2.9	2
3898	ORPA: a fast and efficient phylogenetic analysis method for constructing genome-wide alignments of organelle genomes. <i>Journal of Genetics and Genomics</i> , 2024, 51, 352-358.	3.9	1
3899	The complete chloroplast genome sequences of four <i>Liparis</i> species (Orchidaceae) and phylogenetic implications. <i>Gene</i> , 2023, 888, 147760.	2.2	1
3900	Characterisation and comparative genomics of three new <i>Varanus</i> -associated <i>Borrelia</i> spp. from Indonesia and Australia. <i>Parasites and Vectors</i> , 2023, 16, .	2.5	2
3902	Comparative Analysis of <i>Tylosema esculentum</i> Mitochondrial DNA Revealed Two Distinct Genome Structures. <i>Biology</i> , 2023, 12, 1244.	2.8	0
3905	<i>Enterococcus faecium</i> C171: Modulating the Immune Response to Acute Lethal Viral Challenge. <i>International Journal of Antimicrobial Agents</i> , 2023, 62, 106969.	2.5	0
3907	Chloroplast genome assembly of <i>Serjania erecta</i> Raldk: comparative analysis reveals gene number variation and selection in protein-coding plastid genes of Sapindaceae. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	0
3908	Comparative analyses of Linderniaceae plastomes, with implications for its phylogeny and evolution. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	1
3909	Systematic comparison of genome information processing and boundary recognition tools used for genomic island detection. <i>Computers in Biology and Medicine</i> , 2023, 166, 107550.	7.0	1
3910	Whole genome sequence analysis of the 2018 Persian onager isolate suggests sublineages within the <i>Taylorella asinigenitalis</i> species. <i>Veterinary Microbiology</i> , 2023, 286, 109884.	1.9	0
3911	Genotypic peculiarities of a human brucellosis case caused by <i>Brucella suis</i> biovar 5. <i>Scientific Reports</i> , 2023, 13, .	3.3	0
3912	A new perspective on codon usage, selective pressure, and phylogenetic implications of the plastomes in the <i>Telephium</i> clade (Crassulaceae). <i>Gene</i> , 2024, 892, 147871.	2.2	0
3914	The complete chloroplast genome sequences of six <i>Hylotelephium</i> species: Comparative genomic analysis and phylogenetic relationships. <i>PLoS ONE</i> , 2023, 18, e0292056.	2.5	0
3915	The mitogenomes characterization of two <i>Peltigera</i> species (<i>Peltigera elisabethae</i> and <i>Peltigera</i>) Tj ETQq0 0 0 rgBT /Qverlock 10 Tf 50 10	1.9	0
3916	<i>Pseudomonas aeruginosa</i> strains belonging to phylogroup 3 frequently exhibit an atypical quorum sensing response: the case of MAZ105, a tomato rhizosphere isolate. <i>Microbiology (United Kingdom)</i> , 2023, 169, .	1.8	0

#	ARTICLE	IF	CITATIONS
3917	Genome sequences of <i>bla</i> _{NDM-1} producing <i>Acinetobacter lactucae</i> isolated from immunocompromised patients in India. <i>Microbiology Resource Announcements</i> , 0, , .	0.6	0
3918	Comparative genomics of <i>Mycoplasma feriruminatoris</i> , a fast-growing pathogen of wild Caprinae. <i>Microbial Genomics</i> , 2023, 9, .	2.0	0
3919	Phenotypic and Genomic Characterization of <i>Streptomyces pakalii</i> sp. nov., a Novel Species with Anti-Biofilm and Anti-Quorum Sensing Activity in ESKAPE Bacteria. <i>Microorganisms</i> , 2023, 11, 2551.	3.6	0
3920	Identification and Characterization of ten <i>Escherichia coli</i> Strains Encoding Novel Shiga Toxin 2 Subtypes, Stx2n as Well as Stx2j, Stx2m, and Stx2o, in the United States. <i>Microorganisms</i> , 2023, 11, 2561.	3.6	2
3921	Comparative Analysis of Plastomes in Elsholtzieae: Phylogenetic Relationships and Potential Molecular Markers. <i>International Journal of Molecular Sciences</i> , 2023, 24, 15263.	4.1	1
3922	The genome of <i>Salmacisia buchloëana</i> , the parasitic puppet master pulling strings of sexual phenotypic monstrosities in buffalograss. <i>G3: Genes, Genomes, Genetics</i> , 2024, 14, .	1.8	0
3923	Biosynthetic gene cluster synteny: Orthologous polyketide synthases in <i>Hypogymnia physodes</i> , <i>Hypogymnia tubulosa</i> , and <i>Parmelia sulcata</i> . <i>MicrobiologyOpen</i> , 2023, 12, .	3.0	0
3924	Comparative and phylogenetic analyses of the chloroplast genomes of <i>Filipendula</i> species (Rosoideae.) <i>Tj ETQq1 1 0.784314 ggBT /Over</i>	3.3	0
3926	Characterization and genomic analysis of a novel bacteriophage BUCT_49532 lysing <i>Klebsiella pneumoniae</i> . <i>Virus Genes</i> , 0, , .	1.6	0
3927	The complete chloroplast genome of <i>Cicer reticulatum</i> and comparative analysis against relative <i>Cicer</i> species. <i>Scientific Reports</i> , 2023, 13, .	3.3	0
3928	Country-wide expansion of a VIM-1 carbapenemase-producing <i>Klebsiella oxytoca</i> ST145 lineage in Poland, 2009–2019. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 0, , .	2.9	0
3929	Genomics analysis of KPC-2 and NDM-5-producing Enterobacteriaceae in migratory birds from Qinghai Lake, China. <i>Applied Microbiology and Biotechnology</i> , 0, , .	3.6	0
3930	Genomic characterization and molecular evolution of human monkeypox viruses. <i>Archives of Virology</i> , 2023, 168, .	2.1	0
3931	Comparative Genomics Identifies the Evolutionarily Conserved Gene TPM3 as a Target of eca-miR-1 Involved in the Skeletal Muscle Development of Donkeys. <i>International Journal of Molecular Sciences</i> , 2023, 24, 15440.	4.1	0
3932	A genomic appraisal of invasive <i>Salmonella</i> Typhimurium and associated antibiotic resistance in sub-Saharan Africa. <i>Nature Communications</i> , 2023, 14, .	12.8	0
3933	Taxonomic Re-Classification and Expansion of the Phylum Chloroflexota Based on over 5000 Genomes and Metagenome-Assembled Genomes. <i>Microorganisms</i> , 2023, 11, 2612.	3.6	0
3934	Comparative genomic analysis of <i>Mycoplasma</i> related to cell culture for <i>infB</i> gene-based loop-mediated isothermal amplification. <i>World Journal of Microbiology and Biotechnology</i> , 2023, 39, .	3.6	0
3935	Multiomics analysis reveals the genetic and metabolic characteristics associated with the low prevalence of dental caries. <i>Journal of Oral Microbiology</i> , 2023, 15, .	2.7	0

#	ARTICLE	IF	CITATIONS
3936	The protist <i>Aurantiochytrium</i> has universal subtelomeric rDNAs and is a host for mirusviruses. <i>Current Biology</i> , 2023, 33, 5199-5207.e4.	3.9	3
3937	Complete chloroplast genomes of <i>Cerastium alpinum</i> , <i>C. arcticum</i> and <i>C. nigrescens</i> : genome structures, comparative and phylogenetic analysis. <i>Scientific Reports</i> , 2023, 13, .	3.3	0
3938	Genomic analysis and assessment of pathogenic (toxicogenic) potential of <i>Staphylococcus haemolyticus</i> and <i>Bacillus paranthracis</i> consortia isolated from bovine mastitis in Russia. <i>Scientific Reports</i> , 2023, 13, .	3.3	2
3939	Physiological and genomic characterization of <i>Lactiplantibacillus plantarum</i> isolated from <i>Indri indri</i> in Madagascar. <i>Journal of Applied Microbiology</i> , 2023, 134, .	3.1	0
3940	SDRAP for annotating scrambled or rearranged genomes. <i>NAR Genomics and Bioinformatics</i> , 2023, 5, .	3.2	0
3941	The complete sequence of <i>Lens tomentosus</i> chloroplast genome. <i>Acta Physiologiae Plantarum</i> , 2024, 46, .	2.1	0
3942	Eukaryotic RNA-guided endonucleases evolved from a unique clade of bacterial enzymes. <i>Nucleic Acids Research</i> , 2023, 51, 12414-12427.	14.5	3
3943	Genomic features of a plant growth-promoting endophytic <i>Enterobacter cancerogenus</i> JY65 dominant in microbiota of halophyte <i>Suaeda salsa</i> . <i>Plant and Soil</i> , 0, , .	3.7	0
3944	Identification of a unique conserved region from a kinetoplastid genome of <i>Leishmania orientalis</i> (formerly named <i>Leishmania siamensis</i>) strain PCM2 in Thailand. <i>Scientific Reports</i> , 2023, 13, .	3.3	0
3945	Genome analysis of haloalkaline isolates from the soda saline crater lake of Isabel Island; comparative genomics and potential metabolic analysis within the genus <i>Halomonas</i> . <i>BMC Genomics</i> , 2023, 24, .	2.8	0
3946	The pan-genome of <i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> (Map) confirms ancestral lineage and reveals gene rearrangements within Map Type S. <i>BMC Genomics</i> , 2023, 24, .	2.8	0
3947	Development of molecular assays for the analysis of genetic relationships of <i>Mycoplasma iowae</i> . <i>Veterinary Microbiology</i> , 2023, 287, 109909.	1.9	0
3948	New Insights Into The Evolution of Chloroplast Genomes in <i>Ochna</i> Species (Ochnaceae,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 26	1.2	0
3949	Intragenomic structural variation in organelle genomes from the genus <i>Dystaenia</i> (Apiaceae): genome rearrangement and mitochondrion-to-plastid DNA transfer. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	0
3950	High genomic plasticity and unique features of <i>Xanthomonas translucens</i> pv. <i>graminis</i> revealed through comparative analysis of complete genome sequences. <i>BMC Genomics</i> , 2023, 24, .	2.8	0
3951	Genome characterization and taxonomy of <i>Actinomyces acetigenes</i> sp. nov., and <i>Actinomyces stomatis</i> sp. nov., previously isolated from the human oral cavity. <i>BMC Genomics</i> , 2023, 24, .	2.8	0
3952	The variations of native plasmids greatly affect the cell surface hydrophobicity of sphingomonads. <i>MSystems</i> , 0, , .	3.8	0
3954	Complex interactions between diverse mobile genetic elements drive the evolution of metal-resistant bacterial genomes. <i>Environmental Microbiology</i> , 2023, 25, 3387-3405.	3.8	0

#	ARTICLE	IF	CITATIONS
3956	The complete chloroplast genome sequence of <i>Rhododendron fortunei</i> : Structural comparative and phylogenetic analysis in the ericaceae family. <i>Botanica Serbica</i> , 2023, 47, 279-290.	1.0	0
3957	Characterization of the CMS genetic regulation through comparative complete mitochondrial genome sequencing in <i>Nicotiana tabacum</i> . <i>Plant Genome</i> , 0, , .	2.8	0
3958	Divergences in stem and leaf traits between lianas and coexisting trees in a subtropical montane forest. <i>Journal of Plant Ecology</i> , 2024, 17, .	2.3	0
3959	Comparative genotypic characterization related to antibiotic resistance phenotypes of clinical carbapenem-resistant <i>Acinetobacter baumannii</i> MTC1106 (ST2) and MTC0619 (ST25). <i>BMC Genomics</i> , 2023, 24, .	2.8	1
3960	New Insights into Phylogenetic Relationship of <i>Hydrocotyle</i> (Araliaceae) Based on Plastid Genomes. <i>International Journal of Molecular Sciences</i> , 2023, 24, 16629.	4.1	1
3961	Whole genome sequencing data of <i>Leptospira weilii</i> and <i>Leptospira kirschneri</i> isolated from human subjects of Sri Lanka. <i>Data in Brief</i> , 2024, 52, 109840.	1.0	0
3962	Similar but different: Characterization of <i>dddD</i> gene-mediated DMSP metabolism among coral-associated <i>Endozoicomonas</i> . <i>Science Advances</i> , 2023, 9, .	10.3	0
3964	Characterization and comparative analysis of the complete organelle genomes of three red macroalgae species (<i>Neoporphyra dentata</i> , <i>Neoporphyra seriata</i> , and <i>Neopyropia yezoensis</i>) and development of molecular makers for their identification. <i>Genes and Genomics</i> , 2024, 46, 355-365.	1.4	0
3965	Complete chloroplast genomes of six neotropical palm species, structural comparison, and evolutionary dynamic patterns. <i>Scientific Reports</i> , 2023, 13, .	3.3	1
3966	Mitochondrial genome comparison and phylogenetic analysis of <i>Dendrobium</i> (Orchidaceae) based on whole mitogenomes. <i>BMC Plant Biology</i> , 2023, 23, .	3.6	0
3967	Phylogenomic analysis of <i>Bupleurum</i> in Western Sichuan, China, including an overlooked new species. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	0
3968	<i>Agromyces chromiirensistens</i> sp. nov., <i>Novosphingobium album</i> sp. nov., <i>Sphingobium arsenicirensistens</i> sp. nov., <i>Sphingomonas pollutisoli</i> sp. nov., and <i>Salinibacterium metallirensistens</i> sp. nov.: five new members of Microbacteriaceae and Sphingomonadaceae from polluted soil. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	0
3969	Designing phage cocktails to combat the emergence of bacteriophage-resistant mutants in multidrug-resistant <i>Klebsiella pneumoniae</i> . <i>Microbiology Spectrum</i> , 2024, 12, .	3.0	2
3970	A cytochrome P450 insecticide detoxification mechanism is not conserved across the Megachilidae family of bees. <i>Evolutionary Applications</i> , 0, , .	3.1	0
3971	The complete genome and biological activity of a novel <i>Spodoptera litura</i> multiple nucleopolyhedrovirus for controlling <i>Spodoptera frugiperda</i> . <i>Biological Control</i> , 2024, 188, 105412.	3.0	0
3973	Diversity of <i>Salmonella enterica</i> phages isolated from chicken farms in Kenya. <i>Microbiology Spectrum</i> , 0, , .	3.0	0
3975	Plastome phylogenomics and morphological traits analyses provide new insights into the phylogenetic position, species delimitation and speciation of <i>Triplostegia</i> (Caprifoliaceae). <i>BMC Plant Biology</i> , 2023, 23, .	3.6	0
3976	Liberation of host heme by <i>Clostridioides difficile</i> mediated damage enhances <i>Enterococcus faecalis</i> fitness during infection. <i>MBio</i> , 0, , .	4.1	0

#	ARTICLE	IF	CITATIONS
3979	Identification of an efficient phenanthrene-degrading <i>Pseudarthrobacter</i> sp. L1SW and characterization of its metabolites and catabolic pathway. <i>Journal of Hazardous Materials</i> , 2024, 465, 133138.	12.4	0
3980	Chloroplast Genome Sequences and Phylogenetic Analysis of Eight Newly Sequenced Caryophyllaceae Species. <i>Journal of AOAC INTERNATIONAL</i> , 2024, 107, 345-353.	1.5	0
3981	Symbiotic bacteria confer insecticide resistance by metabolizing buprofezin in the brown planthopper, <i>Nilaparvata lugens</i> (Stål). <i>PLoS Pathogens</i> , 2023, 19, e1011828.	4.7	0
3982	The complete chloroplast genome of <i>Aristolochia fangchi</i> provided insights into the phylogeny and species identification of <i>Aristolochia</i> . <i>Genome</i> , 2024, 67, 90-98.	2.0	0
3983	Comparative genomics analysis of <i>Streptococcus iniae</i> isolated from <i>Trachinotus ovatus</i> : novel insight into antimicrobial resistance and virulence differentiation. <i>BMC Genomics</i> , 2023, 24, .	2.8	0
3984	<i>Escherichia coli</i> O157:H7 tir 255&T&A allele strains differ in chromosomal and plasmid composition. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	0
3986	Clonality and Diversity in the Soft Rot <i>Dickeya solani</i> Phytopathogen. <i>International Journal of Molecular Sciences</i> , 2023, 24, 17553.	4.1	0
3987	A new concept of biocatalytic synthesis of acrylic monomers for obtaining water-soluble acrylic heteropolymers. <i>Metabolic Engineering Communications</i> , 2024, 18, e00231.	3.6	0
3988	A type VII-secreted lipase toxin with reverse domain arrangement. <i>Nature Communications</i> , 2023, 14, .	12.8	1
3989	The population structure of vancomycin-resistant and -susceptible <i>Enterococcus faecium</i> in a low-prevalence antimicrobial resistance setting is highly influenced by circulating global hospital-associated clones. <i>Microbial Genomics</i> , 2023, 9, .	2.0	0
3991	Comparative and phylogenetic analysis of the complete chloroplast genomes of <i>Uncaria</i> (Rubiaceae) species. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	0
3992	Distinctive plastome evolution in carnivorous angiosperms. <i>BMC Plant Biology</i> , 2023, 23, .	3.6	0
3993	Plasmid-encoded toxin defence mediates mutualistic microbial interactions. <i>Nature Microbiology</i> , 2024, 9, 108-119.	13.3	0
3994	Estimation of the Genome Size and Complete Chloroplast Genome in <i>Adenophora remotiflora</i> : Genome Structures, Comparative Genomics, and Phylogenetic Diversity. <i>Applied Sciences (Switzerland)</i> , 2024, 14, 275.	2.5	0
3995	Metabolite profiling and genomic properties of an endophytic <i>Bacillus siamensis</i> strain with anti-tumor activity isolated from medicinal plant <i>Curcuma Wenyujin</i> . <i>Plant Cell, Tissue and Organ Culture</i> , 2024, 156, .	2.3	0
3996	Appelmans protocol “ A directed in vitro evolution enables induction and recombination of prophages with expanded host range. <i>Virus Research</i> , 2024, 339, 199272.	2.2	0
3997	The complete chloroplast genome of the halophyte flowering plant <i>Suaeda monoica</i> from Jeddah, Saudi Arabia. <i>Molecular Biology Reports</i> , 2024, 51, .	2.3	0
3998	The complete plastid genome of <i>Rhamnus leptacantha</i> Schneid. (Rhamnaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2024, 9, 33-36.	0.4	0

#	ARTICLE	IF	CITATIONS
3999	Complete genome sequences of 12 bacterial strains from the honey bee gut, resolved with long-read nanopore sequencing. Microbiology Resource Announcements, 2024, 13, .	0.6	0
4001	A robust yeast chassis: comprehensive characterization of a fast-growing <i>Saccharomyces cerevisiae</i> . MBio, 2024, 15, .	4.1	0
4002	RANAVIRUS (FROG VIRUS 3) INFECTION IN FREE-LIVING THREE-TOED BOX TURTLES (TERRAPENE MEXICANA) Tj ETQq 0 0 0 rgBT /Overl	0.8	0
4003	Identification, comparative and phylogenetic analysis of eight Vitis species based on the chloroplast genome revealed their contribution to heat tolerance in grapevines. Scientia Horticulturae, 2024, 327, 112833.	3.6	0
4004	Towards estimating the number of strains that make up a natural bacterial population. Nature Communications, 2024, 15, .	12.8	2
4006	Comparative genomics of seven genomes of genus Idiomarina reveals important halo adaptations and genes for stress response. 3 Biotech, 2024, 14, .	2.2	0
4007	MAlign: Explainable static raw-byte based malware family classification using sequence alignment. Computers and Security, 2024, 139, 103714.	6.0	0
4008	The Mitogenomic Characterization and Phylogenetic Analysis of the Plant Pathogen Phyllosticta yuccae. Genes, 2024, 15, 111.	2.4	0
4009	Transcriptomic and photosynthetic analyses of Synechocystis sp. PCC6803 and Chlorogloeopsis fritschii sp. PCC6912 exposed to an M-dwarf spectrum under an anoxic atmosphere. Frontiers in Plant Science, 0, 14, .	3.6	0
4010	Plastid genomes provide insights into the phylogeny and chloroplast evolution of the paper daisy tribe Gnaphalieae (Asteraceae). Gene, 2024, 901, 148177.	2.2	0
4011	Characterization and genomic analysis of a broad-spectrum lytic phage PG288: A potential natural therapy candidate for Vibrio infections. Virus Research, 2024, 341, 199320.	2.2	0
4014	Role of membrane vesicles in the transmission of vancomycin resistance in Enterococcus faecium. Scientific Reports, 2024, 14, .	3.3	0
4015	Whole genome sequencing and genotyping Klebsiella pneumoniae multi-drug resistant hospital isolates from Western Kenya. Access Microbiology, 2024, 6, .	0.5	0
4016	A novel conjugative transposon carrying an autonomously amplified plasmid. MBio, 2024, 15, .	4.1	0
4017	Phylogeny and diversification of genus Sanicula L. (Apiaceae): novel insights from plastid phylogenomic analyses. BMC Plant Biology, 2024, 24, .	3.6	0
4018	Phylogenomics and topological conflicts in the tribe Anthospermeae (Rubiaceae). Ecology and Evolution, 2024, 14, .	1.9	0
4019	Live tracking of a plant pathogen outbreak reveals rapid and successive, multidecade plasmid reduction. MSystems, 2024, 9, .	3.8	0
4020	Chloroplast Genome of Medicago lupulina L. var. vulgaris Koch: Structure, Sequences Introduced as a Result of HGT and Viral Nature. Russian Journal of Plant Physiology, 2023, 70, .	1.1	0

#	ARTICLE	IF	CITATIONS
4021	Genomic landscape of NDM-1 producing multidrug-resistant <i>Providencia stuartii</i> causing burn wound infections in Bangladesh. <i>Scientific Reports</i> , 2024, 14, .	3.3	0
4022	Resequencing and characterization of the first <i>Corynebacterium pseudotuberculosis</i> genome isolated from camel. <i>PeerJ</i> , 0, 12, e16513.	2.0	0
4023	Regardless of having identical photosynthetic pathways, chloroplast genomes vary depending on whether the host plant is monocotyledonous or dicotyledonous. <i>Genetic Resources and Crop Evolution</i> , 0, , .	1.6	0
4024	Draft genome of <i>Chloroflexu</i> s sp. MS-CIW-1, of the <i>Chloroflexus</i> sp. MS-G group from Mushroom Spring, Yellowstone National Park. <i>Microbiology Resource Announcements</i> , 2024, 13, .	0.6	0
4025	Genomic Features and Phylogenetic Analysis of Antimicrobial-Resistant <i>Salmonella</i> Mbandaka ST413 Strains. <i>Microorganisms</i> , 2024, 12, 312.	3.6	0
4026	Draft genome sequence of novel <i>Candidatus Ornithobacterium hominis</i> carrying antimicrobial resistance genes in Egypt. <i>BMC Microbiology</i> , 2024, 24, .	3.3	0
4027	Advance typing of <i>Vibrio parahaemolyticus</i> through the <i>mtlA</i> and <i>aer</i> gene: A high-resolution, cost-effective approach. <i>Heliyon</i> , 2024, 10, e25642.	3.2	0
4028	Comparative chloroplast genome analysis of six millet species along with related Poaceae family members. <i>Nucleus (India)</i> , 0, , .	2.2	0
4029	High clonality of <i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> field isolates from red deer revealed by two different methodological approaches of comparative genomic analysis. <i>Frontiers in Veterinary Science</i> , 0, 11, .	2.2	0
4030	Transcriptomic profiles of <i>Mannheimia haemolytica</i> planktonic and biofilm associated cells. <i>PLoS ONE</i> , 2024, 19, e0297692.	2.5	0
4031	Comparative Genome Analysis of Two <i>Streptococcus suis</i> Serotype 8 Strains Identifies Two New Virulence-Associated Genes. <i>Animals</i> , 2024, 14, 572.	2.3	0
4032	The complete plastomes of thirteen <i>Libanotis</i> (Apiaceae, Apioideae) plants: comparative and phylogenetic analyses provide insights into the plastome evolution and taxonomy of <i>Libanotis</i> . <i>BMC Plant Biology</i> , 2024, 24, .	3.6	0
4033	Phenotypic and genetic characterization of <i>Xanthomonas citri</i> pv. <i>malvacearum</i> strains affecting upland cotton in Central India. <i>Indian Phytopathology</i> , 2024, 77, 125-137.	1.2	0
4034	Optical Mapping: Detecting Genomic Resistance Cassettes in MRSA. <i>ACS Omega</i> , 2024, 9, 8862-8873.	3.5	0
4035	Genomic epidemiology reveals geographical clustering of multidrug-resistant <i>Escherichia coli</i> ST131 associated with bacteraemia in Wales. <i>Nature Communications</i> , 2024, 15, .	12.8	0
4036	Extreme Reconfiguration of Plastid Genomes in Papaveraceae: Rearrangements, Gene Loss, Pseudogenization, IR Expansion, and Repeats. <i>International Journal of Molecular Sciences</i> , 2024, 25, 2278.	4.1	0
4037	New reference genomes to distinguish the sympatric malaria parasites, <i>Plasmodium ovale curtisi</i> and <i>Plasmodium ovale wallikeri</i> . <i>Scientific Reports</i> , 2024, 14, .	3.3	0
4038	<i>Corynebacterium pseudotuberculosis</i> biovar <i>ovis</i> strains isolated from small ruminants herds from the Brazilian Amazon present clonal genomic profile. <i>Small Ruminant Research</i> , 2024, 233, 107227.	1.2	0

#	ARTICLE	IF	CITATIONS
4039	Levels of Cytokines in Leptospirosis Patients with Different Serovars and <i>rfb</i> Locus. Journal of Interferon and Cytokine Research, 2024, 44, 80-93.	1.2	0
4040	Phenotypic and genotypic characterization of <i>Campylobacter coli</i> isolates from the Vietnamese poultry production network; a pilot study. , 0, 2, .		0
4041	Diffusion models in text generation: a survey. PeerJ Computer Science, 0, 10, e1905.	4.5	0
4042	Generation of host-pathogen interaction data: an overview of recent technological advancements. , 2024, , 53-79.		0
4043	Study of an <i>Enterococcus faecium</i> strain isolated from an artisanal Mexican cheese, whole-genome sequencing, comparative genomics, and bacteriocin expression. Antonie Van Leeuwenhoek, 2024, 117, .	1.7	0
4044	Tradeoffs Between Evolved Phage Resistance and Antibiotic Susceptibility in a Highly Drug-Resistant Cystic Fibrosis-Derived <i>Pseudomonas aeruginosa</i> Strain. Phage, 0, , .	1.7	0
4045	Perception of the Biocontrol Potential and Palmitic Acid Biosynthesis Pathway of <i>Bacillus subtilis</i> H2 through Merging Genome Mining with Chemical Analysis. Journal of Agricultural and Food Chemistry, 2024, 72, 4834-4848.	5.2	0
4046	<i>Polycladomyces zharkentensis</i> sp. nov., a novel thermophilic cellulose- and starch-degrading member of the Bacillota from a geothermal aquifer in Kazakhstan. International Journal of Systematic and Evolutionary Microbiology, 2024, 74, .	1.7	0
4047	The Complete Chloroplast Genomes of <i>Bulbophyllum</i> (Orchidaceae) Species: Insight into Genome Structure Divergence and Phylogenetic Analysis. International Journal of Molecular Sciences, 2024, 25, 2665.	4.1	0
4048	Plasmid-encoded gene duplications of extended-spectrum β -lactamases in clinical bacterial isolates. Frontiers in Cellular and Infection Microbiology, 0, 14, .	3.9	0
4050	Mutation of <i>wbtJ</i> , a N-formyltransferase involved in O-antigen synthesis, results in biofilm formation, phase variation and attenuation in <i>Francisella tularensis</i> . Microbiology (United Kingdom), 2024, 170, .	1.8	0
4051	Detecting and characterizing new endofungal bacteria in new hosts: <i>Pandora</i> <i>sputorum</i> and <i>Mycetohabitans endofungorum</i> in <i>Rhizopus arrhizus</i> . Frontiers in Microbiology, 0, 15, .	3.5	0
4053	Alcohol dehydrogenase system acts as the sole pathway for methanol oxidation in <i>Desulfofundulus kuznetsovii</i> strain TPOSr. Antonie Van Leeuwenhoek, 2024, 117, .	1.7	0
4054	Pathogenomic analysis and characterization of <i>Pasteurella multocida</i> strains recovered from human infections. Microbiology Spectrum, 2024, 12, .	3.0	0
4055	Comparative Analysis of Six Complete Plastomes of <i>Tripterosperrum</i> spp.. International Journal of Molecular Sciences, 2024, 25, 2534.	4.1	0
4056	A male-specific insert of <i>Opsariichthys bidens</i> identified based on genome-wide association analyses and comparative genomics. Aquaculture Reports, 2024, 35, 101982.	1.7	0
4057	Correction of non-random mutational biases along a linear bacterial chromosome by the mismatch repair endonuclease <i>NucS</i> . Nucleic Acids Research, 0, , .	14.5	0
4058	Whole genome sequencing analysis of <i>Limosilactobacillus reuteri</i> from the intestinal tract of mice recovering from ulcerative colitis and preliminary study on anti-inflammatory effects of its derived peptides. Archives of Microbiology, 2024, 206, .	2.2	0

#	ARTICLE	IF	CITATIONS
4059	Genomics-based analysis of four porcine-derived lactic acid bacteria strains and their evaluation as potential probiotics. Molecular Genetics and Genomics, 2024, 299, .	2.1	0
4060	Genomic insights of a native bacterial consortium for wheat production sustainability. Current Research in Microbial Sciences, 2024, 6, 100230.	2.3	0
4061	Plastid genome data provide new insights into the dynamic evolution of the tribe Ampelopsideae (Vitaceae). BMC Genomics, 2024, 25, .	2.8	0
4062	Bacterial isolation and genome analysis of a novel Klebsiella quasipneumoniae phage in southwest China's karst area. Virology Journal, 2024, 21, .	3.4	0
4063	Organelle genome assembly of Masson pine (Pinus massoniana) geographical germplasms reveal the intraspecific variation of chloroplast genomes in China. Industrial Crops and Products, 2024, 212, 118336.	5.2	0
4064	Genomic insights into local-scale evolution of ocular Chlamydia trachomatis strains within and between individuals in Gambian trachoma-endemic villages. Microbial Genomics, 2024, 10, .	2.0	0
4065	Comparative Mitogenomics Analysis Revealed Evolutionary Divergence among Neopestalotiopsis Species Complex (Fungi: Xylariales). International Journal of Molecular Sciences, 2024, 25, 3093.	4.1	0
4066	Comparative genomics and phylogenomics of the genus Glycyrrhiza (Fabaceae) based on chloroplast genomes. Frontiers in Pharmacology, 0, 15, .	3.5	0
4067	Genetic insights of antibiotic resistance, pathogenicity (virulence) and phylogenetic relationship of Escherichia coli strains isolated from livestock, poultry and their handlers - a one health snapshot. Molecular Biology Reports, 2024, 51, .	2.3	0
4068	Complete Mitochondrial Genome and Phylogenetic Position of Nurudea zhengii Ren (Insecta,) Tj ETQq1 1 0.784314 1.75 / Overlock 10 T	1.75	0
4069	Enterobacter asburiae ST229: an emerging carbapenemases producer. Scientific Reports, 2024, 14, .	3.3	0
4070	Characterisation of colistin resistance in Gram-negative microbiota of pregnant women and neonates in Nigeria. Nature Communications, 2024, 15, .	12.8	0
4071	Comparative genomics analysis reveals sequence characteristics potentially related to host preference in Cryptosporidium xiaoi. International Journal for Parasitology, 2024, , .	3.1	0
4072	Revealing extracellular protein profile and excavating spoilage-related proteases of Aeromonas salmonicida based on multi-omics investigation. International Journal of Biological Macromolecules, 2024, 265, 130916.	7.5	0
4073	Detection of colinear blocks and synteny and evolutionary analyses based on utilization of MCSanX. Nature Protocols, 0, , .	12.0	0
4074	Isolation, identification and whole-genome analysis of an Achromobacter strain with a novel sulfamethazine resistance gene and sulfamethazine degradation gene cluster. Bioresource Technology, 2024, 399, 130598.	9.6	0
4077	Characterization of the complete chloroplast genome of Wolffia arrhiza and comparative genomic analysis with relative Wolffia species. Scientific Reports, 2024, 14, .	3.3	0
4078	Deciphering the genomes of motility-deficient mutants of <i>Vibrio alginolyticus</i> 138-2. PeerJ, 0, 12, e17126.	2.0	0

#	ARTICLE	IF	CITATIONS
4079	DiGAlign: Versatile and Interactive Visualization of Sequence Alignment for Comparative Genomics. Microbes and Environments, 2024, 39, n/a.	1.6	0
4080	A pan-genomic assessment: Delving into the genome of the marine epiphyte Bacillus altitudinis strain 19_A and other very close Bacillus strains from multiple environments. Heliyon, 2024, 10, e27820.	3.2	0
4081	Comparative and phylogenetic analysis of the complete chloroplast genomes of ten Pittosporum species from East Asia. Functional and Integrative Genomics, 2024, 24, .	3.5	0
4082	<i>In vitro</i> development of resistance against antipseudomonal agents: comparison of novel β -lactam/ β -lactamase inhibitor combinations and other β -lactam agents. Antimicrobial Agents and Chemotherapy, 2024, 68, .	3.2	0
4083	Genomic and phenotypic analyses reveal Paenibacillus polymyxa PJH16 is a potential biocontrol agent against cucumber fusarium wilt. Frontiers in Microbiology, 0, 15, .	3.5	0
4084	Molecular epidemiological and antimicrobial-resistant mechanisms analysis of prolonged <i>Neisseria gonorrhoeae</i> collection between 1971 and 2005 in Japan. JAC-Antimicrobial Resistance, 2024, 6, .	2.1	0
4085	Helicobacter pylori glycan biosynthesis modulates host immune cell recognition and response. Frontiers in Cellular and Infection Microbiology, 0, 14, .	3.9	0