# De novo identification of repeat families in large genom

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Citation Report

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Combined Evidence Annotation of Transposable Elements in Genome Sequences. PLoS Computational Biology, 2005, 1, e22. | 1.5 | 347 |
| 2 | Orthologous repeats and mammalian phylogenetic inference. Genome Research, 2005, 15, 998-1006. | 2.4 | 37 |
| 3 | Discovery of Repetitive Patterns in DNA with Accurate Boundaries. , 0, , . | | 8 |
| 4 | Comparison of dot chromosome sequences from D. melanogaster and D. virilisreveals an enrichment of DNA transposon sequences in heterochromatic domains. Genome Biology, 2006, 7, R15. | 3.8 | 50 |
| 5 | Identifying repeat domains in large genomes. Genome Biology, 2006, 7, R7. | 13.9 | 31 |
| 6 | Cluster and Grid Based Classification of Transposable Elements in Eukaryotic Genomes. , 2006, , . | | 6 |
| 7 | Novel porcine repetitive elements. BMC Genomics, 2006, 7, 304. | 1.2 | 7 |
| 8 | Morphological Characters from the Genome: SINE Insertion Polymorphism and Phylogenies. Genome Dynamics and Stability, 2006, , 45-75. | 1.1 | 2 |
| 9 | PLOTREP: a web tool for defragmentation and visual analysis of dispersed genomic repeats. Nucleic Acids Research, 2006, 34, W708-W713. | 6.5 | 17 |
| 10 | DECOMPOSITION OF OVERLAPPING PATTERNS BY CUMULATIVE LOCAL CROSS-CORRELATION. Journal of Bioinformatics and Computational Biology, 2006, 04, 571-587. | 0.3 | 0 |
| 11 | Microinversions in mammalian evolution. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 19824-19829. | 3.3 | 36 |
| 12 | Domain organization within repeated DNA sequences: application to the study of a family of transposable elements. Bioinformatics, 2006, 22, 1948-1954. | 1.8 | 12 |
| 13 | HomologMiner: looking for homologous genomic groups in whole genomes. Bioinformatics, 2007, 23, 917-925. | 1.8 | 7 |
| 14 | Repseek, a tool to retrieve approximate repeats from large DNA sequences. Bioinformatics, 2007, 23, 119-121. | 1.8 | 69 |
| 15 | Discovering and detecting transposable elements in genome sequences. Briefings in Bioinformatics, 2007, 8, 382-392. | 3.2 | 189 |
| 16 | Evolutionary dynamics of transposable elements in the short-tailed opossum Monodelphis domestica. Genome Research, 2007, 17, 992-1004. | 2.4 | 137 |
| 17 | A study of the repetitive structure and distribution of short motifs in human genomic sequences. International Journal of Bioinformatics Research and Applications, 2007, 3, 523. | 0.1 | 5 |
| 18 | Dothideomyceteâ€“Plant Interactions Illuminated by Genome Sequencing and EST Analysis of the Wheat Pathogen Stagonospora nodorum. Plant Cell, 2007, 19, 3347-3368. | 3.1 | 235 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | A Multiscale Model for Efficient Simulation of a Membrane Bound Viral Fusion Peptide. , 2007, , . | | 2 |
| 20 | Micro-repetitive Structure of Genomic Sequences and the Identification of Ancient Repeat Elements. , 2007, , . | | 6 |
| 21 | Genome Assembly, Rearrangement, and Repeats. Chemical Reviews, 2007, 107, 3391-3406. | 23.0 | 23 |
| 22 | Comparative genomic analysis of three Leishmania species that cause diverse human disease. Nature Genetics, 2007, 39, 839-847. | 9.4 | 648 |
| 23 | The grapevine genome sequence suggests ancestral hexaploidization in major angiosperm phyla. Nature, 2007, 449, 463-467. | 13.7 | 3,384 |
| 24 | RepSeq â€“ A database of amino acid repeats present in lower eukaryotic pathogens. BMC Bioinformatics, 2007, 8, 122. | 1.2 | 28 |
| 25 | Diversity and structure of PIF/Harbinger-like elements in the genome of Medicago truncatula. BMC Genomics, 2007, 8, 409. | 1.2 | 25 |
| 26 | De novo identification of LTR retrotransposons in eukaryotic genomes. BMC Genomics, 2007, 8, 90. | 1.2 | 73 |
| 27 | Schistosoma mansoni genome: Closing in on a final gene set. Experimental Parasitology, 2007, 117, 225-228. | 0.5 | 41 |
| 28 | Computational Approaches and Tools Used in Identification of Dispersed Repetitive DNA Sequences. Tropical Plant Biology, 2008, 1, 85-96. | 1.0 | 52 |
| 29 | Genome-Wide Analysis of Repetitive Elements in Papaya. Tropical Plant Biology, 2008, 1, 191-201. | 1.0 | 24 |
| 30 | An automated, high-throughput sequence read classification pipeline for preliminary genome characterization. Analytical Biochemistry, 2008, 373, 78-87. | 1.1 | 5 |
| 31 | Identification of repeat structure in large genomes using repeat probability clouds. Analytical Biochemistry, 2008, 380, 77-83. | 1.1 | 51 |
| 32 | The draft genome of the transgenic tropical fruit tree papaya (Carica papaya Linnaeus). Nature, 2008, 452, 991-996. | 13.7 | 964 |
| 33 | RIPCAL: a tool for alignment-based analysis of repeat-induced point mutations in fungal genomic sequences. BMC Bioinformatics, 2008, 9, 478. | 1.2 | 151 |
| 34 | Discovering relationships among dispersed repeats using spatial association rule mining. BMC Bioinformatics, 2008, 9, . | 1.2 | 1 |
| 35 | Analysis of 90 Mb of the potato genome reveals conservation of gene structures and order with tomato but divergence in repetitive sequence composition. BMC Genomics, 2008, 9, 286. | 1.2 | 37 |
| 36 | A new method to compute K-mer frequencies and its application to annotate large repetitive plant genomes. BMC Genomics, 2008, 9, 517. | 1.2 | 214 |

| # | Article | IF | Citations |
|---|---|---|---|
| 37 | Insights into the Musa genome: Syntenic relationships to rice and between Musa species. BMC Genomics, 2008, 9, 58. | 1.2 | 105 |
| 38 | Genome wide survey, discovery and evolution of repetitive elements in three Entamoeba species. BMC Genomics, 2008, 9, 595. | 1.2 | 53 |
| 39 | Analysis of repetitive DNA distribution patterns in the Tribolium castaneum genome. Genome Biology, 2008, 9, R61. | 13.9 | 50 |
| 40 | Empirical comparison of ab initio repeat finding programs. Nucleic Acids Research, 2008, 36, 2284-2294. | 6.5 | 265 |
| 41 | TEnest: Automated Chronological Annotation and Visualization of Nested Plant Transposable Elements. Plant Physiology, 2008, 146, 45-59. | 2.3 | 61 |
| 42 | Enredo and Pecan: Genome-wide mammalian consistency-based multiple alignment with paralogs. Genome Research, 2008, 18, 1814-1828. | 2.4 | 249 |
| 43 | A Snapshot of the Emerging Tomato Genome Sequence. Plant Genome, 2009, 2, . | 1.6 | 73 |
| 44 | Evolutionary Conservation of Orthoretroviral Long Terminal Repeats (LTRs) and ab initio Detection of Single LTRs in Genomic Data. PLoS ONE, 2009, 4, e5179. | 1.1 | 28 |
| 45 | An Adaptive Suffix Tree Based Algorithm for Repeats Recognition in a DNA Sequence. , 2009, , . | | 3 |
| 46 | Characterization and distribution of retrotransposons and simple sequence repeats in the bovine genome. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 12855-12860. | 3.3 | 108 |
| 47 | Finding genes in Schistosoma japonicum: annotating novel genomes with help of extrinsic evidence. Nucleic Acids Research, 2009, 37, e52-e52. | 6.5 | 13 |
| 48 | Exploring Repetitive DNA Landscapes Using REPCLASS, a Tool That Automates the Classification of Transposable Elements in Eukaryotic Genomes. Genome Biology and Evolution, 2009, 1, 205-220. | 1.1 | 102 |
| 49 | RepPop: a database for repetitive elements in Populus trichocarpa. BMC Genomics, 2009, 10, 14. | 1.2 | 30 |
| 50 | Genome-wide profiling of Populus small RNAs. BMC Genomics, 2009, 10, 620. | 1.2 | 90 |
| 51 | The Schistosoma japonicum genome reveals features of hostâ€“parasite interplay. Nature, 2009, 460, 345-351. | 13.7 | 635 |
| 52 | The genome of the blood fluke Schistosoma mansoni. Nature, 2009, 460, 352-358. | 13.7 | 945 |
| 53 | The genome of the cucumber, Cucumis sativus L.. Nature Genetics, 2009, 41, 1275-1281. | 9.4 | 1,317 |
| 54 | Genesis, effects and fates of repeats in prokaryotic genomes. FEMS Microbiology Reviews, 2009, 33, 539-571. | 3.9 | 137 |

| # | Article | IF | Citations |
|---|---|---|---|
| 55 | TEclassâ€"a tool for automated classification of unknown eukaryotic transposable elements. Bioinformatics, 2009, 25, 1329-1330. | 1.8 | 254 |
| 56 | The DAWGPAWS pipeline for the annotation of genes and transposable elements in plant genomes. Plant Methods, 2009, 5, 8. | 1.9 | 21 |
| 57 | Genomic and genetic analyses of diversity and plant interactions of Pseudomonas fluorescens. Genome Biology, 2009, 10, R51. | 13.9 | 370 |
| 58 | A Novel Heuristic for Local Multiple Alignment of Interspersed DNA Repeats. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2009, 6, 180-189. | 1.9 | 14 |
| 59 | High tandem repeat content in the genome of the short-lived annual fish Nothobranchius furzeri: a new vertebrate model for aging research. Genome Biology, 2009, 10, R16. | 13.9 | 87 |
| 60 | Using RepeatMasker to Identify Repetitive Elements in Genomic Sequences. Current Protocols in Bioinformatics, 2009, 25, Unit 4.10. | 25.8 | 1,548 |
| 61 | An algorithm for the reconstruction of consensus sequences of ancient segmental duplications and transposon copies in eukaryotic genomes. International Journal of Bioinformatics Research and Applications, 2010, 6, 147. | 0.1 | 3 |
| 62 | ModuleOrganizer: detecting modules in families of transposable elements. BMC Bioinformatics, 2010, 11, 474. | 1.2 | 6 |
| 63 | Identifying repeats and transposable elements in sequenced genomes: how to find your way through the dense forest of programs. Heredity, 2010, 104, 520-533. | 1.2 | 194 |
| 64 | Draft genome sequence of the oilseed species Ricinus communis. Nature Biotechnology, 2010, 28, 951-956. | 9.4 | 449 |
| 65 | PiggyBac-ing on a Primate Genome: Novel Elements, Recent Activity and Horizontal Transfer. Genome Biology and Evolution, 2010, 2, 293-303. | 1.1 | 32 |
| 66 | Evolution of a Distinct Genomic Domain in Drosophila: Comparative Analysis of the Dot Chromosome in Drosophila melanogaster and Drosophila virilis. Genetics, 2010, 185, 1519-1534. | 1.2 | 34 |
| 67 | Scaffolding a Caenorhabditis nematode genome with RNA-seq. Genome Research, 2010, 20, 1740-1747. | 2.4 | 83 |
| 68 | Whole-Genome and Chromosome Evolution Associated with Host Adaptation and Speciation of the Wheat Pathogen Mycosphaerella graminicola. PLoS Genetics, 2010, 6, e1001189. | 1.5 | 142 |
| 69 | Multi-Platform Next-Generation Sequencing of the Domestic Turkey (Meleagris gallopavo): Genome Assembly and Analysis. PLoS Biology, 2010, 8, e1000475. | 2.6 | 348 |
| 70 | RepFrag. , 2010, , . | | 0 |
| 71 | Human endogenous retrovirus K14C drove genomic diversification of the Y chromosome during primate evolution. Journal of Human Genetics, 2010, 55, 717-725. | 1.1 | 8 |
| 72 | The Genome of Naegleria gruberi Illuminates Early Eukaryotic Versatility. Cell, 2010, 140, 631-642. | 13.5 | 399 |

| # | Article | IF | Citations |
|---|---|---|---|
| 73 | Genomic characterization of the Yersinia genus. Genome Biology, 2010, 11, R1. | 13.9 | 103 |
| 74 | Population genomic sequencing of Coccidioides fungi reveals recent hybridization and transposon control. Genome Research, 2010, 20, 938-946. | 2.4 | 166 |
| 75 | Identification and quantification of abundant species from pyrosequences of 16S rRNA by consensus alignment. , 2010, 2010, 153-157. | | 83 |
| 76 | The complexity of Rhipicephalus (Boophilus) microplus genome characterised through detailed analysis of two BAC clones. BMC Research Notes, 2011, 4, 254. | 0.6 | 6 |
| 77 | 9 Genomic and Comparative Analysis of the Class Dothideomycetes. , 2011, , 205-229. | | 5 |
| 78 | The draft genome of the carcinogenic human liver fluke Clonorchis sinensis. Genome Biology, 2011, 12, R107. | 13.9 | 183 |
| 79 | Genome sequence of the stramenopile Blastocystis, a human anaerobic parasite. Genome Biology, 2011, 12, R29. | 13.9 | 159 |
| 80 | A cost-effective and universal strategy for complete prokaryotic genome sequencing proposed by computer simulation. Genome Biology, 2011, 12, . | 13.9 | 1 |
| 81 | Endophytic Life Strategies Decoded by Genome and Transcriptome Analyses of the Mutualistic Root Symbiont Piriformospora indica. PLoS Pathogens, 2011, 7, e1002290. | 2.1 | 361 |
| 82 | Considering Transposable Element Diversification in De Novo Annotation Approaches. PLoS ONE, 2011, 6, e16526. | 1.1 | 477 |
| 83 | Discovery of Highly Divergent Repeat Landscapes in Snake Genomes Using High-Throughput Sequencing. Genome Biology and Evolution, 2011, 3, 641-653. | 1.1 | 87 |
| 84 | The Evolution and Diversity of DNA Transposons in the Genome of the Lizard Anolis carolinensis. Genome Biology and Evolution, 2011, 3, 1-14. | 1.1 | 39 |
| 85 | MINING APPROXIMATE REPEATING PATTERNS FROM SEQUENCE DATA WITH GAP CONSTRAINTS. Computational Intelligence, 2011, 27, 336-362. | 2.1 | 5 |
| 86 | Full-length transcriptome assembly from RNA-Seq data without a reference genome. Nature Biotechnology, 2011, 29, 644-652. | 9.4 | 17,264 |
| 87 | Mutation detection in plasmidâ€based biopharmaceuticals. Biotechnology Journal, 2011, 6, 378-391. | 1.8 | 4 |
| 88 | Ascaris suum draft genome. Nature, 2011, 479, 529-533. | 13.7 | 246 |
| 89 | Bioinformatics and genomic analysis of transposable elements in eukaryotic genomes. Chromosome Research, 2011, 19, 787-808. | 1.0 | 49 |
| 90 | Identification, variation and transcription of pneumococcal repeat sequences. BMC Genomics, 2011, 12, 120. | 1.2 | 48 |

| # | Article | IF | Citations |
|---|---|---|---|
| 91 | Genomic insight into the common carp (Cyprinus carpio) genome by sequencing analysis of BAC-end sequences. BMC Genomics, 2011, 12, 188. | 1.2 | 56 |
| 92 | Determination of the melon chloroplast and mitochondrial genome sequences reveals that the largest reported mitochondrial genome in plants contains a significant amount of DNA having a nuclear origin. BMC Genomics, 2011, 12, 424. | 1.2 | 118 |
| 93 | RNA-Seq improves annotation of protein-coding genes in the cucumber genome. BMC Genomics, 2011, 12, 540. | 1.2 | 232 |
| 94 | In search of lost trajectories. Mobile Genetic Elements, 2011, 1, 151-154. | 1.8 | 4 |
| 95 | Discovery of the First Insect Nidovirus, a Missing Evolutionary Link in the Emergence of the Largest RNA Virus Genomes. PLoS Pathogens, 2011, 7, e1002215. | 2.1 | 169 |
| 96 | The genome of the leaf-cutting antAcromyrmex echinatiorsuggests key adaptations to advanced social life and fungus farming. Genome Research, 2011, 21, 1339-1348. | 2.4 | 210 |
| 97 | Restless Genomes. Advances in Genetics, 2011, 73, 219-262. | 0.8 | 19 |
| 98 | Applied Genomics: Data Mining Reveals Species-Specific Malaria Diagnostic Targets More Sensitive than 18S rRNA. Journal of Clinical Microbiology, 2011, 49, 2411-2418. | 1.8 | 74 |
| 99 | Progress towards a reference genome for sunflower. Botany, 2011, 89, 429-437. | 0.5 | 67 |
| 100 | Genome and transcriptome analyses of the mountain pine beetle-fungal symbiont Grosmannia clavigera , a lodgepole pine pathogen. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 2504-2509. | 3.3 | 218 |
| 101 | Short- and Long-term Evolutionary Dynamics of Bacterial Insertion Sequences: Insights from Wolbachia Endosymbionts. Genome Biology and Evolution, 2011, 3, 1175-1186. | 1.1 | 55 |
| 102 | The Genome Sequence of the Leaf-Cutter Ant Atta cephalotes Reveals Insights into Its Obligate Symbiotic Lifestyle. PLoS Genetics, 2011, 7, e1002007. | 1.5 | 231 |
| 103 | Repetitive Elements May Comprise Over Two-Thirds of the Human Genome. PLoS Genetics, 2011, 7, e1002384. | 1.5 | 907 |
| 104 | Diverse Lifestyles and Strategies of Plant Pathogenesis Encoded in the Genomes of Eighteen Dothideomycetes Fungi. PLoS Pathogens, 2012, 8, e1003037. | 2.1 | 595 |
| 105 | Anonymous nuclear loci in non-model organisms: making the most of high-throughput genome surveys. Bioinformatics, 2012, 28, 1807-1810. | 1.8 | 21 |
| 106 | Draft Genome Sequence of Salt-Tolerant Yeast Debaryomyces hansenii var. hansenii MTCC 234. Eukaryotic Cell, 2012, 11, 961-962. | 3.4 | 17 |
| 107 | Slow DNA Loss in the Gigantic Genomes of Salamanders. Genome Biology and Evolution, 2012, 4, 1340-1348. | 1.1 | 55 |
| 108 | Identification of transposable elements of the giant panda (Ailuropoda melanoleuca) genome. , 2012, , . | | 0 |

| # | Article | IF | Citations |
|---|---|---|---|
| 109 | Transposon-Derived and Satellite-Derived Repetitive Sequences Play Distinct Functional Roles in Mammalian Intron Size Expansion. Evolutionary Bioinformatics, 2012, 8, EBO.S9758. | 0.6 | 17 |
| 110 | Rapid divergence and expansion of the X chromosome in papaya. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 13716-13721. | 3.3 | 52 |
| 111 | Sequencing of the smallest Apicomplexan genome from the human pathogen Babesia microtiâ€. Nucleic Acids Research, 2012, 40, 9102-9114. | 6.5 | 179 |
| 112 | LTR Retrotransposons Contribute to Genomic Gigantism in Plethodontid Salamanders. Genome Biology and Evolution, 2012, 4, 168-183. | 1.1 | 152 |
| 113 | Roadmap for Annotating Transposable Elements in Eukaryote Genomes. Methods in Molecular Biology, 2012, 859, 53-68. | 0.4 | 15 |
| 114 | The genome of flax (Linum usitatissimum) assembled de novo from short shotgun sequence reads. Plant Journal, 2012, 72, 461-473. | 2.8 | 415 |
| 115 | A Living Fossil in the Genome of a Living Fossil: Harbinger Transposons in the Coelacanth Genome. Molecular Biology and Evolution, 2012, 29, 985-993. | 3.5 | 36 |
| 117 | Evolution of three Pyrenophora cereal pathogens: Recent divergence, speciation and evolution of non-coding DNA. Fungal Genetics and Biology, 2012, 49, 825-829. | 0.9 | 53 |
| 118 | Transposable Elements and Their Identification. Methods in Molecular Biology, 2012, 855, 337-359. | 0.4 | 26 |
| 119 | Scaling metagenome sequence assembly with probabilistic de Bruijn graphs. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 13272-13277. | 3.3 | 219 |
| 120 | 6â€“10Ã— pyrosequencing is a practical approach for whole prokaryote genome studies. Gene, 2012, 494, 57-64. | 1.0 | 10 |
| 121 | A non-LTR retroelement extinction in Spermophilus tridecemlineatus. Gene, 2012, 500, 47-53. | 1.0 | 28 |
| 122 | Genomic characterization of the conditionally dispensable chromosome in Alternaria arborescens provides evidence for horizontal gene transfer. BMC Genomics, 2012, 13, 171. | 1.2 | 81 |
| 123 | Comparative genomic analysis of human infective Trypanosoma cruzi lineages with the bat-restricted subspecies T. cruzi marinkellei. BMC Genomics, 2012, 13, 531. | 1.2 | 57 |
| 124 | Identification, characterization and distribution of transposable elements in the flax (Linum) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 182 T | 1.2 | 30 |
| 125 | Complete genome sequence of Enterococcus faecium strain TX16 and comparative genomic analysis of Enterococcus faecium genomes. BMC Microbiology, 2012, 12, 135. | 1.3 | 126 |
| 126 | Draft genome sequence of pigeonpea (Cajanus cajan), an orphan legume crop of resource-poor farmers. Nature Biotechnology, 2012, 30, 83-89. | 9.4 | 788 |
| 127 | Transposable Element Annotation in Completely Sequenced Eukaryote Genomes. Topics in Current Genetics, 2012, , 17-39. | 0.7 | 16 |

| # | Article | IF | Citations |
|---|---|---|---|
| 128 | Comparative Genomics of Plant-Associated Pseudomonas spp.: Insights into Diversity and Inheritance of Traits Involved in Multitrophic Interactions. PLoS Genetics, 2012, 8, e1002784. | 1.5 | 578 |
| 129 | Comparing Fungal Genomes: Insight into Functional and Evolutionary Processes. Methods in Molecular Biology, 2012, 835, 531-548. | 0.4 | 7 |
| 131 | Design of a tobacco exon array with application to investigate the differential cadmium accumulation property in two tobacco varieties. BMC Genomics, 2012, 13, 674. | 1.2 | 18 |
| 132 | Sequence Composition and Gene Content of the Short Arm of Rye (Secale cereale) Chromosome 1. PLoS ONE, 2012, 7, e30784. | 1.1 | 20 |
| 133 | The Genome of Ganderma lucidum Provide Insights into Triterpense Biosynthesis and Wood Degradation. PLoS ONE, 2012, 7, e36146. | 1.1 | 78 |
| 134 | Survey of Endosymbionts in the Diaphorina citri Metagenome and Assembly of a Wolbachia wDi Draft Genome. PLoS ONE, 2012, 7, e50067. | 1.1 | 77 |
| 135 | Transposable Elements: From DNA Parasites to Architects of Metazoan Evolution. Genes, 2012, 3, 409-422. | 1.0 | 26 |
| 136 | The predominantly selfing plant Arabidopsis thaliana experienced a recent reduction in transposable element abundance compared to its outcrossing relative Arabidopsis lyrata. Mobile DNA, 2012, 3, 2. | 1.3 | 50 |
| 137 | A beginner's guide to eukaryotic genome annotation. Nature Reviews Genetics, 2012, 13, 329-342. | 7.7 | 553 |
| 138 | Insect Transposable Elements. , 2012, , 57-89. | | 3 |
| 139 | Genome sequence of foxtail millet (Setaria italica) provides insights into grass evolution and biofuel potential. Nature Biotechnology, 2012, 30, 549-554. | 9.4 | 636 |
| 140 | The genome of wine yeast Dekkera bruxellensis provides a tool to explore its food-related properties. International Journal of Food Microbiology, 2012, 157, 202-209. | 2.1 | 102 |
| 141 | EVIDENCE OF ADAPTATION FROM ANCESTRAL VARIATION IN YOUNG POPULATIONS OF BEACH MICE. Evolution; International Journal of Organic Evolution, 2012, 66, 3209-3223. | 1.1 | 64 |
| 142 | The eroded genome of a Psychotria leaf symbiont: hypotheses about lifestyle and interactions with its plant host. Environmental Microbiology, 2012, 14, 2757-2769. | 1.8 | 60 |
| 143 | A cost-effective and universal strategy for complete prokaryotic genomic sequencing proposed by computer simulation. BMC Research Notes, 2012, 5, 80. | 0.6 | 4 |
| 144 | Characterizing the walnut genome through analyses of BAC end sequences. Plant Molecular Biology, 2012, 78, 95-107. | 2.0 | 27 |
| 145 | Reference genomes and transcriptomes of Nicotiana sylvestris and Nicotiana tomentosiformis. Genome Biology, 2013, 14, R60. | 3.8 | 192 |
| 146 | Draft genome of the mountain pine beetle, Dendroctonus ponderosae Hopkins, a major forest pest. Genome Biology, 2013, 14, R27. | 13.9 | 260 |

| # | Article | IF | Citations |
|---|---|---|---|
| 147 | Detection of a novel active transposable element in Caldicellulosiruptor hydrothermalis and a new search for elements in this genus. Journal of Industrial Microbiology and Biotechnology, 2013, 40, 517-521. | 1.4 | 9 |
| 148 | Decoding the Ascaris suum Genome using Massively Parallel Sequencing and Advanced Bioinformatic Methods â€“ Unprecedented Prospects for Fundamental and Applied Research. , 2013, , 287-314. | | 1 |
| 149 | The evolution and pathogenic mechanisms of the rice sheath blight pathogen. Nature Communications, 2013, 4, 1424. | 5.8 | 268 |
| 150 | The miniature genome of a carnivorous plant Genlisea aurea contains a low number of genes and short non-coding sequences. BMC Genomics, 2013, 14, 476. | 1.2 | 58 |
| 151 | KONAGAbase: a genomic and transcriptomic database for the diamondback moth, Plutella xylostella. BMC Genomics, 2013, 14, 464. | 1.2 | 47 |
| 152 | Insights into the evolution of Darwinâ€™s finches from comparative analysis of the Geospiza magnirostris genome sequence. BMC Genomics, 2013, 14, 95. | 1.2 | 38 |
| 153 | Draft genome sequence of chickpea (Cicer arietinum) provides a resource for trait improvement. Nature Biotechnology, 2013, 31, 240-246. | 9.4 | 1,049 |
| 154 | Overview of Repeat Annotation and De Novo Repeat Identification. Methods in Molecular Biology, 2013, 1057, 275-287. | 0.4 | 12 |
| 155 | Sequence organization and evolutionary dynamics of Brachypodium-specific centromere retrotransposons. Chromosome Research, 2013, 21, 507-521. | 1.0 | 14 |
| 156 | The sacred lotus genome provides insights into the evolution of flowering plants. Plant Journal, 2013, 76, 557-567. | 2.8 | 75 |
| 157 | A draft genome sequence of the pulse crop chickpea (<scp>C</scp>icer arietinumÂL.). Plant Journal, 2013, 74, 715-729. | 2.8 | 382 |
| 158 | Adaptive Evolution of Multiple Traits Through Multiple Mutations at a Single Gene. Science, 2013, 339, 1312-1316. | 6.0 | 277 |
| 159 | Genome-wide survey of repetitive DNA elements in the button mushroom Agaricus bisporus. Fungal Genetics and Biology, 2013, 55, 6-21. | 0.9 | 37 |
| 160 | A heterozygous moth genome provides insights into herbivory and detoxification. Nature Genetics, 2013, 45, 220-225. | 9.4 | 472 |
| 161 | The genome of the hydatid tapeworm Echinococcus granulosus. Nature Genetics, 2013, 45, 1168-1175. | 9.4 | 260 |
| 162 | Identification of both copy number variation-type and constant-type core elements in a large segmental duplication region of the mouse genome. BMC Genomics, 2013, 14, 455. | 1.2 | 6 |
| 163 | Developing molecular tools and insights into the Penstemon genome using genomic reduction and next-generation sequencing. BMC Genetics, 2013, 14, 66. | 2.7 | 14 |
| 164 | The genome of Romanomermis culicivorax: revealing fundamental changes in the core developmental genetic toolkit in Nematoda. BMC Genomics, 2013, 14, 923. | 1.2 | 43 |

| # | Article | IF | Citations |
|---|---|---|---|
| 165 | A BAC based physical map and genome survey of the rice false smut fungus Villosiclava virens. BMC Genomics, 2013, 14, 883. | 1.2 | 10 |
| 166 | Tips and tricks for the assembly of a <scp>C</scp>orynebacterium pseudotuberculosis genome using a semiconductor sequencer. Microbial Biotechnology, 2013, 6, 150-156. | 2.0 | 14 |
| 167 | The draft genome of watermelon (Citrullus lanatus) and resequencing of 20 diverse accessions. Nature Genetics, 2013, 45, 51-58. | 9.4 | 731 |
| 168 | The draft genomes of soft-shell turtle and green sea turtle yield insights into the development and evolution of the turtle-specific body plan. Nature Genetics, 2013, 45, 701-706. | 9.4 | 409 |
| 169 | The draft genome of the fast-growing non-timber forest species moso bamboo (Phyllostachys) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 582 | 9.4 | 483 |
| 170 | The high-quality draft genome of peach (Prunus persica) identifies unique patterns of genetic diversity, domestication and genome evolution. Nature Genetics, 2013, 45, 487-494. | 9.4 | 1,031 |
| 171 | Comparative genomic and transcriptomic analyses reveal the hemibiotrophic stage shift of Colletotrichum fungi. New Phytologist, 2013, 197, 1236-1249. | 3.5 | 332 |
| 172 | Comparative Genomics Analysis of Trichoderma reesei Strains. Industrial Biotechnology, 2013, 9, 352-367. | 0.5 | 34 |
| 173 | Deciphering the Cryptic Genome: Genome-wide Analyses of the Rice Pathogen Fusarium fujikuroi Reveal Complex Regulation of Secondary Metabolism and Novel Metabolites. PLoS Pathogens, 2013, 9, e1003475. | 2.1 | 406 |
| 174 | Genomic Mechanisms Accounting for the Adaptation to Parasitism in Nematode-Trapping Fungi. PLoS Genetics, 2013, 9, e1003909. | 1.5 | 97 |
| 175 | Extensive chromosomal reshuffling drives evolution of virulence in an asexual pathogen. Genome Research, 2013, 23, 1271-1282. | 2.4 | 338 |
| 176 | Comparative Genome Structure, Secondary Metabolite, and Effector Coding Capacity across Cochliobolus Pathogens. PLoS Genetics, 2013, 9, e1003233. | 1.5 | 232 |
| 177 | Functional and Evolutionary Analysis of the Genome of an Obligate Fungal Symbiont. Genome Biology and Evolution, 2013, 5, 891-904. | 1.1 | 54 |
| 178 | PRAP: an ab initio software package for automated genome-wide analysis of DNA repeats for prokaryotes. Bioinformatics, 2013, 29, 2683-2689. | 1.8 | 11 |
| 179 | The genome and developmental transcriptome of the strongylid nematode Haemonchus contortus. Genome Biology, 2013, 14, R89. | 13.9 | 192 |
| 180 | Functional characterization of piggyBat from the bat Myotis lucifugus unveils an active mammalian DNA transposon. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 234-239. | 3.3 | 73 |
| 181 | Draft genome sequence of the mulberry tree Morus notabilis. Nature Communications, 2013, 4, 2445. | 5.8 | 277 |
| 182 | The Genome of the Anaerobic Fungus Orpinomyces sp. Strain C1A Reveals the Unique Evolutionary History of a Remarkable Plant Biomass Degrader. Applied and Environmental Microbiology, 2013, 79, 4620-4634. | 1.4 | 224 |

| # | Article | IF | Citations |
|---|---|---|---|
| 183 | Draft genome of the kiwifruit Actinidia chinensis. Nature Communications, 2013, 4, 2640. | 5.8 | 423 |
| 184 | Genomics of Loa loa, a Wolbachia-free filarial parasite of humans. Nature Genetics, 2013, 45, 495-500. | 9.4 | 173 |
| 185 | Improving prokaryotic transposable elements identification using a combination of de novo and profile HMM methods. BMC Genomics, 2013, 14, 700. | 1.2 | 19 |
| 186 | The genome sequence of the colonial chordate, Botryllus schlosseri. ELife, 2013, 2, e00569. | 2.8 | 209 |
| 187 | Studentsâ€™ perspective on genomics: from sample to sequence using the case study of blueberry. Frontiers in Genetics, 2013, 4, 245. | 1.1 | 4 |
| 188 | Genome Re-Sequencing of Semi-Wild Soybean Reveals a Complex Soja Population Structure and Deep Introgression. PLoS ONE, 2014, 9, e108479. | 1.1 | 26 |
| 189 | Genomic takeover by transposable elements in the Strawberry poison frog. Molecular Biology and Evolution, 2014, 35, 2913-2927. | 3.5 | 45 |
| 190 | BengaSaVex: A new computational genetic sequence extraction tool for DNA repeats. African Journal of Biotechnology, 2014, 13, 2103-2112. | 0.3 | 2 |
| 191 | Fungal Genomics. Advances in Botanical Research, 2014, , 1-52. | 0.5 | 25 |
| 192 | The genome sequence of the Antarctic bullhead notothen reveals evolutionary adaptations to a cold environment. Genome Biology, 2014, 15, 468. | 3.8 | 86 |
| 193 | The genome of Eimeria falciformisv - reduction and specialization in a single host apicomplexan parasite. BMC Genomics, 2014, 15, 696. | 1.2 | 44 |
| 194 | Rapid Evolution of piRNA Pathway in the Teleost Fish: Implication for an Adaptation to Transposon Diversity. Genome Biology and Evolution, 2014, 6, 1393-1407. | 1.1 | 46 |
| 195 | Genomes of the rice pest brown planthopper and its endosymbionts reveal complex complementary contributions for host adaptation. Genome Biology, 2014, 15, 521. | 3.8 | 404 |
| 196 | Whole-genome sequence of a flatfish provides insights into ZW sex chromosome evolution and adaptation to a benthic lifestyle. Nature Genetics, 2014, 46, 253-260. | 9.4 | 685 |
| 197 | Genome of the Avirulent Human-Infective Trypanosomeâ€”Trypanosoma rangeli. PLoS Neglected Tropical Diseases, 2014, 8, e3176. | 1.3 | 72 |
| 198 | Genome Sequencing and Comparative Genomics of the Broad Host-Range Pathogen Rhizoctonia solani AG8. PLoS Genetics, 2014, 10, e1004281. | 1.5 | 145 |
| 199 | Big data challenges for estimating genome assembler quality. , 2014, , . | | 1 |
| 200 | Complete Plastome Sequences from Glycine syndetika and Six Additional Perennial Wild Relatives of Soybean. G3: Genes, Genomes, Genetics, 2014, 4, 2023-2033. | 0.8 | 26 |

| # | Article | IF | Citations |
|---|---|---|---|
| 201 | ADe NovoGenome Assembly Algorithm for Repeats and Nonrepeats. BioMed Research International, 2014, 2014, 1-16. | 0.9 | 3 |
| 202 | Single Nucleus Genome Sequencing Reveals High Similarity among Nuclei of an Endomycorrhizal Fungus. PLoS Genetics, 2014, 10, e1004078. | 1.5 | 238 |
| 203 | Mining hidden polymorphic sequence motifs from divergent planthelitrons. Mobile Genetic Elements, 2014, 4, 1-5. | 1.8 | 0 |
| 204 | Sequence-Based Analysis of Structural Organization and Composition of the Cultivated Sunflower (Helianthus annuus L.) Genome. Biology, 2014, 3, 295-319. | 1.3 | 16 |
| 205 | The Draft Genome and Transcriptome of Amaranthus hypochondriacus: A C4 Dicot Producing High-Lysine Edible Pseudo-Cereal. DNA Research, 2014, 21, 585-602. | 1.5 | 52 |
| 206 | Molecular tracing of the emergence, diversification, and transmission of S. aureus sequence type 8 in a New York community. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 6738-6743. | 3.3 | 176 |
| 207 | Deep Investigation of Arabidopsis thaliana Junk DNA Reveals a Continuum between Repetitive Elements and Genomic Dark Matter. PLoS ONE, 2014, 9, e94101. | 1.1 | 62 |
| 208 | The landscape of transposable elements in the finished genome of the fungal wheat pathogen Mycosphaerella graminicola. BMC Genomics, 2014, 15, 1132. | 1.2 | 65 |
| 209 | Genome sequencing of four Aureobasidium pullulans varieties: biotechnological potential, stress tolerance, and description of new species. BMC Genomics, 2014, 15, 549. | 1.2 | 262 |
| 210 | Draft Genome Sequence of Eggplant (Solanum melongena L.): the Representative Solanum Species Indigenous to the Old World. DNA Research, 2014, 21, 649-660. | 1.5 | 254 |
| 211 | Random non-coding fragments of lizard DNA: anonymous nuclear loci for the Australian skink, Tiliqua rugosa, and their utility in other Egernia-group species. Australian Journal of Zoology, 2014, 62, 515. | 0.6 | 2 |
| 212 | The complex jujube genome provides insights into fruit tree biology. Nature Communications, 2014, 5, 5315. | 5.8 | 251 |
| 213 | The complete sequence of the chloroplast genome of the green microalgaLobosphaera(Parietochloris)incisa. Mitochondrial DNA, 2016, 27, 1-3. | 0.6 | 3 |
| 214 | Three crocodilian genomes reveal ancestral patterns of evolution among archosaurs. Science, 2014, 346, 1254449. | 6.0 | 300 |
| 215 | Rolling-Circle Transposons Catalyze Genomic Innovation in a Mammalian Lineage. Genome Biology and Evolution, 2014, 6, 2595-2610. | 1.1 | 53 |
| 216 | Draft Sequences of the Radish (Raphanus sativus L.) Genome. DNA Research, 2014, 21, 481-490. | 1.5 | 165 |
| 217 | TEMP: a computational method for analyzing transposable element polymorphism in populations. Nucleic Acids Research, 2014, 42, 6826-6838. | 6.5 | 124 |
| 218 | Comparative Genomic and Transcriptomic Analysis of Wangiella dermatitidis, A Major Cause of Phaeohyphomycosis and a Model Black Yeast Human Pathogen. G3: Genes, Genomes, Genetics, 2014, 4, 561-578. | 0.8 | 58 |

| # | Article | IF | Citations |
|---|---|---|---|
| 219 | Hellbender Genome Sequences Shed Light on Genomic Expansion at the Base of Crown Salamanders. Genome Biology and Evolution, 2014, 6, 1818-1829. | 1.1 | 57 |
| 220 | ChiloDB: a genomic and transcriptome database for an important rice insect pest Chilo suppressalis. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau065-bau065. | 1.4 | 50 |
| 221 | Ancestral repeats have shaped epigenome and genome composition for millions of years in Arabidopsis thaliana. Nature Communications, 2014, 5, 4104. | 5.8 | 74 |
| 222 | Gene Loss Rather Than Gene Gain Is Associated with a Host Jump from Monocots to Dicots in the Smut Fungus Melanopsichium pennsylvanicum. Genome Biology and Evolution, 2014, 6, 2034-2049. | 1.1 | 146 |
| 223 | Finding the missing honey bee genes: lessons learned from a genome upgrade. BMC Genomics, 2014, 15, 86. | 1.2 | 375 |
| 224 | Genome sequence of Anopheles sinensis provides insight into genetics basis of mosquito competence for malaria parasites. BMC Genomics, 2014, 15, 42. | 1.2 | 56 |
| 225 | The rainbow trout genome provides novel insights into evolution after whole-genome duplication in vertebrates. Nature Communications, 2014, 5, 3657. | 5.8 | 814 |
| 226 | Genome Sequence of the Tsetse Fly ( Glossina morsitans ): Vector of African Trypanosomiasis. Science, 2014, 344, 380-386. | 6.0 | 254 |
| 227 | The tobacco genome sequence and its comparison with those of tomato and potato. Nature Communications, 2014, 5, 3833. | 5.8 | 503 |
| 228 | Population Genomics Reveal Recent Speciation and Rapid Evolutionary Adaptation in Polar Bears. Cell, 2014, 157, 785-794. | 13.5 | 363 |
| 229 | Stick Insect Genomes Reveal Natural Selectionâ€™s Role in Parallel Speciation. Science, 2014, 344, 738-742. | 6.0 | 386 |
| 230 | Papaya Repeat Database. , 2014, , 225-240. | | 1 |
| 231 | Topological organization of multichromosomal regions by the long intergenic noncoding RNA Firre. Nature Structural and Molecular Biology, 2014, 21, 198-206. | 3.6 | 565 |
| 232 | The genome of the recently domesticated crop plant sugar beet (Beta vulgaris). Nature, 2014, 505, 546-549. | 13.7 | 569 |
| 233 | Minke whale genome and aquatic adaptation in cetaceans. Nature Genetics, 2014, 46, 88-92. | 9.4 | 227 |
| 234 | Rapid diversification of five Oryza AA genomes associated with rice adaptation. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E4954-62. | 3.3 | 145 |
| 235 | Evolutionary active transposable elements in the genome of the coelacanth. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2014, 322, 322-333. | 0.6 | 22 |
| 236 | Comparative genome sequencing reveals genomic signature of extreme desiccation tolerance in the anhydrobiotic midge. Nature Communications, 2014, 5, 4784. | 5.8 | 118 |

| # | Article | IF | Citations |
|---|---|---|---|
| 237 | Endogenous florendoviruses are major components of plant genomes and hallmarks of virus evolution. Nature Communications, 2014, 5, 5269. | 5.8 | 99 |
| 238 | RepARKâ€"de novo creation of repeat libraries from whole-genome NGS reads. Nucleic Acids Research, 2014, 42, e80-e80. | 6.5 | 67 |
| 239 | Genome and transcriptome of the porcine whipworm Trichuris suis. Nature Genetics, 2014, 46, 701-706. | 9.4 | 93 |
| 240 | The coffee genome provides insight into the convergent evolution of caffeine biosynthesis. Science, 2014, 345, 1181-1184. | 6.0 | 520 |
| 241 | The genome sequence of African rice (Oryza glaberrima) and evidence for independent domestication. Nature Genetics, 2014, 46, 982-988. | 9.4 | 342 |
| 242 | The genome of the white-rot fungus Pycnoporus cinnabarinus: a basidiomycete model with a versatile arsenal for lignocellulosic biomass breakdown. BMC Genomics, 2014, 15, 486. | 1.2 | 91 |
| 243 | Oil accumulation mechanisms of the oleaginous microalga Chlorella protothecoides revealed through its genome, transcriptomes, and proteomes. BMC Genomics, 2014, 15, 582. | 1.2 | 134 |
| 244 | The genome sequence of the biocontrol fungus Metarhizium anisopliae and comparative genomics of Metarhizium species. BMC Genomics, 2014, 15, 660. | 1.2 | 59 |
| 245 | DINE-1, the highest copy number repeats in Drosophila melanogaster are non-autonomous endonuclease-encoding rolling-circle transposable elements (Helentrons). Mobile DNA, 2014, 5, 18. | 1.3 | 32 |
| 246 | The Architecture of a Scrambled Genome Reveals Massive Levels of Genomic Rearrangement during Development. Cell, 2014, 158, 1187-1198. | 13.5 | 152 |
| 247 | Heterochromatin Controls Î³H2A Localization in Neurospora crassa. Eukaryotic Cell, 2014, 13, 990-1000. | 3.4 | 26 |
| 248 | OMIGA: Optimized Maker-Based Insect Genome Annotation. Molecular Genetics and Genomics, 2014, 289, 567-573. | 1.0 | 24 |
| 249 | Genome sequence of the cultivated cotton Gossypium arboreum. Nature Genetics, 2014, 46, 567-572. | 9.4 | 883 |
| 250 | Billions of basepairs of recently expanded, repetitive sequences are eliminated from the somatic genome during copepod development. BMC Genomics, 2014, 15, 186. | 1.2 | 34 |
| 251 | Accumulation of interspersed and sex-specific repeats in the non-recombining region of papaya sex chromosomes. BMC Genomics, 2014, 15, 335. | 1.2 | 28 |
| 252 | Evolution of gene structure in the conifer Picea glauca: a comparative analysis of the impact of intron size. BMC Plant Biology, 2014, 14, 95. | 1.6 | 46 |
| 253 | Genetic parameters and response to selection in blue mussel (Mytilus galloprovincialis) using a SNP-based pedigree. Aquaculture, 2014, 420-421, 295-301. | 1.7 | 61 |
| 254 | The heterothallic sugarbeet pathogen Cercospora beticola contains exon fragments of both MAT genes that are homogenized by concerted evolution. Fungal Genetics and Biology, 2014, 62, 43-54. | 0.9 | 15 |

| # | Article | IF | Citations |
|---|---|---|---|
| 255 | Mobile elements and mitochondrial genome expansion in the soil fungus and potato pathogenRhizoctonia solaniAG-3. FEMS Microbiology Letters, 2014, 352, 165-173. | 0.7 | 143 |
| 256 | Analysis of the leaf methylomes of parents and their hybrids provides new insight into hybrid vigor in Populus deltoides. BMC Genetics, 2014, 15, S8. | 2.7 | 16 |
| 257 | Feature frequency profiles for automatic sample identification using PySpark. , 2015, , . | | 0 |
| 258 | An advanced draft genome assembly of a desi type chickpea (Cicer arietinum L.). Scientific Reports, 2015, 5, 12806. | 1.6 | 114 |
| 259 | Helitrons , the Eukaryotic Rolling-circle Transposable Elements. Microbiology Spectrum, 2015, 3, . | 1.2 | 81 |
| 260 | Sequencing of plant genomes â€“ a review. Turk Tarim Ve Ormancilik Dergisi/Turkish Journal of Agriculture and Forestry, 2015, 39, 361-376. | 0.8 | 20 |
| 261 | Repbase Update, a database of repetitive elements in eukaryotic genomes. Mobile DNA, 2015, 6, 11. | 1.3 | 2,243 |
| 262 | Draft genome sequences of Chrysoporthe austroafricana, Diplodia scrobiculata, Fusarium nygamai, Leptographium lundbergii, Limonomyces culmigenus, Stagonosporopsis tanaceti, and Thielaviopsis punctulata. IMA Fungus, 2015, 6, 233-248. | 1.7 | 46 |
| 263 | MnTEdb, a collective resource for mulberry transposable elements. Database: the Journal of Biological Databases and Curation, 2015, 2015, . | 1.4 | 25 |
| 264 | Global identification and analysis of long non-coding RNAs in diploid strawberry Fragaria vesca during flower and fruit development. BMC Genomics, 2015, 16, 815. | 1.2 | 106 |
| 265 | Predicting DNA mutations during cancer evolution. International Journal of Bioinformatics Research and Applications, 2015, 11, 200. | 0.1 | 1 |
| 266 | An Introduction to Genome Annotation. Current Protocols in Bioinformatics, 2015, 52, 4.1.1-4.1.17. | 25.8 | 4 |
| 267 | Genome sequence of the plant growth promoting endophytic yeast Rhodotorula graminis WP1. Frontiers in Microbiology, 2015, 6, 978. | 1.5 | 83 |
| 268 | Reproductive Mode and the Evolution of Genome Size and Structure in Caenorhabditis Nematodes. PLoS Genetics, 2015, 11, e1005323. | 1.5 | 102 |
| 269 | A Deluge of Complex Repeats: The Solanum Genome. PLoS ONE, 2015, 10, e0133962. | 1.1 | 23 |
| 270 | The genome of Leishmania panamensis: insights into genomics of the L. (Viannia) subgenus.. Scientific Reports, 2015, 5, 8550. | 1.6 | 63 |
| 271 | Metagenome sequence of <scp>E</scp>laphomyces granulatus from sporocarp tissue reveals <scp>A</scp>scomycota ectomycorrhizal fingerprints of genome expansion and a <scp>P</scp>roteobacteriaâ€rich microbiome. Environmental Microbiology, 2015, 17, 2952-2968. | 1.8 | 34 |
| 272 | High quality reference genome of drumstick tree (Moringa oleifera Lam.), a potential perennial crop. Science China Life Sciences, 2015, 58, 627-638. | 2.3 | 53 |

| # | Article | IF | Citations |
|---|---|---|---|
| 274 | The complete mitochondrial genome sequence of the green microalga Lobosphaera (Parietochloris) incisa reveals a new type of palindromic repetitive repeat. BMC Genomics, 2015, 16, 580. | 1.2 | 9 |
| 275 | Genome sequencing of herb Tulsi (Ocimum tenuiflorum) unravels key genes behind its strong medicinal properties. BMC Plant Biology, 2015, 15, 212. | 1.6 | 80 |
| 276 | Genome of Rhodnius prolixus , an insect vector of Chagas disease, reveals unique adaptations to hematophagy and parasite infection. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 14936-14941. | 3.3 | 329 |
| 277 | Insights into Sex Chromosome Evolution and Aging from the Genome of a Short-Lived Fish. Cell, 2015, 163, 1527-1538. | 13.5 | 251 |
| 278 | Linked selection and recombination rate variation drive the evolution of the genomic landscape of differentiation across the speciation continuum of Ficedula flycatchers. Genome Research, 2015, 25, 1656-1665. | 2.4 | 385 |
| 279 | Single-molecule sequencing of the desiccation-tolerant grass Oropetium thomaeum. Nature, 2015, 527, 508-511. | 13.7 | 291 |
| 280 | De novo genome assembly tool comparison for highly heterozygous species Vitis vinifera cv. Sultanina. , 2015, , . | | 2 |
| 281 | Computational Synteny Block: A framework to identify evolutionary events. , 2015, , . | | 0 |
| 282 | Evolution of novel wood decay mechanisms in Agaricales revealed by the genome sequences of Fistulina hepatica and Cylindrobasidium torrendii. Fungal Genetics and Biology, 2015, 76, 78-92. | 0.9 | 141 |
| 283 | Studying Genome Heterogeneity within the Arbuscular Mycorrhizal Fungal Cytoplasm. Genome Biology and Evolution, 2015, 7, 505-521. | 1.1 | 30 |
| 284 | Integrated genome sequence and linkage map of physic nut (Jatropha curcas L.), a biodiesel plant. Plant Journal, 2015, 81, 810-821. | 2.8 | 149 |
| 285 | The genome and transcriptome of the zoonotic hookworm Ancylostoma ceylanicum identify infection-specific gene families. Nature Genetics, 2015, 47, 416-422. | 9.4 | 91 |
| 286 | Genetic blueprint of the zoonotic pathogen Toxocara canis. Nature Communications, 2015, 6, 6145. | 5.8 | 103 |
| 287 | Genome Sequencing of the Perciform Fish Larimichthys crocea Provides Insights into Molecular and Genetic Mechanisms of Stress Adaptation. PLoS Genetics, 2015, 11, e1005118. | 1.5 | 230 |
| 288 | Characterization and distribution of mating-type genes of the turfgrass pathogen Sclerotinia homoeocarpa on a global scale. Fungal Genetics and Biology, 2015, 81, 25-40. | 0.9 | 15 |
| 289 | DNA transposons have colonized the genome of the giant virus Pandoravirus salinus. BMC Biology, 2015, 13, 38. | 1.7 | 50 |
| 290 | Saccharina genomes provide novel insight into kelp biology. Nature Communications, 2015, 6, 6986. | 5.8 | 222 |
| 291 | Genomic and transcriptomic analysis of the endophytic fungus Pestalotiopsis fici reveals its lifestyle and high potential for synthesis of natural products. BMC Genomics, 2015, 16, 28. | 1.2 | 102 |

| # | Article | IF | Citations |
|---|---|---|---|
| 292 | The genome of the basal agaricomycete Xanthophyllomyces dendrorhous provides insights into the organization of its acetyl-CoA derived pathways and the evolution of Agaricomycotina. BMC Genomics, 2015, 16, 233. | 1.2 | 47 |
| 293 | Local hopping mobile DNA implicated in pseudogene formation and reductive evolution in an obligate cyanobacteria-plant symbiosis. BMC Genomics, 2015, 16, 193. | 1.2 | 20 |
| 294 | The Alternaria genomes database: a comprehensive resource for a fungal genus comprised of saprophytes, plant pathogens, and allergenic species. BMC Genomics, 2015, 16, 239. | 1.2 | 105 |
| 295 | Analyses of random BAC clone sequences of Japanese cedar, Cryptomeria japonica. Tree Genetics and Genomes, 2015, 11, 1. | 0.6 | 4 |
| 296 | The goose genome sequence leads to insights into the evolution of waterfowl and susceptibility to fatty liver. Genome Biology, 2015, 16, 89. | 3.8 | 98 |
| 297 | Impact of transposable elements on insect genomes and biology. Current Opinion in Insect Science, 2015, 7, 30-36. | 2.2 | 45 |
| 298 | The nervous system of Xenacoelomorpha: a genomic perspective. Journal of Experimental Biology, 2015, 218, 618-628. | 0.8 | 36 |
| 299 | Genome Sequences of Three Phytopathogenic Species of the Magnaporthaceae Family of Fungi. G3: Genes, Genomes, Genetics, 2015, 5, 2539-2545. | 0.8 | 33 |
| 300 | The Lingula genome provides insights into brachiopod evolution and the origin of phosphate biomineralization. Nature Communications, 2015, 6, 8301. | 5.8 | 159 |
| 301 | Genome and transcriptome of the regeneration-competent flatworm, Macrostomum lignano. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 12462-12467. | 3.3 | 90 |
| 302 | Red: an intelligent, rapid, accurate tool for detecting repeats de-novo on the genomic scale. BMC Bioinformatics, 2015, 16, 227. | 1.2 | 150 |
| 303 | The Genome and Methylome of a Beetle with Complex Social Behavior,Nicrophorus vespilloides(Coleoptera: Silphidae). Genome Biology and Evolution, 2015, 7, 3383-3396. | 1.1 | 87 |
| 304 | Genome sequence of the Asian Tiger mosquito, Aedes albopictus , reveals insights into its biology, genetics, and evolution. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E5907-15. | 3.3 | 251 |
| 305 | Genome Sequencing of Multiple Isolates Highlights Subtelomeric Genomic Diversity withinFusarium fujikuroi. Genome Biology and Evolution, 2015, 7, 3062-3069. | 1.1 | 36 |
| 306 | The Genome of Winter Moth (Operophtera brumata) Provides a Genomic Perspective on Sexual Dimorphism and Phenology. Genome Biology and Evolution, 2015, 7, 2321-2332. | 1.1 | 70 |
| 307 | RiTE database: a resource database for genus-wide rice genomics and evolutionary biology. BMC Genomics, 2015, 16, 538. | 1.2 | 86 |
| 308 | The genome of the truffle-parasite Tolypocladium ophioglossoides and the evolution of antifungal peptaibiotics. BMC Genomics, 2015, 16, 553. | 1.2 | 46 |
| 309 | Single-Molecule Real-Time Sequencing Combined with Optical Mapping Yields Completely Finished Fungal Genome. MBio, 2015, 6, . | 1.8 | 141 |

| # | Article | IF | Citations |
|---|---|---|---|
| 310 | Comparative Genomics Including the Early-Diverging Smut FungusCeraceosorus bombacisReveals Signatures of Parallel Evolution within Plant and Animal Pathogens of Fungi and Oomycetes. Genome Biology and Evolution, 2015, 7, 2781-2798. | 1.1 | 16 |
| 311 | Comparative Genomics of a Bacterivorous Green Alga Reveals Evolutionary Causalities and Consequences of Phago-Mixotrophic Mode of Nutrition. Genome Biology and Evolution, 2015, 7, 3047-3061. | 1.1 | 36 |
| 312 | A new approach for annotation of transposable elements using small RNA mapping. Nucleic Acids Research, 2015, 43, e84-e84. | 6.5 | 28 |
| 313 | Gene expression during zombie ant biting behavior reflects the complexity underlying fungal parasitic behavioral manipulation. BMC Genomics, 2015, 16, 620. | 1.2 | 107 |
| 314 | A call for benchmarking transposable element annotation methods. Mobile DNA, 2015, 6, 13. | 1.3 | 83 |
| 315 | Hemichordate genomes and deuterostome origins. Nature, 2015, 527, 459-465. | 13.7 | 217 |
| 316 | The genome sequence of the orchid Phalaenopsis equestris. Nature Genetics, 2015, 47, 65-72. | 9.4 | 413 |
| 317 | Highly evolvable malaria vectors: The genomes of 16 Anopheles mosquitoes. Science, 2015, 347, 1258522. | 6.0 | 492 |
| 318 | An evaluation of the ecological relationship between Drosophila species and their parasitoid wasps as an opportunity for horizontal transposon transfer. Molecular Genetics and Genomics, 2015, 290, 67-78. | 1.0 | 18 |
| 319 | Comprehensive repeatome annotation reveals strong potential impact of repetitive elements on tomato ripening. BMC Genomics, 2016, 17, 624. | 1.2 | 29 |
| 320 | Toward a First High-quality Genome Draft for Marker-assisted Breeding in Leaf Chicory, Radicchio (Cichorium intybus L.). , 0, , . | | 11 |
| 321 | Deep landscape update of dispersed and tandem repeats in the genome model of the red jungle fowl, Gallus gallus, using a series of de novo investigating tools. BMC Genomics, 2016, 17, 659. | 1.2 | 14 |
| 322 | A complete toolset for the study of Ustilago bromivora and Brachypodium sp. as a fungal-temperate grass pathosystem. ELife, 2016, 5, . | 2.8 | 49 |
| 323 | Biosynthesis of Antibiotic Leucinostatins in Bio-control Fungus Purpureocillium lilacinum and Their Inhibition on Phytophthora Revealed by Genome Mining. PLoS Pathogens, 2016, 12, e1005685. | 2.1 | 122 |
| 324 | Chromosomal-Level Assembly of the Asian Seabass Genome Using Long Sequence Reads and Multi-layered Scaffolding. PLoS Genetics, 2016, 12, e1005954. | 1.5 | 105 |
| 325 | Comparative Genomics of the Sigatoka Disease Complex on Banana Suggests a Link between Parallel Evolutionary Changes in Pseudocercospora fijiensis and Pseudocercospora eumusae and Increased Virulence on the Banana Host. PLoS Genetics, 2016, 12, e1005904. | 1.5 | 51 |
| 326 | Transposable Elements versus the Fungal Genome: Impact on Whole-Genome Architecture and Transcriptional Profiles. PLoS Genetics, 2016, 12, e1006108. | 1.5 | 177 |
| 327 | Computational Synteny Block: A Framework to Identify Evolutionary Events. IEEE Transactions on Nanobioscience, 2016, 15, 343-353. | 2.2 | 4 |

| # | Article | IF | Citations |
|---|---|---|---|
| 328 | DPTEdb, an integrative database of transposable elements in dioecious plants. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw078. | 1.4 | 23 |
| 329 | The genome of black raspberry (Rubus occidentalis). Plant Journal, 2016, 87, 535-547. | 2.8 | 111 |
| 330 | The genome analysis of <scp>C</scp>andidatusâ€¦<scp>B</scp>urkholderia crenata reveals that secondary metabolism may be a key function of the <scp>A</scp>rdisia crenata leaf nodule symbiosis. Environmental Microbiology, 2016, 18, 2507-2522. | 1.8 | 64 |
| 331 | New resources for genetic studies in Populus nigra: genomeâ€wide <scp>SNP</scp> discovery and development of a 12k Infinium array. Molecular Ecology Resources, 2016, 16, 1023-1036. | 2.2 | 48 |
| 332 | Function and evolution of local repeats in the Firre locus. Nature Communications, 2016, 7, 11021. | 5.8 | 75 |
| 333 | De Novo Annotation of Transposable Elements: Tackling the Fat Genome Issue. Proceedings of the IEEE, 2016, , 1-8. | 16.4 | 8 |
| 334 | Genomes of coral dinoflagellate symbionts highlight evolutionary adaptations conducive to a symbiotic lifestyle. Scientific Reports, 2016, 6, 39734. | 1.6 | 303 |
| 335 | Draft genome sequence ofCicer reticulatumL., the wild progenitor of chickpea provides a resource for agronomic trait improvement. DNA Research, 2017, 24, dsw042. | 1.5 | 73 |
| 336 | The draft genome of whitefly Bemisia tabaci MEAM1, a global crop pest, provides novel insights into virus transmission, host adaptation, and insecticide resistance. BMC Biology, 2016, 14, 110. | 1.7 | 265 |
| 337 | Survey of the genome of Pogostemon cablin provides insights into its evolutionary history and sesquiterpenoid biosynthesis. Scientific Reports, 2016, 6, 26405. | 1.6 | 21 |
| 338 | The Asian arowana (Scleropages formosus) genome provides new insights into the evolution of an early lineage of teleosts. Scientific Reports, 2016, 6, 24501. | 1.6 | 89 |
| 339 | Comparative â€œOmicsâ€•of theFusarium fujikuroiSpecies Complex Highlights Differences in Genetic Potential and Metabolite Synthesis. Genome Biology and Evolution, 2016, 8, 3574-3599. | 1.1 | 124 |
| 340 | Comparative genomics to explore phylogenetic relationship, cryptic sexual potential and host specificity of Rhynchosporium species on grasses. BMC Genomics, 2016, 17, 953. | 1.2 | 33 |
| 341 | Draft genome sequencing and secretome analysis of fungal phytopathogen Ascochyta rabiei provides insight into the necrotrophic effector repertoire. Scientific Reports, 2016, 6, 24638. | 1.6 | 57 |
| 342 | Globally distributed root endophyte Phialocephala subalpina links pathogenic and saprophytic lifestyles. BMC Genomics, 2016, 17, 1015. | 1.2 | 54 |
| 343 | phRAIDER: Pattern-Hunter based Rapid Ab Initio Detection of Elementary Repeats. Bioinformatics, 2016, 32, i209-i215. | 1.8 | 16 |
| 344 | The rubber tree genome shows expansion of gene family associated with rubber biosynthesis. Scientific Reports, 2016, 6, 28594. | 1.6 | 118 |
| 345 | Genetic Drift, Not Life History or RNAi, Determine Long-Term Evolution of Transposable Elements. Genome Biology and Evolution, 2016, 8, 2964-2978. | 1.1 | 58 |

| # | Article | IF | Citations |
|---|---|---|---|
| 346 | A novel method for identifying polymorphic transposable elements via scanning of high-throughput short reads. DNA Research, 2016, 23, 241-251. | 1.5 | 18 |
| 347 | Reconstructing the evolutionary history of gypsy retrotransposons in the PÃ©rigord black truffle (Tuber melanosporum Vittad.). Mycorrhiza, 2016, 26, 553-563. | 1.3 | 7 |
| 348 | X. couchianus and X. hellerii genome models provide genomic variation insight among Xiphophorus species. BMC Genomics, 2016, 17, 37. | 1.2 | 32 |
| 349 | Sequencing and comparative analyses of the genomes of zoysiagrasses. DNA Research, 2016, 23, 171-180. | 1.5 | 68 |
| 350 | Repetitive Sequences. Compendium of Plant Genomes, 2016, , 115-123. | 0.3 | 0 |
| 351 | DNA methylation changes facilitated evolution of genes derived from Mutator-like transposable elements. Genome Biology, 2016, 17, 92. | 3.8 | 14 |
| 352 | The genome sequence of allopolyploid Brassica juncea and analysis of differential homoeolog gene expression influencing selection. Nature Genetics, 2016, 48, 1225-1232. | 9.4 | 479 |
| 353 | Draft genome sequence of an inbred line ofChenopodium quinoa, an allotetraploid crop with great environmental adaptability and outstanding nutritional properties. DNA Research, 2016, 23, 535-546. | 1.5 | 84 |
| 354 | Partial sequencing reveals the transposable element composition of Coffea genomes and provides evidence for distinct evolutionary stories. Molecular Genetics and Genomics, 2016, 291, 1979-1990. | 1.0 | 16 |
| 355 | Fine-scale spatial genetic structure of a fungal parasite of coffee scale insects. Journal of Invertebrate Pathology, 2016, 139, 34-41. | 1.5 | 4 |
| 356 | The Genome of a Southern Hemisphere Seagrass Species (Zostera muelleri). Plant Physiology, 2016, 172, 272-283. | 2.3 | 88 |
| 357 | A draft genome of the brown alga,Cladosiphon okamuranus, S-strain: a platform for future studies of â€˜mozukuâ€™ biology. DNA Research, 2016, 23, 561-570. | 1.5 | 73 |
| 358 | Repeat Sequences in the Tomato Genome. Compendium of Plant Genomes, 2016, , 173-199. | 0.3 | 1 |
| 359 | Genome Analysis of Plants. , 2016, , 1-27. | | 0 |
| 360 | TheDitylenchus destructorgenome provides new insights into the evolution of plant parasitic nematodes. Proceedings of the Royal Society B: Biological Sciences, 2016, 283, 20160942. | 1.2 | 29 |
| 361 | Exome capture from the spruce and pine gigaâ€genomes. Molecular Ecology Resources, 2016, 16, 1136-1146. | 2.2 | 75 |
| 362 | Genomic resources for a unique, low-virulence Babesia taxon from China. Parasites and Vectors, 2016, 9, 564. | 1.0 | 17 |
| 363 | Genome sequence and analysis of the Japanese morning glory Ipomoea nil. Nature Communications, 2016, 7, 13295. | 5.8 | 138 |

| # | Article | IF | Citations |
|---|---|---|---|
| 364 | The future of transposable element annotation and their classification in the light of functional genomics - what we can learn from the fables of Jean de la Fontaine?. Mobile Genetic Elements, 2016, 6, e1256852. | 1.8 | 27 |
| 365 | Ectomycorrhizal ecology is imprinted in the genome of the dominant symbiotic fungus Cenococcum geophilum. Nature Communications, 2016, 7, 12662. | 5.8 | 156 |
| 366 | The genome of the miiuy croaker reveals well-developed innate immune and sensory systems. Scientific Reports, 2016, 6, 21902. | 1.6 | 67 |
| 367 | CRISPRdigger: detecting CRISPRs with better direct repeat annotations. Scientific Reports, 2016, 6, 32942. | 1.6 | 19 |
| 368 | The Lungfish Transcriptome: A Glimpse into Molecular Evolution Events at the Transition from Water to Land. Scientific Reports, 2016, 6, 21571. | 1.6 | 75 |
| 369 | Genomic survey of a hyperparasitic microsporidianAmphiamblyssp. (Metchnikovellidae). Genome Biology and Evolution, 2016, 9, evw235. | 1.1 | 41 |
| 370 | Structural and functional analysis of the finished genome of the recently isolated toxic Anabaena sp. WA102. BMC Genomics, 2016, 17, 457. | 1.2 | 38 |
| 371 | Comparative genomics of Beauveria bassiana: uncovering signatures of virulence against mosquitoes. BMC Genomics, 2016, 17, 986. | 1.2 | 38 |
| 372 | The walnut (Juglans regia) genome sequence reveals diversity in genes coding for the biosynthesis of nonâ€structural polyphenols. Plant Journal, 2016, 87, 507-532. | 2.8 | 233 |
| 373 | Assembly of the draft genome of buckwheat and its applications in identifying agronomically useful genes. DNA Research, 2016, 23, 215-224. | 1.5 | 122 |
| 374 | Genus-Wide Comparative Genome Analyses ofColletotrichumSpecies Reveal Specific Gene Family Losses and Gains during Adaptation to Specific Infection Lifestyles. Genome Biology and Evolution, 2016, 8, 1467-1481. | 1.1 | 69 |
| 375 | Reference sequence (RefSeq) database at NCBI: current status, taxonomic expansion, and functional annotation. Nucleic Acids Research, 2016, 44, D733-D745. | 6.5 | 4,739 |
| 376 | Transcriptome sequencing based annotation and homologous evidence based scaffolding of Anguilla japonica draft genome. BMC Genomics, 2016, 17, 13. | 1.2 | 9 |
| 377 | Comparative genomics and prediction of conditionally dispensable sequences in legumeâ€“infecting Fusarium oxysporum formae speciales facilitates identification of candidate effectors. BMC Genomics, 2016, 17, 191. | 1.2 | 109 |
| 378 | Exploration of the Drosophila buzzatii transposable element content suggests underestimation of repeats in Drosophila genomes. BMC Genomics, 2016, 17, 344. | 1.2 | 22 |
| 379 | Identification and characterization of abundant repetitive sequences in Eragrostis tef cv. Enatite genome. BMC Plant Biology, 2016, 16, 39. | 1.6 | 16 |
| 380 | Identifying the effect of patient sharing on between-hospital genetic differentiation of methicillin-resistant Staphylococcus aureus. Genome Medicine, 2016, 8, 18. | 3.6 | 20 |
| 381 | Genome sequences of Knoxdaviesia capensis and K. proteae (Fungi: Ascomycota) from Protea trees in South Africa. Standards in Genomic Sciences, 2016, 11, 22. | 1.5 | 6 |

| # | Article | IF | Citations |
|---|---|---|---|
| 382 | Mining approximate patterns with frequent locally optimal occurrences. Discrete Applied Mathematics, 2016, 200, 123-152. | 0.5 | 5 |
| 383 | The Dfam database of repetitive DNA families. Nucleic Acids Research, 2016, 44, D81-D89. | 6.5 | 543 |
| 384 | Draft genome sequence of the silver pomfret fish, Pampus argenteus. Genome, 2016, 59, 51-58. | 0.9 | 14 |
| 385 | A Tale of Genome Compartmentalization: The Evolution of Virulence Clusters in Smut Fungi. Genome Biology and Evolution, 2016, 8, 681-704. | 1.1 | 125 |
| 386 | Potential and pitfalls of eukaryotic metagenome skimming: a test case for lichens. Molecular Ecology Resources, 2016, 16, 511-523. | 2.2 | 24 |
| 387 | Impact and insights from ancient repetitive elements in plant genomes. Current Opinion in Plant Biology, 2016, 30, 41-46. | 3.5 | 34 |
| 388 | From NGS assembly challenges to instability of fungal mitochondrial genomes: A case study in genome complexity. Computational Biology and Chemistry, 2016, 61, 258-269. | 1.1 | 13 |
| 389 | High-throughput transcriptome sequencing analysis provides preliminary insights into the biotransformation mechanism of Rhodopseudomonas palustris treated with alpha-rhamnetin-3-rhamnoside. Microbiological Research, 2016, 185, 1-12. | 2.5 | 2 |
| 390 | Evidence of horizontal gene transfer between obligate leaf nodule symbionts. ISME Journal, 2016, 10, 2092-2105. | 4.4 | 63 |
| 391 | Accurate Transposable Element Annotation Is Vital When Analyzing New Genome Assemblies. Genome Biology and Evolution, 2016, 8, 403-410. | 1.1 | 107 |
| 392 | Mind the gap; seven reasons to close fragmented genome assemblies. Fungal Genetics and Biology, 2016, 90, 24-30. | 0.9 | 108 |
| 393 | A Complete and Accurate Ab Initio Repeat Finding Algorithm. Interdisciplinary Sciences, Computational Life Sciences, 2016, 8, 75-83. | 2.2 | 7 |
| 394 | Genome sequencing and analysis of Kloeckera apiculata strain 34-9, a biocontrol agent against postharvest pathogens in citrus. Genes and Genomics, 2017, 39, 87-99. | 0.5 | 6 |
| 395 | Complex modular architecture around a simple toolkit of wing pattern genes. Nature Ecology and Evolution, 2017, 1, 52. | 3.4 | 179 |
| 396 | Improved genome assembly of American alligator genome reveals conserved architecture of estrogen signaling. Genome Research, 2017, 27, 686-696. | 2.4 | 38 |
| 397 | Identification of RAN1 orthologue associated with sex determination through whole genome sequencing analysis in fig (Ficus carica L.). Scientific Reports, 2017, 7, 41124. | 1.6 | 52 |
| 398 | Isolation and characterization of centromeric repetitive DNA sequences in Saccharum spontaneum. Scientific Reports, 2017, 7, 41659. | 1.6 | 31 |
| 399 | Extensive recent secondary contacts between four European white oak species. New Phytologist, 2017, 214, 865-878. | 3.5 | 113 |

| # | Article | IF | Citations |
|---|---|---|---|
| 400 | Biology, dynamics, and applications of transposable elements in basidiomycete fungi. Applied Microbiology and Biotechnology, 2017, 101, 1337-1350. | 1.7 | 35 |
| 401 | Evolutionary genomics of the cold-adapted diatom Fragilariopsis cylindrus. Nature, 2017, 541, 536-540. | 13.7 | 332 |
| 402 | Comparative genomics reveals high biological diversity and specific adaptations in the industrially and medically important fungal genus Aspergillus. Genome Biology, 2017, 18, 28. | 3.8 | 417 |
| 404 | The genome sequence of the wisent (Bison bonasus). GigaScience, 2017, 6, 1-5. | 3.3 | 22 |
| 405 | The Whole-Genome and Transcriptome of the Manila Clam (Ruditapes philippinarum). Genome Biology and Evolution, 2017, 9, 1487-1498. | 1.1 | 75 |
| 406 | Draft genome sequence of the Tibetan medicinal herb Rhodiola crenulata. GigaScience, 2017, 6, 1-5. | 3.3 | 33 |
| 407 | Widespread adenine N6-methylation of active genes in fungi. Nature Genetics, 2017, 49, 964-968. | 9.4 | 292 |
| 408 | The Comparative Analysis of the Repeat Regions from the Assembled Contigs. Lecture Notes in Electrical Engineering, 2017, , 432-439. | 0.3 | 0 |
| 409 | Discovery of SCORs: Anciently derived, highly conserved gene-associated repeats in stony corals. Genomics, 2017, 109, 383-390. | 1.3 | 3 |
| 410 | 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 |
| 411 | Comparative analysis of the predicted secretomes of Rosaceae scab pathogens Venturia inaequalis and V. pirina reveals expanded effector families and putative determinants of host range. BMC Genomics, 2017, 18, 339. | 1.2 | 68 |
| 412 | The genome sequence of sweet cherry (Prunus avium) for use in genomics-assisted breeding. DNA Research, 2017, 24, 499-508. | 1.5 | 212 |
| 413 | Genome sequencing of the sweetpotato whitefly Bemisia tabaci MED/Q. GigaScience, 2017, 6, 1-7. | 3.3 | 90 |
| 414 | Genome sequence of pacific abalone (Haliotis discus hannai): the first draft genome in family Haliotidae. GigaScience, 2017, 6, 1-8. | 3.3 | 84 |
| 415 | Genome sequencing of the winged midge, Parochlus steinenii, from the Antarctic Peninsula. GigaScience, 2017, 6, 1-8. | 3.3 | 15 |
| 416 | Ant-infecting Ophiocordyceps genomes reveal a high diversity of potential behavioral manipulation genes and a possible major role for enterotoxins. Scientific Reports, 2017, 7, 12508. | 1.6 | 52 |
| 417 | Genomic adaptation to polyphagy and insecticides in a major East Asian noctuid pest. Nature Ecology and Evolution, 2017, 1, 1747-1756. | 3.4 | 269 |
| 418 | Linkage mapping aided by de novo genome and transcriptome assembly in Portunus trituberculatus: applications in growth-related QTL and gene identification. Scientific Reports, 2017, 7, 7874. | 1.6 | 50 |

| # | Article | IF | Citations |
|---|---|---|---|
| 419 | Application of Data Mining Algorithms to Classify Biological Data: The Coffea canephora Genome Case. Communications in Computer and Information Science, 2017, , 156-170. | 0.4 | 7 |
| 420 | Analysis of the spotted gar genome suggests absence of causative link between ancestral genome duplication and transposable element diversification in teleost fish. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2017, 328, 629-637. | 0.6 | 16 |
| 421 | Comparative genomics of maize ear rot pathogens reveals expansion of carbohydrate-active enzymes and secondary metabolism backbone genes in Stenocarpella maydis. Fungal Biology, 2017, 121, 966-983. | 1.1 | 8 |
| 422 | The Discovery of Wild Date Palms in Oman Reveals a Complex Domestication History Involving Centers in the Middle East and Africa. Current Biology, 2017, 27, 2211-2218.e8. | 1.8 | 63 |
| 423 | Penelope-like retrotransposons in the genome of the Asian blood fluke Schistosoma japonicum (Trematoda: Schistosomatidae). Molecular Genetics, Microbiology and Virology, 2017, 32, 21-28. | 0.0 | 0 |
| 424 | The genome sequence of Bipolaris cookei reveals mechanisms of pathogenesis underlying target leaf spot of sorghum. Scientific Reports, 2017, 7, 17217. | 1.6 | 29 |
| 425 | Bacterial endosymbionts influence host sexuality and reveal reproductive genes of early divergent fungi. Nature Communications, 2017, 8, 1843. | 5.8 | 85 |
| 426 | Application of Bioinformatics in Understanding of Plant Stress Tolerance. , 2017, , 347-374. | | 8 |
| 427 | Genome-wide mapping and characterization of microsatellites in the swamp eel genome. Scientific Reports, 2017, 7, 3157. | 1.6 | 23 |
| 428 | The pomegranate (Punica granatum L.) genome and the genomics of punicalagin biosynthesis. Plant Journal, 2017, 91, 1108-1128. | 2.8 | 109 |
| 429 | From randomness to traplining: a framework for the study of routine movement behavior. Behavioral Ecology, 2017, 28, 280-287. | 1.0 | 23 |
| 430 | Comprehensive definition of genome features in Spirodela polyrhiza by highâ€depth physical mapping and shortâ€read <scp>DNA</scp> sequencing strategies. Plant Journal, 2017, 89, 617-635. | 2.8 | 115 |
| 431 | Genomic Basis of Adaptive Evolution: The Survival of Amur Ide (Leuciscuswaleckii) in an Extremely Alkaline Environment. Molecular Biology and Evolution, 2017, 34, 145-159. | 3.5 | 66 |
| 432 | Genomic skimming for identification of medium/highly abundant transposable elements in Arundo donax and Arundo plinii. Molecular Genetics and Genomics, 2017, 292, 157-171. | 1.0 | 4 |
| 433 | Complete mitochondrial genomes from the ferns Ophioglossum californicum and Psilotum nudum are highly repetitive with the largest organellar introns. New Phytologist, 2017, 213, 391-403. | 3.5 | 83 |
| 434 | Comparative analysis of the genomes of Stylophora pistillata and Acropora digitifera provides evidence for extensive differences between species of corals. Scientific Reports, 2017, 7, 17583. | 1.6 | 121 |
| 435 | Sequencing the Chickpea Genome. Compendium of Plant Genomes, 2017, , 117-123. | 0.3 | 0 |
| 436 | The Landscape of Extreme Genomic Variation in the Highly Adaptable Atlantic Killifish. Genome Biology and Evolution, 2017, 9, 659-676. | 1.1 | 43 |

| # | Article | IF | Citations |
|---|---|---|---|
| 437 | Genome sequence of the small brown planthopper, Laodelphax striatellus. GigaScience, 2017, 6, 1-12. | 3.3 | 106 |
| 438 | Comparative genomics of the tardigrades Hypsibius dujardini and Ramazzottius varieornatus. PLoS Biology, 2017, 15, e2002266. | 2.6 | 170 |
| 439 | The house spider genome reveals an ancient whole-genome duplication during arachnid evolution. BMC Biology, 2017, 15, 62. | 1.7 | 286 |
| 440 | SilkPathDB: a comprehensive resource for the study of silkworm pathogens. Database: the Journal of Biological Databases and Curation, 2017, 2017, . | 1.4 | 11 |
| 441 | Genome analysis of the foxtail millet pathogen Sclerospora graminicola reveals the complex effector repertoire of graminicolous downy mildews. BMC Genomics, 2017, 18, 897. | 1.2 | 27 |
| 442 | In Silico Approach for Characterization and Comparison of Repeats in the Genomes of Oil and Date Palms. Bioinformatics and Biology Insights, 2017, 11, 117793221770238. | 1.0 | 3 |
| 443 | Improved Genome Assembly and Annotation for the Rock Pigeon (Columba livia). G3: Genes, Genomes, Genetics, 2018, 8, 1391-1398. | 0.8 | 62 |
| 444 | Analysis of the Draft Genome of the Red Seaweed Gracilariopsis chorda Provides Insights into Genome Size Evolution in Rhodophyta. Molecular Biology and Evolution, 2018, 35, 1869-1886. | 3.5 | 71 |
| 445 | The Gastrodia elata genome provides insights into plant adaptation to heterotrophy. Nature Communications, 2018, 9, 1615. | 5.8 | 170 |
| 446 | Chromosome-scale assembly of the Monopterus genome. GigaScience, 2018, 7, . | 3.3 | 30 |
| 447 | The draft genome sequence of forest musk deer (Moschus berezovskii). GigaScience, 2018, 7, . | 3.3 | 26 |
| 448 | The genome sequence of the soft-rot fungus Penicillium purpurogenum reveals a high gene dosage for lignocellulolytic enzymes. Mycology, 2018, 9, 59-69. | 2.0 | 12 |
| 449 | Draft genome sequence of ramie, Boehmeria nivea (L.) Gaudich. Molecular Ecology Resources, 2018, 18, 639-645. | 2.2 | 46 |
| 450 | High intraspecific genome diversity in the model arbuscular mycorrhizal symbiont Rhizophagus irregularis. New Phytologist, 2018, 220, 1161-1171. | 3.5 | 206 |
| 451 | A hybrid-hierarchical genome assembly strategy to sequence the invasive golden mussel, Limnoperna fortunei. GigaScience, 2018, 7, . | 3.3 | 60 |
| 452 | The pomegranate (Punica granatum L.) genome provides insights into fruit quality and ovule developmental biology. Plant Biotechnology Journal, 2018, 16, 1363-1374. | 4.1 | 115 |
| 453 | Comparative genomics and transcriptomics depict ericoid mycorrhizal fungi as versatile saprotrophs and plant mutualists. New Phytologist, 2018, 217, 1213-1229. | 3.5 | 185 |
| 454 | Analysis of the Aedes albopictus C6/36 genome provides insight into cell line utility for viral propagation. GigaScience, 2018, 7, 1-13. | 3.3 | 51 |

| # | Article | IF | Citations |
|---|---|---|---|
| 455 | Genome sequence of the Japanese oak silk moth, Antheraea yamamai: the first draft genome in the family Saturniidae. GigaScience, 2018, 7, 1-11. | 3.3 | 20 |
| 456 | Comparative genome and transcriptome analyses reveal adaptations to opportunistic infections in woody plant degrading pathogens of Botryosphaeriaceae. DNA Research, 2018, 25, 87-102. | 1.5 | 60 |
| 457 | RepLong: de novo repeat identification using long read sequencing data. Bioinformatics, 2018, 34, 1099-1107. | 1.8 | 21 |
| 458 | Rapid genome shrinkage in a self-fertile nematode reveals sperm competition proteins. Science, 2018, 359, 55-61. | 6.0 | 102 |
| 459 | Comparative genome analysis of 52 fish species suggests differential associations of repetitive elements with their living aquatic environments. BMC Genomics, 2018, 19, 141. | 1.2 | 89 |
| 460 | Intraspecific comparative genomics of isolates of the Norway spruce pathogen (Heterobasidion) Tj ETQq1 1 0.784314 rgBT /Overlock | 1.2 | 37 |
| 461 | Comparative genomics of the wheat fungal pathogen Pyrenophora tritici-repentis reveals chromosomal variations and genome plasticity. BMC Genomics, 2018, 19, 279. | 1.2 | 56 |
| 462 | Integrative analysis of large scale transcriptome data draws a comprehensive landscape of Phaeodactylum tricornutum genome and evolutionary origin of diatoms. Scientific Reports, 2018, 8, 4834. | 1.6 | 131 |
| 463 | Draft genome of an iconic Red Sea reef fish, the blacktail butterflyfish (Chaetodon austriacus): current status and its characteristics. Molecular Ecology Resources, 2018, 18, 347-355. | 2.2 | 11 |
| 464 | Genome structure of Rosa multiflora, a wild ancestor of cultivated roses. DNA Research, 2018, 25, 113-121. | 1.5 | 70 |
| 465 | Know your farmer: Ancient origins and multiple independent domestications of ambrosia beetle fungal cultivars. Molecular Ecology, 2018, 27, 2077-2094. | 2.0 | 67 |
| 466 | The repeat structure of two paralogous genes, Yersinia ruckeri invasin (yrlnv) and a â€œY. ruckeri invasin-like moleculeâ€• (yrllm) sheds light on the evolution of adhesive capacities of a fish pathogen. Journal of Structural Biology, 2018, 201, 171-183. | 1.3 | 22 |
| 467 | Genome sequences of Chlorella sorokiniana <scp>UTEX</scp> 1602 and Micractinium conductrix <scp>SAG</scp> 241.80: implications to maltose excretion by a green alga. Plant Journal, 2018, 93, 566-586. | 2.8 | 68 |
| 468 | Nemertean and phoronid genomes reveal lophotrochozoan evolution and the origin of bilaterian heads. Nature Ecology and Evolution, 2018, 2, 141-151. | 3.4 | 98 |
| 469 | Contemporary evolution of a Lepidopteran species, Heliothis virescens, in response to modern agricultural practices. Molecular Ecology, 2018, 27, 167-181. | 2.0 | 28 |
| 470 | ConTEdb: a comprehensive database of transposable elements in conifers. Database: the Journal of Biological Databases and Curation, 2018, 2018, . | 1.4 | 15 |
| 471 | First draft genome sequence of the rock bream in the family Oplegnathidae. Scientific Data, 2018, 5, 180234. | 2.4 | 4 |
| 472 | Patterns of Nucleotide Deletion and Insertion Inferred from Bacterial Pseudogenes. Genome Biology and Evolution, 2018, 10, 1792-1802. | 1.1 | 12 |

| # | Article | IF | Citations |
|---|---|---|---|
| 473 | Predicting Genes in Single Genomes with AUGUSTUS. Current Protocols in Bioinformatics, 2019, 65, e57. | 25.8 | 225 |
| 474 | N6-Methyladenine DNA Methylation in Japonica and Indica Rice Genomes and Its Association with Gene Expression, Plant Development, and Stress Responses. Molecular Plant, 2018, 11, 1492-1508. | 3.9 | 123 |
| 475 | Endangered PÃ¨re Davidâ€™s deer genome provides insights into population recovering. Evolutionary Applications, 2018, 11, 2040-2053. | 1.5 | 19 |
| 476 | FishTEDB: a collective database of transposable elements identified in the complete genomes of fish. Database: the Journal of Biological Databases and Curation, 2018, 2018, . | 1.4 | 40 |
| 477 | First Draft Genome for Red Sea Bream of Family Sparidae. Frontiers in Genetics, 2018, 9, 643. | 1.1 | 22 |
| 478 | Deciphering the evolutionary signatures of pinnipeds using novel genome sequences: The first genomes of Phoca largha, Callorhinus ursinus, and Eumetopias jubatus. Scientific Reports, 2018, 8, 16877. | 1.6 | 7 |
| 479 | Genome sequence of walking catfish (Clarias batrachus) provides insights into terrestrial adaptation. BMC Genomics, 2018, 19, 952. | 1.2 | 36 |
| 480 | Genome survey sequencing for the characterization of genetic background of Dracaena cambodiana and its defense response during dragonâ€™s blood formation. PLoS ONE, 2018, 13, e0209258. | 1.1 | 16 |
| 481 | Downregulation of RdDM during strawberry fruit ripening. Genome Biology, 2018, 19, 212. | 3.8 | 147 |
| 482 | A draft genome of the striped catfish, Pangasianodon hypophthalmus, for comparative analysis of genes relevant to development and a resource for aquaculture improvement. BMC Genomics, 2018, 19, 733. | 1.2 | 34 |
| 483 | Allele-defined genome of the autopolyploid sugarcane Saccharum spontaneum L.. Nature Genetics, 2018, 50, 1565-1573. | 9.4 | 463 |
| 484 | The genome of common long-arm octopus Octopus minor. GigaScience, 2018, 7, . | 3.3 | 43 |
| 485 | Fast construction of a reference genome: challenges and opportunities using â€˜Royal Galaâ€™ apple as a case study. Acta Horticulturae, 2018, , 35-40. | 0.1 | 0 |
| 486 | The annotation of repetitive elements in the genome of channel catfish (Ictalurus punctatus). PLoS ONE, 2018, 13, e0197371. | 1.1 | 13 |
| 487 | PIWI genes and piRNAs are ubiquitously expressed in mollusks and show patterns of lineage-specific adaptation. Communications Biology, 2018, 1, 137. | 2.0 | 54 |
| 488 | Deciphering Genome Organization of the Polyploid Brassica napus. Compendium of Plant Genomes, 2018, , 87-97. | 0.3 | 0 |
| 489 | Genomic comparison of Trypanosoma conorhini and Trypanosoma rangeli to Trypanosoma cruzi strains of high and low virulence. BMC Genomics, 2018, 19, 770. | 1.2 | 14 |
| 490 | An improved approach for reconstructing consensus repeats from short sequence reads. BMC Genomics, 2018, 19, 566. | 1.2 | 1 |

| # | Article | IF | Citations |
|---|---|---|---|
| 491 | A New Reference Genome Shows the One-Speed Genome Structure of the Barley PathogenRamularia collo-cygni. Genome Biology and Evolution, 2018, 10, 3243-3249. | 1.1 | 30 |
| 492 | Firefly genomes illuminate parallel origins of bioluminescence in beetles. ELife, 2018, 7, . | 2.8 | 108 |
| 493 | Genomic overview of closely related fungi with different Protea host ranges. Fungal Biology, 2018, 122, 1201-1214. | 1.1 | 1 |
| 494 | A benchmark study of k-mer counting methods for high-throughput sequencing. GigaScience, 2018, 7, . | 3.3 | 53 |
| 495 | Measuring the Mappability Spectrum of Reference Genome Assemblies. , 2018, , . | | 3 |
| 496 | â€œOut of the Canâ€: A Draft Genome Assembly, Liver Transcriptome, and Nutrigenomics of the European Sardine, Sardina pilchardus. Genes, 2018, 9, 485. | 1.0 | 30 |
| 497 | The genome of Naegleria lovaniensis, the basis for a comparative approach to unravel pathogenicity factors of the human pathogenic amoeba N. fowleri. BMC Genomics, 2018, 19, 654. | 1.2 | 23 |
| 498 | Computational tools to unmask transposable elements. Nature Reviews Genetics, 2018, 19, 688-704. | 7.7 | 173 |
| 499 | Genome sequencing of rice subspecies and genetic analysis of recombinant lines reveals regional yield- and quality-associated loci. BMC Biology, 2018, 16, 102. | 1.7 | 66 |
| 500 | Evolution of the U.S. Biological Select Agent Rathayibacter toxicus. MBio, 2018, 9, . | 1.8 | 10 |
| 501 | Drosophila parasitoid wasps bears a distinct DNA transposon profile. Mobile DNA, 2018, 9, 23. | 1.3 | 7 |
| 502 | Identification of transposons near predicted lncRNA and mRNA pools of Prunus mume using an integrative transposable element database constructed from Rosaceae plant genomes. Molecular Genetics and Genomics, 2018, 293, 1301-1316. | 1.0 | 3 |
| 503 | SPTEdb: a database for transposable elements in salicaceous plants. Database: the Journal of Biological Databases and Curation, 2018, 2018, . | 1.4 | 12 |
| 504 | Whole-genome data reveal the complex history of a diverse ecological community. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E6507-E6515. | 3.3 | 45 |
| 505 | De novo genome assembly of Oryza granulata reveals rapid genome expansion and adaptive evolution. Communications Biology, 2018, 1, 84. | 2.0 | 24 |
| 506 | A transposable element annotation pipeline and expression analysis reveal potentially active elements in the microalga Tisochrysis lutea. BMC Genomics, 2018, 19, 378. | 1.2 | 45 |
| 507 | The genomic features of parasitism, Polyembryony and immune evasion in the endoparasitic wasp Macrocentrus cingulum. BMC Genomics, 2018, 19, 420. | 1.2 | 53 |
| 508 | A High-Quality, Long-Read De Novo Genome Assembly to Aid Conservation of Hawaiiâ€™s Last Remaining Crow Species. Genes, 2018, 9, 393. | 1.0 | 22 |

| # | Article | IF | Citations |
|---|---|---|---|
| 509 | Extensive exchange of transposable elements in the Drosophila pseudoobscura group. Mobile DNA, 2018, 9, 20. | 1.3 | 28 |
| 510 | Genomic signatures of mitonuclear coevolution across populations of Tigriopus californicus. Nature Ecology and Evolution, 2018, 2, 1250-1257. | 3.4 | 154 |
| 511 | Resequencing of 243 diploid cotton accessions based on an updated A genome identifies the genetic basis of key agronomic traits. Nature Genetics, 2018, 50, 796-802. | 9.4 | 401 |
| 512 | Sequencing Plant Genomes. Progress in Botany Fortschritte Der Botanik, 2018, , 109-193. | 0.1 | 4 |
| 513 | Comparison of three assembly strategies for a heterozygous seedless grapevine genome assembly. BMC Genomics, 2018, 19, 57. | 1.2 | 15 |
| 514 | Draft genome of Glyptosternon maculatum, an endemic fish from Tibet Plateau. GigaScience, 2018, 7, . | 3.3 | 18 |
| 515 | Tung Tree (Vernicia fordii, Hemsl.) Genome and Transcriptome Sequencing Reveals Co-Ordinate Up-Regulation of Fatty Acid Î²-Oxidation and Triacylglycerol Biosynthesis Pathways During Eleostearic Acid Accumulation in Seeds. Plant and Cell Physiology, 2018, 59, 1990-2003. | 1.5 | 45 |
| 516 | A reference genome of the European beech (Fagus sylvatica L.). GigaScience, 2018, 7, . | 3.3 | 58 |
| 517 | Superior ab initio identification, annotation and characterisation of TEs and segmental duplications from genome assemblies. PLoS ONE, 2018, 13, e0193588. | 1.1 | 27 |
| 518 | Harnessing the power of phylogenomics to disentangle the directionality and signatures of interkingdom host jumping in the parasitic fungal genus Tolypocladium. Mycologia, 2018, 110, 104-117. | 0.8 | 12 |
| 519 | Fungal Genome Annotation. Methods in Molecular Biology, 2018, 1775, 171-184. | 0.4 | 14 |
| 520 | Oak genome reveals facets of long lifespan. Nature Plants, 2018, 4, 440-452. | 4.7 | 303 |
| 521 | Long-read sequencing and de novo genome assembly of Ammopiptanthus nanus, a desert shrub. GigaScience, 2018, 7, . | 3.3 | 22 |
| 522 | Repeat in Genomes: How and Why You Should Consider Them in Genome Analyses?. , 2019, , 210-220. | | 1 |
| 523 | Dicyemid Mesozoans: A Unique Parasitic Lifestyle and a Reduced Genome. Genome Biology and Evolution, 2019, 11, 2232-2243. | 1.1 | 15 |
| 524 | Draft Genome of the Rice Coral Montipora capitata Obtained from Linked-Read Sequencing. Genome Biology and Evolution, 2019, 11, 2045-2054. | 1.1 | 30 |
| 525 | Retrotransposons in Plant Genomes: Structure, Identification, and Classification through Bioinformatics and Machine Learning. International Journal of Molecular Sciences, 2019, 20, 3837. | 1.8 | 56 |
| 526 | Characterizations of transposable element (TE) landscape in Rhizoctonia solani. AIP Conference Proceedings, 2019, , . | 0.3 | 0 |

| # | Article | IF | Citations |
|---|---|---|---|
| 527 | Rapid evolution of piRNA pathway and its transposon targets in Japanese flounder (Paralichthys) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 7 100609. | 0.4 | 9 |
| 528 | Chromosomal-level assembly of the blood clam, Scapharca (Anadara) broughtonii, using long sequence reads and Hi-C. GigaScience, 2019, 8, . | 3.3 | 63 |
| 529 | PolyCRACKER, a robust method for the unsupervised partitioning of polyploid subgenomes by signatures of repetitive DNA evolution. BMC Genomics, 2019, 20, 580. | 1.2 | 10 |
| 530 | De novo genome assembly of the endangered Acer yangbiense, a plant species with extremely small populations endemic to Yunnan Province, China. GigaScience, 2019, 8, . | 3.3 | 42 |
| 531 | Genome-Wide Identification of Microsatellites and Transposable Elements in the Dromedary Camel Genome Using Whole-Genome Sequencing Data. Frontiers in Genetics, 2019, 10, 692. | 1.1 | 6 |
| 532 | Transposable Elements: Classification, Identification, and Their Use As a Tool For Comparative Genomics. Methods in Molecular Biology, 2019, 1910, 177-207. | 0.4 | 74 |
| 533 | Genome sequence of Isaria javanica and comparative genome analysis insights into family S53 peptidase evolution in fungal entomopathogens. Applied Microbiology and Biotechnology, 2019, 103, 7111-7128. | 1.7 | 14 |
| 534 | Pseudomolecule-level assembly of the Chinese oil tree yellowhorn (Xanthoceras sorbifolium) genome. GigaScience, 2019, 8, . | 3.3 | 47 |
| 535 | Genetic basis of species-specific genitalia reveals role in species diversification. Science Advances, 2019, 5, eaav9939. | 4.7 | 22 |
| 536 | Genome Sequences Provide Insights into the Reticulate Origin and Unique Traits of Woody Bamboos. Molecular Plant, 2019, 12, 1353-1365. | 3.9 | 116 |
| 537 | Draft genome sequence of cauliflower (Brassica oleracea L. var. botrytis) provides new insights into the C genome in Brassica species. Horticulture Research, 2019, 6, 82. | 2.9 | 53 |
| 538 | Extensive intraspecific gene order and gene structural variations in upland cotton cultivars. Nature Communications, 2019, 10, 2989. | 5.8 | 144 |
| 539 | A draft genome for Spatholobus suberectus. Scientific Data, 2019, 6, 113. | 2.4 | 28 |
| 540 | Expansion of phycobilisome linker gene families in mesophilic red algae. Nature Communications, 2019, 10, 4823. | 5.8 | 15 |
| 541 | A high-quality Actinidia chinensis (kiwifruit) genome. Horticulture Research, 2019, 6, 117. | 2.9 | 109 |
| 542 | Chromosomeâ€level genome assembly of the razor clam Sinonovacula constricta (Lamarck, 1818). Molecular Ecology Resources, 2019, 19, 1647-1658. | 2.2 | 45 |
| 543 | The sequence and de novo assembly of hog deer genome. Scientific Data, 2019, 6, 180305. | 2.4 | 10 |
| 544 | The wild sweetpotato (Ipomoea trifida) genome provides insights into storage root development. BMC Plant Biology, 2019, 19, 119. | 1.6 | 33 |

| # | Article | IF | Citations |
|---|---|---|---|
| 545 | Whole Genome Assembly of the Snout Otter Clam, Lutraria rhynchaena, Using Nanopore and Illumina Data, Benchmarked Against Bivalve Genome Assemblies. Frontiers in Genetics, 2019, 10, 1158. | 1.1 | 16 |
| 546 | The Rhododendron Genome and Chromosomal Organization Provide Insight into Shared Whole-Genome Duplications across the Heath Family (Ericaceae). Genome Biology and Evolution, 2019, 11, 3353-3371. | 1.1 | 47 |
| 547 | Early Diverging Fungus Mucor circinelloides Lacks Centromeric Histone CENP-A and Displays a Mosaic of Point and Regional Centromeres. Current Biology, 2019, 29, 3791-3802.e6. | 1.8 | 77 |
| 548 | Chromosome genome assembly and annotation of the yellowbelly pufferfish with PacBio and Hi-C sequencing data. Scientific Data, 2019, 6, 267. | 2.4 | 21 |
| 549 | Genome assembly of the common pheasant Phasianus colchicus, a model for speciation and ecological genomics. Genome Biology and Evolution, 2019, 11, 3326-3331. | 1.1 | 6 |
| 550 | Evolutionary lability inHoxcluster structure and gene expression inAnolislizards. Evolution Letters, 2019, 3, 474-484. | 1.6 | 11 |
| 551 | A high-quality genome assembly for the endangered golden snub-nosed monkey (Rhinopithecus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 5 | 3.3 | 22 |
| 552 | A chromosome-level draft genome of the grain aphid Sitobion miscanthi. GigaScience, 2019, 8, . | 3.3 | 41 |
| 553 | The evolution study on Oryza rufipogon. dw by whole-genome sequencing. Journal of Genetics, 2019, 98, 1. | 0.4 | 3 |
| 554 | Assembly and Annotation of a Draft Genome of the Medicinal Plant Polygonum cuspidatum. Frontiers in Plant Science, 2019, 10, 1274. | 1.7 | 36 |
| 555 | Intraspecific Variation in Protists: Clues for Microevolution from Poteriospumella lacustris (Chrysophyceae). Genome Biology and Evolution, 2019, 11, 2492-2504. | 1.1 | 7 |
| 556 | The sequencing and de novo assembly of the Larimichthys crocea genome using PacBio and Hi-C technologies. Scientific Data, 2019, 6, 188. | 2.4 | 50 |
| 557 | The sequence and de novo assembly of Takifugu bimaculatus genome using PacBio and Hi-C technologies. Scientific Data, 2019, 6, 187. | 2.4 | 29 |
| 558 | Genome sequence ofMalania oleifera, a tree with great value for nervonic acid production. GigaScience, 2019, 8, . | 3.3 | 36 |
| 559 | Comparative analyses identify genomic features potentially involved in the evolution of birds-of-paradise. GigaScience, 2019, 8, . | 3.3 | 22 |
| 560 | The Genome ofArmadillidium vulgare(Crustacea, Isopoda) Provides Insights into Sex Chromosome Evolution in the Context of Cytoplasmic Sex Determination. Molecular Biology and Evolution, 2019, 36, 727-741. | 3.5 | 43 |
| 561 | De Novo Sequencing and Hybrid Assembly of the Biofuel Crop Jatropha curcas L.: Identification of Quantitative Trait Loci for Geminivirus Resistance. Genes, 2019, 10, 69. | 1.0 | 20 |
| 562 | The genome of broomcorn millet. Nature Communications, 2019, 10, 436. | 5.8 | 130 |

| # | Article | IF | Citations |
|---|---|---|---|
| 563 | Genomic changes associated with adaptation to arid environments in cactophilic Drosophila species. BMC Genomics, 2019, 20, 52. | 1.2 | 22 |
| 564 | Heterozygous diploid structure of Amorphotheca resinae ZN1 contributes efficient biodetoxification on solid pretreated corn stover. Biotechnology for Biofuels, 2019, 12, 126. | 6.2 | 24 |
| 565 | Tracing the history of LINE and SINE extinction in sigmodontine rodents. Mobile DNA, 2019, 10, 22. | 1.3 | 17 |
| 566 | Comparative genome analysis indicates high evolutionary potential of pathogenicity genes in Colletotrichum tanaceti. PLoS ONE, 2019, 14, e0212248. | 1.1 | 19 |
| 567 | LtrDetector: A tool-suite for detecting long terminal repeat retrotransposons de-novo. BMC Genomics, 2019, 20, 450. | 1.2 | 19 |
| 568 | Genome Miningâ€“Based Identification of Identical Multirepeat Sequences in Plasmodium falciparum Genome for Highly Sensitive Real-Time Quantitative PCR Assay and Its Application in Malaria Diagnosis. Journal of Molecular Diagnostics, 2019, 21, 824-838. | 1.2 | 12 |
| 569 | De novo Inference of Diversity Genes and Analysis of Non-canonical V(DD)J Recombination in Immunoglobulins. Frontiers in Immunology, 2019, 10, 987. | 2.2 | 22 |
| 570 | Generic Repeat Finder: A High-Sensitivity Tool for Genome-Wide De Novo Repeat Detection. Plant Physiology, 2019, 180, 1803-1815. | 2.3 | 64 |
| 571 | De Novo Genome Sequence Assembly of Dwarf Coconut (Cocos nucifera L. â€˜Catigan Green') Genes, Genomes, Genetics, 2019, 9, 2377-2393. | 0.8 | 55 |
| 572 | The Draft Genome of Eggplant. Compendium of Plant Genomes, 2019, , 55-63. | 0.3 | 0 |
| 573 | The Reference Genome Sequence of Scutellaria baicalensis Provides Insights into the Evolution of Wogonin Biosynthesis. Molecular Plant, 2019, 12, 935-950. | 3.9 | 121 |
| 574 | Insect genomes: progress and challenges. Insect Molecular Biology, 2019, 28, 739-758. | 1.0 | 115 |
| 575 | DeviaTE: Assemblyâ€free analysis and visualization of mobile genetic element composition. Molecular Ecology Resources, 2019, 19, 1346-1354. | 2.2 | 28 |
| 576 | MGERT: a pipeline to retrieve coding sequences of mobile genetic elements from genome assemblies. Mobile DNA, 2019, 10, 21. | 1.3 | 2 |
| 577 | ImtRDB: a database and software for mitochondrial imperfect interspersed repeats annotation. BMC Genomics, 2019, 20, 295. | 1.2 | 10 |
| 578 | Medusozoan genomes inform the evolution of the jellyfish body plan. Nature Ecology and Evolution, 2019, 3, 811-822. | 3.4 | 94 |
| 579 | Whole genomes and transcriptomes reveal adaptation and domestication of pistachio. Genome Biology, 2019, 20, 79. | 3.8 | 81 |
| 580 | Genomic Plasticity Mediated by Transposable Elements in the Plant Pathogenic Fungus Colletotrichum higginsianum. Genome Biology and Evolution, 2019, 11, 1487-1500. | 1.1 | 47 |

| # | Article | IF | Citations |
|---|---|---|---|
| 581 | Whole-Genome Annotation with BRAKER. Methods in Molecular Biology, 2019, 1962, 65-95. | 0.4 | 461 |
| 582 | Chromosome-Level Assembly of the Chinese Seabass (Lateolabrax maculatus) Genome. Frontiers in Genetics, 2019, 10, 275. | 1.1 | 33 |
| 583 | Draft genome of the brown alga, Nemacystus decipiens, Onna-1 strain: Fusion of genes involved in the sulfated fucan biosynthesis pathway. Scientific Reports, 2019, 9, 4607. | 1.6 | 33 |
| 584 | Nanopore sequencing reads improve assembly and gene annotation of the Parochlus steinenii genome. Scientific Reports, 2019, 9, 5095. | 1.6 | 19 |
| 585 | A re-annotation of the Anopheles darlingi mobilome. Genetics and Molecular Biology, 2019, 42, 125-131. | 0.6 | 5 |
| 586 | The genome of the jellyfish Clytia hemisphaerica and the evolution of the cnidarian life-cycle. Nature Ecology and Evolution, 2019, 3, 801-810. | 3.4 | 135 |
| 587 | Population Genomic Analysis and De Novo Assembly Reveal the Origin of Weedy Rice as an Evolutionary Game. Molecular Plant, 2019, 12, 632-647. | 3.9 | 61 |
| 588 | Genome sequence of the corn leaf aphid (Rhopalosiphum maidisFitch). GigaScience, 2019, 8, . | 3.3 | 60 |
| 589 | The genome of the giant Nomuraâ€™s jellyfish sheds light on the early evolution of active predation. BMC Biology, 2019, 17, 28. | 1.7 | 38 |
| 590 | Molecular evolutionary trends and feeding ecology diversification in the Hemiptera, anchored by the milkweed bug genome. Genome Biology, 2019, 20, 64. | 3.8 | 114 |
| 591 | De novo genome assembly of the white-spotted flower chafer (Protaetia brevitarsis). GigaScience, 2019, 8, . | 3.3 | 28 |
| 592 | A Chromosome-Scale Genome Assembly of Paper Mulberry (Broussonetia papyrifera) Provides New Insights into Its Forage and Papermaking Usage. Molecular Plant, 2019, 12, 661-677. | 3.9 | 83 |
| 593 | The genomic basis for colonizing the freezing Southern Ocean revealed by Antarctic toothfish and Patagonian robalo genomes. GigaScience, 2019, 8, . | 3.3 | 47 |
| 594 | Antarctic blackfin icefish genome reveals adaptations to extreme environments. Nature Ecology and Evolution, 2019, 3, 469-478. | 3.4 | 115 |
| 595 | The Galleria mellonella Hologenome Supports Microbiota-Independent Metabolism of Long-Chain Hydrocarbon Beeswax. Cell Reports, 2019, 26, 2451-2464.e5. | 2.9 | 103 |
| 596 | DNA Methylation Patterns in the Social Spider, Stegodyphus dumicola. Genes, 2019, 10, 137. | 1.0 | 46 |
| 597 | Chromosome rearrangements shape the diversification of secondary metabolism in the cyclosporin producing fungus Tolypocladium inflatum. BMC Genomics, 2019, 20, 120. | 1.2 | 22 |
| 598 | IMA Genome-F 11. IMA Fungus, 2019, 10, 13. | 1.7 | 12 |

| # | Article | IF | Citations |
|---|---|---|---|
| 599 | Draft genome assembly of Tenualosa ilisha, Hilsa shad, provides resource for osmoregulation studies. Scientific Reports, 2019, 9, 16511. | 1.6 | 23 |
| 600 | The persimmon (Diospyros oleifera Cheng) genome provides new insights into the inheritance of astringency and ancestral evolution. Horticulture Research, 2019, 6, 138. | 2.9 | 39 |
| 601 | Lipid and DHA-production in Aurantiochytrium sp. â€“ Responses to nitrogen starvation and oxygen limitation revealed by analyses of production kinetics and global transcriptomes. Scientific Reports, 2019, 9, 19470. | 1.6 | 48 |
| 602 | Benchmarking transposable element annotation methods for creation of a streamlined, comprehensive pipeline. Genome Biology, 2019, 20, 275. | 3.8 | 579 |
| 603 | The genetic basis of adaptive evolution in parasitic environment from the Angiostrongylus cantonensis genome. PLoS Neglected Tropical Diseases, 2019, 13, e0007846. | 1.3 | 9 |
| 604 | A chromosome-level genome assembly of the Chinese tupelo Nyssa sinensis. Scientific Data, 2019, 6, 282. | 2.4 | 10 |
| 605 | Trochodendron aralioides, the first chromosome-level draft genome in Trochodendrales and a valuable resource for basal eudicot research. GigaScience, 2019, 8, . | 3.3 | 20 |
| 606 | A de novo genome assembly of the dwarfing pear rootstock Zhongai 1. Scientific Data, 2019, 6, 281. | 2.4 | 28 |
| 607 | Genomic insights into mite phylogeny, fitness, development, and reproduction. BMC Genomics, 2019, 20, 954. | 1.2 | 25 |
| 608 | Liriodendron genome sheds light on angiosperm phylogeny and speciesâ€“pair differentiation. Nature Plants, 2019, 5, 18-25. | 4.7 | 163 |
| 609 | A physical and genetic map of Cannabis sativa identifies extensive rearrangements at the THC/CBD acid synthase loci. Genome Research, 2019, 29, 146-156. | 2.4 | 160 |
| 610 | A highâ€quality chromosomeâ€level genome assembly of a generalist herbivore, Trichoplusia ni. Molecular Ecology Resources, 2019, 19, 485-496. | 2.2 | 47 |
| 611 | Comparative genomics of Rhizophagus irregularis, R.Âcerebriforme, R.Âdiaphanus and Gigaspora rosea highlights specific genetic features in Glomeromycotina. New Phytologist, 2019, 222, 1584-1598. | 3.5 | 133 |
| 612 | Draft Genome Assembly and Population Genetics of an Agricultural Pollinator, the Solitary Alkali Bee (Halictidae: Nomia melanderi). G3: Genes, Genomes, Genetics, 2019, 9, 625-634. | 0.8 | 19 |
| 613 | Alignment-free approaches for predicting novel Nuclear Mitochondrial Segments (NUMTs) in the human genome. Gene, 2019, 691, 141-152. | 1.0 | 14 |
| 614 | Phylogenomics of Endogonaceae and evolution of mycorrhizas within Mucoromycota. New Phytologist, 2019, 222, 511-525. | 3.5 | 81 |
| 615 | Fast and global detection of periodic sequence repeats in large genomic resources. Nucleic Acids Research, 2019, 47, e8-e8. | 6.5 | 7 |
| 616 | A chromosomeâ€level genome assembly reveals the genetic basis of cold tolerance in a notorious rice insect pest, Chilo suppressalis. Molecular Ecology Resources, 2020, 20, 268-282. | 2.2 | 51 |

| # | Article | IF | Citations |
|---|---|---|---|
| 617 | The pomegranate (Punica granatum L.) draft genome dissects genetic divergence between softâ€• and hardâ€seeded cultivars. Plant Biotechnology Journal, 2020, 18, 955-968. | 4.1 | 70 |
| 618 | Genome assembly provides insights into the genome evolution and flowering regulation of orchardgrass. Plant Biotechnology Journal, 2020, 18, 373-388. | 4.1 | 51 |
| 619 | Chromosomeâ€level genome assembly of the predator Propylea japonica to understand its tolerance to insecticides and high temperatures. Molecular Ecology Resources, 2020, 20, 292-307. | 2.2 | 43 |
| 620 | Mesostigma viride Genome and Transcriptome Provide Insights into the Origin and Evolution of Streptophyta. Advanced Science, 2020, 7, 1901850. | 5.6 | 40 |
| 621 | Deciphering the highâ€quality genome sequence of coriander that causes controversial feelings. Plant Biotechnology Journal, 2020, 18, 1444-1456. | 4.1 | 56 |
| 622 | The Coix Genome Provides Insights into Panicoideae Evolution and Papery Hull Domestication. Molecular Plant, 2020, 13, 309-320. | 3.9 | 28 |
| 623 | Comparison of Arachis monticola with Diploid and Cultivated Tetraploid Genomes Reveals Asymmetric Subgenome Evolution and Improvement of Peanut. Advanced Science, 2020, 7, 1901672. | 5.6 | 43 |
| 624 | Longâ€read sequencing and de novo assembly of the Luffa cylindrica (L.) Roem. genome. Molecular Ecology Resources, 2020, 20, 511-519. | 2.2 | 27 |
| 625 | Chromosomalâ€level assembly of Takifugu obscurus (Abe, 1949) genome using thirdâ€generation DNA sequencing and Hiâ€C analysis. Molecular Ecology Resources, 2020, 20, 520-530. | 2.2 | 46 |
| 626 | Draft Genome of a Blister Beetle Mylabris aulica. Frontiers in Genetics, 2020, 10, 1281. | 1.1 | 7 |
| 627 | Large-scale survey reveals pervasiveness and potential function of endogenous geminiviral sequences in plants. Virus Evolution, 2020, 6, veaa071. | 2.2 | 15 |
| 628 | Blue genome: chromosomeâ€scale genome reveals the evolutionary and molecular basis of indigo biosynthesis in Strobilanthes cusia. Plant Journal, 2020, 104, 864-879. | 2.8 | 15 |
| 629 | Reconstruction of ancient homeobox gene linkages inferred from a new high-quality assembly of the Hong Kong oyster (Magallana hongkongensis) genome. BMC Genomics, 2020, 21, 713. | 1.2 | 24 |
| 630 | The genome of Chinese flowering cherry (Cerasus serrulata) provides new insights into Cerasus species. Horticulture Research, 2020, 7, 165. | 2.9 | 22 |
| 631 | High-quality nuclear genome for Sarcoptes scabieiâ€"A critical resource for a neglected parasite. PLoS Neglected Tropical Diseases, 2020, 14, e0008720. | 1.3 | 25 |
| 632 | The mole genome reveals regulatory rearrangements associated with adaptive intersexuality. Science, 2020, 370, 208-214. | 6.0 | 41 |
| 633 | Genomes of the Banyan Tree and Pollinator Wasp Provide Insights into Fig-Wasp Coevolution. Cell, 2020, 183, 875-889.e17. | 13.5 | 71 |
| 634 | Genomic insights of body plan transitions from bilateral to pentameral symmetry in Echinoderms. Communications Biology, 2020, 3, 371. | 2.0 | 34 |

| # | Article | IF | Citations |
|---|---|---|---|
| 635 | The highâ€quality genome of diploid strawberry (Fragaria nilgerrensis) provides new insights into anthocyanin accumulation. Plant Biotechnology Journal, 2020, 18, 1908-1924. | 4.1 | 51 |
| 636 | Comprehensive Chromosome End Remodeling during Programmed DNA Elimination. Current Biology, 2020, 30, 3397-3413.e4. | 1.8 | 39 |
| 637 | Genome-enabled discovery of anthraquinone biosynthesis in Senna tora. Nature Communications, 2020, 11, 5875. | 5.8 | 57 |
| 638 | A highâ€quality reference genome sequence of Salvia miltiorrhiza provides insights into tanshinone synthesis in its red rhizomes. Plant Genome, 2020, 13, e20041. | 1.6 | 45 |
| 639 | The genome and transcriptome analysis of snake gourd provide insights into its evolution and fruit development and ripening. Horticulture Research, 2020, 7, 199. | 2.9 | 22 |
| 640 | The Tetracentron genome provides insight into the early evolution of eudicots and the formation of vessel elements. Genome Biology, 2020, 21, 291. | 3.8 | 23 |
| 641 | The de novo genome assembly of Tapiscia sinensis and the transcriptomic and developmental bases of androdioecy. Horticulture Research, 2020, 7, 191. | 2.9 | 3 |
| 642 | Donkey genomes provide new insights into domestication and selection for coat color. Nature Communications, 2020, 11, 6014. | 5.8 | 63 |
| 643 | The Acer truncatum genome provides insights into nervonic acid biosynthesis. Plant Journal, 2020, 104, 662-678. | 2.8 | 52 |
| 644 | The chromosome-level wintersweet (Chimonanthus praecox) genome provides insights into floral scent biosynthesis and flowering in winter. Genome Biology, 2020, 21, 200. | 3.8 | 69 |
| 645 | The Genome of Microthlaspi erraticum (Brassicaceae) Provides Insights Into the Adaptation to Highly Calcareous Soils. Frontiers in Plant Science, 2020, 11, 943. | 1.7 | 4 |
| 646 | A chromosomeâ€level genome assembly provides new insights into paternal genome elimination in the cotton mealybug Phenacoccus solenopsis. Molecular Ecology Resources, 2020, 20, 1733-1747. | 2.2 | 12 |
| 647 | Reference Genome Assembly for AustralianAscochyta rabieiIsolate ArME14. G3: Genes, Genomes, Genetics, 2020, 10, 2131-2140. | 0.8 | 15 |
| 648 | Improved Reference Genome for Cyclotella cryptica CCMP332, a Model for Cell Wall Morphogenesis, Salinity Adaptation, and Lipid Production in Diatoms (Bacillariophyta). G3: Genes, Genomes, Genetics, 2020, 10, 2965-2974. | 0.8 | 14 |
| 649 | Long-Read Genome Sequencing and Assembly of Leptopilina boulardi: A Specialist Drosophila Parasitoid. G3: Genes, Genomes, Genetics, 2020, 10, 1485-1494. | 0.8 | 3 |
| 650 | De novo Genome Assembly, Annotation, and SNP Identification of an Endangered Rockcress, Boechera fecunda. Frontiers in Ecology and Evolution, 2020, 8, . | 1.1 | 3 |
| 651 | Pacific Biosciences assembly with Hi-C mapping generates an improved, chromosome-level goose genome. GigaScience, 2020, 9, . | 3.3 | 20 |
| 652 | Genome-scale analyses and characteristics of putative pathogenicity genes of Stagonosporopsis cucurbitacearum, a pumpkin gummy stem blight fungus. Scientific Reports, 2020, 10, 18065. | 1.6 | 6 |

| # | Article | IF | Citations |
|---|---|---|---|
| 653 | First Draft Genome Assembly of the Seaweed Sargassum fusiforme. Frontiers in Genetics, 2020, 11, 590065. | 1.1 | 14 |
| 654 | The Phoebe genome sheds light on the evolution of magnoliids. Horticulture Research, 2020, 7, 146. | 2.9 | 41 |
| 655 | The Genome of the Cauliflower Coral Pocillopora verrucosa. Genome Biology and Evolution, 2020, 12, 1911-1917. | 1.1 | 23 |
| 656 | A high-quality chromosome-level genome assembly reveals genetics for important traits in eggplant. Horticulture Research, 2020, 7, 153. | 2.9 | 85 |
| 657 | Long-read sequencing and de novo genome assembly of marine medaka (Oryzias melastigma). BMC Genomics, 2020, 21, 640. | 1.2 | 7 |
| 658 | A mini foxtail millet with an Arabidopsis-like life cycle as a C4 model system. Nature Plants, 2020, 6, 1167-1178. | 4.7 | 111 |
| 659 | Comparative Analysis of Clinical and Environmental Strains of Exophiala spinifera by Long-Reads Sequencing and RNAseq Reveal Adaptive Strategies. Frontiers in Microbiology, 2020, 11, 1880. | 1.5 | 6 |
| 660 | The chromosome-level draft genome of Dalbergia odorifera. GigaScience, 2020, 9, . | 3.3 | 21 |
| 661 | A haplotype-resolved,de novogenome assembly for the wood tiger moth (Arctia) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 422 Td | 3.3 | 20 |
| 662 | Genomic and transcriptomic insights into Raffaelea lauricola pathogenesis. BMC Genomics, 2020, 21, 570. | 1.2 | 6 |
| 663 | Screening of Helicoverpa armigera Mobilome Revealed Transposable Element Insertions in Insecticide Resistance Genes. Insects, 2020, 11, 879. | 1.0 | 25 |
| 664 | Genome sequencing and phylogenetic analysis of allotetraploid Salix matsudana Koidz. Horticulture Research, 2020, 7, 201. | 2.9 | 30 |
| 665 | A phased Vanilla planifolia genome enables genetic improvement of flavour and production. Nature Food, 2020, 1, 811-819. | 6.2 | 52 |
| 666 | Chromosome-level draft genome of a diploid plum (Prunus salicina). GigaScience, 2020, 9, . | 3.3 | 39 |
| 667 | Integrated omics unveil the secondary metabolic landscape of a basal dinoflagellate. BMC Biology, 2020, 18, 139. | 1.7 | 17 |
| 668 | Chromosome-scale genome assembly for the duckweed Spirodela intermedia, integrating cytogenetic maps, PacBio and Oxford Nanopore libraries. Scientific Reports, 2020, 10, 19230. | 1.6 | 23 |
| 669 | Degradation of the Repetitive Genomic Landscape in a Close Relative of Caenorhabditis elegans. Molecular Biology and Evolution, 2020, 37, 2549-2567. | 3.5 | 15 |
| 670 | The draft genome sequence of an upland wild rice species, Oryza granulata. Scientific Data, 2020, 7, 131. | 2.4 | 21 |

| # | Article | IF | Citations |
|---|---|---|---|
| 671 | Genomic re-assessment of the transposable element landscape of the potato genome. Plant Cell Reports, 2020, 39, 1161-1174. | 2.8 | 12 |
| 672 | The Genome of Peronospora belbahrii Reveals High Heterozygosity, a Low Number of Canonical Effectors, and TC-Rich Promoters. Molecular Plant-Microbe Interactions, 2020, 33, 742-753. | 1.4 | 15 |
| 673 | De novo Assembly and Genome-Wide SNP Discovery in Rohu Carp, Labeo rohita. Frontiers in Genetics, 2020, 11, 386. | 1.1 | 17 |
| 674 | A High-Quality Genome Sequence of Model Legume Lotus japonicus (MG-20) Provides Insights into the Evolution of Root Nodule Symbiosis. Genes, 2020, 11, 483. | 1.0 | 31 |
| 675 | Chromosome-scale assembly of the Kandelia obovata genome. Horticulture Research, 2020, 7, 75. | 2.9 | 38 |
| 676 | Chromosomeâ€level genome assembly of the greenfin horseâ€faced filefish (Thamnaconus) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Ecology Resources, 2020, 20, 1069-1079. | 2.2 | 27 |
| 677 | Draft genome of the famous ornamental plant Paeonia suffruticosa. Ecology and Evolution, 2020, 10, 4518-4530. | 0.8 | 34 |
| 678 | A draft genome of sweet cherry (Prunus avium L.) reveals genomeâ€wide and local effects of domestication. Plant Journal, 2020, 103, 1420-1432. | 2.8 | 23 |
| 679 | Chromosome-Scale Assembly of Winter Oilseed Rape Brassica napus. Frontiers in Plant Science, 2020, 11, 496. | 1.7 | 60 |
| 680 | Whole-genome sequence of Phellinus gilvus (mulberry Sanghuang) reveals its unique medicinal values. Journal of Advanced Research, 2020, 24, 325-335. | 4.4 | 24 |
| 681 | De novo sequencing and chromosomalâ€scale genome assembly of leopard coral grouper, Plectropomus leopardus. Molecular Ecology Resources, 2020, 20, 1403-1413. | 2.2 | 32 |
| 682 | Whole-genome sequencing provides insights into the genetic diversity and domestication of bitter gourd (Momordica spp.). Horticulture Research, 2020, 7, 85. | 2.9 | 41 |
| 683 | Genome sequence of Kobresia littledalei, the first chromosome-level genome in the family Cyperaceae. Scientific Data, 2020, 7, 175. | 2.4 | 20 |
| 684 | Dissecting the genome of star fruit (Averrhoa carambola L.). Horticulture Research, 2020, 7, 94. | 2.9 | 16 |
| 685 | Draft genomes of two outcrossing wild rice, Oryza rufipogon and O. longistaminata , reveal genomic features associated with matingâ€system evolution. Plant Direct, 2020, 4, e00232. | 0.8 | 9 |
| 686 | Lowâ€coverage genomic data resolve the population divergence and gene flow history of an Australian rain forest fig wasp. Molecular Ecology, 2020, 29, 3649-3666. | 2.0 | 4 |
| 687 | Recent hybrids recapitulate ancient hybrid outcomes. Nature Communications, 2020, 11, 2179. | 5.8 | 29 |
| 688 | Taro Genome Assembly and Linkage Map Reveal QTLs for Resistance to Taro Leaf Blight. G3: Genes, Genomes, Genetics, 2020, 10, 2763-2775. | 0.8 | 15 |

| # | Article | IF | Citations |
|---|---|---|---|
| 689 | Chromosome Level Genome Assembly of Andrographis paniculata. Frontiers in Genetics, 2020, 11, 701. | 1.1 | 14 |
| 690 | Jellyfish genomes reveal distinct homeobox gene clusters and conservation of small RNA processing. Nature Communications, 2020, 11, 3051. | 5.8 | 47 |
| 691 | Genome of the webworm Hyphantria cunea unveils genetic adaptations supporting its rapid invasion and spread. BMC Genomics, 2020, 21, 242. | 1.2 | 12 |
| 692 | Chromosomalâ€level reference genome of the incense tree Aquilaria sinensis. Molecular Ecology Resources, 2020, 20, 971-979. | 2.2 | 24 |
| 693 | Highly Contiguous Genome Resource of Colletotrichum fructicola Generated Using Long-Read Sequencing. Molecular Plant-Microbe Interactions, 2020, 33, 790-793. | 1.4 | 12 |
| 694 | Chromosome-level genome assembly and annotation of the loquat (Eriobotrya japonica) genome. GigaScience, 2020, 9, . | 3.3 | 43 |
| 695 | Chromosomeâ€level analysis of the Crassostrea hongkongensis genome reveals extensive duplication of immuneâ€related genes in bivalves. Molecular Ecology Resources, 2020, 20, 980-994. | 2.2 | 45 |
| 696 | Chromosomeâ€level genome assembly of the greenhouse whitefly (Trialeurodes vaporariorum) Tj ETQq1 1 0.784314 rgBT /Ov | 2.2 | 21 |
| 697 | A Giant Genome for a Giant Crayfish (Cherax quadricarinatus) With Insights Into cox1 Pseudogenes in Decapod Genomes. Frontiers in Genetics, 2020, 11, 201. | 1.1 | 23 |
| 698 | The chromosome-scale assembly of the willow genome provides insight into Salicaceae genome evolution. Horticulture Research, 2020, 7, 45. | 2.9 | 35 |
| 699 | Draft genomes of female and male turbot Scophthalmus maximus. Scientific Data, 2020, 7, 90. | 2.4 | 15 |
| 700 | Chromosomeâ€level genome assembly of the East Asian common octopus (Octopus sinensis) using PacBio sequencing and Hiâ€C technology. Molecular Ecology Resources, 2020, 20, 1572-1582. | 2.2 | 28 |
| 701 | Adaptation to Extreme Antarctic Environments Revealed by the Genome of a Sea Ice Green Alga. Current Biology, 2020, 30, 3330-3341.e7. | 1.8 | 48 |
| 702 | A High-Quality Genome Assembly of the North American Song Sparrow, Melospiza melodia. G3: Genes, Genomes, Genetics, 2020, 10, 1159-1166. | 0.8 | 8 |
| 703 | Genome sequencing and transcriptome analysis of Geotrichum citri-aurantii on citrus reveal the potential pathogenic- and guazatine-resistance related genes. Genomics, 2020, 112, 4063-4071. | 1.3 | 15 |
| 704 | Comparative genomics of four strains of the edible brown alga, Cladosiphon okamuranus. BMC Genomics, 2020, 21, 422. | 1.2 | 9 |
| 705 | The roles of hybridization and habitat fragmentation in the evolution of Brazilâ€™s enigmatic longwing butterflies, Heliconius nattereri and H. hermathena. BMC Biology, 2020, 18, 84. | 1.7 | 14 |
| 706 | The Genome Assembly and Annotation of the Southern Elephant Seal Mirounga leonina. Genes, 2020, 11, 160. | 1.0 | 3 |

| # | Article | IF | Citations |
|---|---|---|---|
| 707 | Improved genome assembly provides new insights into genome evolution in a desert poplar (Populus euphratica). Molecular Ecology Resources, 2020, 20, 781-794. | 2.2 | 45 |
| 708 | The hornwort genome and early land plant evolution. Nature Plants, 2020, 6, 107-118. | 4.7 | 203 |
| 709 | Characterization of Growth Morphology and Pathology, and Draft Genome Sequencing of Botrytis fabae, the Causal Organism of Chocolate Spot of Faba Bean (Vicia faba L.). Frontiers in Microbiology, 2020, 11, 217. | 1.5 | 9 |
| 710 | Genomic consequences of population decline in critically endangered pangolins and their demographic histories. National Science Review, 2020, 7, 798-814. | 4.6 | 45 |
| 711 | First Draft Genome of the Sable, Martes zibellina. Genome Biology and Evolution, 2020, 12, 59-65. | 1.1 | 5 |
| 712 | Novel de Novo Genome of Cynopterus brachyotis Reveals Evolutionarily Abrupt Shifts in Gene Family Composition across Fruit Bats. Genome Biology and Evolution, 2020, 12, 259-272. | 1.1 | 12 |
| 713 | The persimmon genome reveals clues to the evolution of a lineage-specific sex determination system in plants. PLoS Genetics, 2020, 16, e1008566. | 1.5 | 54 |
| 714 | Extreme Genome and Nervous System Streamlining in the Invertebrate Parasite Intoshia variabili. Current Biology, 2020, 30, 1292-1298.e3. | 1.8 | 35 |
| 715 | A draft genome sequence of the elusive giant squid, Architeuthis dux. GigaScience, 2020, 9, . | 3.3 | 37 |
| 716 | A high-quality chromosomal genome assembly of Diospyros oleifera Cheng. GigaScience, 2020, 9, . | 3.3 | 37 |
| 717 | Counter based suffix tree for DNA pattern repeats. Theoretical Computer Science, 2020, 814, 1-12. | 0.5 | 3 |
| 718 | Genomic analyses of a â€œliving fossilâ€• The endangered doveâ€tree. Molecular Ecology Resources, 2020, 20, 756-769. | 2.2 | 26 |
| 719 | The genome of opportunistic fungal pathogen Fusarium oxysporum carries a unique set of lineage-specific chromosomes. Communications Biology, 2020, 3, 50. | 2.0 | 55 |
| 720 | Field cricket genome reveals the footprint of recent, abrupt adaptation in the wild. Evolution Letters, 2020, 4, 19-33. | 1.6 | 32 |
| 721 | Exploitation of Hi-C sequencing for improvement of genome assembly and in-vitro validation of differentially expressing genes in Jatropha curcas L.. 3 Biotech, 2020, 10, 91. | 1.1 | 3 |
| 722 | The Reference Genome of Tea Plant and Resequencing of 81 Diverse Accessions Provide Insights into Its Genome Evolution and Adaptation. Molecular Plant, 2020, 13, 1013-1026. | 3.9 | 257 |
| 723 | Genome of extreme halophyte Puccinellia tenuiflora. BMC Genomics, 2020, 21, 311. | 1.2 | 8 |
| 724 | RepeatModeler2 for automated genomic discovery of transposable element families. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 9451-9457. | 3.3 | 1,480 |

| # | Article | IF | Citations |
|---|---|---|---|
| 725 | An Annotated Chromosome-Level Reference Genome of the Red-Eared Slider Turtle (Trachemys scripta) Tj ETQq0 0 0 rgBT /Overlock 10 | 1.1 | 25 |
| 726 | De novo assembly of the olive fruit fly (Bactrocera oleae) genome with linked-reads and long-read technologies minimizes gaps and provides exceptional Y chromosome assembly. BMC Genomics, 2020, 21, 259. | 1.2 | 21 |
| 727 | Probing the Mobilome: Discoveries in the Dynamic Microbiome. Trends in Microbiology, 2021, 29, 158-170. | 3.5 | 41 |
| 728 | Sequence repetitiveness quantification and de novo repeat detection by weighted k-mer coverage. Briefings in Bioinformatics, 2021, 22, . | 3.2 | 4 |
| 729 | The chromosomeâ€level genome sequence and karyotypic evolution of Megadenia pygmaea (Brassicaceae). Molecular Ecology Resources, 2021, 21, 871-879. | 2.2 | 7 |
| 730 | A highâ€quality genome of taro (Colocasia esculenta (L.) Schott), one of the world's oldest crops. Molecular Ecology Resources, 2021, 21, 68-77. | 2.2 | 28 |
| 731 | A chromosomeâ€scale reference genome and genomeâ€wide genetic variations elucidate adaptation in yak. Molecular Ecology Resources, 2021, 21, 201-211. | 2.2 | 14 |
| 732 | The genome sequence of Samia ricini , a new model species of lepidopteran insect. Molecular Ecology Resources, 2021, 21, 327-339. | 2.2 | 12 |
| 733 | A chromosomeâ€scale assembly of allotetraploid Brassica juncea (AABB) elucidates comparative architecture of the A and B genomes. Plant Biotechnology Journal, 2021, 19, 602-614. | 4.1 | 62 |
| 734 | Genome Sequence Resource for Colletotrichum scovillei, the Cause of Anthracnose Disease of Chili. Molecular Plant-Microbe Interactions, 2021, 34, 122-126. | 1.4 | 12 |
| 735 | The celery genome sequence reveals sequential paleoâ€polyploidizations, karyotype evolution and resistance gene reduction in apiales. Plant Biotechnology Journal, 2021, 19, 731-744. | 4.1 | 62 |
| 736 | A chromosomeâ€level genome assembly of rice leaffolder, Cnaphalocrocis medinalis. Molecular Ecology Resources, 2021, 21, 561-572. | 2.2 | 15 |
| 737 | A Chromosomal-scale Reference Genome of the Kelp Grouper Epinephelus moara. Marine Biotechnology, 2021, 23, 12-16. | 1.1 | 7 |
| 738 | Wholeâ€genome assembly and resequencing reveal genomic imprint and key genes of rapid domestication in narrowâ€leafed lupin. Plant Journal, 2021, 105, 1192-1210. | 2.8 | 12 |
| 739 | Genomic Analysis Enlightens Agaricales Lifestyle Evolution and Increasing Peroxidase Diversity. Molecular Biology and Evolution, 2021, 38, 1428-1446. | 3.5 | 72 |
| 740 | Chromosomeâ€level reference genome assembly provides insights into aroma biosynthesis in passion fruit (Passiflora edulis). Molecular Ecology Resources, 2021, 21, 955-968. | 2.2 | 31 |
| 741 | Genus-Wide Characterization of Bumblebee Genomes Provides Insights into Their Evolution and Variation in Ecological and Behavioral Traits. Molecular Biology and Evolution, 2021, 38, 486-501. | 3.5 | 58 |
| 742 | Eighteen Coral Genomes Reveal the Evolutionary Origin of Acropora Strategies to Accommodate Environmental Changes. Molecular Biology and Evolution, 2021, 38, 16-30. | 3.5 | 75 |

| # | Article | IF | Citations |
|---|---|---|---|
| 745 | Identifying a melanogenesis-related candidate gene by a high-quality genome assembly and population diversity analysis in Hypsizygus marmoreus. Journal of Genetics and Genomics, 2021, 48, 75-87. | 1.7 | 14 |
| 746 | Genome-wide signatures of mammalian skin covering evolution. Science China Life Sciences, 2021, 64, 1765-1780. | 2.3 | 5 |
| 747 | Draft Genome Sequences of the Black Truffles Tuber brumale Vittad. and Tuber indicum Cook & Massee. Microbiology Resource Announcements, 2021, 10, . | 0.3 | 7 |
| 748 | Horseshoe crab genomes reveal the evolution of genes and microRNAs after three rounds of whole genome duplication. Communications Biology, 2021, 4, 83. | 2.0 | 31 |
| 749 | Combined genomic, transcriptomic, and metabolomic analyses provide insights into chayote (Sechium) Tj ETQq0 0 0 rgBT /Overlock 10 | 2.9 | 39 |
| 750 | Chromosomal assembly of the Antarctic toothfish (<i>Dissostichus mawsoni</i>) genome using third-generation DNA sequencing and Hi-C technology. Zoological Research, 2021, 42, 124-129. | 0.9 | 17 |
| 751 | Genomes of Other Species in Panax Linn. Compendium of Plant Genomes, 2021, , 149-157. | 0.3 | 0 |
| 752 | Genome assemblies for two Neotropical trees: Jacaranda copaia and Handroanthus guayacan. G3: Genes, Genomes, Genetics, 2021, 11, . | 0.8 | 3 |
| 753 | Transposable Elements and Teleost Migratory Behaviour. International Journal of Molecular Sciences, 2021, 22, 602. | 1.8 | 9 |
| 754 | Genome sequence and transcriptome profiles of pathogenic fungus Paecilomyces penicillatus reveal its interactions with edible fungus Morchella importuna. Computational and Structural Biotechnology Journal, 2021, 19, 2607-2617. | 1.9 | 11 |
| 755 | Chromosome-scale genome assembly of brown-spotted flathead <i>Platycephalus</i> sp.1 provides insights into demersal adaptation in flathead fish. Zoological Research, 2021, 42, 660-665. | 0.9 | 2 |
| 756 | How the pan-genome is changing crop genomics and improvement. Genome Biology, 2021, 22, 3. | 3.8 | 142 |
| 757 | Reference genome assembly for Australian Ascochyta lentis isolate Al4. G3: Genes, Genomes, Genetics, 2021, 11, . | 0.8 | 9 |
| 758 | The draft genome sequence of the grove snail Cepaea nemoralis. G3: Genes, Genomes, Genetics, 2021, 11, . | 0.8 | 15 |
| 759 | Genome and population evolution and environmental adaptation of <i>Glyptosternon maculatum</i> on the Qinghai-Tibet Plateau. Zoological Research, 2021, 42, 502-513. | 0.9 | 7 |
| 760 | Chromosome-level genome assembly of the Chinese longsnout catfish <i>Leiocassis longirostris</i>. Zoological Research, 2021, 42, 417-422. | 0.9 | 14 |
| 761 | A mosquito small RNA genomics resource reveals dynamic evolution and host responses to viruses and transposons. Genome Research, 2021, 31, 512-528. | 2.4 | 29 |
| 762 | Chromosome-level genome assembly of Ophiorrhiza pumila reveals the evolution of camptothecin biosynthesis. Nature Communications, 2021, 12, 405. | 5.8 | 77 |

| # | Article | IF | Citations |
|---|---|---|---|
| 763 | Hybridization History and Repetitive Element Content in the Genome of a Homoploid Hybrid, Yucca gloriosa (Asparagaceae). Frontiers in Plant Science, 2020, 11, 573767. | 1.7 | 9 |
| 764 | Wholeâ€Genome Sequence of Synthesized Allopolyploids in Cucumis Reveals Insights into the Genome Evolution of Allopolyploidization. Advanced Science, 2021, 8, 2004222. | 5.6 | 24 |
| 767 | Gene family amplification facilitates adaptation in freshwater unionid bivalve Megalonaias nervosa. Molecular Ecology, 2021, 30, 1155-1173. | 2.0 | 19 |
| 768 | A chromosomeâ€level genome assembly for the tertiary relict plant Tetracentron sinense oliv. (trochodendraceae). Molecular Ecology Resources, 2021, 21, 1186-1199. | 2.2 | 12 |
| 769 | A Chromosome-Level Genome Assembly of the Dark Sleeper Odontobutis potamophila. Genome Biology and Evolution, 2021, 13, . | 1.1 | 7 |
| 770 | Comparative analysis using the draft genome sequence of California poppy (Eschscholzia californica) for exploring the candidate genes involved in benzylisoquinoline alkaloid biosynthesis. Bioscience, Biotechnology and Biochemistry, 2021, 85, 851-859. | 0.6 | 10 |
| 771 | Gene family expansions and transcriptome signatures uncover fungal adaptations to wood decay. Environmental Microbiology, 2021, 23, 5716-5732. | 1.8 | 44 |
| 772 | The genome of Tripterygium wilfordii and characterization of the celastrol biosynthesis pathway. GigaByte, 0, 2021, 1-32. | 0.0 | 3 |
| 773 | A long reads-based de-novo assembly of the genome of the Arlee homozygous line reveals chromosomal rearrangements in rainbow trout. G3: Genes, Genomes, Genetics, 2021, 11, . | 0.8 | 40 |
| 774 | Genome sequences of Tropheus moorii and Petrochromis trewavasae, two eco-morphologically divergent cichlid fishes endemic to Lake Tanganyika. Scientific Reports, 2021, 11, 4309. | 1.6 | 4 |
| 775 | Genome sequence and evolution ofBetula platyphylla. Horticulture Research, 2021, 8, 37. | 2.9 | 53 |
| 778 | TEfinder: A Bioinformatics Pipeline for Detecting New Transposable Element Insertion Events in Next-Generation Sequencing Data. Genes, 2021, 12, 224. | 1.0 | 4 |
| 780 | Search for SINE repeats in the rice genome using correlation-based position weight matrices. BMC Bioinformatics, 2021, 22, 42. | 1.2 | 3 |
| 781 | A large genome with chromosomeâ€scale assembly sheds light on the evolutionary success of a true toad (Bufo gargarizans). Molecular Ecology Resources, 2021, 21, 1256-1273. | 2.2 | 32 |
| 782 | Insights into triterpene synthesis and unsaturated fatty-acid accumulation provided by chromosomal-level genome analysis of Akebia trifoliata subsp. australis. Horticulture Research, 2021, 8, 33. | 2.9 | 23 |
| 784 | The first genomic resources for Phymatotrichopsis omnivora, a soil-borne pezizomycete pathogen with a broad host range. Phytopathology, 2021, , PHYTO01210014A. | 1.1 | 3 |
| 785 | Chromosomeâ€level assembly of the mangrove plant Aegiceras corniculatum genome generated through Illumina, PacBio and Hiâ€C sequencing technologies. Molecular Ecology Resources, 2021, 21, 1593-1607. | 2.2 | 16 |
| 786 | Interplay between genome organization and epigenomic alterations of pericentromeric DNA in cancer. Journal of Genetics and Genomics, 2021, 48, 184-197. | 1.7 | 7 |

| # | Article | IF | Citations |
|---|---|---|---|
| 788 | A route to de novo domestication of wild allotetraploid rice. Cell, 2021, 184, 1156-1170.e14. | 13.5 | 259 |
| 789 | A multi-omic characterization of temperature stress in a halotolerant Scenedesmus strain for algal biotechnology. Communications Biology, 2021, 4, 333. | 2.0 | 22 |
| 790 | Chromosomeâ€level genome of Poropuntius huangchuchieni provides a diploid progenitorâ€like reference genome for the allotetraploid Cyprinus carpio. Molecular Ecology Resources, 2021, 21, 1658-1669. | 2.2 | 13 |
| 791 | A chromosome level genome assembly of Propsilocerus akamusi to understand its response to heavy metal exposure. Molecular Ecology Resources, 2021, 21, 1996-2012. | 2.2 | 11 |
| 795 | A Genomic Blueprint of Flax Fungal Parasite Fusarium oxysporum f. sp. lini. International Journal of Molecular Sciences, 2021, 22, 2665. | 1.8 | 6 |
| 797 | High-Quality Genome Resource of Diaporthe destruens Causing Foot Rot Disease of Sweet Potato. Plant Disease, 2021, 105, 3279-3281. | 0.7 | 4 |
| 798 | Nutrient-driven genome evolution revealed by comparative genomics of chrysomonad flagellates. Communications Biology, 2021, 4, 328. | 2.0 | 7 |
| 799 | Gigantic Genomes Provide Empirical Tests of Transposable Element Dynamics Models. Genomics, Proteomics and Bioinformatics, 2021, 19, 123-139. | 3.0 | 13 |
| 800 | The draft genome of the specialist flea beetle Altica viridicyanea (Coleoptera: Chrysomelidae). BMC Genomics, 2021, 22, 243. | 1.2 | 6 |
| 801 | An Annotated Draft Genome for the Andean Bear,Tremarctos ornatus. Journal of Heredity, 2021, 112, 377-384. | 1.0 | 6 |
| 802 | A Chromosomeâ€"Level Genome Assembly of the Spotted Scat (Scatophagus argus). Genome Biology and Evolution, 2021, 13, . | 1.1 | 17 |
| 803 | Comparative genome analyses of four rice-infecting Rhizoctonia solani isolates reveal extensive enrichment of homogalacturonan modification genes. BMC Genomics, 2021, 22, 242. | 1.2 | 18 |
| 804 | Chromosomeâ€level genome assembly of the Arctic fox (Vulpes lagopus) using PacBio sequencing and Hiâ€C technology. Molecular Ecology Resources, 2021, 21, 2093-2108. | 2.2 | 15 |
| 805 | Sequencing, assembly and annotation of the whole-insect genome of Lymantria dispar dispar, the European gypsy moth. G3: Genes, Genomes, Genetics, 2021, 11, . | 0.8 | 5 |
| 806 | Whole-genome resequencing of 445 Lactuca accessions reveals the domestication history of cultivated lettuce. Nature Genetics, 2021, 53, 752-760. | 9.4 | 64 |
| 807 | Comparative genomics of the coconut crab and other decapod crustaceans: exploring the molecular basis of terrestrial adaptation. BMC Genomics, 2021, 22, 313. | 1.2 | 11 |
| 808 | Engineered sex ratio distortion by X-shredding in the global agricultural pest Ceratitis capitata. BMC Biology, 2021, 19, 78. | 1.7 | 29 |
| 810 | The Meishan pig genome reveals structural variationâ€mediated gene expression and phenotypic divergence underlying Asian pig domestication. Molecular Ecology Resources, 2021, 21, 2077-2092. | 2.2 | 20 |

| # | Article | IF | Citations |
|---|---|---|---|
| 811 | A chromosome-level reference genome of the hazelnut, Corylus heterophylla Fisch. GigaScience, 2021, 10, . | 3.3 | 13 |
| 812 | Genome-wide analyses of the relict gull (Larus relictus): insights and evolutionary implications. BMC Genomics, 2021, 22, 311. | 1.2 | 6 |
| 813 | De novo assembly of a new Olea europaea genome accession using nanopore sequencing. Horticulture Research, 2021, 8, 64. | 2.9 | 41 |
| 815 | Chromosomal-Level Reference Genome of the Neotropical Tree Jacaranda mimosifolia D. Don. Genome Biology and Evolution, 2021, 13, . | 1.1 | 7 |
| 816 | Highâ€quality chromosomeâ€level genomes of Cucumis metuliferus and Cucumis melo provide insight into Cucumis genome evolution. Plant Journal, 2021, 107, 136-148. | 2.8 | 20 |
| 817 | K-mer-based machine learning method to classify LTR-retrotransposons in plant genomes. PeerJ, 2021, 9, e11456. | 0.9 | 13 |
| 818 | Comparative Genome Analyses Highlight Transposon-Mediated Genome Expansion and the Evolutionary Architecture of 3D Genomic Folding in Cotton. Molecular Biology and Evolution, 2021, 38, 3621-3636. | 3.5 | 41 |
| 819 | Chorus2: design of genomeâ€scale oligonucleotideâ€based probes for fluorescence inÂsitu hybridization. Plant Biotechnology Journal, 2021, 19, 1967-1978. | 4.1 | 31 |
| 820 | Chromosome-scale assembly of the Sparassis latifolia genome obtained using long-read and Hi-C sequencing. G3: Genes, Genomes, Genetics, 2021, 11, . | 0.8 | 4 |
| 821 | The genome of the venomous snail Lautoconus ventricosus sheds light on the origin of conotoxin diversity. GigaScience, 2021, 10, . | 3.3 | 29 |
| 822 | The genome of Nautilus pompilius illuminates eye evolution and biomineralization. Nature Ecology and Evolution, 2021, 5, 927-938. | 3.4 | 40 |
| 823 | Whole-genome resequencing of Osmanthus fragrans provides insights into flower color evolution. Horticulture Research, 2021, 8, 98. | 2.9 | 35 |
| 824 | Molecular mechanisms of mutualistic and antagonistic interactions in a plantâ€“pollinator association. Nature Ecology and Evolution, 2021, 5, 974-986. | 3.4 | 30 |
| 825 | Genetic basis of high aroma and stress tolerance in the oolong tea cultivar genome. Horticulture Research, 2021, 8, 107. | 2.9 | 80 |
| 826 | The reference genome of Miscanthus floridulus illuminates the evolution of Saccharinae. Nature Plants, 2021, 7, 608-618. | 4.7 | 23 |
| 827 | The Genomic Signature of Allopatric Speciation in a Songbird Is Shaped by Genome Architecture (Aves:) Tj ETQq1 1 0.784314 rgBT /O | 1.1 | 10 |
| 829 | Whole genome sequencing of a snailfish from the Yap Trench (~7,000 m) clarifies the molecular mechanisms underlying adaptation to the deep sea. PLoS Genetics, 2021, 17, e1009530. | 1.5 | 26 |
| 831 | The chromosome-level reference genome of Coptis chinensis provides insights into genomic evolution and berberine biosynthesis. Horticulture Research, 2021, 8, 121. | 2.9 | 25 |

| # | Article | IF | Citations |
|---|---|---|---|
| 832 | Gapless indica rice genome reveals synergistic contributions of active transposable elements and segmental duplications to rice genome evolution. Molecular Plant, 2021, 14, 1745-1756. | 3.9 | 50 |
| 833 | A chromosome-level Camptotheca acuminata genome assembly provides insights into the evolutionary origin of camptothecin biosynthesis. Nature Communications, 2021, 12, 3531. | 5.8 | 66 |
| 834 | De novo genome assembly of a foxtail millet cultivar Huagu11 uncovered the genetic difference to the cultivar Yugu1, and the genetic mechanism of imazethapyr tolerance. BMC Plant Biology, 2021, 21, 271. | 1.6 | 9 |
| 836 | Chromosome assembled and annotated genome sequence of Aspergillus flavus NRRL 3357. G3: Genes, Genomes, Genetics, 2021, 11, . | 0.8 | 19 |
| 837 | The chromosome-level Stevia genome provides insights into steviol glycoside biosynthesis. Horticulture Research, 2021, 8, 129. | 2.9 | 35 |
| 838 | The nearly complete genome of Ginkgo biloba illuminates gymnosperm evolution. Nature Plants, 2021, 7, 748-756. | 4.7 | 98 |
| 839 | Genomic insights into the adaptation and evolution of the nautilus, an ancient but evolving â€œliving fossilâ€• Molecular Ecology Resources, 2022, 22, 15-27. | 2.2 | 15 |
| 841 | Investigation of the activity of transposable elements and genes involved in their silencing in the newt Cynops orientalis, a species with a giant genome. Scientific Reports, 2021, 11, 14743. | 1.6 | 7 |
| 842 | Dissecting the chromosome-level genome of the Asian Clam (Corbicula fluminea). Scientific Reports, 2021, 11, 15021. | 1.6 | 5 |
| 843 | Chromosomeâ€level genome assembly of Sichuan pepper provides insights into apomixis, drought tolerance, and alkaloid biosynthesis. Molecular Ecology Resources, 2021, 21, 2533-2545. | 2.2 | 30 |
| 844 | Diploidy within a Haploid Genus of Entomopathogenic Fungi. Genome Biology and Evolution, 2021, 13, . | 1.1 | 5 |
| 845 | The first draft genome of feather grasses using SMRT sequencing and its implications in molecular studies of Stipa. Scientific Reports, 2021, 11, 15345. | 1.6 | 6 |
| 846 | The Welwitschia genome reveals aÂunique biology underpinning extreme longevity in deserts. Nature Communications, 2021, 12, 4247. | 5.8 | 51 |
| 847 | Evolutionary transition to XY sex chromosomes associated with Y-linked duplication of a male hormone gene in a terrestrial isopod. Heredity, 2021, 127, 266-277. | 1.2 | 5 |
| 848 | Chromosomalâ€scale genome assembly of Eleutherococcus senticosus provides insights into chromosome evolution in Araliaceae. Molecular Ecology Resources, 2021, 21, 2204-2220. | 2.2 | 10 |
| 849 | Genome of the Southern Giant Petrel Assembled Using Third-Generation DNA Sequencing and Linked Reads Reveals Evolutionary Traits of Southern Avian. Animals, 2021, 11, 2046. | 1.0 | 1 |
| 850 | De Novo Sequencing and High-Contiguity Genome Assembly of Moniezia expansa Reveals Its Specific Fatty Acid Metabolism and Reproductive Stem Cell Regulatory Network. Frontiers in Cellular and Infection Microbiology, 2021, 11, 693914. | 1.8 | 3 |
| 851 | Gossypium tomentosum genome and interspecific ultra-dense genetic maps reveal genomic structures, recombination landscape and flowering depression in cotton. Genomics, 2021, 113, 1999-2009. | 1.3 | 8 |

| # | Article | IF | Citations |
|---|---|---|---|
| 852 | Draft genome of Puya raimondii (Bromeliaceae), the Queen of the Andes. Genomics, 2021, 113, 2537-2546. | 1.3 | 4 |
| 854 | The first draft genome of Picrorhiza kurrooa, an endangered medicinal herb from Himalayas. Scientific Reports, 2021, 11, 14944. | 1.6 | 10 |
| 856 | Tracking the transition to agriculture in Southern Europe through ancient DNA analysis of dental calculus. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, . | 3.3 | 29 |
| 857 | Whole genome sequencing and bulked segregant analysis suggest a new mechanism of amitraz resistance in the citrus red mite, Panonychus citri ( Acari: Tetranychidae ). Pest Management Science, 2021, 77, 5032-5048. | 1.7 | 6 |
| 858 | Impact of Repetitive DNA Elements on Snake Genome Biology and Evolution. Cells, 2021, 10, 1707. | 1.8 | 11 |
| 859 | A sensitive repeat identification framework based on short and long reads. Nucleic Acids Research, 2021, 49, e100-e100. | 6.5 | 10 |
| 861 | Genome assembly of Scorias spongiosa and comparative genomics provide insights into ecological adaptation of honeydew-dependent sooty mould fungi. Genomics, 2021, 113, 2189-2198. | 1.3 | 2 |
| 862 | Genome assembly of primitive cultivated potato Solanum stenotomum provides insights into potato evolution. G3: Genes, Genomes, Genetics, 2021, 11, . | 0.8 | 5 |
| 863 | Seadragon genome analysis provides insights into its phenotype and sex determination locus. Science Advances, 2021, 7, . | 4.7 | 32 |
| 864 | The genome of the thin-necked bladder worm Taenia hydatigena reveals evolutionary strategies for helminth survival. Communications Biology, 2021, 4, 1004. | 2.0 | 2 |
| 865 | High-quality genome assembly and resequencing of modern cotton cultivars provide resources for crop improvement. Nature Genetics, 2021, 53, 1385-1391. | 9.4 | 76 |
| 866 | Transposable elements expression in Rhinella marina (cane toad) specimens submitted to immune and stress challenge. Genetica, 2021, 149, 335-342. | 0.5 | 1 |
| 867 | The Cardamine enshiensis genome reveals whole genome duplication and insight into selenium hyperaccumulation and tolerance. Cell Discovery, 2021, 7, 62. | 3.1 | 15 |
| 868 | Transposable elements and introgression introduce genetic variation in the invasive ant Cardiocondyla obscurior. Molecular Ecology, 2021, 30, 6211-6228. | 2.0 | 20 |
| 870 | Insights into the Host Specificity of a New Oomycete Root Pathogen, Pythium brassicum P1: Whole Genome Sequencing and Comparative Analysis Reveals Contracted Regulation of Metabolism, Protein Families, and Distinct Pathogenicity Repertoire. International Journal of Molecular Sciences, 2021, 22, 9002. | 1.8 | 3 |
| 871 | Chromosome-scale assembly and evolution of the tetraploid Salvia splendens (Lamiaceae) genome. Horticulture Research, 2021, 8, 177. | 2.9 | 27 |
| 872 | High-quality genome assembly of 'Cuiguan' pear (Pyrus pyrifolia) as a reference genome for identifying regulatory genes and epigenetic modifications responsible for bud dormancy. Horticulture Research, 2021, 8, 197. | 2.9 | 44 |
| 873 | Chromosome-scale assembly of the Dendrobium chrysotoxum genome enhances the understanding of orchid evolution. Horticulture Research, 2021, 8, 183. | 2.9 | 41 |

| # | Article | IF | Citations |
|---|---|---|---|
| 874 | Genome-Wide Transcriptional Changes of Rhodosporidium kratochvilovae at Low Temperature. Frontiers in Microbiology, 2021, 12, 727105. | 1.5 | 5 |
| 875 | Chromosomeâ€level genome assembly of the mirid predator Cyrtorhinus lividipennis Reuter (Hemiptera: Miridae), an important natural enemy in the rice ecosystem. Molecular Ecology Resources, 2022, 22, 1086-1099. | 2.2 | 7 |
| 876 | Whole-genome assembly ofGanoderma leucocontextum(Ganodermataceae, Fungi) discovered from the Tibetan Plateau of China. G3: Genes, Genomes, Genetics, 2021, 11, . | 0.8 | 11 |
| 877 | Chromosome-Level Genome Assembly and Annotation of the Fiber Flax (Linum usitatissimum) Genome. Frontiers in Genetics, 2021, 12, 735690. | 1.1 | 15 |
| 878 | Comparative Mitogenomic Analysis and the Evolution of Rhizoctonia solani Anastomosis Groups. Frontiers in Microbiology, 2021, 12, 707281. | 1.5 | 5 |
| 880 | Chromosome-level assembly of the Hypophthalmichthys molitrix (Cypriniformes: Cyprinidae) genome provides insights into its ecological adaptation. Genomics, 2021, 113, 2944-2952. | 1.3 | 5 |
| 881 | A chromosome-level reference genome of red swamp crayfish Procambarus clarkii provides insights into the gene families regarding growth or development in crustaceans. Genomics, 2021, 113, 3274-3284. | 1.3 | 20 |
| 882 | Zanthoxylum-specific whole genome duplication and recent activity of transposable elements in the highly repetitive paleotetraploid Z. bungeanum genome. Horticulture Research, 2021, 8, 205. | 2.9 | 19 |
| 883 | The chromosome-scale genome of Magnolia officinalis provides insight into the evolutionary position of magnoliids. IScience, 2021, 24, 102997. | 1.9 | 14 |
| 884 | The evolutionary puzzle solution for the origins of the partial loss of the CÏ„2 exon in notothenioid fishes. Fish and Shellfish Immunology, 2021, 116, 124-139. | 1.6 | 2 |
| 885 | Genome Sequence Resource for Stagonosporopsis cucurbitacearum, a Cause of Gummy Stem Blight Disease of Watermelon. Molecular Plant-Microbe Interactions, 2021, 34, 977-980. | 1.4 | 3 |
| 887 | The Clausena lansium (Wampee) genome reveal new insights into the carbazole alkaloids biosynthesis pathway. Genomics, 2021, 113, 3696-3704. | 1.3 | 11 |
| 888 | The evolution and genetics of sexually dimorphic â€˜dualâ€™ mimicry in the butterflyElymnias hypermnestra. Proceedings of the Royal Society B: Biological Sciences, 2021, 288, 20202192. | 1.2 | 6 |
| 889 | Rapid protein evolution, organellar reductions, and invasive intronic elements in the marine aerobic parasite dinoflagellate Amoebophrya spp. BMC Biology, 2021, 19, 1. | 1.7 | 135 |
| 890 | The Dfam community resource of transposable element families, sequence models, and genome annotations. Mobile DNA, 2021, 12, 2. | 1.3 | 279 |
| 891 | A Practical Guide on Computational Tools and Databases for Transposable Elements in Plants. Methods in Molecular Biology, 2021, 2250, 31-53. | 0.4 | 2 |
| 892 | De novowhole-genome assembly and resequencing resources for the roan (Hippotragus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 | 0.8 | 4 |
| 893 | Draft genome of the herbaceous bamboo Raddia distichophylla. G3: Genes, Genomes, Genetics, 2021, 11, . | 0.8 | 6 |

| # | Article | IF | Citations |
|---|---|---|---|
| 894 | The hard clam genome reveals massive expansion and diversification of inhibitors of apoptosis in Bivalvia. BMC Biology, 2021, 19, 15. | 1.7 | 52 |
| 895 | The <i>Cymbidium goeringii</i> genome provides insight into organ development and adaptive evolution in orchids. Ornamental Plant Research, 2021, 1, 1-13. | 0.2 | 7 |
| 896 | Finding and Characterizing Repeats in Plant Genomes. Methods in Molecular Biology, 2016, 1374, 293-337. | 0.4 | 7 |
| 897 | Computational Methods for the Analysis of Primate Mobile Elements. Methods in Molecular Biology, 2010, 628, 137-151. | 0.4 | 9 |
| 898 | Citrus Genomes: From Sequence Variations to Epigenetic Modifications. Compendium of Plant Genomes, 2020, , 141-165. | 0.3 | 1 |
| 899 | RAIDER: Rapid Ab Initio Detection of Elementary Repeats. Lecture Notes in Computer Science, 2013, , 170-180. | 1.0 | 1 |
| 900 | A New Approach to String Pattern Mining with Approximate Match. Lecture Notes in Computer Science, 2013, , 110-125. | 1.0 | 3 |
| 901 | Crop Genome Annotation: A Case Study for the Brassica rapa Genome. Compendium of Plant Genomes, 2015, , 53-64. | 0.3 | 1 |
| 902 | Genomics and Transcriptomics Advance in Plant Sciences. Energy, Environment, and Sustainability, 2019, , 419-448. | 0.6 | 5 |
| 904 | A chromosome-level reference genome of non-heading Chinese cabbage [Brassica campestris (syn.) Tj ETQq1 1 0.784314 rgBT /Overl | 2.9 | 51 |
| 905 | A chromosome-scale genome assembly of Isatis indigotica, an important medicinal plant used in traditional Chinese medicine. Horticulture Research, 2020, 7, 18. | 2.9 | 58 |
| 906 | The sequence and de novo assembly of Oxygymnocypris stewartii genome. Scientific Data, 2019, 6, 190009. | 2.4 | 29 |
| 907 | The evolutionary origin and domestication history of goldfish ( Carassius auratus ). Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 29775-29785. | 3.3 | 47 |
| 908 | Approaches to Fungal Genome Annotation. Mycology, 2011, 2, 118-141. | 2.0 | 109 |
| 909 | A high-quality de novo genome assembly of one swamp eel (Monopterus albus) strain with PacBio and Hi-C sequencing data. G3: Genes, Genomes, Genetics, 2021, 11, 1-9. | 0.8 | 15 |
| 910 | Chromosomal-Level Genome Assembly of Silver Sillago (Sillago sihama). Genome Biology and Evolution, 2021, 13, . | 1.1 | 6 |
| 911 | Assembly of highly repetitive genomes using short reads: the genome of discrete typing unit III Trypanosoma cruzi strain 231. Microbial Genomics, 2018, 4, . | 1.0 | 24 |
| 937 | Helitrons, the Eukaryotic Rolling-circle Transposable Elements. , 0, , 891-924. | | 8 |

| # | Article | IF | Citations |
|---|---|---|---|
| 938 | Millipede genomes reveal unique adaptations during myriapod evolution. PLoS Biology, 2020, 18, e3000636. | 2.6 | 18 |
| 939 | Combating a Global Threat to a Clonal Crop: Banana Black Sigatoka Pathogen Pseudocercospora fijiensis (Synonym Mycosphaerella fijiensis) Genomes Reveal Clues for Disease Control. PLoS Genetics, 2016, 12, e1005876. | 1.5 | 77 |
| 940 | Comparative Genomic Analysis of Drechmeria coniospora Reveals Core and Specific Genetic Requirements for Fungal Endoparasitism of Nematodes. PLoS Genetics, 2016, 12, e1006017. | 1.5 | 45 |
| 941 | Mosquito genomes are frequently invaded by transposable elements through horizontal transfer. PLoS Genetics, 2020, 16, e1008946. | 1.5 | 31 |
| 942 | Genome Erosion in a Nitrogen-Fixing Vertically Transmitted Endosymbiotic Multicellular Cyanobacterium. PLoS ONE, 2010, 5, e11486. | 1.1 | 178 |
| 943 | The First Symbiont-Free Genome Sequence of Marine Red Alga, Susabi-nori (Pyropia yezoensis). PLoS ONE, 2013, 8, e57122. | 1.1 | 150 |
| 944 | Sequencing and Comparative Analysis of the Straw Mushroom (Volvariella volvacea) Genome. PLoS ONE, 2013, 8, e58294. | 1.1 | 143 |
| 945 | Genome Survey Sequencing and Genetic Background Characterization of Gracilariopsis lemaneiformis (Rhodophyta) Based on Next-Generation Sequencing. PLoS ONE, 2013, 8, e69909. | 1.1 | 52 |
| 946 | The Draft Genome Sequence of European Pear (Pyrus communis L. â€˜Bartlettâ€™). PLoS ONE, 2014, 9, e92644. | 1.1 | 241 |
| 947 | Candidatus Frankia Datiscae Dg1, the Actinobacterial Microsymbiont of Datisca glomerata, Expresses the Canonical nod Genes nodABC in Symbiosis with Its Host Plant. PLoS ONE, 2015, 10, e0127630. | 1.1 | 131 |
| 948 | Genome Filtering for New DNA Biomarkers of Loa loa Infection Suitable for Loop-Mediated Isothermal Amplification. PLoS ONE, 2015, 10, e0139286. | 1.1 | 16 |
| 949 | Genome Survey Sequencing for the Characterization of the Genetic Background of Rosa roxburghii Tratt and Leaf Ascorbate Metabolism Genes. PLoS ONE, 2016, 11, e0147530. | 1.1 | 60 |
| 950 | Comparative Genomics of Pathogens Causing Brown Spot Disease of Tobacco: Alternaria longipes and Alternaria alternata. PLoS ONE, 2016, 11, e0155258. | 1.1 | 42 |
| 951 | Draft Genomes of Anopheles cracens and Anopheles maculatus: Comparison of Simian Malaria and Human Malaria Vectors in Peninsular Malaysia. PLoS ONE, 2016, 11, e0157893. | 1.1 | 8 |
| 952 | Deciphering the Draft Genome of Toxoplasma gondii RH Strain. PLoS ONE, 2016, 11, e0157901. | 1.1 | 28 |
| 953 | Comprehensive analysis of small RNAs expressed in developing male strobili of Cryptomeria japonica. PLoS ONE, 2018, 13, e0193665. | 1.1 | 14 |
| 954 | Estimating the k-mer Coverage Frequencies in Genomic Datasets: A Comparative Assessment of the State-of-the-art. Current Genomics, 2019, 20, 2-15. | 0.7 | 10 |
| 955 | An Efficient Tool for Searching Maximal and Super Maximal Repeats in Large DNA/Protein Sequences via Induced-Enhanced Suffix Array. Recent Patents on Computer Science, 2019, 12, 128-134. | 0.5 | 2 |

| # | Article | IF | Citations |
|---|---|---|---|
| 956 | Molecular analysis of commercial date palm cultivars in Lybia using ISSR and SRAP PCR-based markers. Genetika, 2016, 48, 307-322. | 0.1 | 2 |
| 958 | Asymptotic Analysis of the kth Subword Complexity. Entropy, 2020, 22, 207. | 1.1 | 1 |
| 959 | The draft genome assembly of the critically endangered Nyssa yunnanensis, a plant species with extremely small populations endemic to Yunnan Province, China. GigaByte, 0, 2020, 1-12. | 0.0 | 3 |
| 960 | Draft genome of the aquatic moss Fontinalis antipyretica (Fontinalaceae, Bryophyta). GigaByte, 0, 2020, 1-9. | 0.0 | 12 |
| 961 | Evidence for suppression of immunity as a driver for genomic introgressions and host range expansion in races of Albugo candida, a generalist parasite. ELife, 2015, 4, . | 2.8 | 71 |
| 962 | Structure of the germline genome of Tetrahymena thermophila and relationship to the massively rearranged somatic genome. ELife, 2016, 5, . | 2.8 | 130 |
| 963 | The genome of an intranuclear parasite, Paramicrosporidium saccamoebae, reveals alternative adaptations to obligate intracellular parasitism. ELife, 2017, 6, . | 2.8 | 63 |
| 964 | Genome streamlining in a minute herbivore that manipulates its host plant. ELife, 2020, 9, . | 2.8 | 33 |
| 965 | A draft genome and transcriptome of common milkweed (Asclepias syriaca) as resources for evolutionary, ecological, and molecular studies in milkweeds and Apocynaceae. PeerJ, 2019, 7, e7649. | 0.9 | 19 |
| 966 | msRepDB: a comprehensive repetitive sequence database of over 80 000 species. Nucleic Acids Research, 2022, 50, D236-D245. | 6.5 | 8 |
| 967 | Chromosome Level Genome Assembly and Annotation of Highly Invasive Japanese Stiltgrass (Microstegium vimineum). Genome Biology and Evolution, 2021, 13, . | 1.1 | 4 |
| 968 | A chromosomeâ€scale genome assembly and annotation of the spring orchid (Cymbidium) Tj ETQq1 1 0.784314 rgBT /Overlock 1 | 2.2 | 9 |
| 969 | High-quality genome assembly of an important biodiesel plant, Euphorbia lathyris L. DNA Research, 2021, 28, . | 1.5 | 11 |
| 970 | A chromosome-scale draft genome sequence of horsegram (Macrotyloma uniflorum). GigaByte, 0, 2021, 1-23. | 0.0 | 7 |
| 971 | Evolutionary history and pan-genome dynamics of strawberry ( Fragaria spp.). Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, . | 3.3 | 43 |
| 972 | Chromosome-Level Genome Assembly of Cyrtotrachelus buqueti and Mining of Its Specific Genes. Frontiers in Ecology and Evolution, 2021, 9, . | 1.1 | 2 |
| 973 | Chromosomeâ€level genome assemblies of two cottonâ€melon aphid Aphis gossypii biotypes unveil mechanisms of host adaption. Molecular Ecology Resources, 2022, 22, 1120-1134. | 2.2 | 10 |
| 974 | Chromosome-Scale Genome and Comparative Transcriptomic Analysis Reveal Transcriptional Regulators of Î²-Carotene Biosynthesis in Mango. Frontiers in Plant Science, 2021, 12, 749108. | 1.7 | 8 |

| # | Article | IF | Citations |
|---|---|---|---|
| 975 | The chromosomeâ€scale genome assembly, annotation and evolution of Rhododendron henanense subsp. lingbaoense. Molecular Ecology Resources, 2022, 22, 988-1001. | 2.2 | 14 |
| 976 | Chromosome-level genome assemblies ofChanna argusandChanna maculataand comparative analysis of their temperature adaptability. GigaScience, 2021, 10, . | 3.3 | 5 |
| 977 | Genome features of common vetch (<scp>Vicia sativa</scp>) in natural habitats. Plant Direct, 2021, 5, e352. | 0.8 | 12 |
| 978 | Draft genome sequence of Diaporthe batatatis causing dry rot disease in sweetpotato. Plant Disease, 2021, , . | 0.7 | 2 |
| 980 | Image and Fractal Information Processing for Large-Scale Chemoinformatics, Genomics Analyses and Pattern Discovery. Lecture Notes in Computer Science, 2006, , 163-173. | 1.0 | 3 |
| 981 | An Algorithm for Identification of Repeats with Accurate Boundaries. Jisuanji Xuebao/Chinese Journal of Computers, 2009, 31, 214-219. | 0.3 | 0 |
| 982 | An Adaptive Suffix Tree Based Algorithm for Repeats Identification in a DNA Sequence. Jisuanji Xuebao/Chinese Journal of Computers, 2010, 33, 747-754. | 0.3 | 0 |
| 983 | Rice Genome Initiative. , 2010, , 205-242. | | 0 |
| 985 | LCR_Finder: A de Novo Low Copy Repeat Finder for Human Genome. Lecture Notes in Computer Science, 2013, , 125-136. | 1.0 | 0 |
| 986 | Alternaria Comparative Genomics: The Secret Life of Rots. , 2014, , 45-63. | | 3 |
| 991 | Penelope-like retrotransposons in the genome of asian blood fluke Schisto-soma Japonicum (Trematoda: Schistosomatidae). Molekuliarnaia Genetika, Mikrobiologiia I Virusologiia, 2017, 35, 20. | 0.1 | 0 |
| 1029 | Comprehensive understanding of Tn5 insertion preference improves transcription regulatory element identification. NAR Genomics and Bioinformatics, 2021, 3, lqab094. | 1.5 | 8 |
| 1030 | The Melastoma dodecandrum genome and the evolution of Myrtales. Journal of Genetics and Genomics, 2022, 49, 120-131. | 1.7 | 14 |
| 1031 | The Aphelenchus avenae genome highlights evolutionary adaptation to desiccation. Communications Biology, 2021, 4, 1232. | 2.0 | 19 |
| 1033 | Genome and systems biology of Melilotus albus provides insights into coumarins biosynthesis. Plant Biotechnology Journal, 2022, 20, 592-609. | 4.1 | 24 |
| 1034 | A draft genome, resequencing, and metabolomes reveal the genetic background and molecular basis of the nutritional and medicinal properties of loquat (Eriobotrya japonica (Thunb.) Lindl). Horticulture Research, 2021, 8, 231. | 2.9 | 14 |
| 1035 | De novo assembly of a chromosome-scale reference genome for the northern flicker Colaptes auratus. G3: Genes, Genomes, Genetics, 2021, 11, . | 0.8 | 4 |
| 1039 | Identification of Transposable Elements in Schistosoma mansoni. Methods in Molecular Biology, 2020, 2151, 135-144. | 0.4 | 0 |

| # | Article | IF | Citations |
|---|---|---|---|
| 1040 | Transposable Elements in Anopheles Species: Refining Annotation Strategies Towards Population Genomics Analyses. Population Genomics, 2020, , 1. | 0.2 | 1 |
| 1041 | 9 FungalÂGenomics. , 2020, , 207-224. | | 0 |
| 1050 | Proteome and strain analysis of cyanobacterium Candidatus â€œPhormidium alkaliphilumâ€•reveals traits for success in biotechnology. IScience, 2021, 24, 103405. | 1.9 | 13 |
| 1055 | Genome Sequence ofElaeagnus mollis, the First Chromosome-Level Genome of the Family Elaeagnaceae. Genome Biology and Evolution, 2021, 13, . | 1.1 | 2 |
| 1057 | Chromosomeâ€level de novo genome assembly and wholeâ€genome resequencing of the threatened species Acanthochlamys bracteata (Velloziaceae) provide insights into alpine plant divergence in a biodiversity hotspot. Molecular Ecology Resources, 2022, 22, 1582-1595. | 2.2 | 5 |
| 1058 | Long-Read Assembly and Annotation of the Parasitoid Wasp Muscidifurax raptorellus, a Biological Control Agent for Filth Flies. Frontiers in Genetics, 2021, 12, 748135. | 1.1 | 3 |
| 1059 | Phylogenomic analyses of the genusDrosophilareveals genomic signals of climate adaptation. Molecular Ecology Resources, 2022, 22, 1559-1581. | 2.2 | 15 |
| 1060 | The Draft Genome of the Centric Diatom Conticribra weissflogii (Coscinodiscophyceae, Ochrophyta). Protist, 2021, 172, 125845. | 0.6 | 4 |
| 1061 | Ecological generalism drives hyperdiversity of secondary metabolite gene clusters in xylarialean endophytes. New Phytologist, 2022, 233, 1317-1330. | 3.5 | 23 |
| 1063 | Transcriptional activity and epigenetic regulation of transposable elements in the symbiotic fungus Rhizophagus irregularis. Genome Research, 2021, 31, 2290-2302. | 2.4 | 19 |
| 1064 | The first highâ€quality chromosomal genome assembly of a medicinal and edible plant Arctium lappa. Molecular Ecology Resources, 2021, , . | 2.2 | 11 |
| 1065 | Multiomics study of a heterotardigrade, Echinisicus testudo, suggests the possibility of convergent evolution of abundant heat-soluble proteins in Tardigrada. BMC Genomics, 2021, 22, 813. | 1.2 | 24 |
| 1066 | Chromosome-Scale Genome Assembly for Chinese Sour Jujube and Insights Into Its Genome Evolution and Domestication Signature. Frontiers in Plant Science, 2021, 12, 773090. | 1.7 | 20 |
| 1067 | The Cymbidium genome reveals the evolution of unique morphological traits. Horticulture Research, 2021, 8, 255. | 2.9 | 33 |
| 1068 | A chromosomeâ€level genome of Portunus trituberculatus provides insights into its evolution, salinity adaptation and sex determination. Molecular Ecology Resources, 2022, 22, 1606-1625. | 2.2 | 11 |
| 1069 | The chromosomeâ€level genome provides insight into the molecular mechanism underlying the tortuousâ€branch phenotype of Prunus mume. New Phytologist, 2022, 235, 141-156. | 3.5 | 15 |
| 1071 | Alleleâ€aware chromosomeâ€scale assembly of the allopolyploid genome of hexaploid Ma bamboo (Dendrocalamus latiflorus Munro). Journal of Integrative Plant Biology, 2022, 64, 649-670. | 4.1 | 24 |
| 1072 | Genome sequences ofÂfive Sitopsis species of Aegilops and the origin of polyploid wheat B subgenome. Molecular Plant, 2022, 15, 488-503. | 3.9 | 84 |

| # | Article | IF | Citations |
|---|---|---|---|
| 1073 | First Draft Genome of a Mud Loach (Misgurnus mizolepis) in the Family Cobitidae. Frontiers in Marine Science, 2022, 8, . | 1.2 | 0 |
| 1074 | A highâ€quality chromosomeâ€level genome of the endangered roughskin sculpin provides insights into its evolution and adaptation. Molecular Ecology Resources, 2022, 22, 1892-1905. | 2.2 | 1 |
| 1076 | Chromosomal-level genome and multi-omics dataset of Pueraria lobata var. thomsonii provide new insights into legume family and the isoflavone and puerarin biosynthesis pathways. Horticulture Research, 2022, 9, . | 2.9 | 10 |
| 1077 | Chromosome-level genome assembly of the fully mycoheterotrophic orchid Gastrodia elata. G3: Genes, Genomes, Genetics, 2022, 12, . | 0.8 | 15 |
| 1078 | Finding and Characterizing Repeats in Plant Genomes. Methods in Molecular Biology, 2022, 2443, 327-385. | 0.4 | 2 |
| 1079 | A bacterial type three secretion-based delivery system for functional characterization ofÂSporisorium scitamineumÂplant immune suppressing effector proteins. Phytopathology, 2022, , . | 1.1 | 2 |
| 1080 | A chromosome-scale genome assembly for the holly (Ilex polyneura) provides insights into genomic adaptations to elevation in Southwest China. Horticulture Research, 2022, 9, . | 2.9 | 12 |
| 1081 | A Chromosome-Level Genome Assembly of the Pygmy Mole Cricket Xya riparia. Genome Biology and Evolution, 2022, 14, . | 1.1 | 0 |
| 1082 | Genome sequence and transcriptome of Sorbus pohuashanensis provide insights into population evolution and leaf sunburn response. Journal of Genetics and Genomics, 2022, 49, 547-558. | 1.7 | 9 |
| 1083 | Hybrid Assembly Improves Genome Quality and Completeness of Trametes villosa CCMB561 and Reveals a Huge Potential for Lignocellulose Breakdown. Journal of Fungi (Basel, Switzerland), 2022, 8, 142. | 1.5 | 8 |
| 1084 | Chromosome-level genome assembly of Zizania latifolia provides insights into its seed shattering and phytocassane biosynthesis. Communications Biology, 2022, 5, 36. | 2.0 | 11 |
| 1085 | Chromosome-level genome assembly of Bactrocera dorsalis reveals its adaptation and invasion mechanisms. Communications Biology, 2022, 5, 25. | 2.0 | 17 |
| 1086 | Genome survey sequence of black carp provides insights into developmentâ€related gene duplications. Journal of the World Aquaculture Society, 2022, 53, 1197-1214. | 1.2 | 0 |
| 1087 | Describing biodiversity in the genomics era: A new species of Nearctic Cynipidae gall wasp and its genome. Systematic Entomology, 2022, 47, 94-112. | 1.7 | 12 |
| 1088 | A chromosome-level genome assembly of an alpine plant Crucihimalaya lasiocarpa provides insights into high-altitude adaptation. DNA Research, 2022, 29, . | 1.5 | 13 |
| 1089 | Annotation of Protein-Coding Genes in Plant Genomes. Methods in Molecular Biology, 2022, 2443, 309-326. | 0.4 | 0 |
| 1090 | A Genome forBidens hawaiensis: A Member of a Hexaploid Hawaiian Plant Adaptive Radiation. Journal of Heredity, 2022, 113, 205-214. | 1.0 | 11 |
| 1091 | Chromosome-Level Genome Assemblies of Two Hypnales (Mosses) Reveal High Intergeneric Synteny. Genome Biology and Evolution, 2022, 14, . | 1.1 | 11 |

| # | Article | IF | Citations |
|---|---|---|---|
| 1092 | OUP accepted manuscript. DNA Research, 2022, , . | 1.5 | 4 |
| 1093 | The roles of recombination and selection in shaping genomic divergence in an incipient ecological species complex. Molecular Ecology, 2023, 32, 1478-1496. | 2.0 | 10 |
| 1094 | Chromosome-level genome assembly of Aristolochia contorta provides insights into the biosynthesis of benzylisoquinoline alkaloids and aristolochic acids. Horticulture Research, 2022, 9, . | 2.9 | 11 |
| 1095 | A Chromosome-Level Genome Assembly of the European Beech (Fagus sylvatica) Reveals Anomalies for Organelle DNA Integration, Repeat Content and Distribution of SNPs. Frontiers in Genetics, 2021, 12, 691058. | 1.1 | 17 |
| 1096 | Haplotype-Resolved Genome Analyses Reveal Genetically Distinct Nuclei within a Commercial Cultivar of Lentinula edodes. Journal of Fungi (Basel, Switzerland), 2022, 8, 167. | 1.5 | 5 |
| 1097 | Small RNA pathways in the nematode Ascaris in the absence of piRNAs. Nature Communications, 2022, 13, 837. | 5.8 | 11 |
| 1100 | The evolution study on by whole-genome sequencing. Journal of Genetics, 2019, 98, . | 0.4 | 0 |
| 1101 | A high-quality assembled genome and its comparative analysis decode the adaptive molecular mechanism of the number one Chinese cotton variety CRI-12. GigaScience, 2022, 11, . | 3.3 | 6 |
| 1102 | A high-quality assembly reveals genomic characteristics, phylogenetic status, and causal genes for leucism plumage of Indian peafowl. GigaScience, 2022, 11, . | 3.3 | 10 |
| 1103 | Chromosome-Scale Cerasus Humilis Genome Assembly Reveals Gene Family Evolution and Possible Genomic Basis of Calcium Accumulation in Fruits. SSRN Electronic Journal, 0, , . | 0.4 | 0 |
| 1104 | Draft Genome Sequence of an Unusual Ectomycorrhizal Fungus, Pseudotulostoma volvatum. Microbiology Resource Announcements, 2022, 11, e0080121. | 0.3 | 1 |
| 1105 | Chromosome-level genome assembly of a xerophytic plant, Haloxylon ammodendron. DNA Research, 2022, 29, . | 1.5 | 15 |
| 1106 | A myxozoan genome reveals mosaic evolution in a parasitic cnidarian. BMC Biology, 2022, 20, 51. | 1.7 | 8 |
| 1107 | Chromosome-level genome assembly of the diploid blueberry Vaccinium darrowii provides insights into its subtropical adaptation and cuticle synthesis. Plant Communications, 2022, 3, 100307. | 3.6 | 10 |
| 1108 | Draft Assembled Genome of Walleye Pollock (Gadus chalcogrammus). Frontiers in Marine Science, 2022, 9, . | 1.2 | 2 |
| 1109 | The Chromosome-Scale Reference Genome of Macadamia tetraphylla Provides Insights Into Fatty Acid Biosynthesis. Frontiers in Genetics, 2022, 13, 835363. | 1.1 | 4 |
| 1110 | Migrators within migrators: exploring transposable element dynamics in the monarch butterfly, Danaus plexippus. Mobile DNA, 2022, 13, 5. | 1.3 | 17 |
| 1111 | The genome of Hibiscus hamabo reveals its adaptation to saline and waterlogged habitat. Horticulture Research, 2022, 9, uhac067. | 2.9 | 12 |

| # | Article | IF | Citations |
|---|---|---|---|
| 1112 | Chromosomeâ€level pepino genome provides insights into genome evolution and anthocyanin biosynthesis in Solanaceae. Plant Journal, 2022, 110, 1128-1143. | 2.8 | 9 |
| 1113 | A beginnerâ€™s guide to manual curation of transposable elements. Mobile DNA, 2022, 13, 7. | 1.3 | 36 |
| 1114 | Chromosome-Level Genome Assembly for Acer pseudosieboldianum and Highlights to Mechanisms for Leaf Color and Shape Change. Frontiers in Plant Science, 2022, 13, 850054. | 1.7 | 7 |
| 1115 | Genome Sequence Resource of Colletotrichum horii, an Important Pathogenic Fungus Threatening Persimmon Production. Plant Disease, 2022, 106, 1052-1055. | 0.7 | 1 |
| 1116 | Onset and stepwise extensions of recombination suppression are common in matingâ€type chromosomes of Microbotryum antherâ€smut fungi. Journal of Evolutionary Biology, 2022, 35, 1619-1634. | 0.8 | 11 |
| 1117 | The adaptive evolution of Euryale ferox to the aquatic environment through paleoâ€hexaploidization. Plant Journal, 2022, 110, 627-645. | 2.8 | 12 |
| 1118 | Chromosome-scale Echinococcus granulosus (genotype G1) genome reveals the Eg95 gene family and conservation of the EG95-vaccine molecule. Communications Biology, 2022, 5, 199. | 2.0 | 7 |
| 1119 | Genome sequence and population genomics provide insights into chromosomal evolution and phytochemical innovation of Hippophae rhamnoides. Plant Biotechnology Journal, 2022, 20, 1257-1273. | 4.1 | 17 |
| 1120 | The spinach YY genome reveals sex chromosome evolution, domestication, and introgression history of the species. Genome Biology, 2022, 23, 75. | 3.8 | 15 |
| 1121 | The new Haemaphysalis longicornis genome provides insights into its requisite biological traits. Genomics, 2022, 114, 110317. | 1.3 | 9 |
| 1122 | Tracking of Diversity and Evolution in the Brown Rot Fungi Monilinia fructicola, Monilinia fructigena, and Monilinia laxa. Frontiers in Microbiology, 2022, 13, 854852. | 1.5 | 14 |
| 1123 | Phylogenomics and Comparative Genomics Highlight Specific Genetic Features in Ganoderma Species. Journal of Fungi (Basel, Switzerland), 2022, 8, 311. | 1.5 | 10 |
| 1124 | Do Ty3/Gypsy Transposable Elements Play Preferential Roles in Sex Chromosome Differentiation?. Life, 2022, 12, 522. | 1.1 | 8 |
| 1125 | Reshuffling of the ancestral core-eudicot genome shaped chromatin topology and epigenetic modification in Panax. Nature Communications, 2022, 13, 1902. | 5.8 | 30 |
| 1126 | Comparative analyses of American and Asian lotus genomes reveal insights into petal color, carpel thermogenesis and domestication. Plant Journal, 2022, 110, 1498-1515. | 2.8 | 21 |
| 1127 | A Chromosome-Level Reference Genome of Chinese Balloon Flower (Platycodon grandiflorus). Frontiers in Genetics, 2022, 13, 869784. | 1.1 | 7 |
| 1128 | Supercomputing of reducing sequenced bases in de novo sequencing of the human genome. Journal of Supercomputing, 0, , 1. | 2.4 | 4 |
| 1129 | The chromosome-level genome assembly of Gentiana dahurica (Gentianaceae) provides insights into gentiopicroside biosynthesis. DNA Research, 2022, 29, . | 1.5 | 12 |

| # | Article | IF | Citations |
|---|---|---|---|
| 1130 | De novo genome assembly of Bradysia cellarum (Diptera: Sciaridae), a notorious pest in traditional special vegetables in China. Insect Molecular Biology, 2022, 31, 508-518. | 1.0 | 3 |
| 1131 | Chromosome-scale Cerasus humilis genome assembly reveals gene family evolution and possible genomic basis of calcium accumulation in fruits. Scientia Horticulturae, 2022, 299, 111012. | 1.7 | 5 |
| 1132 | Genome Analysis of Lagocephalus sceleratus: Unraveling the Genomic Landscape of a Successful Invader. Frontiers in Genetics, 2021, 12, 790850. | 1.1 | 6 |
| 1133 | Chromosomal-Level Assembly of Antarctic Scaly Rockcod, Trematomus loennbergii Genome Using Long-Read Sequencing and Chromosome Conformation Capture (Hi-C) Technologies. Diversity, 2021, 13, 668. | 0.7 | 3 |
| 1134 | Exploring transposable element-based markers to identify allelic variations underlying agronomic traits in rice. Plant Communications, 2021, 3, 100270. | 3.6 | 13 |
| 1135 | Genomic analysis of ElsinoÃ« arachidis reveals its potential pathogenic mechanism and the biosynthesis pathway of elsinochrome toxin. PLoS ONE, 2021, 16, e0261487. | 1.1 | 3 |
| 1136 | A masculinizing supergene underlies an exaggerated male reproductive morph in a spider. Nature Ecology and Evolution, 2022, 6, 195-206. | 3.4 | 18 |
| 1138 | Genome sequence of the English grain aphid,Sitobion avenaeand its endosymbiontBuchnera aphidicola. G3: Genes, Genomes, Genetics, 2022, 12, . | 0.8 | 4 |
| 1139 | Genetic and Molecular Characterization of a Self-Compatible Brassica rapa Line Possessing a New Class II S Haplotype. Plants, 2021, 10, 2815. | 1.6 | 5 |
| 1140 | Genome sequencing and transcriptome analyses provide insights into the origin and domestication of water caltrop (Trapa spp., Lythraceae). Plant Biotechnology Journal, 2022, 20, 761-776. | 4.1 | 16 |
| 1141 | Genomic Analysis Based on Chromosome-Level Genome Assembly Reveals an Expansion of Terpene Biosynthesis of Azadirachta indica. Frontiers in Plant Science, 2022, 13, 853861. | 1.7 | 5 |
| 1142 | Methodologies for the De novo Discovery of Transposable Element Families. Genes, 2022, 13, 709. | 1.0 | 10 |
| 1143 | Incomplete lineage sorting and phenotypic evolution in marsupials. Cell, 2022, 185, 1646-1660.e18. | 13.5 | 43 |
| 1144 | A chromosome-level genome of the kuruma shrimp (Marsupenaeus japonicus) provides insights into its evolution and cold-resistance mechanism. Genomics, 2022, 114, 110373. | 1.3 | 8 |
| 1210 | Deletion and tandem duplications of biosynthetic genes drive the diversity of triterpenoids in Aralia elata. Nature Communications, 2022, 13, 2224. | 5.8 | 34 |
| 1211 | Genome of the ramshorn snail Biomphalaria straminea-an obligate intermediate host of schistosomiasis.. GigaScience, 2022, 11, . | 3.3 | 11 |
| 1212 | A High-Quality Haplotype-Resolved Genome of Common Bermudagrass (Cynodon dactylon L.) Provides Insights Into Polyploid Genome Stability and Prostrate Growth. Frontiers in Plant Science, 2022, 13, 890980. | 1.7 | 4 |
| 1213 | Software evaluation for de novo detection of transposons. Mobile DNA, 2022, 13, 14. | 1.3 | 14 |

| # | Article | IF | Citations |
|---|---|---|---|
| 1214 | Chromosome-Scale, Haplotype-Resolved Genome Assembly of Suaeda Glauca. Frontiers in Genetics, 2022, 13, . | 1.1 | 3 |
| 1215 | Tolypocladamide H and the Proposed Tolypocladamide NRPS in Tolypocladium Species. Journal of Natural Products, 2022, 85, 1363-1373. | 1.5 | 10 |
| 1216 | Comparative Genomics Reveals Insights into the Divergent Evolution of Astigmatic Mites and Household Pest Adaptations. Molecular Biology and Evolution, 2022, 39, . | 3.5 | 13 |
| 1219 | Chromosome-level genome assembly of Asian yellow pond turtle (Mauremys mutica) with temperature-dependent sex determination system. Scientific Reports, 2022, 12, 7905. | 1.6 | 7 |
| 1220 | SunUp and Sunset genomes revealed impact of particle bombardment mediated transformation and domestication history in papaya. Nature Genetics, 2022, 54, 715-724. | 9.4 | 26 |
| 1221 | A haploid pseudo-chromosome genome assembly for a keystone sagebrush species of western North American rangelands. G3: Genes, Genomes, Genetics, 2022, 12, . | 0.8 | 3 |
| 1222 | The chromosomeâ€level genome assembly of the Japanese yellowtail jack Seriola aureovittata provides insights into genome evolution and efficient oxygen transport. Molecular Ecology Resources, 2022, 22, 2701-2712. | 2.2 | 5 |
| 1227 | Comparative genomics highlight the importance of lineage-specific gene families in evolutionary divergence of the coral genus, Montipora. Bmc Ecology and Evolution, 2022, 22, . | 0.7 | 7 |
| 1228 | Chromosome-scale genome assembly of an important medicinal plant honeysuckle. Scientific Data, 2022, 9, . | 2.4 | 7 |
| 1229 | The chromosome-level genome for Toxicodendron vernicifluum provides crucial insights into Anacardiaceae evolution and urushiol biosynthesis. IScience, 2022, 25, 104512. | 1.9 | 6 |
| 1230 | Genomic insights into the recent chromosome reduction of autopolyploid sugarcane Saccharum spontaneum. Nature Genetics, 2022, 54, 885-896. | 9.4 | 33 |
| 1232 | Full-length transcripts facilitates Portunus trituberculatus genome structure annotation. Journal of Oceanology and Limnology, 2022, 40, 2042-2051. | 0.6 | 3 |
| 1233 | Genomes and demographic histories of the endangeredBretschneidera sinensis(Akaniaceae). GigaScience, 2022, 11, . | 3.3 | 6 |
| 1235 | A chromosome-level genome assembly of Artocarpus nanchuanensis (Moraceae), an extremely endangered fruit tree. GigaScience, 2022, 11, . | 3.3 | 3 |
| 1236 | The Genetic Adaptations of Toxoptera Aurantia Facilitated its Rapid Multiple Plant Hosts Dispersal and Invasion. SSRN Electronic Journal, 0, , . | 0.4 | 0 |
| 1237 | A chromosomeâ€level Populus qiongdaoensis genome assembly provides insights into tropical adaptation and a cryptic turnover of sex determination. Molecular Ecology, 2023, 32, 1366-1380. | 2.0 | 10 |
| 1238 | A chromosome-level genome assembly for the rabbit tapeworm Taenia pisiformis. Gene, 2022, 834, 146650. | 1.0 | 2 |
| 1239 | High sorbic acid resistance of Penicillium roqueforti is mediated by the SORBUS gene cluster. PLoS Genetics, 2022, 18, e1010086. | 1.5 | 4 |

| # | Article | IF | Citations |
|---|---|---|---|
| 1240 | The genome of a mangrove plant, Avicennia marina, provides insights into adaptation to coastal intertidal habitats. Planta, 2022, 256, . | 1.6 | 5 |
| 1241 | Comparative Genomic Analyses Provide Insight Into the Pathogenicity of Metschnikowia bicuspidata LNES0119. Frontiers in Microbiology, 0, 13, . | 1.5 | 7 |
| 1242 | Genome sequence of Gossypium anomalum facilitates interspecific introgression breeding. Plant Communications, 2022, 3, 100350. | 3.6 | 14 |
| 1243 | A chromosome-level genome assembly and annotation of the maize elite breeding line Dan340. GigaByte, 0, 2022, 1-8. | 0.0 | 2 |
| 1244 | Chromosome-scale assembly with a phased sex-determining region resolves features of early Z and W chromosome differentiation in a wild octoploid strawberry. G3: Genes, Genomes, Genetics, 2022, 12, . | 0.8 | 11 |
| 1245 | Comparative genomics reveals low levels of inter- and intraspecies diversity in the causal agents of dwarf and common bunt of wheat and hint at conspecificity of Tilletia caries and T. laevis. IMA Fungus, 2022, 13, . | 1.7 | 5 |
| 1246 | Loci underlying leaf agronomic traits identified by re-sequencing celery accessions based on an assembled genome. IScience, 2022, 25, 104565. | 1.9 | 6 |
| 1247 | Chromosome-level genome assembly and annotation of the native Chinese wild blueberry <i>Vaccinium bracteatum</i>. Fruit Research, 2022, 2, 1-14. | 0.9 | 5 |
| 1248 | Bioinformatics Approaches for Determining the Functional Impact of Repetitive Elements on Non-coding RNAs. Methods in Molecular Biology, 2022, , 315-340. | 0.4 | 2 |
| 1249 | Impact of host demography and evolutionary history on endosymbiont molecular evolution: A test in carpenter ants (genus Camponotus) and their Blochmannia endosymbionts. Ecology and Evolution, 2022, 12, . | 0.8 | 7 |
| 1250 | A de novo assembled high-quality chromosome-scale Trifolium pratense genome and fine-scale phylogenetic analysis. BMC Plant Biology, 2022, 22, . | 1.6 | 6 |
| 1251 | Lilac (Syringa oblata) genome provides insights into its evolution and molecular mechanism of petal color change. Communications Biology, 2022, 5, . | 2.0 | 13 |
| 1252 | Comparative genomic analysis of Babesia duncani responsible for human babesiosis. BMC Biology, 2022, 20, . | 1.7 | 11 |
| 1254 | Highâ€quality ice plant reference genome analysis provides insights into genome evolution and allows exploration of genes involved in the transition from <scp>C3</scp> to <scp>CAM</scp> pathways. Plant Biotechnology Journal, 2022, 20, 2107-2122. | 4.1 | 17 |
| 1255 | Chromosome-scale genome assembly of Rhododendron molle provides insights into its evolution and terpenoid biosynthesis. BMC Plant Biology, 2022, 22, . | 1.6 | 6 |
| 1256 | Chromosome-Level Genome Assembly and Transcriptome Comparison Analysis of Cephalopholis sonnerati and Its Related Grouper Species. Biology, 2022, 11, 1053. | 1.3 | 4 |
| 1257 | Chromosome-level assembly and analysis of the Thymus genome provide insights into glandular secretory trichome formation and monoterpenoid biosynthesis in thyme. Plant Communications, 2022, 3, 100413. | 3.6 | 20 |
| 1258 | DNA Methylome and LncRNAome Analysis Provide Insights Into Mechanisms of Genome-Dosage Effects in Autotetraploid Cassava. Frontiers in Plant Science, 0, 13, . | 1.7 | 6 |

| # | Article | IF | Citations |
|---|---|---|---|
| 1259 | A Chromosome-Level Genome Assembly ofToona ciliata(Meliaceae). Genome Biology and Evolution, 2022, 14, . | 1.1 | 7 |
| 1260 | Chromosome-level genome of Tibetan naked carp (Gymnocypris przewalskii) provides insights into Tibetan highland adaptation. DNA Research, 2022, 29, . | 1.5 | 9 |
| 1261 | An Updated Genome Assembly Improves Understanding of the Transcriptional Regulation of Coloration in Midas Cichlid. Frontiers in Marine Science, 0, 9, . | 1.2 | 2 |
| 1262 | New insights into the evolutionary dynamic and lineage divergence of gasdermin E in metazoa. Frontiers in Cell and Developmental Biology, 0, 10, . | 1.8 | 13 |
| 1264 | Multi-omics profiling of the cold tolerant Monoraphidium minutum 26B-AM in response to abiotic stress. Algal Research, 2022, 66, 102794. | 2.4 | 3 |
| 1265 | Chromosome-level Genome Assembly of the High-altitude Leopard (Panthera pardus) Sheds Light on Its Environmental Adaptation. Genome Biology and Evolution, 0, , . | 1.1 | 1 |
| 1266 | Chromosome-level genome assembly of largemouth bass (Micropterus salmoides) using PacBio and Hi-C technologies. Scientific Data, 2022, 9, . | 2.4 | 4 |
| 1268 | The chromosome-level holly (Ilex latifolia) genome reveals key enzymes in triterpenoid saponin biosynthesis and fruit color change. Frontiers in Plant Science, 0, 13, . | 1.7 | 7 |
| 1269 | Chromosome-level genome assembly and population genomic analyses provide insights into adaptive evolution of the red turpentine beetle, Dendroctonus valens. BMC Biology, 2022, 20, . | 1.7 | 5 |
| 1270 | Revealing Landscapes of Transposable Elements in Apis Species by Meta-Analysis. Insects, 2022, 13, 698. | 1.0 | 8 |
| 1271 | Behavioral innovation and genomic novelty are associated with the exploitation of a challenging dietary opportunity by an avivorous bat. IScience, 2022, 25, 104973. | 1.9 | 7 |
| 1273 | The nearly complete assembly of the Cercis chinensis genome and Fabaceae phylogenomic studies provide insights into new gene evolution. Plant Communications, 2023, 4, 100422. | 3.6 | 4 |
| 1274 | A reference-grade genome assembly for Gossypium bickii and insights into its genome evolution and formation of pigment glands and gossypol. Plant Communications, 2023, 4, 100421. | 3.6 | 10 |
| 1275 | Chromosome-Level Genome Assembly of Callitettix versicolor (Rice Spittlebug). Genome Biology and Evolution, 2022, 14, . | 1.1 | 2 |
| 1276 | Assembly of highâ€quality genomes of the locoweed Oxytropis ochrocephala and its endophyte Alternaria oxytropis provides new evidence for their symbiotic relationship and swainsonine biosynthesis. Molecular Ecology Resources, 2023, 23, 253-272. | 2.2 | 4 |
| 1277 | The improved genome of the nematode Parapristionchus giblindavisi provides insights into lineage-specific gene family evolution. G3: Genes, Genomes, Genetics, 2022, 12, . | 0.8 | 2 |
| 1278 | Annotation of Siberian Larch (Larix sibirica Ledeb.) Nuclear Genomeâ€”One of the Most Cold-Resistant Tree Species in the Only Deciduous GENUS in Pinaceae. Plants, 2022, 11, 2062. | 1.6 | 7 |
| 1279 | Transposons and non-coding regions drive the intrafamily differences of genome size in insects. IScience, 2022, 25, 104873. | 1.9 | 9 |

| # | Article | IF | Citations |
|---|---|---|---|
| 1280 | Genomic and transcriptomic analyses provide insights into valuable fatty acid biosynthesis and environmental adaptation of yellowhorn. Frontiers in Plant Science, 0, 13, . | 1.7 | 2 |
| 1281 | Functional genomics analysis reveals the evolutionary adaptation and demographic history of pygmy lorises. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, . | 3.3 | 5 |
| 1282 | Roles of Species-Specific Legumains in Pathogenicity of the Pinewood Nematode Bursaphelenchus xylophilus. International Journal of Molecular Sciences, 2022, 23, 10437. | 1.8 | 2 |
| 1283 | The genetic adaptations of Toxoptera aurantii facilitated its rapid multiple plant hosts dispersal and invasion. Genomics, 2022, 114, 110472. | 1.3 | 2 |
| 1284 | A Chromosome-Level Genome Assembly of the <i>Rhus</i> Gall Aphid <i>Schlechtendalia chinensis</i> Provides Insight into the Endogenization of <i>Parvovirus</i>-Like DNA Sequences. SSRN Electronic Journal, 0, , . | 0.4 | 0 |
| 1285 | Genome Assembly of the Polyclad Flatworm Prostheceraeus crozieri. Genome Biology and Evolution, 2022, 14, . | 1.1 | 3 |
| 1286 | Chromosome-level Genomes Reveal the Genetic Basis of Descending Dysploidy and Sex Determination in Morus Plants. Genomics, Proteomics and Bioinformatics, 2022, 20, 1119-1137. | 3.0 | 6 |
| 1287 | Chromosome-scale genome assembly of Camellia sinensis combined with multi-omics provides insights into its responses to infestation with green leafhoppers. Frontiers in Plant Science, 0, 13, . | 1.7 | 6 |
| 1288 | Differences in pseudogene evolution contributed to the contrasting flavors of turnip and Chiifu, two Brassica rapa subspecies. Plant Communications, 2023, 4, 100427. | 3.6 | 5 |
| 1289 | Genomic adaptation of the picoeukaryote Pelagomonas calceolata to iron-poor oceans revealed by a chromosome-scale genome sequence. Communications Biology, 2022, 5, . | 2.0 | 6 |
| 1291 | Whole-genome assembly and analysis of a medicinal fungus: Inonotus hispidus. Frontiers in Microbiology, 0, 13, . | 1.5 | 4 |
| 1292 | The genome of Orychophragmus violaceus provides genomic insights into the evolution of Brassicaceae polyploidization and its distinct traits. Plant Communications, 2023, 4, 100431. | 3.6 | 4 |
| 1293 | The genetic architecture of phenotypic diversity in the Betta fish ( Betta splendens ). Science Advances, 2022, 8, . | 4.7 | 10 |
| 1294 | A chromosome-level genome assembly of the Chinese cork oak (Quercus variabilis). Frontiers in Plant Science, 0, 13, . | 1.7 | 16 |
| 1295 | A de novo assembled genome of the Tibetan Partridge (Perdix hodgsoniae) and its highâ€altitude adaptation. Integrative Zoology, 2023, 18, 225-236. | 1.3 | 8 |
| 1296 | Genome-wide characterization of two Aubrieta taxa: Aubrieta canescens subsp. canescens and Au. macrostyla (Brassicaceae). AoB PLANTS, 2022, 14, . | 1.2 | 0 |
| 1297 | A chromosome-level genome assembly of the redfin culter (Chanodichthys erythropterus). Scientific Data, 2022, 9, . | 2.4 | 3 |
| 1299 | Genome sequencing reveals the evolution and pathogenic mechanisms of the wheat sharp eyespot pathogen Rhizoctonia cerealis. Crop Journal, 2023, 11, 405-416. | 2.3 | 1 |

| # | Article | IF | Citations |
|---|---|---|---|
| 1300 | Repeated turnovers keep sex chromosomes young in willows. Genome Biology, 2022, 23, . | 3.8 | 14 |
| 1301 | A chromosome-level genome assembly of the potato grouper (Epinephelus tukula). Genomics, 2022, 114, 110473. | 1.3 | 2 |
| 1302 | Chromosomal-scale genome assembly of the near-extinction big-head schizothorcin (Aspiorhynchus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf | 2.4 | 4 |
| 1303 | De novo genome assembly of the medicinal plant Gentiana macrophylla provides insights into the genomic evolution and biosynthesis of iridoids. DNA Research, 2022, 29, . | 1.5 | 10 |
| 1304 | Comparative genomics of Sarcoptes scabiei provide new insights into adaptation to permanent parasitism and withinâ€host species divergence. Transboundary and Emerging Diseases, 2022, 69, 3468-3484. | 1.3 | 4 |
| 1305 | Timeâ€ordering japonica/geng genomes analysis indicates the importance of large structural variants in rice breeding. Plant Biotechnology Journal, 2023, 21, 202-218. | 4.1 | 5 |
| 1306 | Chromosome-level genome assembly for the Aldabra giant tortoise enables insights into the genetic health of a threatened population. GigaScience, 2022, 11, . | 3.3 | 5 |
| 1307 | Chinese Jujube: Crop Background and Genome Sequencing. Compendium of Plant Genomes, 2022, , 69-86. | 0.3 | 0 |
| 1310 | Chromosome-Level Assembly of Male Opsariichthys bidens Genome Provides Insights into the Regulation of the GnRH Signaling Pathway and Genome Evolution. Biology, 2022, 11, 1500. | 1.3 | 3 |
| 1311 | A reference-grade genome assembly for Astragalus mongholicus and insights into the biosynthesis and high accumulation of triterpenoids and flavonoids in its roots. Plant Communications, 2023, 4, 100469. | 3.6 | 8 |
| 1313 | Whole-Genome Sequencing and Transcriptome Analysis of Ganoderma lucidum Strain Yw-1-5 Provides New Insights into the Enhanced Effect of Tween80 on Exopolysaccharide Production. Journal of Fungi (Basel, Switzerland), 2022, 8, 1081. | 1.5 | 4 |
| 1314 | Whole genome and transcriptome reveal flavone accumulation in Scutellaria baicalensis roots. Frontiers in Plant Science, 0, 13, . | 1.7 | 4 |
| 1316 | The chromosomeâ€level genome of Akebia trifoliata as an important resource to study plant evolution and environmental adaptation in the Cretaceous. Plant Journal, 2022, 112, 1316-1330. | 2.8 | 14 |
| 1317 | Diploid chromosome-level reference genome and population genomic analyses provide insights into Gypenoside biosynthesis and demographic evolution of Gynostemma pentaphyllum (Cucurbitaceae). Horticulture Research, 2023, 10, . | 2.9 | 3 |
| 1319 | Telomere-to-telomere genome assembly of bitter melon (Momordica charantia L. var.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 187 T<br>Horticulture Research, 2023, 10, . | 2.9 | 16 |
| 1320 | Draft genome of the bluefin tuna blood fluke, Cardicola forsteri. PLoS ONE, 2022, 17, e0276287. | 1.1 | 0 |
| 1321 | Pathogenicity Variation in Two Genomes of Cercospora Species Causing Gray Leaf Spot in Maize. Molecular Plant-Microbe Interactions, 2023, 36, 14-25. | 1.4 | 4 |
| 1322 | De novo genome assembly and annotation of Holothuria scabra (Jaeger, 1833) from nanopore sequencing reads. Genes and Genomics, 2022, 44, 1487-1498. | 0.5 | 3 |

| # | Article | IF | Citations |
|---|---|---|---|
| 1323 | De-novo genome assembly and annotation of sobaity seabream Sparidentex hasta. Frontiers in Genetics, 0, 13, . | 1.1 | 1 |
| 1324 | A Chromosome-Scale Genome Assembly of Mitragyna speciosa (Kratom) and the Assessment of Its Genetic Diversity in Thailand. Biology, 2022, 11, 1492. | 1.3 | 2 |
| 1325 | Thirteen Dipterocarpoideae genomes provide insights into their evolution and borneol biosynthesis. Plant Communications, 2022, 3, 100464. | 3.6 | 6 |
| 1327 | Comparative Genomic Analysis of 31 Phytophthora Genomes Reveals Genome Plasticity and Horizontal Gene Transfer. Molecular Plant-Microbe Interactions, 2023, 36, 26-46. | 1.4 | 6 |
| 1328 | An improved, chromosome-level genome of the giant panda (Ailuropoda melanoleuca). Genomics, 2022, 114, 110501. | 1.3 | 5 |
| 1329 | High-quality genome assemblies from key Hawaiian coral species. GigaScience, 2022, 11, . | 3.3 | 11 |
| 1330 | metaMIC: reference-free misassembly identification and correction of de novo metagenomic assemblies. Genome Biology, 2022, 23, . | 3.8 | 12 |
| 1331 | Wholeâ€genome assembly and annotation for the little yellow croaker (Larimichthys polyactis) provide insights into the evolution of hermaphroditism and gonochorism. Molecular Ecology Resources, 2023, 23, 632-658. | 2.2 | 4 |
| 1332 | A high-quality chromosome-level genome assembly of Pelteobagrus vachelli provides insights into its environmental adaptation and population history. Frontiers in Genetics, 0, 13, . | 1.1 | 0 |
| 1333 | Improved assembly and annotation of the sesame genome. DNA Research, 2022, 29, . | 1.5 | 11 |
| 1334 | A high-quality, haplotype-phased genome reconstruction reveals unexpected haplotype diversity in a pearl oyster. DNA Research, 2022, 29, . | 1.5 | 10 |
| 1335 | Long-read assembly of major histocompatibility complex and killer cell immunoglobulin-like receptor genome regions in cynomolgus macaque. Biology Direct, 2022, 17, . | 1.9 | 2 |
| 1336 | African Suid Genomes Provide Insights into the Local Adaptation to Diverse African Environments. Molecular Biology and Evolution, 2022, 39, . | 3.5 | 9 |
| 1337 | The first genome sequence of Phomopsis vexans: a fungal pathogen causing Phomopsis blight in eggplant. , 0, , . | | 1 |
| 1339 | Chromosomal-level genome assembly of potato tuberworm, Phthorimaea operculella: a pest of solanaceous crops. Scientific Data, 2022, 9, . | 2.4 | 5 |
| 1340 | The chromosome-level genome assembly of goldstripe ponyfish (Karalla daura) reveals its similarity to Chinese sillago on contracted immune gene families. Frontiers in Marine Science, 0, 9, . | 1.2 | 0 |
| 1341 | Karyotype evolution of the Asterids insights from the first genome sequences of the family Cornaceae. DNA Research, 2023, 30, . | 1.5 | 2 |
| 1342 | MycoCosm, the JGIâ€™s Fungal Genome Portal for Comparative Genomic and Multiomics Data Analyses. Methods in Molecular Biology, 2023, , 271-291. | 0.4 | 7 |

| # | Article | IF | Citations |
|---|---|---|---|
| 1343 | CAULIFINDER: a pipeline for the automated detection and annotation of caulimovirid endogenous viral elements in plant genomes. Mobile DNA, 2022, 13, . | 1.3 | 2 |
| 1344 | An Overview of Best Practices for Transposable Element Identification, Classification, and Annotation in Eukaryotic Genomes. Methods in Molecular Biology, 2023, , 1-23. | 0.4 | 1 |
| 1345 | Genome Sequence Resource of Fusarium graminearum TaB10 and Fusarium avenaceum KA13, Causal Agents of Stored Apple Rot. Molecular Plant-Microbe Interactions, 0, , . | 1.4 | 0 |
| 1346 | How to survive in the worldâ€™s third poplar: Insights from the genome of the highest altitude woody plant, Hippophae tibetana (Elaeagnaceae). Frontiers in Plant Science, 0, 13, . | 1.7 | 2 |
| 1348 | Genome assembly of wild loquat (Eriobotrya japonica) and resequencing provide new insights into the genomic evolution and fruit domestication in loquat. Horticulture Research, 2023, 10, . | 2.9 | 12 |
| 1349 | Mobilome of the Rhus Gall Aphid Schlechtendalia chinensis Provides Insight into TE Insertion-Related Inactivation of Functional Genes. International Journal of Molecular Sciences, 2022, 23, 15967. | 1.8 | 1 |
| 1350 | Immunogenetic losses co-occurred with seahorse male pregnancy and mutation in tlx1 accompanied functional asplenia. Nature Communications, 2022, 13, . | 5.8 | 9 |
| 1351 | Sinapis genomes provide insights into wholeâ€genome triplication and divergence patterns within tribe Brassiceae. Plant Journal, 2023, 113, 246-261. | 2.8 | 5 |
| 1352 | Syringa oblata genome provides new insights into molecular mechanism of flower color differences among individuals and biosynthesis of its flower volatiles. Frontiers in Plant Science, 0, 13, . | 1.7 | 0 |
| 1355 | The draft genome of the Tibetan partridge (Perdix hodgsoniae) provides insights into its phylogenetic position and high-altitude adaptation. Journal of Heredity, 0, , . | 1.0 | 2 |
| 1357 | Gapless genome assembly of East Asian finless porpoise. Scientific Data, 2022, 9, . | 2.4 | 1 |
| 1358 | High-quality genome of Diaphanosoma dubium provides insights into molecular basis of its broad ecological adaptation. IScience, 2023, 26, 106006. | 1.9 | 0 |
| 1359 | Similar adaptative mechanism but divergent demographic history of four sympatric desert rodents in Eurasian inland. Communications Biology, 2023, 6, . | 2.0 | 2 |
| 1360 | High-quality haplotype-resolved genome assembly of cultivated octoploid strawberry. Horticulture Research, 2023, 10, . | 2.9 | 11 |
| 1361 | A chromosome-scale genome assembly of Artemisia argyi reveals unbiased subgenome evolution and key contributions of gene duplication to volatile terpenoid diversity. Plant Communications, 2023, 4, 100516. | 3.6 | 16 |
| 1362 | Genome sequencing and resequencing identified three horizontal gene transfers and uncovered the genetic mechanism on the intraspecies adaptive evolution of Gastrodia elata Blume. Frontiers in Plant Science, 0, 13, . | 1.7 | 1 |
| 1363 | Small RNAs and Karma methylation in Elaeis guineensis mother palms are linked to high clonal mantling. Plant Molecular Biology, 2023, 111, 345-363. | 2.0 | 2 |
| 1364 | Chromosome-level genome assembly of a high-altitude-adapted frog (Rana kukunoris) from the Tibetan plateau provides insight into amphibian genome evolution and adaptation. Frontiers in Zoology, 2023, 20, . | 0.9 | 3 |

| # | Article | IF | Citations |
|---|---|---|---|
| 1365 | Large-Scale Chromosomal Changes Lead to Genome-Level Expression Alterations, Environmental Adaptation, and Speciation in the Gayal (Bos frontalis). Molecular Biology and Evolution, 2023, 40, . | 3.5 | 5 |
| 1366 | Two-speed genome evolution drives pathogenicity in fungal pathogens of animals. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, . | 3.3 | 12 |
| 1367 | Nuclear Genome Sequence and Gene Expression of an Intracellular Fungal Endophyte Stimulating the Growth of Cranberry Plants. Journal of Fungi (Basel, Switzerland), 2023, 9, 126. | 1.5 | 2 |
| 1368 | The Jasmine (Jasminum sambac) Genome Provides Insight into the Biosynthesis of Flower Fragrances and Jasmonates. Genomics, Proteomics and Bioinformatics, 2023, 21, 127-149. | 3.0 | 5 |
| 1369 | Chromosome-scale genomics, metabolomics, and transcriptomics provide insight into the synthesis and regulation of phenols in Vitis adenoclada grapes. Frontiers in Plant Science, 0, 14, . | 1.7 | 1 |
| 1370 | Chromosome fusions repatterned recombination rate and facilitated reproductive isolation during Pristionchus nematode speciation. Nature Ecology and Evolution, 0, , . | 3.4 | 11 |
| 1371 | Complete genome sequencing of nematode Aphelenchoides besseyi, an economically important pest causing rice white-tip disease. Phytopathology Research, 2023, 5, . | 0.9 | 3 |
| 1374 | Chromosome-Level Genome Assembly of Herpetospermum pedunculosum (Cucurbitaceae). Genome Biology and Evolution, 2023, 15, . | 1.1 | 1 |
| 1375 | Epigenetic and Genetic Population Structure is Coupled in a Marine Invertebrate. Genome Biology and Evolution, 2023, 15, . | 1.1 | 4 |
| 1378 | Chromosome-level genome of the bean bug Megacopta cribraria in native range, provides insights into adaptation and pest management. International Journal of Biological Macromolecules, 2023, 237, 123989. | 3.6 | 0 |
| 1379 | Reference genomes of channel catfish and blue catfish reveal multiple pericentric chromosome inversions. BMC Biology, 2023, 21, . | 1.7 | 1 |
| 1380 | Chromosome-Level Assembly of Flowering Cherry (Prunus campanulata) Provides Insight into Anthocyanin Accumulation. Genes, 2023, 14, 389. | 1.0 | 1 |
| 1381 | Genome and haplotype provide insights into the population differentiation and breeding improvement of Gossypium barbadense. Journal of Advanced Research, 2023, 54, 15-27. | 4.4 | 2 |
| 1382 | The genome of a vestimentiferan tubeworm (Ridgeia piscesae) provides insights into its adaptation to a deep-sea environment. BMC Genomics, 2023, 24, . | 1.2 | 4 |
| 1383 | Chromosomal-level genome assembly of the high-quality Xian/Indica rice (Oryza sativa L.) Xiangyaxiangzhan. BMC Plant Biology, 2023, 23, . | 1.6 | 0 |
| 1384 | Genome survey and genetic characterization of Acacia pachyceras O. Schwartz. Frontiers in Plant Science, 0, 14, . | 1.7 | 2 |
| 1385 | A chromosome-level genome assembly for Erianthus fulvus provides insights into its biofuel potential and facilitates breeding for improvement of sugarcane. Plant Communications, 2023, 4, 100562. | 3.6 | 4 |
| 1386 | A chromosome-level genome assembly of an early matured aromatic Japonica rice variety Qigeng10 to accelerate rice breeding for high grain quality in Northeast China. Frontiers in Plant Science, 0, 14, . | 1.7 | 0 |

| # | Article | IF | Citations |
|---|---|---|---|
| 1388 | Transposable element and host silencing activity in gigantic genomes. Frontiers in Cell and Developmental Biology, 0, 11, . | 1.8 | 3 |
| 1390 | Repeat DNA Sequences in Flax Genomes. Compendium of Plant Genomes, 2023, , 19-36. | 0.3 | 0 |
| 1391 | Pangenomic analysis identifies structural variation associated with heat tolerance in pearl millet. Nature Genetics, 2023, 55, 507-518. | 9.4 | 31 |
| 1392 | Chromosomeâ€level reference genome of Tetrastigma hemsleyanum (Vitaceae) provides insights into genomic evolution and the biosynthesis of phenylpropanoids and flavonoids. Plant Journal, 2023, 114, 805-823. | 2.8 | 5 |
| 1393 | The chromosome-scale genome assembly of Jasminum sambac var. unifoliatum provides insights into the formation of floral fragrance. Horticultural Plant Journal, 2023, 9, 1131-1148. | 2.3 | 2 |
| 1394 | Genome assembly of the deep-sea coral Lophelia pertusa. GigaByte, 0, 2023, 1-12. | 0.0 | 1 |
| 1395 | Insights into the genomic evolution and the alkali tolerance mechanisms of Agaricus sinodeliciosus by comparative genomic and transcriptomic analyses. Microbial Genomics, 2023, 9, . | 1.0 | 0 |
| 1396 | Biocatalytic potential of Pseudolycoriella CAZymes (Sciaroidea, Diptera) in degrading plant and fungal cell wall polysaccharides. IScience, 2023, 26, 106449. | 1.9 | 3 |
| 1397 | Intraspecific Comparative Analysis Reveals Genomic Variation of Didymella arachidicola and Pathogenicity Factors Potentially Related to Lesion Phenotype. Biology, 2023, 12, 476. | 1.3 | 0 |
| 1398 | Transposable Element Interactions Shape the Ecology of the Deer Mouse Genome. Molecular Biology and Evolution, 2023, 40, . | 3.5 | 6 |
| 1399 | Chromosome-level analysis of the Colletotrichum graminicola genome reveals the unique characteristics of core and minichromosomes. Frontiers in Microbiology, 0, 14, . | 1.5 | 4 |
| 1401 | Improved chromosomal-level genome assembly and re-annotation of leopard coral grouper. Scientific Data, 2023, 10, . | 2.4 | 2 |
| 1402 | LTR Retroelements and Bird Adaptation to Arid Environments. International Journal of Molecular Sciences, 2023, 24, 6332. | 1.8 | 0 |
| 1403 | The genome of Lactuca saligna, a wild relative of lettuce, provides insight into nonâ€host resistance to the downy mildew Bremia lactucae. Plant Journal, 2023, 115, 108-126. | 2.8 | 2 |
| 1404 | Chromosome-level genome assembly of the critically endangered Baerâ€™s pochard (Aythya baeri). Scientific Data, 2023, 10, . | 2.4 | 1 |
| 1405 | Comparative genomics reveals unique features of two Babesia motasi subspecies: Babesia motasi lintanensis and Babesia motasi hebeiensis. International Journal for Parasitology, 2023, 53, 265-283. | 1.3 | 2 |
| 1406 | Genomic Analysis of Amphioxus Reveals a Wide Range of Fragments Homologous to Viral Sequences. Viruses, 2023, 15, 909. | 1.5 | 1 |
| 1407 | Abundance of Transgene Transcript Variants Associated with Somatically Active Transgenic Helitrons from Multiple T-DNA Integration Sites in Maize. International Journal of Molecular Sciences, 2023, 24, 6574. | 1.8 | 1 |

| # | Article | IF | Citations |
|---|---|---|---|
| 1408 | A complete gap-free diploid genome in Saccharum complex and the genomic footprints of evolution in the highly polyploid Saccharum genus. Nature Plants, 2023, 9, 554-571. | 4.7 | 7 |
| 1409 | Super-pangenome analyses highlight genomic diversity and structural variation across wild and cultivated tomato species. Nature Genetics, 2023, 55, 852-860. | 9.4 | 43 |
| 1410 | Chromosome-scale genome assembly of Prunus pusilliflora provides novel insights into genome evolution, disease resistance, and dormancy release in Cerasus L.. Horticulture Research, 0, , . | 2.9 | 1 |
| 1411 | Chromosome-level genome assembly of Salvia miltiorrhiza with orange roots uncovers the role of Sm2OGD3 in catalyzing 15,16-dehydrogenation of tanshinones. Horticulture Research, 2023, 10, . | 2.9 | 4 |
| 1412 | New insights into the genome and transmission of the microsporidian pathogen Nosema muscidifuracis. Frontiers in Microbiology, 0, 14, . | 1.5 | 2 |
| 1413 | Haplotype-resolved genomes of two buckwheat crops provide insights into their contrasted rutin concentrations and reproductive systems. BMC Biology, 2023, 21, . | 1.7 | 4 |
| 1414 | Genomics reveals broad hybridization in deeply divergent Palearctic grass and water snakes (Natrix) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 | 1.2 | 3 |
| 1501 | Computational Genomics Approaches for Livestock Improvement and Management. Livestock Diseases and Management, 2023, , 351-376. | 0.5 | 0 |