Ray: Simultaneous Assembly of Reads from a Mix of Hig Technologies

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Citation Report

#	Article	IF	CITATIONS
1	A Practical Comparison of De Novo Genome Assembly Software Tools for Next-Generation Sequencing Technologies. PLoS ONE, 2011, 6, e17915.	1.1	194
2	Pathogen comparative genomics in the next-generation sequencing era: genome alignments, pangenomics and metagenomics. Briefings in Functional Genomics, 2011, 10, 322-333.	1.3	41
4	A Draft Sequence of the Puerto Rican Parrot Genome (Amazona vittata) – a Genome Project funded by a Local Community Effort. Nature Precedings, 2011, , .	0.1	0
5	Comparing De Novo Genome Assembly: The Long and Short of It. PLoS ONE, 2011, 6, e19175.	1.1	95
6	An integer programming approach to DNA sequence assembly. Computational Biology and Chemistry, 2011, 35, 251-258.	1.1	7
7	Genomics for Key Players in the N Cycle. Methods in Enzymology, 2011, 496, 289-318.	0.4	3
8	Draft Genome Sequences of Two Pseudomonas aeruginosa Clinical Isolates with Different Antibiotic Susceptibilities. Journal of Bacteriology, 2011, 193, 5573-5573.	1.0	7
9	Draft Genome Sequence of the Pseudomonas aeruginosa Bloodstream Isolate PABL056. Journal of Bacteriology, 2012, 194, 5999-5999.	1.0	2
10	Draft Genome Sequence of the Quality Control Strain Enterococcus faecalis ATCC 29212. Journal of Bacteriology, 2012, 194, 6006-6007.	1.0	27
11	Draft Genome Sequence of Thermus sp. Strain RL, Isolated from a Hot Water Spring Located atop the Himalayan Ranges at Manikaran, India. Journal of Bacteriology, 2012, 194, 3534-3534.	1.0	31
12	Genome Sequence of Moraxella catarrhalis RH4, an Isolate of Seroresistant Lineage. Journal of Bacteriology, 2012, 194, 6969-6969.	1.0	12
13	Efficient de novo assembly of large genomes using compressed data structures. Genome Research, 2012, 22, 549-556.	2.4	649
14	Genome Sequence of Acinetobacter sp. Strain HA, Isolated from the Gut of the Polyphagous Insect Pest Helicoverpa armigera. Journal of Bacteriology, 2012, 194, 5156-5156.	1.0	22
15	Genome sequencing of the lizard parasite Leishmania tarentolae reveals loss of genes associated to the intracellular stage of human pathogenic species. Nucleic Acids Research, 2012, 40, 1131-1147.	6.5	135
16	Extensive variation in surface lipoprotein gene content and genomic changes associated with virulence during evolution of a novel North American house finch epizootic strain of Mycoplasma gallisepticum. Microbiology (United Kingdom), 2012, 158, 2073-2088.	0.7	43
17	The simple fool's guide to population genomics via <scp>RNA</scp> ‣eq: an introduction to highâ€throughput sequencing data analysis. Molecular Ecology Resources, 2012, 12, 1058-1067.	2.2	229
18	The <i>ARC1</i> E3 Ligase Gene Is Frequently Deleted in Self-Compatible Brassicaceae Species and Has a Conserved Role in <i>Arabidopsis lyrata</i> Self-Pollen Rejection. Plant Cell, 2012, 24, 4607-4620.	3.1	94
19	A locally funded Puerto Rican parrot (Amazona vittata) genome sequencing project increases avian data and advances young researcher education. GigaScience, 2012, 1, 14.	3.3	40

#	Article	IF	CITATIONS
20	Library Preparation and Data Analysis Packages for Rapid Genome Sequencing. Methods in Molecular Biology, 2012, 944, 1-22.	0.4	17
21	Ray Meta: scalable de novo metagenome assembly and profiling. Genome Biology, 2012, 13, R122.	13.9	549
22	Feature-by-Feature – Evaluating De Novo Sequence Assembly. PLoS ONE, 2012, 7, e31002.	1.1	50
23	Sequencing Intractable DNA to Close Microbial Genomes. PLoS ONE, 2012, 7, e41295.	1.1	11
24	Evidence for Transitional Stages in the Evolution of Euglenid Group II Introns and Twintrons in the Monomorphina aenigmatica Plastid Genome. PLoS ONE, 2012, 7, e53433.	1.1	27
25	Gain and loss of multiple functionally related, horizontally transferred genes in the reduced genomes of two microsporidian parasites. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 12638-12643.	3.3	97
26	Next generation sequencing and bioinformatic bottlenecks: the current state of metagenomic data analysis. Current Opinion in Biotechnology, 2012, 23, 9-15.	3.3	296
27	Referenceâ€free transcriptome assembly in nonâ€model animals from nextâ€generation sequencing data. Molecular Ecology Resources, 2012, 12, 834-845.	2.2	142
28	An atlas of over 90,000 conserved noncoding sequences provides insight into crucifer regulatory regions. Nature Genetics, 2013, 45, 891-898.	9.4	350
29	Human milk metagenome: a functional capacity analysis. BMC Microbiology, 2013, 13, 116.	1.3	176
30	Correlation between Clostridium difficile Bacterial Load, Commercial Real-Time PCR Cycle Thresholds, and Results of Diagnostic Tests Based on Enzyme Immunoassay and Cell Culture Cytotoxicity Assay. Journal of Clinical Microbiology, 2013, 51, 3624-3630.	1.8	69
31	Assembling Genomes and Mini-metagenomes from Highly Chimeric Reads. Lecture Notes in Computer Science, 2013, , 158-170.	1.0	439
32	Assembling Single-Cell Genomes and Mini-Metagenomes From Chimeric MDA Products. Journal of Computational Biology, 2013, 20, 714-737.	0.8	1,235
33	Efficient and accurate whole genome assembly and methylome profiling of E. coli. BMC Genomics, 2013, 14, 675.	1.2	38
34	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. GigaScience, 2013, 2, 10.	3.3	582
36	Human Analysts at Superhuman Scales: What Has Friendly Software To Do?. Big Data, 2013, 1, 227-236.	2.1	1
37	Research in Computational Molecular Biology. Lecture Notes in Computer Science, 2013, , .	1.0	17
38	Draft Genome Sequence of the Phyllosphere Model Bacterium Pantoea agglomerans 299R. Genome Announcements, 2013, 1, .	0.8	36

#	Article	IF	CITATIONS
39	Draft Genome Sequence of <i>Ralstonia</i> sp. Strain GA3-3, Isolated from Australian Suburban Soil. Genome Announcements, 2013, 1, .	0.8	1
40	Draft Genome Sequence of Pandoraea sp. Strain SD6-2, Isolated from Lindane-Contaminated Australian Soil. Genome Announcements, 2013, 1, .	0.8	10
41	Draft Genome Sequence of the Fast-Growing Marine Bacterium Vibrio natriegens Strain ATCC 14048. Genome Announcements, 2013, 1, .	0.8	28
42	Draft Genome Sequence of <i>Exiguobacterium pavilionensis</i> Strain RW-2, with Wide Thermal, Salinity, and pH Tolerance, Isolated from Modern Freshwater Microbialites. Genome Announcements, 2013, 1, .	0.8	32
43	Complete Genome Sequence of the Mesoplasma florum W37 Strain. Genome Announcements, 2013, 1, .	0.8	7
44	Secondary Evolution of a Self-Incompatibility Locus in the Brassicaceae Genus Leavenworthia. PLoS Biology, 2013, 11, e1001560.	2.6	54
45	Organelle Genome Complexity Scales Positively with Organism Size in Volvocine Green Algae. Molecular Biology and Evolution, 2013, 30, 793-797.	3.5	52
46	Hammondia hammondi, an avirulent relative of Toxoplasma gondii, has functional orthologs of known T. gondii virulence genes. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 7446-7451.	3.3	49
47	Phylogenetic Diversity of the Enteric Pathogen Salmonella enterica subsp. enterica Inferred from Genome-Wide Reference-Free SNP Characters. Genome Biology and Evolution, 2013, 5, 2109-2123.	1.1	139
48	Palindromic Genes in the Linear Mitochondrial Genome of the Nonphotosynthetic Green Alga Polytomella magna. Genome Biology and Evolution, 2013, 5, 1661-1667.	1.1	22
49	Complete Genome Sequences from Three Genetically Distinct Strains Reveal High Intraspecies Genetic Diversity in the Microsporidian Encephalitozoon cuniculi. Eukaryotic Cell, 2013, 12, 503-511.	3.4	57
50	The complete mitochondrial genome from an unidentified Phalansterium species Protist Genomics, 2013, 1, .	1.7	5
51	Genome Assembly on a Multicore System. , 2013, , .		1
53	Hemichordate Molecular Phylogeny Reveals a Novel Cold-Water Clade of Harrimaniid Acorn Worms. Biological Bulletin, 2013, 225, 194-204.	0.7	25
54	Genome Sequence of <i>Moraxella macacae</i> 0408225, a Novel Bacterial Species Isolated from a Cynomolgus Macaque with Epistaxis. Genome Announcements, 2013, 1, .	0.8	5
55	The Draft Genome Sequence of Sphingomonas paucimobilis Strain HER1398 (<i>Proteobacteria</i>), Host to the Giant PAU Phage, Indicates That It Is a Member of the Genus <i>Sphingobacterium</i> () Tj ETQq1 1	0.70884314	rg B 3T /Overlo
56	3DScapeCS: application of three dimensional, parallel, dynamic network visualization in Cytoscape. BMC Bioinformatics, 2013, 14, 322.	1.2	14
57	Draft genome sequence of Francisella tularensis subsp. holarctica BD11-00177. Standards in Genomic Sciences, 2013, 8, 539-547.	1.5	5

#	Article	IF	CITATIONS
58	Genomic Evaluation of Thermoanaerobacter spp. for the Construction of Designer Co-Cultures to Improve Lignocellulosic Biofuel Production. PLoS ONE, 2013, 8, e59362.	1.1	39
59	Genomic Characterization of a Large Outbreak of Legionella pneumophila Serogroup 1 Strains in Quebec City, 2012. PLoS ONE, 2014, 9, e103852.	1.1	58
60	Parallel De Bruijn Graph Construction and Traversal for De Novo Genome Assembly. , 2014, , .		58
62	The Genome of the Chicken DT40 Bursal Lymphoma Cell Line. G3: Genes, Genomes, Genetics, 2014, 4, 2231-2240.	0.8	25
63	Next-Generation Sequence Assemblers. SpringerBriefs in Systems Biology, 2014, , 103-116.	0.1	2
64	Konnector: Connecting paired-end reads using a bloom filter de Bruijn graph. , 2014, , .		8
65	A Lack of Parasitic Reduction in the Obligate Parasitic Green Alga Helicosporidium. PLoS Genetics, 2014, 10, e1004355.	1.5	57
66	Draft genomes of Amanita jacksonii, Ceratocystis albifundus, Fusarium circinatum, Huntiella omanensis, Leptographium procerum, Rutstroemia sydowiana, and Sclerotinia echinophila. IMA Fungus, 2014, 5, 472-486.	1.7	56
67	Big data challenges for estimating genome assembler quality. , 2014, , .		1
68	Complete Genome Sequence of Haemophilus influenzae Strain 375 from the Middle Ear of a Pediatric Patient with Otitis Media. Genome Announcements, 2014, 2, .	0.8	14
69	Safety of the Surrogate Microorganism <i>Enterococcus faecium</i> NRRL B-2354 for Use in Thermal Process Validation. Applied and Environmental Microbiology, 2014, 80, 1899-1909.	1.4	107
70	Complete Genome Sequence of a Rabies Virus Isolated from a Human in Central African Republic. Genome Announcements, 2014, 2, .	0.8	4
71	Genome Sequence of Oenococcus oeni OM27, the First Fully Assembled Genome of a Strain Isolated from an Italian Wine. Genome Announcements, 2014, 2, .	0.8	28
72	Draft Genome Sequence of Acinetobacter baumannii Strain ABBL099, a Multidrug-Resistant Clinical Outbreak Isolate with a Novel Multilocus Sequence Type. Genome Announcements, 2014, 2, .	0.8	5
73	Draft Genome Sequence of <i>Serratia</i> sp. Strain DD3, Isolated from the Guts of <i>Daphnia magna</i> . Genome Announcements, 2014, 2, .	0.8	4
74	Genome Sequences of Five Oenococcus oeni Strains Isolated from Nero Di Troia Wine from the Same Terroir in Apulia, Southern Italy. Genome Announcements, 2014, 2, .	0.8	35
75	Detection of Variants of the pRAS3, pAB5S9, and pSN254 Plasmids in Aeromonas salmonicida subsp. salmonicida: Multidrug Resistance, Interspecies Exchanges, and Plasmid Reshaping. Antimicrobial Agents and Chemotherapy, 2014, 58, 7367-7374.	1.4	50
76	The Mitochondrial Genomes of the Glaucophytes Gloeochaete wittrockiana and Cyanoptyche gloeocystis: Multilocus Phylogenetics Suggests a Monophyletic Archaeplastida. Genome Biology and Evolution, 2014, 6, 2774-2785.	1.1	37

#	Article	IF	CITATIONS
77	Six newly sequenced chloroplast genomes from prasinophyte green algae provide insights into the relationships among prasinophyte lineages and the diversity of streamlined genome architecture in picoplanktonic species. BMC Genomics, 2014, 15, 857.	1.2	82
78	Chloroplast phylogenomic analysis resolves deep-level relationships within the green algal class Trebouxiophyceae. BMC Evolutionary Biology, 2014, 14, 211.	3.2	107
79	ExSPAnder: a universal repeat resolver for DNA fragment assembly. Bioinformatics, 2014, 30, i293-i301.	1.8	103
80	Parallelization of the Trinity Pipeline for De Novo Transcriptome Assembly. , 2014, , .		6
81	Massive difference in synonymous substitution rates among mitochondrial, plastid, and nuclear genes of Phaeocystis algae. Molecular Phylogenetics and Evolution, 2014, 71, 36-40.	1.2	47
82	Phenotypic and genomic characterization of the Antarctic bacterium Gillisia sp. CAL575, a producer of antimicrobial compounds. Extremophiles, 2014, 18, 35-49.	0.9	22
83	Use of Whole Genome Shotgun Metagenomics: A Practical Guide for the Microbiome-Minded Physician Scientist. Seminars in Reproductive Medicine, 2014, 32, 005-013.	0.5	19
84	<i>De no</i> vo finished 2.8 Mbp <i>Staphylococcus aureus</i> genome assembly from 100 bp short and long range paired-end reads. Bioinformatics, 2014, 30, 40-49.	1.8	50
86	Complete genome sequence of Salmonella enterica serovar Typhimurium VNP20009, a strain engineered for tumor targeting. Journal of Biotechnology, 2014, 192, 177-178.	1.9	22
87	AblaVIM-2Plasmid Disseminating in Extensively Drug-Resistant Clinical Pseudomonas aeruginosa and Serratia marcescens Isolates. Antimicrobial Agents and Chemotherapy, 2014, 58, 7017-7018.	1.4	18
88	Nucleotide substitution analyses of the glaucophyte Cyanophora suggest an ancestrally lower mutation rate in plastid vs mitochondrial DNA for the Archaeplastida. Molecular Phylogenetics and Evolution, 2014, 79, 380-384.	1.2	14
89	Evolution of Oseltamivir Resistance Mutations in Influenza A(H1N1) and A(H3N2) Viruses during Selection in Experimentally Infected Mice. Antimicrobial Agents and Chemotherapy, 2014, 58, 6398-6405.	1.4	26
90	A New Microviridae Phage Isolated from a Failed Biotechnological Process Driven by Escherichia coli. Applied and Environmental Microbiology, 2014, 80, 6992-7000.	1.4	14
91	SSPACE-LongRead: scaffolding bacterial draft genomes using long read sequence information. BMC Bioinformatics, 2014, 15, 211.	1.2	474
92	Mating system shifts and transposable element evolution in the plant genus Capsella. BMC Genomics, 2014, 15, 602.	1.2	61
93	Characterization of the core and accessory genomes of Pseudomonas aeruginosa using bioinformatic tools Spine and AGEnt. BMC Genomics, 2014, 15, 737.	1.2	184
94	High-coverage sequencing and annotated assemblies of the budgerigar genome. GigaScience, 2014, 3, 11.	3.3	75
95	A field guide to wholeâ€genome sequencing, assembly and annotation. Evolutionary Applications, 2014, 7, 1026-1042.	1.5	296

	Сітат	CITATION REPORT	
#	Article	IF	Citations
96	Automated ensemble assembly and validation of microbial genomes. BMC Bioinformatics, 2014, 15, 126.	1.2	60
97	Novel gammaherpesvirus functions encoded by bovine herpesvirus 6 (bovine lymphotropic virus). Journal of General Virology, 2014, 95, 1790-1798.	1.3	12
98	Serial Gene Losses and Foreign DNA Underlie Size and Sequence Variation in the Plastid Genomes of Diatoms. Genome Biology and Evolution, 2014, 6, 644-654.	1.1	72
99	What is the difference between the breakpoint graph and the de Bruijn graph?. BMC Genomics, 2014, 15, S6.	, <u>1.2</u>	14
100	SWAP-Assembler: scalable and efficient genome assembly towards thousands of cores. BMC Bioinformatics, 2014, 15, S2.	1.2	35
101	HipMer. , 2015, , .		57
102	Konnector v2.0: pseudo-long reads from paired-end sequencing data. BMC Medical Genomics, 2015, 8, S1.	0.7	19
103	Chloroplast phylogenomic analysis of chlorophyte green algae identifies a novel lineage sister to the Sphaeropleales (Chlorophyceae). BMC Evolutionary Biology, 2015, 15, 264.	3.2	69
104	Draft Genome Sequence of Lactobacillus kunkeei AR114 Isolated from Honey Bee Gut. Genome Announcements, 2015, 3, .	0.8	6
105	Draft genome sequence and characterization of Desulfitobacterium hafniense PCE-S. Standards in Genomic Sciences, 2015, 10, 15.	1.5	25
106	Exploring the genomic traits of fungus-feeding bacterial genus Collimonas. BMC Genomics, 2015, 16, 1103.	1.2	57
107	Genome Sequence Analysis of <i>Mycoplasma</i> sp <i>.</i> HU2014, Isolated from Tissue Culture. Genome Announcements, 2015, 3, .	0.8	3
108	Auxotrophy and intrapopulation complementary in the â€~interactome' of a cultivated freshwater mo community. Molecular Ecology, 2015, 24, 4449-4459.	del 2.0	97
109	Draft Genome Sequence of Lactobacillus plantarum Strain SNU.Lp177 from Pig Feces in South Korea. Genome Announcements, 2015, 3, .	0.8	0
110	Diversity of acid stress resistant variants of Listeria monocytogenes and the potential role of ribosomal protein S21 encoded by rpsU. Frontiers in Microbiology, 2015, 6, 422.	1.5	35
111	Metagenomic analysis reveals that modern microbialites and polar microbial mats have similar taxonomic and functional potential. Frontiers in Microbiology, 2015, 6, 966.	1.5	62
112	Investigation of a Large Collection of Pseudomonas aeruginosa Bacteriophages Collected from a Single Environmental Source in Abidjan, Côte d'Ivoire. PLoS ONE, 2015, 10, e0130548.	1.1	62
113	Assembling short reads from jumping libraries with large insert sizes. Bioinformatics, 2015, 31, 3262-3268.	1.8	40

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#		IF	CITATIONS
114	Draft Genome Sequence of Lactobacillus plantarum Lp90 Isolated from Wine. Genome Announcements, 2015, 3, .	0.8	17
115	Identification of candidate mimicry proteins involved in parasite-driven phenotypic changes. Parasites and Vectors, 2015, 8, 225.	1.0	20
116	Next generation sequence assembler mis-assembly of phage genomes with terminal redundancy. , 2015, , \cdot		0
117	<i>De novo</i> meta-assembly of ultra-deep sequencing data. Bioinformatics, 2015, 31, i9-i16.	1.8	25
118	Next-Generation Sequencing (NGS) Tools and Impact in Plant Breeding. , 2015, , 563-612.		8
119	Spaler: Spark and GraphX based de novo genome assembler. , 2015, , .		19
120	DNA assembly with de bruijn graphs on FPGA. , 2015, 2015, 6489-92.		1
121	Influence of ACB complex genospecies on clinical outcomes in a U.S. hospital with high rates of multidrug resistance. Journal of Infection, 2015, 70, 144-152.	1.7	56
122	Phages of dairy Leuconostoc mesenteroides: Genomics and factors influencing their adsorption. International Journal of Food Microbiology, 2015, 201, 58-65.	2.1	16
123	Hybrid origins and the earliest stages of diploidization in the highly successful recent polyploid <i>Capsella bursa-pastoris</i> . Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 2806-2811.	3.3	128
124	Eye-like ocelloids are built from different endosymbiotically acquired components. Nature, 2015, 523, 204-207.	13.7	74
125	Genomic characteristics and environmental distributions of the uncultivated Far-T4 phages. Frontiers in Microbiology, 2015, 6, 199.	1.5	24
126	Massive and Widespread Organelle Genomic Expansion in the Green Algal Genus Dunaliella. Genome Biology and Evolution, 2015, 7, 656-663.	1.1	31
127	Genetics, structure, and prevalence of FP967 (CDC Triffid) T-DNA in flax. SpringerPlus, 2015, 4, 146.	1.2	12
128	Mitogenomics reveals phylogeny and repeated motifs in control regions of the deep-sea family Siboglinidae (Annelida). Molecular Phylogenetics and Evolution, 2015, 85, 221-229.	1.2	62
129	A Virulent Phage Infecting Lactococcus garvieae, with Homology to Lactococcus lactis Phages. Applied and Environmental Microbiology, 2015, 81, 8358-8365.	1.4	10
130	Evolutionary insights from de novo transcriptome assembly and SNP discovery in California white oaks. BMC Genomics, 2015, 16, 552.	1.2	31
131	Single-cell transcriptomics using spliced leader PCR: Evidence for multiple losses of photosynthesis in polykrikoid dinoflagellates. BMC Genomics, 2015, 16, 528.	1.2	20

#	Article	IF	CITATIONS
132	Maternal transmission, sex ratio distortion, and mitochondria. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 10162-10168.	3.3	49
133	Regulation of Bioluminescence in Photobacterium leiognathi Strain KNH6. Journal of Bacteriology, 2015, 197, 3676-3685.	1.0	19
134	SWAP-Assembler 2: Scalable Genome Assembler towards Millions of Cores Practice and Experience. , 2015, , .		1
135	Draft Genome Sequences of Leptospira santarosai Strains U160, U164, and U233, Isolated from Asymptomatic Cattle. Genome Announcements, 2015, 3, .	0.8	6
136	Microbiome analyses of pacific white shrimp (Litopenaeus vannamei) collected from disparate geographical locations. Genomics Data, 2015, 6, 67-69.	1.3	9
137	Drug resistance analysis by next generation sequencing in Leishmania. International Journal for Parasitology: Drugs and Drug Resistance, 2015, 5, 26-35.	1.4	66
138	First Complete Genome Sequence of a Probiotic Enterococcus faecium Strain T-110 and Its Comparative Genome Analysis with Pathogenic and Non-pathogenic Enterococcus faecium Genomes. Journal of Genetics and Genomics, 2015, 42, 43-46.	1.7	33
139	The Resistome of Pseudomonas aeruginosa in Relationship to Phenotypic Susceptibility. Antimicrobial Agents and Chemotherapy, 2015, 59, 427-436.	1.4	242
140	Genetic characterization of strains of Saccharomyces uvarum from New Zealand wineries. Food Microbiology, 2015, 46, 92-99.	2.1	40
141	Draft Genome Sequence of <i>Capniomyces stellatus</i> , the Obligate Gut Fungal Symbiont of Stonefly. Genome Announcements, 2016, 4, .	0.8	5
142	Mitochondrion-to-Chloroplast DNA Transfers and Intragenomic Proliferation of Chloroplast Group II Introns in <i>Gloeotilopsis</i> Green Algae (Ulotrichales, Ulvophyceae). Genome Biology and Evolution, 2016, 8, 2789-2805.	1.1	34
143	Draft genome of the Leptospira interrogans strains, Acegua, RCA, Prea, and Capivara, obtained from wildlife maintenance hosts and infected domestic animals. Memorias Do Instituto Oswaldo Cruz, 2016, 111, 280-283.	0.8	15
144	Comparison of Acceleration Techniques for Selected Low-Level Bioinformatics Operations. Frontiers in Genetics, 2016, 7, 5.	1.1	4
145	Metagenomic Analysis Suggests Modern Freshwater Microbialites Harbor a Distinct Core Microbial Community. Frontiers in Microbiology, 2016, 6, 1531.	1.5	78
146	Tricking Arthrinium malaysianum into Producing Industrially Important Enzymes Under 2-Deoxy D-Glucose Treatment. Frontiers in Microbiology, 2016, 7, 596.	1.5	10
147	A Terpene Synthase Is Involved in the Synthesis of the Volatile Organic Compound Sodorifen of Serratia plymuthica 4Rx13. Frontiers in Microbiology, 2016, 7, 737.	1.5	29
148	Salmonella Enteritidis Isolate Harboring Multiple Efflux Pumps and Pathogenicity Factors, Shows Absence of O Antigen Polymerase Gene. Frontiers in Microbiology, 2016, 7, 1130.	1.5	1
149	Genomic Analysis of Storage Protein Deficiency in Genetically Related Lines of Common Bean (Phaseolus vulgaris). Frontiers in Plant Science, 2016, 7, 389.	1.7	10

#	Article	IF	CITATIONS
150	Comparative Chloroplast Genome Analyses of Streptophyte Green Algae Uncover Major Structural Alterations in the Klebsormidiophyceae, Coleochaetophyceae and Zygnematophyceae. Frontiers in Plant Science, 2016, 7, 697.	1.7	62
151	Development of highly reliable in silico SNP resource and genotyping assay from exome capture and sequencing: an example from black spruce (<i>Picea mariana</i>). Molecular Ecology Resources, 2016, 16, 588-598.	2.2	32
152	Genome Sequences of Five Arboviruses in Field-Captured Mosquitoes in a Unique Rural Environment of South Korea. Genome Announcements, 2016, 4, .	0.8	35
153	Genome and proteome analysis of <scp> <i>P</i></scp> <i>seudomonas chloritidismutans</i> â€ <scp>AW</scp> â€l <scp> ^T</scp> that grows on <i>n</i> â€decane with chlorate or oxygen as electron acceptor. Environmental Microbiology, 2016, 18, 3247-3257.	1.8	21
154	Methanogenic paraffin degradation proceeds via alkane addition to fumarate by <i>â€~Smithella'</i> spp. mediated by a syntrophic coupling with hydrogenotrophic methanogens. Environmental Microbiology, 2016, 18, 2604-2619.	1.8	71
155	Mitochondrial genomes and comparative genomics of Aphanomyces astaci and Aphanomyces invadans. Scientific Reports, 2016, 6, 36089.	1.6	18
156	Predictive computational phenotyping and biomarker discovery using reference-free genome comparisons. BMC Genomics, 2016, 17, 754.	1.2	97
157	Lazer: Distributed memory-efficient assembly of large-scale genomes. , 2016, , .		4
158	Lowâ€coverage, wholeâ€genome sequencing of <i>Artocarpus camansi</i> (Moraceae) for phylogenetic marker development and gene discovery. Applications in Plant Sciences, 2016, 4, 1600017.	0.8	38
159	Draft Genome Sequence of Criibacterium bergeronii gen. nov., sp. nov., Strain CCRI-22567 T , Isolated from a Vaginal Sample from a Woman with Bacterial Vaginosis. Genome Announcements, 2016, 4, .	0.8	2
160	Deduplication Potential of HPC Applicationsâ \in M Checkpoints. , 2016, , .		6
161	Comparative genomics of mitochondria in chlorarachniophyte algae: endosymbiotic gene transfer and organellar genome dynamics. Scientific Reports, 2016, 6, 21016.	1.6	23
162	A Scalable Pipeline for Transcriptome Profiling Tasks with On-Demand Computing Clouds. , 2016, , .		0
163	Compacting de Bruijn graphs from sequencing data quickly and in low memory. Bioinformatics, 2016, 32, i201-i208.	1.8	170
164	Metagenomic Profiling, Interaction of Genomics with Meta-genomics. Translational Bioinformatics, 2016, , 241-267.	0.0	0
165	SWAP-Assembler 2: Optimization of De Novo Genome Assembler at Extreme Scale. , 2016, , .		13
166	Precultivation of Bacillus coagulans DSM2314 in the presence of furfural decreases inhibitory effects of lignocellulosic by-products during l(+)-lactic acid fermentation. Applied Microbiology and Biotechnology, 2016, 100, 10307-10319.	1.7	15
167	Identifying wrong assemblies in de novo short read primary sequence assembly contigs. Journal of Biosciences, 2016, 41, 455-474.	0.5	0

#	Article	IF	CITATIONS
168	Repeated replacement of an intrabacterial symbiont in the tripartite nested mealybug symbiosis. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E5416-24.	3.3	222
169	Genix: a new online automated pipeline for bacterial genome annotation. FEMS Microbiology Letters, 2016, 363, fnw263.	0.7	14
170	Resolving evolutionary relationships in lichen-forming fungi using diverse phylogenomic datasets and analytical approaches. Scientific Reports, 2016, 6, 22262.	1.6	42
171	Evidence for the sexual origin of heterokaryosis in arbuscular mycorrhizal fungi. Nature Microbiology, 2016, 1, 16033.	5.9	137
172	Draft Genome Sequences of Four Thermophilic Spore Formers Isolated from a Dairy-Processing Environment. Genome Announcements, 2016, 4, .	0.8	3
173	<i>Moramonas marocensis</i> gen. nov., sp. nov.: a jakobid flagellate isolated from desert soil with a bacteria-like, but bloated mitochondrial genome. Open Biology, 2016, 6, 150239.	1.5	12
174	Recovering complete and draft population genomes from metagenome datasets. Microbiome, 2016, 4, 8.	4.9	254
175	Genome Evolution and Nitrogen Fixation in Bacterial Ectosymbionts of a Protist Inhabiting Wood-Feeding Cockroaches. Applied and Environmental Microbiology, 2016, 82, 4682-4695.	1.4	41
176	Genome-Wide Survey of Gut Fungi (Harpellales) Reveals the First Horizontally Transferred Ubiquitin Gene from a Mosquito Host. Molecular Biology and Evolution, 2016, 33, 2544-2554.	3.5	28
177	Unravelling core microbial metabolisms in the hypersaline microbial mats of Shark Bay using high-throughput metagenomics. ISME Journal, 2016, 10, 183-196.	4.4	147
178	MEGAnnotator: a user-friendly pipeline for microbial genomes assembly and annotation. FEMS Microbiology Letters, 2016, 363, fnw049.	0.7	94
179	The genome of an Encephalitozoon cuniculi type III strain reveals insights into the genetic diversity and mode of reproduction of a ubiquitous vertebrate pathogen. Heredity, 2016, 116, 458-465.	1.2	16
180	Genomic Comparison of Two O111:Hâ^'Enterohemorrhagic Escherichia coli Isolates from a Historic Hemolytic-Uremic Syndrome Outbreak in Australia. Infection and Immunity, 2016, 84, 775-781.	1.0	14
181	Draft Genome Sequence of a Strictly Anaerobic Dichloromethane-Degrading Bacterium. Genome Announcements, 2016, 4, .	0.8	13
182	Utility of Whole-Genome Sequencing in Characterizing Acinetobacter Epidemiology and Analyzing Hospital Outbreaks. Journal of Clinical Microbiology, 2016, 54, 593-612.	1.8	103
183	<scp>hybrid</scp> SPA <scp>des</scp> : an algorithm for hybrid assembly of short and long reads. Bioinformatics, 2016, 32, 1009-1015.	1.8	463
184	The initial state of the human gut microbiome determines its reshaping by antibiotics. ISME Journal, 2016, 10, 707-720.	4.4	251
185	Genomic Diversity of Phages Infecting Probiotic Strains of Lactobacillus paracasei. Applied and Environmental Microbiology, 2016, 82, 95-105.	1.4	36

#	Article	IF	CITATIONS
186	Phylogenetic utility, and variability in structure and content, of complete mitochondrial genomes among genetic lineages of the Hawaiian anchialine shrimp <i>Halocaridina rubra</i> Holthuis 1963 (Atyidae:Decapoda). Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 2710-2718.	0.7	2
187	Next-generation sequencing (NGS) in the microbiological world: How to make the most of your money. Journal of Microbiological Methods, 2017, 138, 60-71.	0.7	123
188	ISEA: Iterative Seed-Extension Algorithm for De Novo Assembly Using Paired-End Information and Insert Size Distribution. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 916-925.	1.9	20
189	Unraveling the microbial processes of black band disease in corals through integrated genomics. Scientific Reports, 2017, 7, 40455.	1.6	36
190	Multiple horizontal transfers of nuclear ribosomal genes between phylogenetically distinct grass lineages. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 1726-1731.	3.3	34
191	Fast and simple protein-alignment-guided assembly of orthologous gene families from microbiome sequencing reads. Microbiome, 2017, 5, 11.	4.9	31
192	Building and Improving Reference Genome Assemblies. Proceedings of the IEEE, 2017, , 1-14.	16.4	6
193	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. Plant Physiology, 2017, 173, 932-943.	2.3	33
194	Obtaining the Most Accurate de novo Transcriptomes for Non-model Organisms: The Case of Castanea sativa. Lecture Notes in Computer Science, 2017, , 489-499.	1.0	0
195	The complete chloroplast genome of the green microalgae <i>Dunaliella salina</i> strain SQ. Mitochondrial DNA Part B: Resources, 2017, 2, 225-226.	0.2	2
196	Mitochondrial Genome Evolution and a Novel RNA Editing System in Deep-Branching Heteroloboseids. Genome Biology and Evolution, 2017, 9, 1161-1174.	1.1	19
197	Complete plastid genome sequence of goosegrass (Eleusine indica) and comparison with other Poaceae. Gene, 2017, 600, 36-43.	1.0	15
198	Sequence Assembly. Methods in Molecular Biology, 2017, 1525, 35-45.	0.4	2
199	Large-scale parallel genome assembler over cloud computing environment. Journal of Bioinformatics and Computational Biology, 2017, 15, 1740003.	0.3	5
200	Draft Genome Sequences of Mycobacterium kansasii Clinical Strains. Genome Announcements, 2017, 5, .	0.8	6
201	Gene-enriched draft genome of the cattle tick Rhipicephalus microplus: assembly by the hybrid Pacific Biosciences/Illumina approach enabled analysis of the highly repetitive genome. International Journal for Parasitology, 2017, 47, 569-583.	1.3	48
202	Phenotypic diversity and genotypic flexibility of <i>Burkholderia cenocepacia</i> during long-term chronic infection of cystic fibrosis lungs. Genome Research, 2017, 27, 650-662.	2.4	64
203	Genome Sequence of Deinococcus marmoris PAMC 26562 Isolated from Antarctic Lichen. Genome Announcements, 2017, 5, .	0.8	3

#	Article	IF	CITATIONS
204	Outlier analyses to test for local adaptation to breeding grounds in a migratory arctic seabird. Ecology and Evolution, 2017, 7, 2370-2381.	0.8	30
205	Parallelizing the Searching for K-mers and the Alignment of Reads to Edges to Speedup the Pregraph Construction in SOAPdenovo2. , 2017, , 81-105.		Ο
206	Critical Assessment of Metagenome Interpretation—a benchmark of metagenomics software. Nature Methods, 2017, 14, 1063-1071.	9.0	635
207	Whole-Genome Sequencing of Bacterial Pathogens: the Future of Nosocomial Outbreak Analysis. Clinical Microbiology Reviews, 2017, 30, 1015-1063.	5.7	310
208	Reference-based RADseq resolves robust relationships among closely related species of lichen-forming fungi using metagenomic DNA. Scientific Reports, 2017, 7, 9884.	1.6	33
209	Homeodomain-like DNA binding proteins control the haploid-to-diploid transition in <i>Dictyostelium</i> . Science Advances, 2017, 3, e1602937.	4.7	21
210	Scalable Genomic Assembly through Parallel <i>de Bruijn</i> Graph Construction for Multiple K-mers. , 2017, , .		7
211	Ninety-nine <i>de novo</i> assembled genomes from the moose (<i>Alces alces</i>) rumen microbiome provide new insights into microbial plant biomass degradation. ISME Journal, 2017, 11, 2538-2551.	4.4	120
212	Divergent copies of the large inverted repeat in the chloroplast genomes of ulvophycean green algae. Scientific Reports, 2017, 7, 994.	1.6	77
213	Phenetic Comparison of Prokaryotic Genomes Using k-mers. Molecular Biology and Evolution, 2017, 34, 2716-2729.	3.5	20
214	The complete mitochondrial genome of the green microalgae <i>Dunaliella salina</i> strain SQ. Mitochondrial DNA Part B: Resources, 2017, 2, 311-312.	0.2	2
215	Complete chloroplast genomes of the Chlamydomonas reinhardtii nonphotosynthetic mutants CC-1375, CC-373, CC-4199, CC-2359 and CC-1051. Mitochondrial DNA Part B: Resources, 2017, 2, 405-407.	0.2	2
216	Toward Universal Forward Genetics: Using a Draft Genome Sequence of the Nematode <i>Oscheius tipulae</i> To Identify Mutations Affecting Vulva Development. Genetics, 2017, 206, 1747-1761.	1.2	18
217	The complete mitochondrial genome of the copepod Calanus glacialis. Mitochondrial DNA Part B: Resources, 2017, 2, 506-507.	0.2	2
218	Mitochondrial genome of Dinophilus gyrociliatus (Annelida: Dinophilidae). Mitochondrial DNA Part B: Resources, 2017, 2, 831-832.	0.2	3
219	A New Lineage of Eukaryotes Illuminates Early Mitochondrial Genome Reduction. Current Biology, 2017, 27, 3717-3724.e5.	1.8	109
220	Ardissonea crystallina has a type of sexual reproduction that is unusual for centric diatoms. Scientific Reports, 2017, 7, 14670.	1.6	16
221	Monophyletic Origin and Evolution of the Largest Crucifer Genomes. Plant Physiology, 2017, 174, 2062-2071.	2.3	34

		CITATION REF	PORT	
#	Article		IF	CITATIONS
222	Nitrogen fixation in a chemoautotrophic lucinid symbiosis. Nature Microbiology, 2017, 2,	16193.	5.9	56
223	Draft genome of the American Eel (<i>Anguilla rostrata</i>). Molecular Ecology Resource 806-811.	s, 2017, 17,	2.2	21
224	Safe and Complete Contig Assembly Through Omnitigs. Journal of Computational Biology 590-602.	ı, 2017, 24,	0.8	20
225	Isolation and characterization of Lactobacillus helveticus DSM 20075 variants with impro autolytic capacity. International Journal of Food Microbiology, 2017, 241, 173-180.	ved	2.1	13
226	Hoarding and horizontal transfer led to an expanded gene and intron repertoire in the pla genome of the diatom, Toxarium undulatum (Bacillariophyta). Current Genetics, 2017, 63		0.8	21
227	Identification of a novel aviadenovirus, designated pigeon adenovirus 2 in domestic pigeo	ons (Columba) Tj ETQq1	1,0.78431 1.1	.4 rgBT /O
228	Phylogenomics solves a long-standing evolutionary puzzle in the ciliate world: The subcla Peritrichia is monophyletic. Molecular Phylogenetics and Evolution, 2017, 106, 1-5.	SS	1.2	82
229	Exploration of de Bruijn Graph Filtering for de novo Assembly Using GraphLab. , 2017, , .			0
230	Draft Genome Sequence of <i>Romboutsia weinsteinii</i> sp. nov. Strain CCRI-19649 <se Isolated from Surface Water. Genome Announcements, 2017, 5, .</se 	up>T	0.8	8
231	The complete mitochondrial genome of the scorpion Centruroides vittatus (Arachnida: So Mitochondrial DNA Part B: Resources, 2017, 2, 841-842.	torpiones).	0.2	Ο
232	Draft Genome Sequence of Marinobacter vinifirmus Type Strain FB1. Genome Announcer	nents, 2017, 5, .	0.8	0
233	Strategies and Tools for Sequencing and Assembly of Plant Genomes. Compendium of Pla 2017, , 81-93.	ant Genomes,	0.3	4
234	Draft Genome Sequence of <i>Romboutsia maritimum</i> sp. nov. Strain CCRI-22766 <s Isolated from Coastal Estuarine Mud. Genome Announcements, 2017, 5, .</s 	up>T ,	0.8	3
235	Metabolomic and Metagenomic Analysis of Two Crude Oil Production Pipelines Experience Differential Rates of Corrosion. Frontiers in Microbiology, 2017, 8, 99.	ing	1.5	38
236	Genome Sequence of Desulfurella amilsii Strain TR1 and Comparative Genomics of Desult Family. Frontiers in Microbiology, 2017, 8, 222.	urellaceae	1.5	35
237	Holm Oak (Quercus ilex) Transcriptome. De novo Sequencing and Assembly Analysis. Fro Molecular Biosciences, 2017, 4, 70.	ntiers in	1.6	46
238	Comparing and Evaluating Metagenome Assembly Tools from a Microbiologist's Pers Size Matters!. PLoS ONE, 2017, 12, e0169662.	pective - Not Only	1.1	186
239	Shifts in coastal sediment oxygenation cause pronounced changes in microbial communi composition and associated metabolism. Microbiome, 2017, 5, 96.	ty	4.9	52

#	Article	IF	CITATIONS
240	Parallel NGS Assembly Using Distributed Assembly Graphs Enriched with Biological Knowledge. , 2017, ,		0
241	Scalable Assembly for Massive Genomic Graphs. , 2017, , .		2
242	Draft Genome Sequence of a Sporulating and Motile Strain of Lachnotalea glycerini Isolated from Water in Québec City, Canada. Genome Announcements, 2017, 5, .	0.8	0
243	Approaches for in silico finishing of microbial genome sequences. Genetics and Molecular Biology, 2017, 40, 553-576.	0.6	17
244	Use of a draft genome of coffee (C <i>offea arabica</i>) to identify <scp>SNP</scp> s associated with caffeine content. Plant Biotechnology Journal, 2018, 16, 1756-1766.	4.1	48
245	Multiscale Evolutionary Dynamics of Host-Associated Microbiomes. Cell, 2018, 172, 1216-1227.	13.5	85
246	Fast Metagenomic Binning via Hashing and Bayesian Clustering. Journal of Computational Biology, 2018, 25, 677-688.	0.8	5
247	Isolation of <i>Crithidia</i> spp. from lesions of immunocompetent patients with suspected cutaneous leishmaniasis in Iran. Tropical Medicine and International Health, 2019, 24, 116-126.	1.0	30
248	Oryza glumaepatula Steud Compendium of Plant Genomes, 2018, , 127-135.	0.3	0
249	A multi-omics study of the grapevine-downy mildew (Plasmopara viticola) pathosystem unveils a complex protein coding- and noncoding-based arms race during infection. Scientific Reports, 2018, 8, 757.	1.6	70
250	Assembly of the Lactuca sativa, L. cv. Tizian draft genome sequence reveals differences within major resistance complex 1 as compared to the cv. Salinas reference genome. Journal of Biotechnology, 2018, 267, 12-18.	1.9	13
251	Analyzing large scale genomic data on the cloud with Sparkhit. Bioinformatics, 2018, 34, 1457-1465.	1.8	14
252	DNA Assembly with De Bruijn Graphs Using an FPGA Platform. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1003-1009.	1.9	1
253	Assembly and <scp>RNA</scp> â€free annotation of highly heterozygous genomes: The case of the thickâ€billed murre (<i>Uria lomvia</i>). Molecular Ecology Resources, 2018, 18, 79-90.	2.2	13
254	Oral microbiomes from hunterâ€gatherers and traditional farmers reveal shifts in commensal balance and pathogen load linked to diet. Molecular Ecology, 2018, 27, 182-195.	2.0	85
255	Complete Sequence and Annotation of the Mycoplasma phocidae Strain 105 ^T Genome. Microbiology Resource Announcements, 2018, 7, .	0.3	2
256	SORA: Scalable Overlap-graph Reduction Algorithms for Genome Assembly using Apache Spark in the Cloud. , 2018, , .		2
257	CLAME: a new alignment-based binning algorithm allows the genomic description of a novel Xanthomonadaceae from the Colombian Andes. BMC Genomics, 2018, 19, 858.	1.2	2

#	Article	IF	Citations
258	Scalable De Novo Genome Assembly Using Pregel. , 2018, , .		7
259	Maser: one-stop platform for NGS big data from analysis to visualization. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	42
260	TransFlow: a modular framework for assembling and assessing accurate de novo transcriptomes in non-model organisms. BMC Bioinformatics, 2018, 19, 416.	1.2	16
261	ImproveAssembly - Tool for identifying new gene products and improving genome assembly. PLoS ONE, 2018, 13, e0206000.	1.1	0
262	Complete Genome Sequence of Ebrios, a Novel T7virus Isolated from the Ebrie Lagoon in Abidjan, Côte d'Ivoire. Genome Announcements, 2018, 6, .	0.8	4
263	A Novel Inorganic Sulfur Compound Metabolizing Ferroplasma-Like Population Is Suggested to Mediate Extracellular Electron Transfer. Frontiers in Microbiology, 2018, 9, 2945.	1.5	18
264	Inferring the Minimal Genome of <i>Mesoplasma florum</i> by Comparative Genomics and Transposon Mutagenesis. MSystems, 2018, 3, .	1.7	15
265	Nuclear genome sequence of the plastid-lacking cryptomonad Goniomonas avonlea provides insights into the evolution of secondary plastids. BMC Biology, 2018, 16, 137.	1.7	42
266	Microbiome Analysis. Methods in Molecular Biology, 2018, , .	0.4	13
267	Subsampled Assemblies and Hybrid Nucleotide Composition/Differential Coverage Binning for Genome-Resolved Metagenomics. Methods in Molecular Biology, 2018, 1849, 215-225.	0.4	2
268	A Comprehensive Study of De Novo Genome Assemblers: Current Challenges and Future Prospective. Evolutionary Bioinformatics, 2018, 14, 117693431875865.	0.6	37
269	The draft genome sequence of cork oak. Scientific Data, 2018, 5, 180069.	2.4	98
270	Comparative Genomics Reveals the Core Gene Toolbox for the Fungus-Insect Symbiosis. MBio, 2018, 9, .	1.8	17
271	Whole-genome sequencing identification of a multidrug-resistant Listeria monocytogenes serotype 1/2a isolated from fresh mixed sausage in southern Brazil. Infection, Genetics and Evolution, 2018, 65, 127-130.	1.0	9
272	Viral Communities of Shark Bay Modern Stromatolites. Frontiers in Microbiology, 2018, 9, 1223.	1.5	32
273	Species delimitation and mitogenome phylogenetics in the subterranean genus Pseudoniphargus (Crustacea: Amphipoda). Molecular Phylogenetics and Evolution, 2018, 127, 988-999.	1.2	25
274	Canine caliciviruses of four serotypes from military and research dogs recovered in 1963â^'1978 belong to two phylogenetic clades in the Vesivirus genus. Virology Journal, 2018, 15, 39.	1.4	8
275	Strategies for Taxonomic and Functional Annotation of Metagenomes. , 2018, , 55-79.		11

#	Article	IF	CITATIONS
276	The complete mitochondrial DNA of the tropical oyster <i>Crassostrea belcheri</i> from the Cần Giò' mangrove in Vietnam. Mitochondrial DNA Part B: Resources, 2018, 3, 462-463.	0.2	4
277	GPU-Accelerated Large-Scale Genome Assembly. , 2018, , .		5
278	Novel Autotrophic Organisms Contribute Significantly to the Internal Carbon Cycling Potential of a Boreal Lake. MBio, 2018, 9, .	1.8	18
279	Bioinformatics applications on Apache Spark. GigaScience, 2018, 7, .	3.3	55
280	<i>panlSa: ab initio</i> detection of insertion sequences in bacterial genomes from short read sequence data. Bioinformatics, 2018, 34, 3795-3800.	1.8	29
281	The complete mitogenome of <i>Sydowia polyspora</i> . Mitochondrial DNA Part B: Resources, 2019, 4, 1992-1993.	0.2	1
282	Mobilome of Brevibacterium aurantiacum Sheds Light on Its Genetic Diversity and Its Adaptation to Smear-Ripened Cheeses. Frontiers in Microbiology, 2019, 10, 1270.	1.5	12
283	The Population Structure of Pseudomonas aeruginosa Is Characterized by Genetic Isolation of exoU+ and exoS+ Lineages. Genome Biology and Evolution, 2019, 11, 1780-1796.	1.1	74
284	Cell-Fusing Agent Virus Reduces Arbovirus Dissemination in Aedes aegypti Mosquitoes <i>In Vivo</i> . Journal of Virology, 2019, 93, .	1.5	86
285	Scalable Genome Assembly through Parallel de Bruijn Graph Construction for Multiple k-mers. Scientific Reports, 2019, 9, 14882.	1.6	8
286	An "omic―approach to Pyrocystis lunula: New insights related with this bioluminescent dinoflagellate. Journal of Proteomics, 2019, 209, 103502.	1.2	11
287	Using Apache Spark on genome assembly for scalable overlap-graph reduction. Human Genomics, 2019, 13, 48.	1.4	2
288	Machine Learning Approaches for Epidemiological Investigations of Food-Borne Disease Outbreaks. Frontiers in Microbiology, 2019, 10, 1722.	1.5	22
289	Diversity and Host Specificity Revealed by Biological Characterization and Whole Genome Sequencing of Bacteriophages Infecting Salmonella enterica. Viruses, 2019, 11, 854.	1.5	32
290	Plastid Genomes from Diverse Glaucophyte Genera Reveal a Largely Conserved Gene Content and Limited Architectural Diversity. Genome Biology and Evolution, 2019, 11, 174-188.	1.1	16
291	Ion Torrent and Illumina, two complementary RNA-seq platforms for constructing the holm oak (Quercus ilex) transcriptome. PLoS ONE, 2019, 14, e0210356.	1.1	28
292	Dynamic Interactions Between the Genome and an Endogenous Retrovirus: <i>Tirant</i> in <i>Drosophila simulans</i> Wild-Type Strains. G3: Genes, Genomes, Genetics, 2019, 9, 855-865.	0.8	5
293	Complete Genome Sequence of Escherichia coli Siphophage BRET. Microbiology Resource Announcements, 2019, 8, .	0.3	4

#	Article	IF	CITATIONS
294	Complete Sequence and Annotation of the Mycoplasma phocicerebrale Strain 1049 T Genome. Microbiology Resource Announcements, 2019, 8, .	0.3	0
295	Genome of the tropical plant Marchantia inflexa: implications for sex chromosome evolution and dehydration tolerance. Scientific Reports, 2019, 9, 8722.	1.6	25
296	Accessing a Russian Wheat Aphid Resistance Gene in Bread Wheat by Longâ€Read Technologies. Plant Genome, 2019, 12, 180065.	1.6	15
297	Unraveling the phylogenetic relationships of the extinct bovid Myotragus balearicus Bate 1909 from the Balearic Islands. Quaternary Science Reviews, 2019, 215, 185-195.	1.4	21
298	Mitochondrial genome of Parborlasia corrugatus (Nemertea: Lineidae). Mitochondrial DNA Part B: Resources, 2019, 4, 332-334.	0.2	1
299	Draft Genome Sequence of Enterococcus plantarum Strain TRW2, Isolated from Lettuce. Microbiology Resource Announcements, 2019, 8, .	0.3	0
300	Genome sequence of Xanthomonas fuscans subsp. fuscans strain Xff49: a new isolate obtained from common beans in Southern Brazil. Brazilian Journal of Microbiology, 2019, 50, 357-367.	0.8	3
301	Nitric oxide-dependent regulation of sweet pepper fruit ripening. Journal of Experimental Botany, 2019, 70, 4557-4570.	2.4	84
302	Complete Sequence and Annotation of the Mycoplasma phocirhinis Strain 852 T Genome. Microbiology Resource Announcements, 2019, 8, .	0.3	2
303	Culture-enriched human gut microbiomes reveal core and accessory resistance genes. Microbiome, 2019, 7, 56.	4.9	23
304	Genome Improvement and Genetic Map Construction for <i>Aethionema arabicum</i> , the First Divergent Branch in the Brassicaceae Family. G3: Genes, Genomes, Genetics, 2019, 9, 3521-3530.	0.8	17
305	Complete mitogenome of the streptophyte green alga <i>Coleochaete scutata</i> (Coleochaetophyceae). Mitochondrial DNA Part B: Resources, 2019, 4, 4209-4210.	0.2	3
306	6. Practical overview of bioinformatics data mining in environmental genomics. , 2019, , 127-150.		0
307	The Mitochondrial Genome of Eleusine indica and Characterization of Gene Content Within Poaceae. Genome Biology and Evolution, 2019, 12, 3684-3697.	1.1	3
308	PaKman: Scalable Assembly of Large Genomes on Distributed Memory Machines. , 2019, , .		4
309	Divergence between bread wheat and Triticum militinae in the powdery mildew resistance QPm.tut-4A locus and its implications for cloning of the resistance gene. Theoretical and Applied Genetics, 2019, 132, 1061-1072.	1.8	11
310	Sunflower pan-genome analysis shows that hybridization altered gene content and disease resistance. Nature Plants, 2019, 5, 54-62.	4.7	172
311	Complete mitochondrial genome of a rare diatom (Bacillariophyta) <i>Proschkinia</i> and its phylogenetic and taxonomic implications. Mitochondrial DNA Part B: Resources, 2019, 4, 25-26.	0.2	11

#	Article	IF	CITATIONS
312	Enlarged and highly repetitive plastome of Lagarostrobos and plastid phylogenomics of Podocarpaceae. Molecular Phylogenetics and Evolution, 2019, 133, 24-32.	1.2	8
313	Mitogenomics Reveals a Novel Genetic Code in Hemichordata. Genome Biology and Evolution, 2019, 11, 29-40.	1.1	20
314	FastEtch: A Fast Sketch-Based Assembler for Genomes. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1091-1106.	1.9	4
315	Prospective Cohort Study of Next-Generation Sequencing as a Diagnostic Modality for Unexplained Encephalitis in Children. Journal of the Pediatric Infectious Diseases Society, 2020, 9, 326-333.	0.6	32
316	Assessment of metagenomic assemblers based on hybrid reads of real and simulated metagenomic sequences. Briefings in Bioinformatics, 2020, 21, 777-790.	3.2	18
317	Microsporidia with Vertical Transmission Were Likely Shaped by Nonadaptive Processes. Genome Biology and Evolution, 2020, 12, 3599-3614.	1.1	27
318	Combined Transcriptome Sequencing of Mycoplasma hyopneumoniae and Infected Pig Lung Tissue Reveals Up-Regulation of Bacterial F1-Like ATPase and Down-Regulation of the P102 Cilium Adhesin in vivo. Frontiers in Microbiology, 2020, 11, 1679.	1.5	4
319	Non-retroviral Endogenous Viral Element Limits Cognate Virus Replication in Aedes aegypti Ovaries. Current Biology, 2020, 30, 3495-3506.e6.	1.8	88
320	The Most Frequently Used Sequencing Technologies and Assembly Methods in Different Time Segments of the Bacterial Surveillance and RefSeq Genome Databases. Frontiers in Cellular and Infection Microbiology, 2020, 10, 527102.	1.8	32
321	Bacterial Genome Wide Association Studies (bGWAS) and Transcriptomics Identifies Cryptic Antimicrobial Resistance Mechanisms in Acinetobacter baumannii. Frontiers in Public Health, 2020, 8, 451.	1.3	9
322	Regional sequence expansion or collapse in heterozygous genome assemblies. PLoS Computational Biology, 2020, 16, e1008104.	1.5	31
323	Novel genome sequences of cell-fusing agent virus allow comparison of virus phylogeny with the genetic structure of Aedes aegypti populations. Virus Evolution, 2020, 6, veaa018.	2.2	24
324	Mitogenomics reveals phylogenetic relationships of Arcoida (Mollusca, Bivalvia) and multiple independent expansions and contractions in mitochondrial genome size. Molecular Phylogenetics and Evolution, 2020, 150, 106857.	1.2	32
325	<scp>DNA</scp> <scp>tandem</scp> repeats contribute to the genetic diversity of <i>Brevibacterium aurantiacum</i> phages. Environmental Microbiology, 2020, 22, 3413-3428.	1.8	10
326	The phylogeny of Nereididae (Annelida) based on mitochondrial genomes. Zoologica Scripta, 2020, 49, 366-378.	0.7	22
327	The Origin and Evolution of Plastid Genome Downsizing in Southern Hemispheric Cypresses (Cupressaceae). Frontiers in Plant Science, 2020, 11, 901.	1.7	6
328	Characterization of a Type II-A CRISPR-Cas System in <i>Streptococcus mutans</i> . MSphere, 2020, 5, .	1.3	14
329	Mitogenomic phylogeny of the Naticidae (Gastropoda: Littorinimorpha) reveals monophyly of the Polinicinae. Zoologica Scripta, 2020, 49, 295-306.	0.7	5

ARTICLE IF CITATIONS # Novel Genus of Phages Infecting Streptococcus thermophilus: Genomic and Morphological 331 1.4 22 Characterization. Applied and Environmental Microbiology, 2020, 86, . Levenshtein Distance, Sequence Comparison and Biological Database Search. IEEE Transactions on 1.5 Information Theory, 2021, 67, 3287-3294. Scalable De Novo Genome Assembly Using a Pregel-Like Graph-Parallel System. IEEE/ACM Transactions 333 1.9 2 on Computational Biology and Bioinformatics, 2021, 18, 731-744. High Sequence Divergence but Limited Architectural Rearrangements in Organelle Genomes of 334 Cyanophora (Glaucophyta) Species. Journal of Eukaryotic Microbiology, 2021, 68, e12831. PaKman: A Scalable Algorithm for Generating Genomic Contigs on Distributed Memory Machines. IEEE 335 4.0 3 Transactions on Parallel and Distributed Systems, 2021, 32, 1191-1209. Mitogenomic phylogeny of Trochoidea (Gastropoda: Vetigastropoda): New insights from increased complete genomes. Zoologica Scripta, 2021, 50, 43-57. 337 The complete mitogenome of Diaporthe nobilis. Mitochondrial DNA Part B: Resources, 2021, 6, 6-7. 0.2 1 Methods for Proteogenomics Data Analysis, Challenges, and Scalability Bottlenecks: A Survey. IEEE 338 2.6 14 Access, 2021, 9, 5497-5516. Cloud Computing Enabled Big Multi-Omics Data Analytics. Bioinformatics and Biology Insights, 2021, 339 23 1.0 15, 117793222110359. Assessment of mitochondrial genomes for heterobranch gastropod phylogenetics. Bmc Ecology and 340 Evolution, 2021, 21, 6. Complete Chloroplast Genome Sequences of Coconut cv. Kopyor Green Dwarf and Comparative 341 0 Genome Analysis to Oil Palm, Date Palm, Sago Palm, and Miniature Sugar Palm., 2021, 189-216. NexGen Sequencing Data: Bioinformatic Tools for Visualization and Analysis. , 2021, , 47-90. Hybridization History and Repetitive Element Content in the Genome of a Homoploid Hybrid, Yucca 343 1.7 9 gloriosa (Asparagaceae). Frontiers in Plant Science, 2020, 11, 573767. Genome-Scale Profiling Reveals Noncoding Loci Carry Higher Proportions of Concordant Data. Molecular Biology and Evolution, 2021, 38, 2306-2318. 344 3.5 First finding of free-living representatives of Prokinetoplastina and their nuclear and mitochondrial 345 1.6 13 genomes. Scientific Reports, 2021, 11, 2946. Recent African strains of Zika virus display higher transmissibility and fetal pathogenicity than Asian 346 5.8 strains. Nature Communications, 2021, 12, 916. Complete and Draft Genome Sequences of Aerobic Methanotrophs Isolated from a Riparian Wetland. 348 0.3 0 Microbiology Resource Announcements, 2021, 10, . RMI-DBG algorithm: A more agile iterative de Bruijn graph algorithm in short read genome assembly. 349 Journal of Bioinformatics and Computational Biology, 2021, 19, 2150005.

#	Article	IF	CITATIONS
350	Complete Genome Sequences of 10 Lactococcal Skunavirus Phages Isolated from Cheddar Cheese Whey Samples in Canada. Microbiology Resource Announcements, 2021, 10, .	0.3	2
351	Constructing a de novo transcriptome and a reference proteome for the bivalve Scrobicularia plana: Comparative analysis of different assembly strategies and proteomic analysis. Genomics, 2021, 113, 1543-1553.	1.3	5
352	Haploflow: strain-resolved de novo assembly of viral genomes. Genome Biology, 2021, 22, 212.	3.8	16
353	Empirical evaluation of methods for <i>de novo</i> genome assembly. PeerJ Computer Science, 2021, 7, e636.	2.7	15
354	Changes in the transcript and protein profiles of Quercus ilex seedlings in response to drought stress. Journal of Proteomics, 2021, 243, 104263.	1.2	13
355	The Evidential Statistics of Genetic Assembly: Bootstrapping a Reference Sequence. Frontiers in Ecology and Evolution, 2021, 9, .	1.1	1
356	Further Characterization of Rio Grande Virus and Potential for Cross Reactivity with Rift Valley Fever Virus Assays. Viruses, 2021, 13, 1719.	1.5	1
357	Plastome Structural Evolution and Homoplastic Inversions in Neo-Astragalus (Fabaceae). Genome Biology and Evolution, 2021, 13, .	1.1	13
359	Genomic Analyses of Phenotypic Differences Between Native and Invasive Populations of Diffuse Knapweed (Centaurea diffusa). Frontiers in Ecology and Evolution, 2021, 8, .	1.1	7
360	Specific Protein Database Creation from Transcriptomics Data in Nonmodel Species: Holm Oak (Quercus ilex L.). Methods in Molecular Biology, 2020, 2139, 57-68.	0.4	3
361	Methods for Assembling Reads and Producing Contigs. Methods in Molecular Biology, 2015, 1231, 151-161.	0.4	1
362	Performance Characterization of De Novo Genome Assembly on Leading Parallel Systems. Lecture Notes in Computer Science, 2017, , 79-91.	1.0	5
363	Genomics and Transcriptomics Advance in Plant Sciences. Energy, Environment, and Sustainability, 2019, , 419-448.	0.6	5
364	Assembly Graph Browser: interactive visualization of assembly graphs. Bioinformatics, 2019, 35, 3476-3478.	1.8	12
375	Extreme genome diversity in the hyper-prevalent parasitic eukaryote Blastocystis. PLoS Biology, 2017, 15, e2003769.	2.6	99
376	Identification of Optimum Sequencing Depth Especially for De Novo Genome Assembly of Small Genomes Using Next Generation Sequencing Data. PLoS ONE, 2013, 8, e60204.	1.1	73
377	The Susceptibility of Pseudomonas aeruginosa Strains from Cystic Fibrosis Patients to Bacteriophages. PLoS ONE, 2013, 8, e60575.	1.1	73
378	Genomic Features and Niche-Adaptation of Enterococcus faecium Strains from Korean Soybean-Fermented Foods. PLoS ONE, 2016, 11, e0153279.	1.1	20

#	Article	IF	CITATIONS
379	Experimental Evolution of Mycobacterium tuberculosis in Human Macrophages Results in Low-Frequency Mutations Not Associated with Selective Advantage. PLoS ONE, 2016, 11, e0167989.	1.1	6
380	A new method of evaluating genome assemblies based on kmers frequencies. Keldysh Institute Preprints, 2017, , 1-24.	0.1	2
381	Gammaproteobacterial methanotrophs dominate methanotrophy in aerobic and anaerobic layers of boreal lake waters. Aquatic Microbial Ecology, 2018, 81, 257-276.	0.9	72
382	A novice's guide to analyzing NGS-derived organelle and metagenome data. Algae, 2016, 31, 137-154.	0.9	17
383	Assessing Illumina technology for the high-throughput sequencing of bacteriophage genomes. PeerJ, 2016, 4, e2055.	0.9	38
384	The evolutionary history and diagnostic utility of the CRISPR-Cas system within <i>Salmonella enterica</i> ssp. <i>enterica</i> . PeerJ, 2014, 2, e340.	0.9	31
385	The New Omics Era into Systems Approaches: What Is the Importance of Separation Techniques?. Advances in Experimental Medicine and Biology, 2021, 1336, 1-15.	0.8	0
386	Ultra Efficient Acceleration for De Novo Genome Assembly via Near-Memory Computing. , 2021, , .		5
388	The genetic variation and relationship among the natural hybrids of Mangifera casturi Kosterm. Scientific Reports, 2021, 11, 19766.	1.6	11
389	Parallel and Memory-Efficient Reads Indexing for Genome Assembly. Lecture Notes in Computer Science, 2012, , 272-280.	1.0	0
390	Genetics and breeding for next generation. Ikushugaku Kenkyu, 2013, 15, 115-121.	0.1	0
391	Challenge of Metagenome Assembly and Possible Standards. , 2013, , 1-10.		0
392	Tapping the Wealth of Microbial Data in High-Throughput Metabolic Model Reconstruction. Methods in Molecular Biology, 2014, 1191, 19-45.	0.4	0
394	De novo assembly of ultra-deep sequencing data. , 2014, , .		0
395	Challenge of Metagenome Assembly and Possible Standards. , 2015, , 84-93.		2
401	OBSOLETE: NexGen Sequencing Data: Bioinformatic Tools for Visualization and Analysis. , 2020, , .		0
407	Metagenomic Assembly: Overview, Challenges and Applications. Yale Journal of Biology and Medicine, 2016, 89, 353-362.	0.2	71
409	Referenceâ€free discovery of nuclear SNPs permits accurate, sensitive identification of Carya (hickory) species and hybrids. Applications in Plant Sciences, 2022, 10, e11455.	0.8	1

#	Article	IF	CITATIONS
410	MetaCRS: unsupervised clustering of contigs with the recursive strategy of reducing metagenomic dataset's complexity. BMC Bioinformatics, 2021, 22, 315.	1.2	1
411	Complete mitochondrial genomes of three fairy shrimps from snowmelt pools in Japan. BMC Zoology, 2022, 7, .	0.3	3
412	Genomic sequencing of Thinopyrum elongatum chromosome arm 7EL, carrying fusarium head blight resistance, and characterization of its impact on the transcriptome of the introgressed line CS-7EL. BMC Genomics, 2022, 23, 228.	1.2	8
414	Draft Sequencing Crested Wheatgrass Chromosomes Identified Evolutionary Structural Changes and Genes and Facilitated the Development of SSR Markers. International Journal of Molecular Sciences, 2022, 23, 3191.	1.8	6
415	A Genomic Perspective on the Evolutionary Diversification of Turtles. Systematic Biology, 2022, 71, 1331-1347.	2.7	2
416	Recovering metagenome-assembled genomes from shotgun metagenomic sequencing data: Methods, applications, challenges, and opportunities. Microbiological Research, 2022, 260, 127023.	2.5	17
417	Phage Genome Annotation: Where to Begin and End. Phage, 2021, 2, 183-193.	0.8	17
418	Comparative Genomics and Physiological Investigation of a New Arthrospira/Limnospira Strain O9.13F Isolated from an Alkaline, Winter Freezing, Siberian Lake. Cells, 2021, 10, 3411.	1.8	6
449	Parallel decay of vision genes in subterranean water beetles. Molecular Phylogenetics and Evolution, 2022, 173, 107522.	1.2	14
450	A deep dive into genome assemblies of non-vertebrate animals. , 0, 2, .		4
450 451		5.8	4
	A deep dive into genome assemblies of non-vertebrate animals. , 0, 2, . A truncated anti-CRISPR protein prevents spacer acquisition but not interference. Nature	5.8	
451	A deep dive into genome assemblies of non-vertebrate animals. , 0, 2, . A truncated anti-CRISPR protein prevents spacer acquisition but not interference. Nature Communications, 2022, 13, 2802. Contrasting Modes of Mitochondrial Genome Evolution in Sister Taxa of Wood-Eating Marine		8
451 453	 A deep dive into genome assemblies of non-vertebrate animals., 0, 2, . A truncated anti-CRISPR protein prevents spacer acquisition but not interference. Nature Communications, 2022, 13, 2802. Contrasting Modes of Mitochondrial Genome Evolution in Sister Taxa of Wood-Eating Marine Bivalves (Teredinidae and Xylophagaidae). Genome Biology and Evolution, 2022, 14, . Introduction to the principles and methods underlying the recovery of metagenomeâ€essembled 	1.1	8
451 453 454	A deep dive into genome assemblies of non-vertebrate animals. , 0, 2, . A truncated anti-CRISPR protein prevents spacer acquisition but not interference. Nature Communications, 2022, 13, 2802. Contrasting Modes of Mitochondrial Genome Evolution in Sister Taxa of Wood-Eating Marine Bivalves (Teredinidae and Xylophagaidae). Genome Biology and Evolution, 2022, 14, . Introduction to the principles and methods underlying the recovery of metagenomeâ€assembled genomes from metagenomic data. MicrobiologyOpen, 2022, 11, . Comparative Plastid Genomics of Green-Colored Dinoflagellates Unveils Parallel Genome Compaction	1.1 1.2	8 2 8
451 453 454 455	A deep dive into genome assemblies of non-vertebrate animals. , 0, 2, . A truncated anti-CRISPR protein prevents spacer acquisition but not interference. Nature Communications, 2022, 13, 2802. Contrasting Modes of Mitochondrial Genome Evolution in Sister Taxa of Wood-Eating Marine Bivalves (Teredinidae and Xylophagaidae). Genome Biology and Evolution, 2022, 14, . Introduction to the principles and methods underlying the recovery of metagenomeâ€assembled genomes from metagenomic data. MicrobiologyOpen, 2022, 11, . Comparative Plastid Genomics of Green-Colored Dinoflagellates Unveils Parallel Genome Compaction and RNA Editing. Frontiers in Plant Science, 0, 13, . Antimicrobial Resistance in the Environment: Towards Elucidating the Roles of Bioaerosols in	1.1 1.2 1.7	8 2 8 4
451 453 454 455 456	A deep dive into genome assemblies of non-vertebrate animals., 0, 2, . A truncated anti-CRISPR protein prevents spacer acquisition but not interference. Nature Communications, 2022, 13, 2802. Contrasting Modes of Mitochondrial Genome Evolution in Sister Taxa of Wood-Eating Marine Bivalves (Teredinidae and Xylophagaidae). Genome Biology and Evolution, 2022, 14, . Introduction to the principles and methods underlying the recovery of metagenomeâ€assembled genomes from metagenomic data. MicrobiologyOpen, 2022, 11, . Comparative Plastid Genomics of Green-Colored Dinoflagellates Unveils Parallel Genome Compaction and RNA Editing. Frontiers in Plant Science, 0, 13, . Antimicrobial Resistance in the Environment: Towards Elucidating the Roles of Bioaerosols in Transmission and Detection of Antibacterial Resistance Genes. Antibiotics, 2022, 11, 974. Mitogenomics supports the monophyly of Mysidacea and Peracarida (Malacostraca). Zoologica	1.1 1.2 1.7 1.5	8 2 8 4 5

#	Article	IF	CITATIONS
460	Screening the PRISM Library against <i>Staphylococcus aureus</i> Reveals a Sesquiterpene Lactone from <i>Liriodendron tulipifera</i> with Inhibitory Activity. ACS Omega, 2022, 7, 35677-35685.	1.6	0
461	Genome analysis of Psilogramma increta granulovirus and its intrapopulation diversity. Virus Research, 2022, 322, 198946.	1.1	0
462	In through the Out Door: A Functional Virulence Factor Secretion System Is Necessary for Phage Infection in Ralstonia solanacearum. MBio, 2022, 13, .	1.8	2
463	Improving RNA Assembly via Safety and Completeness in Flow Decompositions. Journal of Computational Biology, 2022, 29, 1270-1287.	0.8	6
464	The plastomes of <i>Hyalomonas oviformis</i> and <i>Hyalogonium fusiforme</i> evolved dissimilar architectures after the loss of photosynthesis. Plant Direct, 2022, 6, .	0.8	0
465	Pathogenesis and Genomic Analysis of a Virulent Leptospira Interrogans Serovar Copenhageni Isolated from a Dog with Lethal Infection. Tropical Medicine and Infectious Disease, 2022, 7, 333.	0.9	1
466	Multiomic Data Integration in the Analysis of Drought-Responsive Mechanisms in Quercus ilex Seedlings. Plants, 2022, 11, 3067.	1.6	8
467	TopKmer: Parallel High Frequency K-mer Counting onÂDistributed Memory. Lecture Notes in Computer Science, 2022, , 96-107.	1.0	0
468	Isolation, Characterization, and Comparative Genomic Analysis of vB_Pd_C23, a Novel Bacteriophage of Pantoea dispersa. Current Microbiology, 2023, 80, .	1.0	1
469	Using low-coverage whole genome sequencing (genome skimming) to delineate three introgressed species of buffalofish (Ictiobus). Molecular Phylogenetics and Evolution, 2023, 182, 107715.	1.2	1
470	Characterization of vancomycin-resistance <i>vanD</i> gene clusters in the human intestinal microbiota by metagenomics and culture-enriched metagenomics. JAC-Antimicrobial Resistance, 2023, 5,	0.9	0
471	The phylogeny and evolutionary ecology of hoverflies (Diptera: Syrphidae) inferred from mitochondrial genomes. Molecular Phylogenetics and Evolution, 2023, 184, 107759.	1.2	4