

GenomeTools: A Comprehensive Software Library for E Genome Annotations

IEEE/ACM Transactions on Computational Biology and Bioinfo
10, 645-656

DOI: [10.1109/tcbb.2013.68](https://doi.org/10.1109/tcbb.2013.68)

Citation Report

#	ARTICLE	IF	CITATIONS
1	LTRsift: a graphical user interface for semi-automatic classification and postprocessing of de novo detected LTR retrotransposons. <i>Mobile DNA</i> , 2012, 3, 18.	3.6	10
2	Long-Range Genomic Enrichment, Sequencing, and Assembly to Determine Unknown Sequences Flanking a Known microRNA. <i>PLoS ONE</i> , 2013, 8, e83721.	2.5	4
3	Genome sequencing of four <i>Aureobasidium pullulans</i> varieties: biotechnological potential, stress tolerance, and description of new species. <i>BMC Genomics</i> , 2014, 15, 549.	2.8	262
4	A cloud-compatible bioinformatics pipeline for ultrarapid pathogen identification from next-generation sequencing of clinical samples. <i>Genome Research</i> , 2014, 24, 1180-1192.	5.5	421
5	The genome of the sparganosis tapeworm <i>Spirometra erinaceieuropaei</i> isolated from the biopsy of a migrating brain lesion. <i>Genome Biology</i> , 2014, 15, 510.	8.8	47
6	FISH Oracle 2: a web server for integrative visualization of genomic data in cancer research. <i>Journal of Clinical Bioinformatics</i> , 2014, 4, 5.	1.2	5
7	High-throughput parallel proteogenomics: A bacterial case study. <i>Proteomics</i> , 2014, 14, 2780-2789.	2.2	21
8	Community-driven development for computational biology at Sprints, Hackathons and Codefests. <i>BMC Bioinformatics</i> , 2014, 15, S7.	2.6	42
9	At RTD – a comprehensive reference transcript dataset resource for accurate quantification of transcript-specific expression in <i>Arabidopsis thaliana</i> . <i>New Phytologist</i> , 2015, 208, 96-101.	7.3	50
10	Characterization of the Avian Trojan Gene Family Reveals Contrasting Evolutionary Constraints. <i>PLoS ONE</i> , 2015, 10, e0121672.	2.5	3
11	Transcriptome analysis of HIV-1 virus in understanding the effect of antiretroviral drugs (cART) and methamphetamine on the virus. , 2015, , .		0
12	GO2TR: a gene ontology-based workflow to generate target regions for target enrichment experiments. <i>Conservation Genetics Resources</i> , 2015, 7, 851-857.	0.8	5
13	A new look at the LTR retrotransposon content of the chicken genome. <i>BMC Genomics</i> , 2016, 17, 688.	2.8	35
14	An Improved microRNA Annotation of the Canine Genome. <i>PLoS ONE</i> , 2016, 11, e0153453.	2.5	20
15	A Tale of Tails: Dissecting the Enhancing Effect of Tailed Primers in Real-Time PCR. <i>PLoS ONE</i> , 2016, 11, e0164463.	2.5	6
16	Comparative genomics provides new insights into the diversity, physiology, and sexuality of the only industrially exploited tremellomycete: <i>Phaffia rhodozyma</i> . <i>BMC Genomics</i> , 2016, 17, 901.	2.8	35
17	SARVAVID. , 2016, , .		14
18	From sequence reads to evolutionary inferences. , 0, , 305-335.		0

#	ARTICLE	IF	CITATIONS
19	The draft genome of MD-2 pineapple using hybrid error correction of long reads. DNA Research, 2016, 23, 427-439.	3.4	35
20	Non-excitable fluorescent protein orthologs found in ctenophores. BMC Evolutionary Biology, 2016, 16, 167.	3.2	7
21	Aligning the unalignable: bacteriophage whole genome alignments. BMC Bioinformatics, 2016, 17, 30.	2.6	8
22	Visual programming for next-generation sequencing data analytics. BioData Mining, 2016, 9, 16.	4.0	14
23	The genome of the yellow potato cyst nematode, <i>Globodera rostochiensis</i> , reveals insights into the basis of parasitism and virulence. Genome Biology, 2016, 17, 124.	8.8	156
24	An introduction to plant phylogenomics with a focus on palms. Botanical Journal of the Linnean Society, 2016, 182, 234-255.	1.6	42
25	Organellar Genomes of White Spruce (<i>Picea glauca</i>): Assembly and Annotation. Genome Biology and Evolution, 2016, 8, 29-41.	2.5	46
26	Finding a partner in the ocean: molecular and evolutionary bases of the response to sexual cues in a planktonic diatom. New Phytologist, 2017, 215, 140-156.	7.3	115
27	A chromosome conformation capture ordered sequence of the barley genome. Nature, 2017, 544, 427-433.	27.8	1,365
28	De Novo Transcriptome Characterization of a Sterilizing Trematode Parasite (<i>Microphallus</i> sp.) from Two Species of New Zealand Snails. G3: Genes, Genomes, Genetics, 2017, 7, 871-880.	1.8	6
29	The sunflower genome provides insights into oil metabolism, flowering and Asterid evolution. Nature, 2017, 546, 148-152.	27.8	579
30	Seqping: gene prediction pipeline for plant genomes using self-training gene models and transcriptomic data. BMC Bioinformatics, 2017, 18, 1-7.	2.6	25
31	POTAGE: A Visualisation Tool for Speeding up Gene Discovery in Wheat. Scientific Reports, 2017, 7, 14315.	3.3	11
32	The genome sequence and insights into the immunogenetics of the bananaquit (Passeriformes: Coereba) Tj ETQq1.1.0.784314 rgBT /Dv	2.4	8
33	Lipid Metabolic Versatility in <i>Malassezia</i> spp. Yeasts Studied through Metabolic Modeling. Frontiers in Microbiology, 2017, 8, 1772.	3.5	31
34	Proteogenomics produces comprehensive and highly accurate protein-coding gene annotation in a complete genome assembly of <i>Malassezia sympodialis</i> . Nucleic Acids Research, 2017, 45, gkx006.	14.5	47
35	"Stealth dissemination" of macrophage-tumor cell fusions cultured from blood of patients with pancreatic ductal adenocarcinoma. PLoS ONE, 2017, 12, e0184451.	2.5	51
36	Plant-RRBS, a bisulfite and next-generation sequencing-based methylome profiling method enriching for coverage of cytosine positions. BMC Plant Biology, 2017, 17, 115.	3.6	13

#	ARTICLE	IF	CITATIONS
37	GFF3sort: a novel tool to sort GFF3 files for tabix indexing. BMC Bioinformatics, 2017, 18, 482.	2.6	6
38	Evolutionary thrift: mycobacteria repurpose plasmid diversity during adaptation of type VII secretion systems. Genome Biology and Evolution, 2017, 9, 398-413.	2.5	33
39	Northern Spotted Owl (<i>Strix occidentalis caurina</i>) Genome: Divergence with the Barred Owl (<i>Strix</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 2522-2545.	2.5	27
40	COGNATE: comparative gene annotation characterizer. BMC Genomics, 2017, 18, 535.	2.8	7
41	Fine-Scale Recombination Maps of Fungal Plant Pathogens Reveal Dynamic Recombination Landscapes and Intragenic Hotspots. Genetics, 2018, 208, 1209-1229.	2.9	61
42	Genome-resolved metagenomics identifies genetic mobility, metabolic interactions, and unexpected diversity in perchlorate-reducing communities. ISME Journal, 2018, 12, 1568-1581.	9.8	82
43	A Whole Genome Assembly of the Horn Fly, <i>Haematobia irritans</i> , and Prediction of Genes with Roles in Metabolism and Sex Determination. G3: Genes, Genomes, Genetics, 2018, 8, 1675-1686.	1.8	12
44	LTR_retriever: A Highly Accurate and Sensitive Program for Identification of Long Terminal Repeat Retrotransposons. Plant Physiology, 2018, 176, 1410-1422.	4.8	694
45	Comparative genomics of the wheat fungal pathogen <i>Pyrenophora tritici-repentis</i> reveals chromosomal variations and genome plasticity. BMC Genomics, 2018, 19, 279.	2.8	56
46	Improving the annotation of the <i>Heterorhabditis bacteriophora</i> genome. GigaScience, 2018, 7, .	6.4	18
47	Refined ab initio gene predictions of <i>Heterorhabditis bacteriophora</i> using RNA-seq. International Journal for Parasitology, 2018, 48, 585-590.	3.1	6
48	Universal correction of enzymatic sequence bias reveals molecular signatures of protein/DNA interactions. Nucleic Acids Research, 2018, 46, e9-e9.	14.5	39
49	TE-nester: a recursive software tool for structure-based discovery of nested transposable elements. , 2018, , .		4
50	DAWN: a resource for yielding insights into the diversity among wheat genomes. BMC Genomics, 2018, 19, 941.	2.8	23
51	Highly Continuous Genome Assembly of Eurasian Perch (<i>Perca fluviatilis</i>) Using Linked-Read Sequencing. G3: Genes, Genomes, Genetics, 2018, 8, 3737-3743.	1.8	42
52	Genomic distribution of a novel <i>Pyrenophora tritici-repentis</i> ToxA insertion element. PLoS ONE, 2018, 13, e0206586.	2.5	16
53	Firefly genomes illuminate parallel origins of bioluminescence in beetles. ELife, 2018, 7, .	6.0	108
54	Out of the Canals: A Draft Genome Assembly, Liver Transcriptome, and Nutrigenomics of the European Sardine, <i>Sardina pilchardus</i> . Genes, 2018, 9, 485.	2.4	30

#	ARTICLE	IF	CITATIONS
55	Genomics as a service: A joint computing and networking perspective. <i>Computer Networks</i> , 2018, 145, 27-51.	5.1	8
56	Integrating embryonic development and evolutionary history to characterize tentacle-specific cell types in a ctenophore. <i>Molecular Biology and Evolution</i> , 2018, 35, 2940-2956.	8.9	29
57	Phylogenomics reveals multiple losses of nitrogen-fixing root nodule symbiosis. <i>Science</i> , 2018, 361, .	12.6	339
58	Fern genomes elucidate land plant evolution and cyanobacterial symbioses. <i>Nature Plants</i> , 2018, 4, 460-472.	9.3	391
59	Transposable Element Genomic Fissuring in <i>Pyrenophora teres</i> Is Associated With Genome Expansion and Dynamics of Host-Pathogen Genetic Interactions. <i>Frontiers in Genetics</i> , 2018, 9, 130.	2.3	45
60	Molecular evolution of DNMT1 in vertebrates: Duplications in marsupials followed by positive selection. <i>PLoS ONE</i> , 2018, 13, e0195162.	2.5	14
61	Genomic signatures of mitonuclear coevolution across populations of <i>Tigriopus californicus</i> . <i>Nature Ecology and Evolution</i> , 2018, 2, 1250-1257.	7.8	154
62	Comparative genomics of the nonlegume <i>Parasponia</i> reveals insights into evolution of nitrogen-fixing rhizobium symbioses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E4700-E4709.	7.1	253
63	Related Endogenous Retrovirus-K Elements Harbor Distinct Protease Active Site Motifs. <i>Frontiers in Microbiology</i> , 2018, 9, 1577.	3.5	6
64	Insect Retroelements Provide Novel Insights into the Origin of Hepatitis B Viruses. <i>Molecular Biology and Evolution</i> , 2018, 35, 2254-2259.	8.9	13
65	The chromosome-scale reference genome of black pepper provides insight into piperine biosynthesis. <i>Nature Communications</i> , 2019, 10, 4702.	12.8	115
66	Orthologous nuclear markers and new transcriptomes that broadly cover the phylogenetic diversity of Acanthaceae. <i>Applications in Plant Sciences</i> , 2019, 7, e11290.	2.1	4
67	A Bidimensional Segregation Mode Maintains Symbiont Chromosome Orientation toward Its Host. <i>Current Biology</i> , 2019, 29, 3018-3028.e4.	3.9	7
68	Effector gene reshuffling involves dispensable mini-chromosomes in the wheat blast fungus. <i>PLoS Genetics</i> , 2019, 15, e1008272.	3.5	103
69	Recompleting the <i>Caenorhabditis elegans</i> genome. <i>Genome Research</i> , 2019, 29, 1009-1022.	5.5	108
70	The Impact of Protein Architecture on Adaptive Evolution. <i>Molecular Biology and Evolution</i> , 2019, 36, 2013-2028.	8.9	42
71	Coding palindromes in mitochondrial genes of Nematomorpha. <i>Nucleic Acids Research</i> , 2019, 47, 6858-6870.	14.5	8
72	Genetic Identification of Species Responsible for Depredation in Commercial and Recreational Fisheries. <i>North American Journal of Fisheries Management</i> , 2019, 39, 524-534.	1.0	18

#	ARTICLE	IF	CITATIONS
73	A High-Quality Grapevine Downy Mildew Genome Assembly Reveals Rapidly Evolving and Lineage-Specific Putative Host Adaptation Genes. <i>Genome Biology and Evolution</i> , 2019, 11, 954-969.	2.5	61
74	Long-Term Population Studies Uncover the Genome Structure and Genetic Basis of Xenobiotic and Host Plant Adaptation in the Herbivore <i>Tetranychus urticae</i> . <i>Genetics</i> , 2019, 211, 1409-1427.	2.9	70
75	Chromosome-scale genome assembly of kiwifruit <i>Actinidia eriantha</i> with single-molecule sequencing and chromatin interaction mapping. <i>GigaScience</i> , 2019, 8, .	6.4	65
76	Genomic content of a novel yeast species <i>Hanseniaspora gamundiae</i> sp. nov. from fungal stromata (Cyttaria) associated with a unique fermented beverage in Andean Patagonia, Argentina. <i>PLoS ONE</i> , 2019, 14, e0210792.	2.5	37
77	Mechanistic insights into the evolution of DUF26-containing proteins in land plants. <i>Communications Biology</i> , 2019, 2, 56.	4.4	75
78	Explore, edit and leverage genomic annotations using Python GTF toolkit. <i>Bioinformatics</i> , 2019, 35, 3487-3488.	4.1	12
79	High throughput genotyping of structural variations in a complex plant genome using an original Affymetrix [®] axion [®] array. <i>BMC Genomics</i> , 2019, 20, 848.	2.8	9
80	Benchmarking transposable element annotation methods for creation of a streamlined, comprehensive pipeline. <i>Genome Biology</i> , 2019, 20, 275.	8.8	579
81	VARUS: sampling complementary RNA reads from the sequence read archive. <i>BMC Bioinformatics</i> , 2019, 20, 558.	2.6	10
82	The C-Fern (<i>Ceratopteris richardii</i>) genome: insights into plant genome evolution with the first partial homosporous fern genome assembly. <i>Scientific Reports</i> , 2019, 9, 18181.	3.3	79
83	Variation in abundance of predicted resistance genes in the <i>Brassica oleracea</i> pangenome. <i>Plant Biotechnology Journal</i> , 2019, 17, 789-800.	8.3	92
84	Finding Nemo's Genes: A chromosome-scale reference assembly of the genome of the orange clownfish <i>Amphiprion percula</i> . <i>Molecular Ecology Resources</i> , 2019, 19, 570-585.	4.8	55
85	Comparative genomics of the major parasitic worms. <i>Nature Genetics</i> , 2019, 51, 163-174.	21.4	377
86	Long-Read Annotation: Automated Eukaryotic Genome Annotation Based on Long-Read cDNA Sequencing. <i>Plant Physiology</i> , 2019, 179, 38-54.	4.8	45
87	The GFF3toolkit: QC and Merge Pipeline for Genome Annotation. <i>Methods in Molecular Biology</i> , 2019, 1858, 75-87.	0.9	10
88	The draft genomes of five agriculturally important African orphan crops. <i>GigaScience</i> , 2019, 8, .	6.4	108
89	Bioinformatics of nanopore sequencing. <i>Journal of Human Genetics</i> , 2020, 65, 61-67.	2.3	28
90	Vegetative desiccation tolerance in the resurrection plant <i>Xerophyta humilis</i> has not evolved through reactivation of the seed canonical LAFL regulatory network. <i>Plant Journal</i> , 2020, 101, 1349-1367.	5.7	19

#	ARTICLE	IF	CITATIONS
91	Transcriptional changes in the aphid species <i>Myzus cerasi</i> under different host and environmental conditions. <i>Insect Molecular Biology</i> , 2020, 29, 271-282.	2.0	10
92	Draft Genomes of Two Artocarpus Plants, Jackfruit (<i>A. heterophyllus</i>) and Breadfruit (<i>A. altilis</i>). <i>Genes</i> , 2020, 11, 27.	2.4	30
93	Draft Genome Assembly of the Freshwater Apex Predator Wels Catfish (<i>Silurus glanis</i>) Using Linked-Read Sequencing. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3897-3906.	1.8	9
94	TE-greedy-nester: structure-based detection of LTR retrotransposons and their nesting. <i>Bioinformatics</i> , 2020, 36, 4991-4999.	4.1	11
95	Whole genome resequencing of four Italian sweet pepper landraces provides insights on sequence variation in genes of agronomic value. <i>Scientific Reports</i> , 2020, 10, 9189.	3.3	18
96	Genome Size Versus Genome Assemblies: Are the Genomes Truly Expanded in Polyploid Fungal Symbionts?. <i>Genome Biology and Evolution</i> , 2020, 12, 2384-2390.	2.5	6
97	Genomic and transcriptomic variation defines the chromosome-scale assembly of <i>Haemonchus contortus</i> , a model gastrointestinal worm. <i>Communications Biology</i> , 2020, 3, 656.	4.4	91
98	The Untapped Australasian Diversity of Astaxanthin-Producing Yeasts with Biotechnological Potential— <i>Phaffia australis</i> sp. nov. and <i>Phaffia tasmanica</i> sp. nov.. <i>Microorganisms</i> , 2020, 8, 1651.	3.6	9
99	Nucleotide diversity of functionally different groups of immune response genes in Old World camels based on newly annotated and reference-guided assemblies. <i>BMC Genomics</i> , 2020, 21, 606.	2.8	15
100	PacBio genome sequencing reveals new insights into the genomic organisation of the multi-copy <i>ToxB</i> gene of the wheat fungal pathogen <i>Pyrenophora tritici-repentis</i> . <i>BMC Genomics</i> , 2020, 21, 645.	2.8	15
101	Genome compartmentalization predates species divergence in the plant pathogen genus <i>Zymoseptoria</i> . <i>BMC Genomics</i> , 2020, 21, 588.	2.8	34
102	Genomic re-assessment of the transposable element landscape of the potato genome. <i>Plant Cell Reports</i> , 2020, 39, 1161-1174.	5.6	12
103	The genome evolution and domestication of tropical fruit mango. <i>Genome Biology</i> , 2020, 21, 60.	8.8	104
104	Can we use it? On the utility of de novo and reference-based assembly of Nanopore data for plant plastome sequencing. <i>PLoS ONE</i> , 2020, 15, e0226234.	2.5	33
105	Genome comparisons suggest an association between <i>Ceratocystis</i> host adaptations and effector clusters in unique transposable element families. <i>Fungal Genetics and Biology</i> , 2020, 143, 103433.	2.1	9
106	The genome of pest <i>Rhynchophorus ferrugineus</i> reveals gene families important at the plant-beetle interface. <i>Communications Biology</i> , 2020, 3, 323.	4.4	44
107	Into the wild: new yeast genomes from natural environments and new tools for their analysis. <i>FEMS Yeast Research</i> , 2020, 20, .	2.3	29
108	Chromosome-Level Assembly of the <i>Caenorhabditis remanei</i> Genome Reveals Conserved Patterns of Nematode Genome Organization. <i>Genetics</i> , 2020, 214, 769-780.	2.9	28

#	ARTICLE	IF	CITATIONS
109	Conservation and Divergence in the Meioocyte sRNAs of Arabidopsis, Soybean, and Cucumber. <i>Plant Physiology</i> , 2020, 182, 301-317.	4.8	13
110	The genome of <i>Draba nivalis</i> shows signatures of adaptation to the extreme environmental stresses of the Arctic. <i>Molecular Ecology Resources</i> , 2021, 21, 661-676.	4.8	14
111	Unique genomic traits for cold adaptation in <i>Naganishia vishniacii</i> , a polyextremophile yeast isolated from Antarctica. <i>FEMS Yeast Research</i> , 2021, 21, .	2.3	14
112	Whole-genome assembly and resequencing reveal genomic imprint and key genes of rapid domestication in narrow-leaved lupin. <i>Plant Journal</i> , 2021, 105, 1192-1210.	5.7	12
113	The digital biomarker discovery pipeline: An open-source software platform for the development of digital biomarkers using mHealth and wearables data. <i>Journal of Clinical and Translational Science</i> , 2021, 5, e19.	0.6	44
114	A Predictive Approach to Infer the Activity and Natural Variation of Retrotransposon Families in Plants. <i>Methods in Molecular Biology</i> , 2021, 2250, 1-14.	0.9	7
121	Comparative genomics of the coconut crab and other decapod crustaceans: exploring the molecular basis of terrestrial adaptation. <i>BMC Genomics</i> , 2021, 22, 313.	2.8	11
122	Impaired viral infection and reduced mortality of diatoms in iron-limited oceanic regions. <i>Nature Geoscience</i> , 2021, 14, 231-237.	12.9	17
123	The <i>Gossypium stocksii</i> genome as a novel resource for cotton improvement. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	8
125	Genome sequencing sheds light on the contribution of structural variants to <i>Brassica oleracea</i> diversification. <i>BMC Biology</i> , 2021, 19, 93.	3.8	41
126	Haplotype-resolved genome assembly enables gene discovery in the red palm weevil <i>Rhynchophorus ferrugineus</i> . <i>Scientific Reports</i> , 2021, 11, 9987.	3.3	20
127	Innate and Adaptive Immune Genes Associated with MERS-CoV Infection in Dromedaries. <i>Cells</i> , 2021, 10, 1291.	4.1	6
128	Chromosome-level genome assembly and manually-curated proteome of model necrotroph <i>Parastagonospora nodorum</i> Sn15 reveals a genome-wide trove of candidate effector homologs, and redundancy of virulence-related functions within an accessory chromosome. <i>BMC Genomics</i> , 2021, 22, 382.	2.8	12
129	The genome of the Pyrenean desman and the effects of bottlenecks and inbreeding on the genomic landscape of an endangered species. <i>Evolutionary Applications</i> , 2021, 14, 1898-1913.	3.1	11
130	Assembly and characterization of the genome of chard (<i>Beta vulgaris</i> ssp. <i>vulgaris</i> var. <i>cicla</i>). <i>Journal of Biotechnology</i> , 2021, 333, 67-76.	3.8	7
131	Sequence of the supernumerary B chromosome of maize provides insight into its drive mechanism and evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	25
133	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
134	A comprehensive annotation dataset of intact LTR retrotransposons of 300 plant genomes. <i>Scientific Data</i> , 2021, 8, 174.	5.3	14

#	ARTICLE	IF	CITATIONS
135	Distinct Retrotransposon Evolution Profile in the Genome of Rabbit (<i>Oryctolagus cuniculus</i>). <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	6
136	LGAAP: Leishmaniinae Genome Assembly and Annotation Pipeline. <i>Microbiology Resource Announcements</i> , 2021, 10, e0043921.	0.6	8
137	GenoVault: a cloud based genomics repository. <i>BioData Mining</i> , 2021, 14, 36.	4.0	0
138	Haplotype-resolved genome of diploid ginger (<i>Zingiber officinale</i>) and its unique gingerol biosynthetic pathway. <i>Horticulture Research</i> , 2021, 8, 189.	6.3	53
139	High-quality genome assembly of the soybean fungal pathogen <i>Cercospora kikuchii</i> . <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	5
140	Diversity and Paleodemography of the Addax (<i>Addax nasomaculatus</i>), a Saharan Antelope on the Verge of Extinction. <i>Genes</i> , 2021, 12, 1236.	2.4	8
142	Genome and transcriptome assemblies of the kuruma shrimp, <i>Marsupenaeus japonicus</i> . <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	20
145	Chromosome-scale genome sequencing, assembly and annotation of six genomes from subfamily Leishmaniinae. <i>Scientific Data</i> , 2021, 8, 234.	5.3	5
146	Chromosome-Level Genome Assembly and Annotation of the Fiber Flax (<i>Linum usitatissimum</i>) Genome. <i>Frontiers in Genetics</i> , 2021, 12, 735690.	2.3	15
147	Role of Dicer-Dependent RNA Interference in Regulating Mycoparasitic Interactions. <i>Microbiology Spectrum</i> , 2021, 9, e0109921.	3.0	12
148	Novel genome reveals susceptibility of popular gamebird, the red-legged partridge (<i>Alectoris rufa</i>). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50</i>	2.9	6
149	Genomic analysis unveils mechanisms of northward invasion and signatures of plateau adaptation in the Asian house rat. <i>Molecular Ecology</i> , 2021, 30, 6596-6610.	3.9	10
150	<i>De novo</i> genome assembly of the tobacco hornworm moth (<i>Manduca sexta</i>). <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	20
151	<i>De novo</i> whole-genome assembly and resequencing resources for the roan (<i>Hippotragus</i>). <i>Tj ETQq1 1 0.784314 rgBT /Overlock</i>	1.8	4
152	Finding and Characterizing Repeats in Plant Genomes. <i>Methods in Molecular Biology</i> , 2016, 1374, 293-337.	0.9	7
153	A high-quality genome assembly and annotation of the gray mangrove, <i>Avicennia marina</i> . <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	16
154	Transcriptome-wide expression profiling of <i>Sporothrix schenckii</i> yeast and mycelial forms and the establishment of the <i>Sporothrix</i> Genome DataBase. <i>Microbial Genomics</i> , 2020, 6, .	2.0	12
169	Combating a Global Threat to a Clonal Crop: Banana Black Sigatoka Pathogen <i>Pseudocercospora fijiensis</i> (Synonym <i>Mycosphaerella fijiensis</i>) Genomes Reveal Clues for Disease Control. <i>PLoS Genetics</i> , 2016, 12, e1005876.	3.5	77

#	ARTICLE	IF	CITATIONS
170	Occurrence of Isopenicillin-N-Synthase Homologs in Bioluminescent Ctenophores and Implications for Coelenterazine Biosynthesis. <i>PLoS ONE</i> , 2015, 10, e0128742.	2.5	21
171	Epigenetic silencing of V(D)J recombination is a major determinant for selective differentiation of mucosal-associated invariant t cells from induced pluripotent stem cells. <i>PLoS ONE</i> , 2017, 12, e0174699.	2.5	8
172	GFF3toEMBL: Preparing annotated assemblies for submission to EMBL. <i>Journal of Open Source Software</i> , 2016, 1, 80.	4.6	3
173	LTRpred: de novo annotation of intact retrotransposons. <i>Journal of Open Source Software</i> , 2020, 5, 2170.	4.6	17
174	The first Antechinus reference genome provides a resource for investigating the genetic basis of semelparity and age-related neuropathologies. <i>GigaByte</i> , 0, 2020, 1-22.	0.0	18
176	Genome streamlining in a minute herbivore that manipulates its host plant. <i>ELife</i> , 2020, 9, .	6.0	33
178	Genome report: a draft genome of <i>Alliaria petiolata</i> (garlic mustard) as a model system for invasion genetics. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	5
179	Taxus yunnanensis genome offers insights into gymnosperm phylogeny and taxol production. <i>Communications Biology</i> , 2021, 4, 1203.	4.4	15
181	Genome sequencing of turmeric provides evolutionary insights into its medicinal properties. <i>Communications Biology</i> , 2021, 4, 1193.	4.4	23
192	Applications of Supercomputers in Sequence Analysis and Genome Annotation. , 2019, , 625-652.		0
201	The <i>Gillenia trifoliata</i> genome reveals dynamics correlated with growth and reproduction in Rosaceae. <i>Horticulture Research</i> , 2021, 8, 233.	6.3	4
203	Integrated Genome-Scale Analysis and Northern Blot Detection of Retrotransposon siRNAs Across Plant Species. <i>Methods in Molecular Biology</i> , 2020, 2166, 387-411.	0.9	3
205	Applications of Supercomputers in Sequence Analysis and Genome Annotation. <i>Advances in Systems Analysis, Software Engineering, and High Performance Computing Book Series</i> , 0, , 149-175.	0.5	2
214	Comparative analysis of transposable elements provides insights into genome evolution in the genus <i>Camelus</i> . <i>BMC Genomics</i> , 2021, 22, 842.	2.8	4
217	Genome Assembly of Alfalfa Cultivar Zhongmu-4 and Identification of SNPs Associated with Agronomic Traits. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 14-28.	6.9	26
218	The highly continuous reference genome of a leaf-chimeric red pineapple (<i>Ananas comosus</i> var.) Tj ETQq1 1.0.784314 rgBT /Overlock 1.0.2022, 12, .	1.8	1
219	Finding and Characterizing Repeats in Plant Genomes. <i>Methods in Molecular Biology</i> , 2022, 2443, 327-385.	0.9	2
220	Chromosome restructuring and number change during the evolution of <i>Morus notabilis</i> and <i>Morus alba</i> . <i>Horticulture Research</i> , 2022, 9, .	6.3	16

#	ARTICLE	IF	CITATIONS
224	A large accessory genome and high recombination rates may influence global distribution and broad host range of the fungal plant pathogen <i>Claviceps purpurea</i> . <i>PLoS ONE</i> , 2022, 17, e0263496.	2.5	8
225	Comparative Population Genomics of Cryptic Speciation and Adaptive Divergence in Bicknell's and Gray-Cheeked Thrushes (<i>Aves: Catharus bicknelli</i> and <i>Catharus minimus</i>). <i>Genome Biology and Evolution</i> , 2022, 14, .	2.5	7
226	iLoci: robust evaluation of genome content and organization for provisional and mature genome assemblies. <i>NAR Genomics and Bioinformatics</i> , 2022, 4, lqac013.	3.2	0
227	The haplotype-resolved chromosome pairs of a heterozygous diploid African cassava cultivar reveal novel pan-genome and allele-specific transcriptome features. <i>GigaScience</i> , 2022, 11, .	6.4	29
228	Amplicon sequencing of <i>Fusarium</i> translation elongation factor 1 \pm reveals that soil communities of <i>Fusarium</i> species are resilient to disturbances caused by crop and tillage practices. <i>Phytobiomes Journal</i> , 0, , .	2.7	1
229	A genome assembly of the Atlantic chub mackerel (<i>Scomber colias</i>): a valuable teleost fishing resource. <i>GigaByte</i> , 0, 2022, 1-21.	0.0	3
230	Genomic insights into longan evolution from a chromosome-level genome assembly and population genomics of longan accessions. <i>Horticulture Research</i> , 2022, 9, .	6.3	14
231	Genome assembly of the JD17 soybean provides a new reference genome for comparative genomics. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	7
232	A chromosome-scale genome assembly of the false clownfish, <i>Amphiprion ocellaris</i> . <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	11
233	The genome sequence of the lesser marbled fritillary, <i>Brenthis ino</i> , and evidence for a segregating neo-Z chromosome. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	8
234	Genome assembly of the roundjaw bonefish (<i>Albula glossodonta</i>), a vulnerable circumtropical sportfish. <i>GigaByte</i> , 0, 2022, 1-29.	0.0	1
235	TransposonUltimate: software for transposon classification, annotation and detection. <i>Nucleic Acids Research</i> , 2022, 50, e64-e64.	14.5	30
237	Chromosome-Level Reference Genomes for Two Strains of <i>Caenorhabditis briggsae</i> : An Improved Platform for Comparative Genomics. <i>Genome Biology and Evolution</i> , 2022, 14, .	2.5	20
242	Genome assembly of <i>Danaus chrysippus</i> and comparison with the Monarch <i>Danaus plexippus</i> . <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	8
243	A high-quality genome assembly and annotation of the dark-eyed junco <i>Junco hyemalis</i> , a recently diversified songbird. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	5
244	High-quality chromosome-scale de novo assembly of the <i>Paspalum notatum</i> "Flugge" genome. <i>BMC Genomics</i> , 2022, 23, 293.	2.8	1
253	Identifying small RNAs and Analyzing Their Association with Gene Expression Using Isolated Arabidopsis Male Meiocytes. <i>Methods in Molecular Biology</i> , 2022, 2484, 23-41.	0.9	0
254	The genome of the sparganosis tapeworm <i>Spirometra erinaceieuropaei</i> isolated from the biopsy of a migrating brain lesion. <i>Genome Biology</i> , 2014, 15, 510.	9.6	15

#	ARTICLE	IF	CITATIONS
255	Near Chromosome-Level Genome Assembly and Annotation of <i>Rhodotorula babjevae</i> Strains Reveals High Intraspecific Divergence. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 323.	3.5	1
256	Chromosomal rearrangements with stable repertoires of genes and transposable elements in an invasive forest-pathogenic fungus. , 0, 2, .		1
257	Assessing and assuring interoperability of a genomics file format. <i>Bioinformatics</i> , 2022, 38, 3327-3336.	4.1	3
259	TextFormats: Simplifying the definition and parsing of text formats in bioinformatics. <i>PLoS ONE</i> , 2022, 17, e0268910.	2.5	0
260	Triobinned genomes of the woodrats <i>Neotoma bryanti</i> and <i>Neotoma lepida</i> reveal novel gene islands and rapid copy number evolution of xenobiotic metabolizing genes. <i>Molecular Ecology Resources</i> , 2022, 22, 2713-2731.	4.8	13
261	A High-Quality Genome of the Dobsonfly <i>Neoneuromus Ignobilis</i> Reveals Molecular Convergences in Aquatic Insects. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
262	Characterising genome architectures using genome decomposition analysis. <i>BMC Genomics</i> , 2022, 23, .	2.8	2
263	De Novo Assembly of <i>Plasmodium knowlesi</i> Genomes From Clinical Samples Explains the Counterintuitive Intrachromosomal Organization of Variant SICAvir and kir Multiple Gene Family Members. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	3
266	Genome of <i>Lindera glauca</i> provides insights into the evolution of biosynthesis genes for aromatic compounds. <i>IScience</i> , 2022, 25, 104761.	4.1	2
268	Evolution of woody plants to the land-sea interface – The atypical genomic features of mangroves with atypical phenotypic adaptation. <i>Molecular Ecology</i> , 2023, 32, 1351-1365.	3.9	8
269	Spruce gigabased genomes: structurally similar yet distinctive with differentially expanding gene families and rapidly evolving genes. <i>Plant Journal</i> , 2022, 111, 1469-1485.	5.7	17
270	Automatic curation of LTR retrotransposon libraries from plant genomes through machine learning. <i>Journal of Integrative Bioinformatics</i> , 2022, .	1.5	1
272	Transcriptome variation in human tissues revealed by long-read sequencing. <i>Nature</i> , 2022, 608, 353-359.	27.8	103
273	The genome sequence of the scarce swallowtail, <i>Iphiclides podalirius</i> . <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	5
275	A high-quality genome of the dobsonfly <i>Neoneuromus ignobilis</i> reveals molecular convergences in aquatic insects. <i>Genomics</i> , 2022, 114, 110437.	2.9	0
276	Genome Assembly of the Polyclad Flatworm <i>Prostheceraeus crozieri</i> . <i>Genome Biology and Evolution</i> , 2022, 14, .	2.5	3
277	Local assembly of long reads enables phylogenomics of transposable elements in a polyploid cell line. <i>Nucleic Acids Research</i> , 2022, 50, e124-e124.	14.5	8
280	The reference genome of the Vernal Pool Tadpole Shrimp, <i>Lepidurus packardii</i> . <i>Journal of Heredity</i> , 0, , .	2.4	1

#	ARTICLE	IF	CITATIONS
281	A draft reference genome of the Vernal Pool Fairy Shrimp, <i>Branchinecta lynchi</i> . Journal of Heredity, 0, , .	2.4	0
282	The genome and lifestage-specific transcriptomes of a plant-parasitic nematode and its host reveal susceptibility genes involved in trans-kingdom synthesis of vitamin B5. Nature Communications, 2022, 13, .	12.8	28
283	Genome Sequence of the Diploid Yeast <i>Debaryomyces hansenii</i> TMW 3.1188. Microbiology Resource Announcements, 2022, 11, .	0.6	2
284	A chromosome-level reference genome for the Versatile Fairy Shrimp, <i>Branchinecta lindahli</i> . Journal of Heredity, 0, , .	2.4	0
286	Eusocial Transition in Blattodea: Transposable Elements and Shifts of Gene Expression. Genes, 2022, 13, 1948.	2.4	2
288	Rounding up the annual ryegrass genome: High-quality reference genome of <i>Lolium rigidum</i> . Frontiers in Genetics, 0, 13, .	2.3	9
289	A highly contiguous genome assembly of red perilla (<i>Perilla frutescens</i>) domesticated in Japan. DNA Research, 2023, 30, .	3.4	7
291	Jack of all trades: Genome assembly of Wild Jack and comparative genomics of <i>Artocarpus</i> . Frontiers in Plant Science, 0, 13, .	3.6	1
292	Global phylogenomic novelty of the Cas1 gene from hot spring microbial communities. Frontiers in Microbiology, 0, 13, .	3.5	0
293	An improved assembly of the "Cascade" hop (<i>Humulus lupulus</i>) genome uncovers signatures of molecular evolution and refines time of divergence estimates for the Cannabaceae family. Horticulture Research, 2023, 10, .	6.3	2
295	Biased mutations and gene losses underlying diploidization of the tetraploid broomcorn millet genome. Plant Journal, 2023, 113, 787-801.	5.7	4
296	The chromosome-scale genome assembly of the yellowtail clownfish <i>Amphiprion clarkii</i> provides insights into the melanic pigmentation of anemonefish. G3: Genes, Genomes, Genetics, 2023, 13, .	1.8	4
297	Phylogenomic resolution of order- and family-level monocot relationships using 602 single-copy nuclear genes and 1375 BUSCO genes. Frontiers in Plant Science, 0, 13, .	3.6	10
298	PlantTribes2: Tools for comparative gene family analysis in plant genomics. Frontiers in Plant Science, 0, 13, .	3.6	5
299	Chromosome-level genome assembly and population genomic resource to accelerate orphan crop lablab breeding. Nature Communications, 2023, 14, .	12.8	10
300	Genomic, transcriptomic, and metabolomic analysis of <i>Oldenlandia corymbosa</i> reveals the biosynthesis and mode of action of anti-cancer metabolites. Journal of Integrative Plant Biology, 2023, 65, 1442-1466.	8.5	7
302	An improved assembly of the pearl millet reference genome using Oxford Nanopore long reads and optical mapping. G3: Genes, Genomes, Genetics, 2023, 13, .	1.8	1
305	RNA silencing proteins and small RNAs in oomycete plant pathogens and biocontrol agents. Frontiers in Microbiology, 0, 14, .	3.5	2

#	ARTICLE	IF	CITATIONS
308	Whole genome assemblies of <i>Zophobas morio</i> and <i>Tenebrio molitor</i> . G3: Genes, Genomes, Genetics, 2023, 13, .	1.8	8
309	Population genomic analysis provides evidence of the past success and future potential of South China tiger captive conservation. BMC Biology, 2023, 21, .	3.8	3
310	A network of DZF proteins controls alternative splicing regulation and fidelity. Nucleic Acids Research, 2023, 51, 6411-6429.	14.5	2
311	A high-quality assembled genome of a representative peach landrace, "Feichenghongli"™, and analysis of distinct late florescence and narrow leaf traits. BMC Plant Biology, 2023, 23, .	3.6	0
312	High-quality chromosome-level de novo assembly of the <i>Trifolium repens</i> . BMC Genomics, 2023, 24, .	2.8	3
313	Circular RNAs modulate the floral fate acquisition in soybean shoot apical meristem. BMC Plant Biology, 2023, 23, .	3.6	3
315	Assembly and comparative genome analysis of a Patagonian <i>Aureobasidium pullulans</i> isolate reveals unexpected intraspecific variation. Yeast, 2023, 40, 197-213.	1.7	0
318	The <i>Metasequoia</i> genome and evolutionary relationships among redwoods. Plant Communications, 2023, 4, 100643.	7.7	4
320	High-Quality Genome Assembly and Genome-Wide Association Study of Male Sterility Provide Resources for Flax Improvement. Plants, 2023, 12, 2773.	3.5	2
321	Genomic Analysis of <i>Yersinia pestis</i> Strains from Brazil: Search for Virulence Factors and Association with Epidemiological Data. Pathogens, 2023, 12, 991.	2.8	0
322	LoCoLotive: In silico mining for low-copy nuclear loci based on target capture probe sets and arbitrary reference genomes. Applications in Plant Sciences, 2023, 11, .	2.1	0
324	Deep serological profiling of the <i>Trypanosoma cruzi</i> TSSA antigen reveals different epitopes and modes of recognition by Chagas disease patients. PLoS Neglected Tropical Diseases, 2023, 17, e0011542.	3.0	1
325	Genome mining shows that retroviruses are pervasively invading vertebrate genomes. Nature Communications, 2023, 14, .	12.8	2
326	Novel and improved <i>Caenorhabditis briggsae</i> gene models generated by community curation. BMC Genomics, 2023, 24, .	2.8	4
327	A haplotype resolved chromosome-scale assembly of North American wild apple <i>Malus fusca</i> and comparative genomics of the fire blight <i>Mfu10</i> locus. Plant Journal, 2023, 116, 989-1002.	5.7	2
329	The first high-quality genome assembly and annotation of <i>Patiria pectinifera</i> . Scientific Data, 2023, 10, .	5.3	0
330	High-quality genome of a pioneer mangrove <i>Laguncularia racemosa</i> explains its advantages for intertidal zone reforestation. Molecular Ecology Resources, 0, , .	4.8	1
331	<i>Sophora</i> genomes provide insight into the evolution of alkaloid metabolites along with small-scale gene duplication. BMC Genomics, 2023, 24, .	2.8	0

#	ARTICLE	IF	CITATIONS
332	Genome sequencing of <i>Syzygium cumini</i> (jamun) reveals adaptive evolution in secondary metabolism pathways associated with its medicinal properties. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	1
335	Do chromosome rearrangements fix by genetic drift or natural selection? Insights from <i>Brenthis</i> butterflies. <i>Molecular Ecology</i> , 0, , .	3.9	3
336	Plants acquired mitochondrial linear plasmids horizontally from fungi likely during the conquest of land. <i>Mobile DNA</i> , 2023, 14, .	3.6	0
338	Dietary Habits of Hardhead (<i>Ariopsis felis</i>) and Gafftopsail (<i>Bagre marinus</i>) Catfish Revealed through DNA Barcoding of Stomach Contents. <i>Fishes</i> , 2023, 8, 539.	1.7	0
339	Representing true plant genomes: haplotype-resolved hybrid pepper genome with trio-binning. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	0
340	Introduction of Plant Transposon Annotation for Beginners. <i>Biology</i> , 2023, 12, 1468.	2.8	0
341	Structural and Functional Annotation of the Wheat Genome. <i>Compendium of Plant Genomes</i> , 2024, , 51-73.	0.5	0
342	Space Efficient Sequence Alignment for SRAM-Based Computing: X-Drop on the Graphcore IPU. , 2023, , .		0
343	Two novel <i>Bartonella</i> (sub)species isolated from edible dormice (<i>Glis glis</i>): hints of cultivation stress-induced genomic changes. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	0
347	Comparative analysis of <i>Lithocarpus</i> chloroplast genomes reveals candidate DNA barcoding loci. <i>IOP Conference Series: Earth and Environmental Science</i> , 2023, 1271, 012083.	0.3	0
348	Seagrass genomes reveal ancient polyploidy and adaptations to the marine environment. <i>Nature Plants</i> , 2024, 10, 240-255.	9.3	0
349	Near telomere-to-telomere genome of the model plant <i>Physcomitrium patens</i> . <i>Nature Plants</i> , 2024, 10, 327-343.	9.3	1
351	Revisiting genomes of non-model species with long reads yields new insights into their biology and evolution. <i>Frontiers in Genetics</i> , 0, 15, .	2.3	0
352	Chromosome-level genome assembly of the silver pomfret <i>Pampus argenteus</i> . <i>Scientific Data</i> , 2024, 11, .	5.3	0
353	Evolution of Endogenous Retroviruses in the Subfamily of Caprinae. <i>Viruses</i> , 2024, 16, 398.	3.3	0