

BUSCO: assessing genome assembly and annotation completeness using single-copy orthologs

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Combined de novo and genome guided assembly and annotation of the <i>Pinus patula</i> juvenile shoot transcriptome. <i>BMC Genomics</i> , 2015, 16, 1057.	1.2	44
2	Optimizing and benchmarking de novo transcriptome sequencing: from library preparation to assembly evaluation. <i>BMC Genomics</i> , 2015, 16, 977.	1.2	82
3	Draft genome sequences of <i>Chrysosporthe austroafricana</i> , <i>Diplodia scrobiculata</i> , <i>Fusarium nygamai</i> , <i>Leptographium lundbergii</i> , <i>Limonomyces culmigenus</i> , <i>Stagonosporopsis tanacetii</i> , and <i>Thielaviopsis punctulata</i> . <i>IMA Fungus</i> , 2015, 6, 233-248.	1.7	46
4	Draft genome of the scabies mite. <i>Parasites and Vectors</i> , 2015, 8, 585.	1.0	94
5	Quality Assessment of Domesticated Animal Genome Assemblies. <i>Bioinformatics and Biology Insights</i> , 2015, 9S4, BBI.S29333.	1.0	11
6	The White-Nose Syndrome Transcriptome: Activation of Anti-fungal Host Responses in Wing Tissue of Hibernating Little Brown Myotis. <i>PLoS Pathogens</i> , 2015, 11, e1005168.	2.1	88
7	NCBI-compliant genome submissions: tips and tricks to save time and money: Table 1. <i>Briefings in Bioinformatics</i> , 2015, 18, bbv104.	3.2	14
8	Insights from the genome of <i>Ophiocordyceps polyrhachis-furcata</i> to pathogenicity and host specificity in insect fungi. <i>BMC Genomics</i> , 2015, 16, 881.	1.2	34
9	Draft genome sequences of <i>Ceratocystis eucalypticola</i> , <i>Chrysosporthe cubensis</i> , <i>C. deuterocubensis</i> , <i>Davidsoniella virescens</i> , <i>Fusarium temperatum</i> , <i>Graphilbum fragrans</i> , <i>Penicillium nordicum</i> , and <i>Thielaviopsis musarum</i> . <i>IMA Fungus</i> , 2015, 6, 493-506.	1.7	57
10	OGS2: genome re-annotation of the jewel wasp <i>Nasonia vitripennis</i> . <i>BMC Genomics</i> , 2016, 17, 678.	1.2	35
11	De novo assembly and analysis of changes in the protein-coding transcriptome of the freshwater shrimp <i>Paratya australiensis</i> (Decapoda: Atyidae) in response to acid sulfate drainage water. <i>BMC Genomics</i> , 2016, 17, 890.	1.2	12
12	IMA Genome-F 6. <i>IMA Fungus</i> , 2016, 7, 217-227.	1.7	39
13	Draft genome sequences for <i>Ceratocystis fagacearum</i> , <i>C. harringtonii</i> , <i>Grosmannia penicillata</i> , and <i>Huntia bhutanensis</i> . <i>IMA Fungus</i> , 2016, 7, 317-323.	1.7	31
14	Draft Whole-Genome Sequence of a <i>Haemophilus</i> <i>quentini</i> Strain Isolated from an Infant in the United Kingdom. <i>Genome Announcements</i> , 2016, 4, .	0.8	3
15	Assessing the Gene Content of the Megagenome: Sugar Pine (<i>Pinus lambertiana</i>). <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 3787-3802.	0.8	51
16	Gene family expansions and contractions are associated with host range in plant pathogens of the genus <i>Colletotrichum</i> . <i>BMC Genomics</i> , 2016, 17, 555.	1.2	151
17	A transcriptional blueprint for a spiral-cleaving embryo. <i>BMC Genomics</i> , 2016, 17, 552.	1.2	20
18	Assembly, Assessment, and Availability of De novo Generated Eukaryotic Transcriptomes. <i>Frontiers in Genetics</i> , 2015, 6, 361.	1.1	57

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19	A Survey of the Gene Repertoire of <i>Gigaspora rosea</i> Unravels Conserved Features among Glomeromycota for Obligate Biotrophy. <i>Frontiers in Microbiology</i> , 2016, 7, 233.	1.5	113
20	Transcriptome Analysis of the Tadpole Shrimp (<i>Triops longicaudatus</i>) by Illumina Paired-End Sequencing: Assembly, Annotation, and Marker Discovery. <i>Genes</i> , 2016, 7, 114.	1.0	15
21	De Novo Assembly and Characterization of the Transcriptome of Grasshopper <i>Shirakiacris shirakii</i> . <i>International Journal of Molecular Sciences</i> , 2016, 17, 1110.	1.8	10
22	On the reversibility of parasitism: adaptation to a free-living lifestyle via gene acquisitions in the diplomonad <i>Trepomonas</i> sp. PC1. <i>BMC Biology</i> , 2016, 14, 62.	1.7	38
23	The Jujube Genome Provides Insights into Genome Evolution and the Domestication of Sweetness/Acidity Taste in Fruit Trees. <i>PLoS Genetics</i> , 2016, 12, e1006433.	1.5	136
24	Deep sequencing of transcriptomes from the nervous systems of two decapod crustaceans to characterize genes important for neural circuit function and modulation. <i>BMC Genomics</i> , 2016, 17, 868.	1.2	62
25	De novo and comparative transcriptome analysis of cultivated and wild spinach. <i>Scientific Reports</i> , 2016, 5, 17706.	1.6	41
26	Genome Sequence of <i>Madurella mycetomatis</i> mm55, Isolated from a Human Mycetoma Case in Sudan. <i>Genome Announcements</i> , 2016, 4, .	0.8	22
27	Genetic and Genomic Tools for <i>Cannabis sativa</i> . <i>Critical Reviews in Plant Sciences</i> , 2016, 35, 364-377.	2.7	70
28	Genomes of <i>Candidatus</i> <i>Wolbachia bourtzisii</i> <i>w</i> DacA and <i>Candidatus</i> <i>Wolbachia pipientis</i> <i>w</i> DacB from the Cochineal Insect <i>Dactylopius coccus</i> (Hemiptera): Tj ETQq1 1 0.784314 rgBT / Overlock 10 Tf 50	1.2	23
29	Comparative transcriptomics enlarges the toolkit of known developmental genes in mollusks. <i>BMC Genomics</i> , 2016, 17, 905.	1.2	41
30	Emerging Genomics of Angiosperm Trees. <i>Plant Genetics and Genomics: Crops and Models</i> , 2016, , 85-99.	0.3	0
31	Genome sequence, population history, and pelage genetics of the endangered African wild dog (<i>Lycaon</i>) Tj ETQq0 0 0 rgBT / Overlock 10 Tf 50	1.2	23
32	Sequencing, de novo assembly and annotation of a pink bollworm larval midgut transcriptome. <i>GigaScience</i> , 2016, 5, 28.	3.3	12
33	Genome analysis of <i>Hibiscus syriacus</i> provides insights of polyploidization and indeterminate flowering in woody plants. <i>DNA Research</i> , 2017, 24, dsw049.	1.5	38
34	Global map of oxytocin/vasopressin-like neuropeptide signalling in insects. <i>Scientific Reports</i> , 2016, 6, 39177.	1.6	35
35	The draft genome of whitefly <i>Bemisia tabaci</i> MEAM1, a global crop pest, provides novel insights into virus transmission, host adaptation, and insecticide resistance. <i>BMC Biology</i> , 2016, 14, 110.	1.7	265
36	First Draft Assembly and Annotation of the Genome of a California Endemic Oak <i>Quercus lobata</i> (Fagaceae). <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 3485-3495.	0.8	95

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37	Draft whole-genome sequence of the <i>Diaporthe helianthi</i> 7/96 strain, causal agent of sunflower stem canker. <i>Genomics Data</i> , 2016, 10, 151-152.	1.3	16
38	The retardant effect of 2-Tridecanone, mediated by Cytochrome P450, on the Development of Cotton bollworm, <i>Helicoverpa armigera</i> . <i>BMC Genomics</i> , 2016, 17, 954.	1.2	32
39	Expansion and diversification of the MSDIN family of cyclic peptide genes in the poisonous agarics <i>Amanita phalloides</i> and <i>A. bisporigera</i> . <i>BMC Genomics</i> , 2016, 17, 1038.	1.2	37
40	Gene Family Evolution Reflects Adaptation to Soil Environmental Stressors in the Genome of the Collembolan <i>Orchesella cincta</i> . <i>Genome Biology and Evolution</i> , 2016, 8, 2106-2117.	1.1	56
41	Genome Update. Let the consumer beware: <i>Streptomyces</i> genome sequence quality. <i>Microbial Biotechnology</i> , 2016, 9, 3-7.	2.0	19
42	Population genomics of the filarial nematode parasite <i>Wuchereria bancrofti</i> from mosquitoes. <i>Molecular Ecology</i> , 2016, 25, 1465-1477.	2.0	38
43	The Genome and Methylome of a Subsocial Small Carpenter Bee, <i>Ceratina calcarata</i> . <i>Genome Biology and Evolution</i> , 2016, 8, 1401-1410.	1.1	71
44	Genome Sequencing of the Phytoseiid Predatory Mite <i>Metaseiulus occidentalis</i> Reveals Completely Atomized <i>Hox</i> Genes and Superdynamic Intron Evolution. <i>Genome Biology and Evolution</i> , 2016, 8, 1762-1775.	1.1	102
45	rnaQUAST: a quality assessment tool for <i>de novo</i> transcriptome assemblies. <i>Bioinformatics</i> , 2016, 32, 2210-2212.	1.8	106
46	Genomic analysis and D-xylose fermentation of three novel <i>Spathaspora</i> species: <i>Spathaspora girioi</i> sp. nov., <i>Spathaspora hagerdaliae</i> f. a., sp. nov. and <i>Spathaspora gorwiae</i> f. a., sp. nov.. <i>FEMS Yeast Research</i> , 2016, 16, fow044.	1.1	47
47	DOGMA: domain-based transcriptome and proteome quality assessment. <i>Bioinformatics</i> , 2016, 32, 2577-2581.	1.8	39
48	Gene Body Methylation Patterns in <i>Daphnia</i> Are Associated with Gene Family Size. <i>Genome Biology and Evolution</i> , 2016, 8, 1185-1196.	1.1	39
49	A Workflow for Studying Specialized Metabolism in Nonmodel Eukaryotic Organisms. <i>Methods in Enzymology</i> , 2016, 576, 69-97.	0.4	18
50	Venus flytrap carnivorous lifestyle builds on herbivore defense strategies. <i>Genome Research</i> , 2016, 26, 812-825.	2.4	88
51	The genome of the largest bony fish, ocean sunfish (<i>Mola mola</i>), provides insights into its fast growth rate. <i>GigaScience</i> , 2016, 5, 36.	3.3	32
52	Towards integration of population and comparative genomics in forest trees. <i>New Phytologist</i> , 2016, 212, 338-344.	3.5	31
53	Computational Considerations in Transcriptome Assemblies and Their Evaluation, using High Quality Human RNA-Seq data. , 2016, , .		1
54	Genome sequences of six <i>Phytophthora</i> species threatening forest ecosystems. <i>Genomics Data</i> , 2016, 10, 85-88.	1.3	29

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55	The whole genome sequence of the Mediterranean fruit fly, <i>Ceratitis capitata</i> (Wiedemann), reveals insights into the biology and adaptive evolution of a highly invasive pest species. <i>Genome Biology</i> , 2016, 17, 192.	3.8	130
56	Multifaceted biological insights from a draft genome sequence of the tobacco hornworm moth, <i>Manduca sexta</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2016, 76, 118-147.	1.2	154
57	Hox and ParaHox gene expression in early body plan patterning of polyplacophoran mollusks. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2016, 326, 89-104.	0.6	34
58	Living apart together: crosstalk between the core and supernumerary genomes in a fungal plant pathogen. <i>BMC Genomics</i> , 2016, 17, 670.	1.2	53
59	Repeated replacement of an intrabacterial symbiont in the tripartite nested mealybug symbiosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E5416-24.	3.3	222
60	The Genome of a Southern Hemisphere Seagrass Species (<i>Zostera muelleri</i>). <i>Plant Physiology</i> , 2016, 172, 272-283.	2.3	88
61	Evolution of the immune system influences speciation rates in teleost fishes. <i>Nature Genetics</i> , 2016, 48, 1204-1210.	9.4	226
62	Are We There Yet? Reliably Estimating the Completeness of Plant Genome Sequences. <i>Plant Cell</i> , 2016, 28, 1759-1768.	3.1	89
63	Transcriptomic and functional resources for the small hive beetle <i>Aethina tumida</i> , a worldwide parasite of honey bees. <i>Genomics Data</i> , 2016, 9, 97-99.	1.3	12
64	Morphological Identification and Single-Cell Genomics of Marine Diplonemids. <i>Current Biology</i> , 2016, 26, 3053-3059.	1.8	83
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66	Draft genome of the living fossil <i>Ginkgo biloba</i> . <i>GigaScience</i> , 2016, 5, 49.	3.3	232
67	Transcriptomic Resources for the Rocky Intertidal Blue Mussel <i>Mytilus edulis</i> from the Gulf of Maine. <i>Journal of Shellfish Research</i> , 2016, 35, 435-465.	0.3	6
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69	Evolutionary Dynamics of Abundant Stop Codon Readthrough. <i>Molecular Biology and Evolution</i> , 2016, 33, 3108-3132.	3.5	53
70	The present and future of <i>de novo</i> whole-genome assembly. <i>Briefings in Bioinformatics</i> , 2018, 19, bbw096.	3.2	139
71	Genome-scale comparison of expanded gene families in <i>Plasmodium ovale wallikeri</i> and <i>Plasmodium ovale curtisi</i> with <i>Plasmodium malariae</i> and with other <i>Plasmodium</i> species. <i>International Journal for Parasitology</i> , 2016, 46, 685-696.	1.3	59
72	Phased diploid genome assembly with single-molecule real-time sequencing. <i>Nature Methods</i> , 2016, 13, 1050-1054.	9.0	1,658

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74	Genomic resources for a unique, low-virulence <i>Babesia</i> taxon from China. <i>Parasites and Vectors</i> , 2016, 9, 564.	1.0	17
75	<i>Daphnia magna</i> transcriptome by RNA-Seq across 12 environmental stressors. <i>Scientific Data</i> , 2016, 3, 160030.	2.4	89
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77	Genome of the Asian longhorned beetle (<i>Anoplophora glabripennis</i>), a globally significant invasive species, reveals key functional and evolutionary innovations at the beetle–plant interface. <i>Genome Biology</i> , 2016, 17, 227.	3.8	244
78	<i>Penicillium arizonense</i> , a new, genome sequenced fungal species, reveals a high chemical diversity in secreted metabolites. <i>Scientific Reports</i> , 2016, 6, 35112.	1.6	33
79	Draft Genome Sequence of <i>Alternaria alternata</i> Isolated from Onion Leaves in South Africa. <i>Genome Announcements</i> , 2016, 4, .	0.8	16
80	Head Transcriptomes of Two Closely Related Species of Fruit Flies of the <i>Anastrepha fraterculus</i> Group Reveals Divergent Genes in Species with Extensive Gene Flow. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 3283-3295.	0.8	18
81	Transcriptomic data from panarthropods shed new light on the evolution of insulator binding proteins in insects. <i>BMC Genomics</i> , 2016, 17, 861.	1.2	23
82	Comparison of carnivore, omnivore, and herbivore mammalian genomes with a new leopard assembly. <i>Genome Biology</i> , 2016, 17, 211.	3.8	101
83	Evidence for the sexual origin of heterokaryosis in arbuscular mycorrhizal fungi. <i>Nature Microbiology</i> , 2016, 1, 16033.	5.9	137
84	Characterisation of the immune compounds in koala milk using a combined transcriptomic and proteomic approach. <i>Scientific Reports</i> , 2016, 6, 35011.	1.6	25
85	Genomic survey of a hyperparasitic microsporidian <i>Amphiamblysp.</i> (Metchnikovellidae). <i>Genome Biology and Evolution</i> , 2016, 9, eww235.	1.1	41
86	Sequence of the Sugar Pine Megagenome. <i>Genetics</i> , 2016, 204, 1613-1626.	1.2	169
87	Genome and transcriptome sequencing characterises the gene space of <i>Macadamia integrifolia</i> (Proteaceae). <i>BMC Genomics</i> , 2016, 17, 937.	1.2	45
88	Reconstructing the Backbone of the Saccharomycotina Yeast Phylogeny Using Genome-Scale Data. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 3927-3939.	0.8	187
89	Comparative Genomics of a Parthenogenesis-Inducing <i>Wolbachia</i> Symbiont. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2113-2123.	0.8	56
90	Combining independent de novo assemblies optimizes the coding transcriptome for nonconventional model eukaryotic organisms. <i>BMC Bioinformatics</i> , 2016, 17, 525.	1.2	63

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91	Comparative genomics of <i>Beauveria bassiana</i> : uncovering signatures of virulence against mosquitoes. <i>BMC Genomics</i> , 2016, 17, 986.	1.2	38
92	Genomic resources and draft assemblies of the human and porcine varieties of scabies mites, <i>Sarcoptes scabiei</i> var. <i>hominis</i> and var. <i>suis</i> . <i>GigaScience</i> , 2016, 5, 23.	3.3	28
93	Draft genome of the leopard gecko, <i>Eublepharis macularius</i> . <i>GigaScience</i> , 2016, 5, 47.	3.3	55
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99	Thermal reactionomes reveal divergent responses to thermal extremes in warm and cool-climate ant species. <i>BMC Genomics</i> , 2016, 17, 171.	1.2	19
100	The effector candidate repertoire of the arbuscular mycorrhizal fungus <i>Rhizophagus clarus</i> . <i>BMC Genomics</i> , 2016, 17, 101.	1.2	76
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102	De novo construction of an expanded transcriptome assembly for the western tarnished plant bug, <i>Lygus hesperus</i> . <i>GigaScience</i> , 2016, 5, 6.	3.3	26
103	Genome sequences of <i>Knoxdaviesia capensis</i> and <i>K. proteae</i> (Fungi: Ascomycota) from Protea trees in South Africa. <i>Standards in Genomic Sciences</i> , 2016, 11, 22.	1.5	6
104	PhyloPro2.0: a database for the dynamic exploration of phylogenetically conserved proteins and their domain architectures across the Eukarya. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw013.	1.4	12
105	Comparative genomics reveals genes significantly associated with woody hosts in the plant pathogen <i>Pseudomonas syringae</i> . <i>Molecular Plant Pathology</i> , 2016, 17, 1409-1424.	2.0	56
106	Draft Genome Sequence of Biocontrol Agent <i>Pythium oligandrum</i> Strain Po37, an Oomycota. <i>Genome Announcements</i> , 2016, 4, .	0.8	21
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108	Genome sequence of the olive tree, <i>Olea europaea</i> . <i>GigaScience</i> , 2016, 5, 29.	3.3	201

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109	A phylotranscriptomic analysis of gene family expansion and evolution in the largest order of pleurocarpous mosses (Hypnales, Bryophyta). <i>Molecular Phylogenetics and Evolution</i> , 2016, 98, 29-40.	1.2	29
110	The mid-developmental transition and the evolution of animal body plans. <i>Nature</i> , 2016, 531, 637-641.	13.7	231
111	Unique features of a global human ectoparasite identified through sequencing of the bed bug genome. <i>Nature Communications</i> , 2016, 7, 10165.	5.8	184
112	Major Improvements to the <i>Heliconius melpomene</i> Genome Assembly Used to Confirm 10 Chromosome Fusion Events in 6 Million Years of Butterfly Evolution. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 695-708.	0.8	149
113	The SIB Swiss Institute of Bioinformatics's resources: focus on curated databases. <i>Nucleic Acids Research</i> , 2016, 44, D27-D37.	6.5	64
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115	MetaQUAST: evaluation of metagenome assemblies. <i>Bioinformatics</i> , 2016, 32, 1088-1090.	1.8	447
116	Iterative error correction of long sequencing reads maximizes accuracy and improves contig assembly. <i>Briefings in Bioinformatics</i> , 2017, 18, 1-8.	3.2	31
117	Characterization and analysis of a <i>de novo</i> transcriptome from the pygmy grasshopper <i>Tetrix japonica</i> . <i>Molecular Ecology Resources</i> , 2017, 17, 381-392.	2.2	33
118	Comparative genomics reveals convergent evolution between the bamboo-eating giant and red pandas. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 1081-1086.	3.3	196
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120	WormBase ParaSite - a comprehensive resource for helminth genomics. <i>Molecular and Biochemical Parasitology</i> , 2017, 215, 2-10.	0.5	527
121	Phylogenetic Origin and Diversification of RNAi Pathway Genes in Insects. <i>Genome Biology and Evolution</i> , 2016, 8, evw281.	1.1	92
122	Complex modular architecture around a simple toolkit of wing pattern genes. <i>Nature Ecology and Evolution</i> , 2017, 1, 52.	3.4	179
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126	De novo genome assembly of <i>Cercospora beticola</i> for microsatellite marker development and validation. <i>Fungal Ecology</i> , 2017, 26, 125-134.	0.7	24

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128	Genome-resolved metagenomics of a bioremediation system for degradation of thiocyanate in mine water containing suspended solid tailings. <i>MicrobiologyOpen</i> , 2017, 6, e00446.	1.2	22
129	Loggerhead sea turtle embryos (<i>Caretta caretta</i>) regulate expression of stress response and developmental genes when exposed to a biologically realistic heat stress. <i>Molecular Ecology</i> , 2017, 26, 2978-2992.	2.0	39
130	An improved genome assembly uncovers prolific tandem repeats in Atlantic cod. <i>BMC Genomics</i> , 2017, 18, 95.	1.2	153
131	De novo transcriptome assemblies of four accessions of the metal hyperaccumulator plant <i>Noccaea caerulescens</i> . <i>Scientific Data</i> , 2017, 4, 160131.	2.4	38
132	De novo hybrid assembly of the rubber tree genome reveals evidence of paleotetraploidy in <i>Hevea</i> species. <i>Scientific Reports</i> , 2017, 7, 41457.	1.6	95
133	Populus as a Model Tree. <i>Plant Genetics and Genomics: Crops and Models</i> , 2017, , 61-84.	0.3	5
134	De Novo Genome and Transcriptome Assembly of the Canadian Beaver (<i>Castor canadensis</i>). <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 755-773.	0.8	18
135	The genome of <i>Chenopodium quinoa</i> . <i>Nature</i> , 2017, 542, 307-312.	13.7	569
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137	Draft Genome Sequence of Sorghum Grain Mold Fungus <i>Epicoccum sorghinum</i> , a Producer of Tenuazonic Acid. <i>Genome Announcements</i> , 2017, 5, .	0.8	19
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559	Adaptation to high zinc depends on distinct mechanisms in metalicolous populations of <i>Arabidopsis halleri</i> . <i>New Phytologist</i> , 2018, 218, 269-282.	3.5	90
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562	Extreme sensitivity to ultraviolet light in the fungal pathogen causing white-nose syndrome of bats. <i>Nature Communications</i> , 2018, 9, 35.	5.8	56
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577	Population-specific transcriptional differences associated with freeze tolerance in a terrestrial worm. <i>Ecology and Evolution</i> , 2018, 8, 3774-3786.	0.8	12
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581	Reconstruction of the ancestral metazoan genome reveals an increase in genomic novelty. <i>Nature Communications</i> , 2018, 9, 1730.	5.8	101
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591	Dispersal and speciation: The cross Atlantic relationship of two parasitic cnidarians. <i>Molecular Phylogenetics and Evolution</i> , 2018, 126, 346-355.	1.2	6
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595	Characterisation of major histocompatibility complex class I transcripts in an Australian dragon lizard. <i>Developmental and Comparative Immunology</i> , 2018, 84, 164-171.	1.0	3
596	Genome analysis reveals evolutionary mechanisms of adaptation in systemic dimorphic fungi. <i>Scientific Reports</i> , 2018, 8, 4473.	1.6	28

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621	Know your farmer: Ancient origins and multiple independent domestications of ambrosia beetle fungal cultivars. <i>Molecular Ecology</i> , 2018, 27, 2077-2094.	2.0	67
622	Multiple hybrid de novo genome assembly of finger millet, an orphan allotetraploid crop. <i>DNA Research</i> , 2018, 25, 39-47.	1.5	85
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639	De novo transcriptome analysis of <i>Ammopiptanthus nanus</i> and its comparative analysis with <i>A. mongolicus</i> . <i>Trees - Structure and Function</i> , 2018, 32, 287-300.	0.9	15
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647	Global transcriptome analysis of the aphelid <i>Paraphelidium tribonemae</i> supports the phagotrophic origin of fungi. <i>Communications Biology</i> , 2018, 1, 231.	2.0	63
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653	Annotated Draft Genome Sequence of the Apple Scab Pathogen <i>Venturia inaequalis</i> . <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	14
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660	Comprehensive transcriptome analysis of <i>Sarcophaga peregrina</i> , a forensically important fly species. <i>Scientific Data</i> , 2018, 5, 180220.	2.4	15
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662	Nine draft genome sequences of <i>Claviceps purpurea</i> s.lat., including <i>C. arundinis</i> , <i>C. humidiphila</i> , and <i>C. cf. spartinae</i> , pseudomolecules for the pitch canker pathogen <i>Fusarium circinatum</i> , draft genome of <i>Davidsoniella eucalypti</i> , <i>Grosmannia galeiformis</i> , <i>Quambalaria eucalypti</i> , and <i>Teratosphaeria destructans</i> . <i>IMA Fungus</i> , 2018, 9, 401-418.	1.7	31
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689	Draft Genome Sequence of <i>Scytalidium lignicola</i> DSM 105466, a Ubiquitous Saprotrophic Fungus. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	5
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956	Inferring synteny between genome assemblies: a systematic evaluation. <i>BMC Bioinformatics</i> , 2018, 19, 26.	1.2	84
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969	Sequence analysis of European maize inbred line F2 provides new insights into molecular and chromosomal characteristics of presence/absence variants. <i>BMC Genomics</i> , 2018, 19, 119.	1.2	27
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975	The Rise and Rise of <i>Nicotiana benthamiana</i> : A Plant for All Reasons. <i>Annual Review of Phytopathology</i> , 2018, 56, 405-426.	3.5	201

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978	The chromosome-level genome assemblies of two rattans (<i>Calamus simplicifolius</i> and <i>Daemonorops</i>) Tj ETQq0 0 0 ggBT /Overlock 10 Tf 3.3 28	3.3	28
979	Improved <i>Brassica rapa</i> reference genome by single-molecule sequencing and chromosome conformation capture technologies. <i>Horticulture Research</i> , 2018, 5, 50.	2.9	224
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988	Expression of <i>vasa</i> , <i>piwi</i> , and <i>nanos</i> during gametogenesis in <i>Typosyllis antoni</i> (Annelida, Syllidae). <i>Evolution & Development</i> , 2018, 20, 132-145.	1.1	20
989	Algorithm for Physiological Interpretation of Transcriptome Profiling Data for Non-Model Organisms. <i>Molecular Biology</i> , 2018, 52, 497-509.	0.4	1
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1014	Oak genome reveals facets of long lifespan. <i>Nature Plants</i> , 2018, 4, 440-452.	4.7	303
1015	Pinaceae show elevated rates of gene turnover that are robust to incomplete gene annotation. <i>Plant Journal</i> , 2018, 95, 862-876.	2.8	12
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1018	The first draft genome of <i>Lophophorus</i> : A step forward for Phasianidae genomic diversity and conservation. <i>Genomics</i> , 2019, 111, 1209-1215.	1.3	9
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1023	Transcriptome Informatics. , 2019, , 324-340.		8
1024	Genome Annotation. , 2019, , 195-209.		3
1025	Trends in herbgenomics. <i>Science China Life Sciences</i> , 2019, 62, 288-308.	2.3	46
1026	Gene expression analysis of bud burst process in European hazelnut (<i>Corylus avellana</i> L.) using RNA-Seq. <i>Physiology and Molecular Biology of Plants</i> , 2019, 25, 13-29.	1.4	10
1027	Genome Sequence and Antifungal Activity of Two Niche-Sharing <i>Pseudomonas protegens</i> Related Strains Isolated from Hydroponics. <i>Microbial Ecology</i> , 2019, 77, 1025-1035.	1.4	2
1028	Structural variation during dog domestication: insights from gray wolf and dhole genomes. <i>National Science Review</i> , 2019, 6, 110-122.	4.6	30
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1032	An improved genome assembly of the fluke <i>Schistosoma japonicum</i> . <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007612.	1.3	50
1033	Comparative genomics of <i>Staphylococcus aureus</i> associated with subclinical and clinical bovine mastitis. <i>PLoS ONE</i> , 2019, 14, e0220804.	1.1	27
1034	Physiological status of silver carp (<i>Hypophthalmichthys molitrix</i>) in the Illinois River: An assessment of fish at the leading edge of the invasion front. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2019, 32, 100614.	0.4	11
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1043	RNA-Seq Analysis Reveals Genes Related to Photoreception, Nutrient Uptake, and Toxicity in a Noxious Red-Tide Raphidophyte <i>Chattonella antiqua</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 1764.	1.5	16
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1049	Transcriptome Surveys in Silverfish Suggest a Multistep Origin of the Insect Odorant Receptor Gene Family. <i>Frontiers in Ecology and Evolution</i> , 2019, 7, .	1.1	17
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1051	Genome assembly of <i>Nannochloropsis oceanica</i> provides evidence of host nucleus overthrow by the symbiont nucleus during speciation. <i>Communications Biology</i> , 2019, 2, 249.	2.0	29
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1053	The biosynthetic origin of psychoactive kavalactones in kava. <i>Nature Plants</i> , 2019, 5, 867-878.	4.7	58
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1055	The draft genome sequence of the spider <i>Dysdera silvatica</i> (Araneae, Dysderidae): A valuable resource for functional and evolutionary genomic studies in chelicerates. <i>GigaScience</i> , 2019, 8, .	3.3	25
1056	Genome Sequence Data of Six Isolates of <i>Phytophthora capsici</i> from Mexico. <i>Molecular Plant-Microbe Interactions</i> , 2019, 32, 1267-1269.	1.4	11
1057	Construction and comparison of three reference-quality genome assemblies for soybean. <i>Plant Journal</i> , 2019, 100, 1066-1082.	2.8	113
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1059	The tea plant reference genome and improved gene annotation using long-read and paired-end sequencing data. <i>Scientific Data</i> , 2019, 6, 122.	2.4	29
1060	Transcriptome analysis of virulence-differentiated <i>Fusarium oxysporum</i> f. sp. <i>cucumerinum</i> isolates during cucumber colonisation reveals pathogenicity profiles. <i>BMC Genomics</i> , 2019, 20, 570.	1.2	13
1061	A high-quality genome of <i>Eragrostis curvula</i> grass provides insights into Poaceae evolution and supports new strategies to enhance forage quality. <i>Scientific Reports</i> , 2019, 9, 10250.	1.6	27
1062	De novo Assembly and Characterization of the Floral Transcriptomes of Two Varieties of <i>Melastoma malabathricum</i> . <i>Frontiers in Genetics</i> , 2019, 10, 521.	1.1	4
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1064	Speciation in <i>Howea</i> Palms Occurred in Sympatry, Was Preceded by Ancestral Admixture, and Was Associated with Edaphic and Phenological Adaptation. <i>Molecular Biology and Evolution</i> , 2019, 36, 2682-2697.	3.5	17
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1068	Updated Assembly of <i>Phytophthora ramorum</i> pr102 Isolate Incorporating Long Reads from PacBio Sequencing. Molecular Plant-Microbe Interactions, 2019, 32, 1472-1474.	1.4	23
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1075	Chromosomal-level assembly of the blood clam, <i>Scapharca (Anadara) broughtonii</i> , using long sequence reads and Hi-C. GigaScience, 2019, 8, .	3.3	63
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1078	Pangloss: A Tool for Pan-Genome Analysis of Microbial Eukaryotes. Genes, 2019, 10, 521.	1.0	14
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1080	Ecological speciation in sympatric palms: 3. Genetic map reveals genomic islands underlying species divergence in <i>Howea</i> . Evolution; International Journal of Organic Evolution, 2019, 73, 1986-1995.	1.1	13
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1089	<i>Wolbachia</i> Acquisition by <i>Drosophila yakuba</i> -Clade Hosts and Transfer of Incompatibility Loci Between Distantly Related <i>Wolbachia</i> . <i>Genetics</i> , 2019, 212, 1399-1419.	1.2	62
1090	Ultraconserved element (UCE) probe set design: Base genome and initial design parameters critical for optimization. <i>Ecology and Evolution</i> , 2019, 9, 6933-6948.	0.8	19
1091	Comparative genome analysis of <i>Phyllosticta citricarpa</i> and <i>Phyllosticta capitalensis</i> , two fungi species that share the same host. <i>BMC Genomics</i> , 2019, 20, 554.	1.2	20
1092	Genome sequence of <i>Isaria javanica</i> and comparative genome analysis insights into family S53 peptidase evolution in fungal entomopathogens. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 7111-7128.	1.7	14
1093	The genome assembly of asparagus bean, <i>Vigna unguiculata</i> ssp. <i>sesquipedialis</i> . <i>Scientific Data</i> , 2019, 6, 124.	2.4	18
1094	Whole Genome Sequence Resource of the Asian Pear Scab Pathogen <i>Venturia nashicola</i> . <i>Molecular Plant-Microbe Interactions</i> , 2019, 32, 1463-1467.	1.4	13
1095	De novo assembly of a chromosome-level reference genome of red-spotted grouper (<i>Epinephelus</i>) Tj ETQq1 1 0.784314 rgBT / Overl	2.2	48
1096	Genome and transcriptome characterization of the glycoengineered <i>Nicotiana benthamiana</i> line $\hat{\Gamma}$ XT/FT. <i>BMC Genomics</i> , 2019, 20, 594.	1.2	20
1097	Insights into cryptic diversity and adaptive evolution of the clam <i>Coelomactra antiquata</i> (Spengler.) Tj ETQq1 1 0.784314 rgBT / Overl	0.3	2
1098	De novo phased assembly of the <i>Vitis riparia</i> grape genome. <i>Scientific Data</i> , 2019, 6, 127.	2.4	71
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1102	Phased genome sequence of an interspecific hybrid flowering cherry, "Somei-Yoshino"™ (Cerasus <i>sp.</i>) Tj ETQq 0 0 rgBT /Overlock of	1.5	59
1103	Genome Sequencing of the Japanese Eel (<i>Anguilla japonica</i>) for Comparative Genomic Studies on <i>tbx4</i> and a <i>tbx4</i> Gene Cluster in Teleost Fishes. <i>Marine Drugs</i> , 2019, 17, 426.	2.2	9
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1105	The transcriptome of Darwin's bark spider silk glands predicts proteins contributing to dragline silk toughness. <i>Communications Biology</i> , 2019, 2, 275.	2.0	46
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1107	Stem cell differentiation trajectories in <i>Hydra</i> resolved at single-cell resolution. <i>Science</i> , 2019, 365, .	6.0	253
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1110	SQUAT: a Sequencing Quality Assessment Tool for data quality assessments of genome assemblies. <i>BMC Genomics</i> , 2019, 19, 238.	1.2	29
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1112	Whole-Genome Sequences of <i>Pantoea agglomerans</i> BL3, <i>Pseudomonas fluorescens</i> BL, and <i>Pseudomonas stutzeri</i> CM14, Isolated from Hops (<i>Humulus lupulus</i>). <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	5
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1116	Draft Genome Sequence of the Yeast <i>Pichia manshurica</i> YM63, a Participant in Secondary Fermentation of Ishizuchi-Kurocha, a Japanese Fermented Tea. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	3
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1118	Genome sequencing and comparison of five <i>Tilletia</i> species to identify candidate genes for the detection of regulated species infecting wheat. <i>IMA Fungus</i> , 2019, 10, 11.	1.7	21
1119	Transcriptome-wide analysis of immune responses in <i>Eriocheir sinensis</i> hemocytes after challenge with different microbial derivatives. <i>Developmental and Comparative Immunology</i> , 2019, 101, 103457.	1.0	4

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1356	Back to the Salt Mines: Genome and Transcriptome Comparisons of the Halophilic Fungus <i>Aspergillus salisburgensis</i> and Its Halotolerant Relative <i>Aspergillus sclerotialis</i> . <i>Genes</i> , 2019, 10, 381.	1.0	17
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1371	The Impact of cDNA Normalization on Long-Read Sequencing of a Complex Transcriptome. <i>Frontiers in Genetics</i> , 2019, 10, 654.	1.1	8

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1374	Embryonic development of a parthenogenetic vertebrate, the mourning gecko (<i>Lepidodactylus</i>). <i>Development</i> , 2019, 146, 1919.	0.8	19
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1376	Genomics of Antarctic Fungi: A New Frontier. <i>Genetics</i> , 2019, 209, 319-338.		0
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1395	Transcriptome Analysis of Gene Families Involved in Chemosensory Function in <i>Spodoptera littoralis</i> (Lepidoptera: Noctuidae). BMC Genomics, 2019, 20, 428.	1.2	69
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1656	Population Genome Sequencing of the Scab Fungal Species <i>Venturia inaequalis</i> , <i>Venturia pirina</i> , <i>Venturia aucupariae</i> and <i>Venturia asperata</i> . <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2405-2414.	0.8	33
1657	The Genome Sequence of the Eastern Woodchuck (<i>Marmota monax</i>) – A Preclinical Animal Model for Chronic Hepatitis B. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3943-3952.	0.8	13
1658	Temporary adhesion of the proseriate flatworm <i>Minona ileanae</i> . <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20190194.	1.8	14
1659	Transcriptome Atlas by Long-Read RNA Sequencing: Contribution to a Reference Transcriptome. , 2019, , .		0
1660	Draft Genome Sequence of <i>Saccharomyces cerevisiae</i> Strain Pf-1, Isolated from <i>Prunus mume</i> . <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	2

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1662	The avocado genome informs deep angiosperm phylogeny, highlights introgressive hybridization, and reveals pathogen-influenced gene space adaptation. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 17081-17089.	3.3	134
1663	A partial genome assembly of the miniature parasitoid wasp, <i>Megaphragma amalphanum</i> . PLoS ONE, 2019, 14, e0226485.	1.1	10
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1665	The <i>de Novo</i> Reference Genome and Transcriptome Assemblies of the Wild Tomato Species <i>Solanum chilense</i> Highlights Birth and Death of NLR Genes Between Tomato Species. G3: Genes, Genomes, Genetics, 2019, 9, 3933-3941.	0.8	37
1666	Construction of High-Resolution RAD-Seq Based Linkage Map, Anchoring Reference Genome, and QTL Mapping of the Sex Chromosome in the Marine Medaka <i>Oryzias melastigma</i> . G3: Genes, Genomes, Genetics, 2019, 9, 3537-3545.	0.8	14
1667	Hybrid <i>de novo</i> whole-genome assembly and annotation of the model tapeworm <i>Hymenolepis diminuta</i> . Scientific Data, 2019, 6, 302.	2.4	21
1668	<i>Solenodon</i> genome reveals convergent evolution of venom in eulipotyphlan mammals. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 25745-25755.	3.3	42
1669	Greenlip Abalone (<i>Haliotis laevigata</i>) Genome and Protein Analysis Provides Insights into Maturation and Spawning. G3: Genes, Genomes, Genetics, 2019, 9, 3067-3078.	0.8	14
1670	Characterization of Core Microbiomes and Functional Profiles of Mesophilic Anaerobic Digesters Fed With <i>Chlorella vulgaris</i> Green Microalgae and Maize Silage. Frontiers in Energy Research, 2019, 7, .	1.2	19
1671	Tung Tree (<i>Vernicia fordii</i>) Genome Provides A Resource for Understanding Genome Evolution and Improved Oil Production. Genomics, Proteomics and Bioinformatics, 2019, 17, 558-575.	3.0	43
1672	Draft Genome Sequence of <i>Xylaria hypoxylon</i> DSM 108379, a Ubiquitous Fungus on Hardwood. Microbiology Resource Announcements, 2019, 8, .	0.3	2
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1674	IMA Genome-F 11. IMA Fungus, 2019, 10, 13.	1.7	12
1675	Closed Complete Annotated Genome Sequences of Five <i>Haemophilus influenzae</i> Biogroup <i>aegyptius</i> Strains. Microbiology Resource Announcements, 2019, 8, .	0.3	2
1676	Genome Sequences of Two Strains of the Food Spoilage Mold <i>Aspergillus fischeri</i> . Microbiology Resource Announcements, 2019, 8, .	0.3	9
1677	<i>De Novo</i> Genome Assembly and Comparative Genomics of the Barley Leaf Rust Pathogen <i>Puccinia hordei</i> Identifies Candidates for Three Avirulence Genes. G3: Genes, Genomes, Genetics, 2019, 9, 3263-3271.	0.8	25
1678	Draft Genome Assembly and Annotation of the Gila Topminnow <i>Poeciliopsis occidentalis</i> . Frontiers in Ecology and Evolution, 2019, 7, .	1.1	3

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1680	Capture of complete ciliate chromosomes in single sequencing reads reveals widespread chromosome isoforms. <i>BMC Genomics</i> , 2019, 20, 1037.	1.2	12
1681	Updated Genome Assembly and Annotation for <i>Metrosideros polymorpha</i> , an Emerging Model Tree Species of Ecological Divergence. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3513-3520.	0.8	4
1682	Genome Sequencing of <i>Pleurozium schreberi</i> : The Assembled and Annotated Draft Genome of a Pleurocarpous Feather Moss. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2791-2797.	0.8	35
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1684	Genome of <i>Spea multiplicata</i> , a Rapidly Developing, Phenotypically Plastic, and Desert-Adapted Spadefoot Toad. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3909-3919.	0.8	23
1685	Utilization of Tissue Ploidy Level Variation in <i>de Novo</i> Transcriptome Assembly of <i>Pinus sylvestris</i> . <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3409-3421.	0.8	16
1686	<i>De Novo</i> Genome Sequence Assemblies of <i>Gossypium raimondii</i> and <i>Gossypium turneri</i> . <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3079-3085.	0.8	72
1687	Host-Microbe Interactions in the Chemosynthetic <i>Riftia pachyptila</i> Symbiosis. <i>MBio</i> , 2019, 10, .	1.8	38
1688	Transcriptome Characterization of Reverse Development in <i>Turritopsis dohrnii</i> (Hydrozoa,) Tj ETQq1 1 0.784314 rgBT /Overloc	0.8	15
1689	The genome of <i>Chenopodium pallidicaule</i> : An emerging Andean super grain. <i>Applications in Plant Sciences</i> , 2019, 7, e11300.	0.8	19
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1692	The genome of a subterrestrial nematode reveals adaptations to heat. <i>Nature Communications</i> , 2019, 10, 5268.	5.8	22
1693	An influential meal: host plant dependent transcriptional variation in the beet armyworm, <i>Spodoptera exigua</i> (Lepidoptera: Noctuidae). <i>BMC Genomics</i> , 2019, 20, 845.	1.2	5
1694	Reanalysis of <i>Lactobacillus paracasei</i> Lbs2 Strain and Large-Scale Comparative Genomics Places Many Strains into Their Correct Taxonomic Position. <i>Microorganisms</i> , 2019, 7, 487.	1.6	14
1695	Fungal Adaptation to the Advanced Stages of Wood Decomposition: Insights from the <i>Steccherinum ochraceum</i> . <i>Microorganisms</i> , 2019, 7, 527.	1.6	13
1696	A High-Quality Melon Genome Assembly Provides Insights into Genetic Basis of Fruit Trait Improvement. <i>IScience</i> , 2019, 22, 16-27.	1.9	37

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1698	Comparative transcriptomics in Syllidae (Annelida) indicates that posterior regeneration and regular growth are comparable, while anterior regeneration is a distinct process. <i>BMC Genomics</i> , 2019, 20, 855.	1.2	27
1699	Integrated transcriptome and miRNA analysis uncovers molecular regulators of aerial stem-to-rhizome transition in the medical herb <i>Gynostemma pentaphyllum</i> . <i>BMC Genomics</i> , 2019, 20, 865.	1.2	9
1700	Demographic Histories and Genome-Wide Patterns of Divergence in Incipient Species of Shorebirds. <i>Frontiers in Genetics</i> , 2019, 10, 919.	1.1	14
1701	Disparate responses to salinity across species and organizational levels in anchialine shrimps. <i>Journal of Experimental Biology</i> , 2019, 222, .	0.8	5
1702	The Endophytic Fungus <i>Chaetomium cupreum</i> Regulates Expression of Genes Involved in the Tolerance to Metals and Plant Growth Promotion in <i>Eucalyptus globulus</i> Roots. <i>Microorganisms</i> , 2019, 7, 490.	1.6	28
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1705	Draft genome sequences of five <i>Calonectria</i> species from <i>Eucalyptus</i> plantations in China, <i>Celoporthe dispersa</i> , <i>Sporothrix phasma</i> and <i>Alectoria sarmentosa</i> . <i>IMA Fungus</i> , 2019, 10, 22.	1.7	17
1706	The persimmon (<i>Diospyros oleifera</i> Cheng) genome provides new insights into the inheritance of astringency and ancestral evolution. <i>Horticulture Research</i> , 2019, 6, 138.	2.9	39
1707	Integrative transcriptome analysis discloses the molecular basis of a heterogeneous fungal phytopathogen complex, <i>Rhizoctonia solani</i> AG-1 subgroups. <i>Scientific Reports</i> , 2019, 9, 19626.	1.6	20
1708	De novo Assembly of the <i>Brugia malayi</i> Genome Using Long Reads from a Single MinION Flowcell. <i>Scientific Reports</i> , 2019, 9, 19521.	1.6	9
1709	Local adaptation of a dominant coastal tree to freshwater availability and solar radiation suggested by genomic and ecophysiological approaches. <i>Scientific Reports</i> , 2019, 9, 19936.	1.6	19
1710	Novel findings to the biosynthetic pathway of magnoflorine and taspine through transcriptomic and metabolomic analysis of <i>Croton draco</i> (Euphorbiaceae). <i>BMC Plant Biology</i> , 2019, 19, 560.	1.6	7
1711	Conjoint Analysis of SMRT- and Illumina-Based RNA-Sequencing Data of <i>Fenneropenaeus chinensis</i> Provides Insight Into Sex-Biased Expression Genes Involved in Sexual Dimorphism. <i>Frontiers in Genetics</i> , 2019, 10, 1175.	1.1	5
1712	A Phylogenomic Analysis of the Floral Transcriptomes of Sexually Deceptive and Rewarding European Orchids, <i>Ophrys</i> and <i>Gymnadenia</i> . <i>Frontiers in Plant Science</i> , 2019, 10, 1553.	1.7	26
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1714	Full-length transcriptome sequencing from multiple tissues of duck, <i>Anas platyrhynchos</i> . <i>Scientific Data</i> , 2019, 6, 275.	2.4	26

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1716	Genome analyses of a placozoan rickettsial endosymbiont show a combination of mutualistic and parasitic traits. <i>Scientific Reports</i> , 2019, 9, 17561.	1.6	11
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1719	The genetic basis of adaptive evolution in parasitic environment from the <i>Angiostrongylus cantonensis</i> genome. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007846.	1.3	9
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1721	Structural and functional insights into the <i>Diabrotica virgifera virgifera</i> ATP-binding cassette transporter gene family. <i>BMC Genomics</i> , 2019, 20, 899.	1.2	8
1722	Full-Length Transcriptome Survey and Expression Analysis of Parasitoid Wasp <i>Chouioia cunea</i> upon Exposure to 1-Dodecene. <i>Scientific Reports</i> , 2019, 9, 18167.	1.6	4
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1727	Comprehensive Stress-Based De Novo Transcriptome Assembly and Annotation of Guar (<i>Cyamopsis) Tj ETQq0 0.0 rgBT /Overlock 10 <i>Genomics</i> , 2019, 2019, 1-14.	0.8	23
1728	Genome draft of the <i>Arabidopsis</i> relative <i>Pachycladon cheesemanii</i> reveals novel strategies to tolerate New Zealand's high ultraviolet B radiation environment. <i>BMC Genomics</i> , 2019, 20, 838.	1.2	9
1729	Assembly, annotation, and comparison of <i>Macrophomina phaseolina</i> isolates from strawberry and other hosts. <i>BMC Genomics</i> , 2019, 20, 802.	1.2	16
1730	Organ transcriptomes of the lucinid clam <i>Loripes orbiculatus</i> (Poli, 1791) provide insights into their specialised roles in the biology of a chemosymbiotic bivalve. <i>BMC Genomics</i> , 2019, 20, 820.	1.2	13
1731	Functional categorization of de novo transcriptome assembly of <i>Vanilla planifolia</i> Jacks. potentially points to a translational regulation during early stages of infection by <i>Fusarium oxysporum</i> f. sp. <i>vanillae</i> . <i>BMC Genomics</i> , 2019, 20, 826.	1.2	14
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1734	Genomic insights from the first chromosome-scale assemblies of oat (<i>Avena</i> spp.) diploid species. <i>BMC Biology</i> , 2019, 17, 92.	1.7	58
1735	Environmental transcriptomes of invasive dreissena, a model species in ecotoxicology and invasion biology. <i>Scientific Data</i> , 2019, 6, 234.	2.4	6
1736	A de novo genome assembly of the dwarfing pear rootstock Zhongai 1. <i>Scientific Data</i> , 2019, 6, 281.	2.4	28
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1741	Microbial Community Rearrangements in Power-to-Biomethane Reactors Employing Mesophilic Biogas Digestate. <i>Frontiers in Energy Research</i> , 2019, 7, .	1.2	19
1742	Full-length transcriptome sequences of <i>Agropyron cristatum</i> facilitate the prediction of putative genes for thousand-grain weight in a wheat-A. cristatum translocation line. <i>BMC Genomics</i> , 2019, 20, 1025.	1.2	12
1743	Transcriptome analysis of <i>Pueraria candollei</i> var. <i>mirifica</i> for gene discovery in the biosyntheses of isoflavones and miroestrol. <i>BMC Plant Biology</i> , 2019, 19, 581.	1.6	15
1744	Draft genome of <i>Ompok bimaculatus</i> (Pabda fish). <i>BMC Research Notes</i> , 2019, 12, 825.	0.6	3
1745	Hybridization promotes asexual reproduction in <i>Caenorhabditis</i> nematodes. <i>PLoS Genetics</i> , 2019, 15, e1008520.	1.5	10
1746	Genomic and transcriptomic insights into molecular basis of sexually dimorphic nuptial spines in <i>Leptobranchium leishanense</i> . <i>Nature Communications</i> , 2019, 10, 5551.	5.8	52
1747	TRITEX: chromosome-scale sequence assembly of Triticeae genomes with open-source tools. <i>Genome Biology</i> , 2019, 20, 284.	3.8	179
1748	Comparative Analysis of Strategies for De Novo Transcriptome Assembly in Prokaryotes: <i>Streptomyces clavuligerus</i> as a Case Study. <i>High-Throughput</i> , 2019, 8, 20.	4.4	1
1749	A transposable element insertion is associated with an alternative life history strategy. <i>Nature Communications</i> , 2019, 10, 5757.	5.8	41
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1756	Transcriptome Analysis Reveals the Molecular Mechanisms Underlying Adenosine Biosynthesis in Anamorph Strain of Caterpillar Fungus. <i>BioMed Research International</i> , 2019, 2019, 1-12.	0.9	8
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1759	Transcriptomic Evidence of Adaptive Evolution of the Epiphytic Fern <i>Asplenium nidus</i> . <i>International Journal of Genomics</i> , 2019, 2019, 1-9.	0.8	15
1760	Crowdsourcing and the feasibility of manual gene annotation: A pilot study in the nematode <i>Pristionchus pacificus</i> . <i>Scientific Reports</i> , 2019, 9, 18789.	1.6	22
1761	Genomic insights into mite phylogeny, fitness, development, and reproduction. <i>BMC Genomics</i> , 2019, 20, 954.	1.2	25
1762	Novel redox-active enzymes for ligninolytic applications revealed from multiomics analyses of <i>Peniophora</i> sp. CBMAI 1063, a laccase hyper-producer strain. <i>Scientific Reports</i> , 2019, 9, 17564.	1.6	24
1763	A whole genome assembly of <i>Leptospermum scoparium</i> (Myrtaceae) for mānuka research. <i>New Zealand Journal of Crop and Horticultural Science</i> , 2019, 47, 233-260.	0.7	31
1764	Basal Rot of Narcissus: Understanding Pathogenicity in <i>Fusarium oxysporum</i> f. sp. <i>narcissi</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 2905.	1.5	8
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1766	An integrated analysis of mRNA and sRNA transcriptional profiles in <i>Coffea arabica</i> L. roots: insights on nitrogen starvation responses. <i>Functional and Integrative Genomics</i> , 2019, 19, 151-169.	1.4	28
1767	Finding Nemo's Genes: A chromosome-scale reference assembly of the genome of the orange clownfish <i>Amphiprion percula</i> . <i>Molecular Ecology Resources</i> , 2019, 19, 570-585.	2.2	55
1768	Cost-effective assembly of the African wild dog (<i>Lycaon pictus</i>) genome using linked reads. <i>GigaScience</i> , 2019, 8, .	3.3	22

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1770	The Coiled-Coil NLR <i><i>Rph1</i></i> , Confers Leaf Rust Resistance in Barley Cultivar Sudan. <i>Plant Physiology</i> , 2019, 179, 1362-1372.	2.3	53
1771	Adaptation of Proteins to the Cold in Antarctic Fish: A Role for Methionine?. <i>Genome Biology and Evolution</i> , 2019, 11, 220-231.	1.1	25
1772	Genomics of forest trees. <i>Advances in Botanical Research</i> , 2019, 89, 1-37.	0.5	4
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1774	<i>Liriodendron</i> genome sheds light on angiosperm phylogeny and speciesâ€pair differentiation. <i>Nature Plants</i> , 2019, 5, 18-25.	4.7	163
1775	Detoxification Genes Differ Between Cactus-, Fruit-, and Flower-Feeding <i><i>Drosophila</i></i> . <i>Journal of Heredity</i> , 2019, 110, 80-91.	1.0	17
1776	Comparative transcriptome analysis identifies genes associated with papilla development in the sea cucumber <i>Apostichopus japonicus</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2019, 29, 255-263.	0.4	4
1777	Taxonomic and functional heterogeneity of the gill microbiome in a symbiotic coastal mangrove lucinid species. <i>ISME Journal</i> , 2019, 13, 902-920.	4.4	38
1778	Sunflower pan-genome analysis shows that hybridization altered gene content and disease resistance. <i>Nature Plants</i> , 2019, 5, 54-62.	4.7	172
1779	Chromosomal level reference genome of <i><i>Tachypleus tridentatus</i></i> provides insights into evolution and adaptation of horseshoe crabs. <i>Molecular Ecology Resources</i> , 2019, 19, 744-756.	2.2	25
1780	Differential introgression of a female competitive trait in a hybrid zone between sexâ€role reversed species. <i>Evolution; International Journal of Organic Evolution</i> , 2019, 73, 188-201.	1.1	25
1781	Transcriptome-wide analysis of <i>Chlorella</i> reveals auxin-induced carotenogenesis pathway in green microalgae. <i>Algal Research</i> , 2019, 37, 320-335.	2.4	25
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1783	Hypoxic and Cold Adaptation Insights from the Himalayan Marmot Genome. <i>IScience</i> , 2019, 11, 519-530.	1.9	34
1784	Re-assembly, quality evaluation, and annotation of 678 microbial eukaryotic reference transcriptomes. <i>GigaScience</i> , 2019, 8, .	3.3	61
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1786	Transcriptome-wide analysis of wild Asari (=Manila) clams affected by the Brown Muscle Disease: Etiology and impacts of the disease. <i>Fish and Shellfish Immunology</i> , 2019, 86, 179-185.	1.6	4

#	ARTICLE	IF	CITATIONS
1787	A Malvaceae mystery: A mallow maelstrom of genome multiplications and maybe misleading methods?. <i>Journal of Integrative Plant Biology</i> , 2019, 61, 12-31.	4.1	25
1788	A physical and genetic map of <i>Cannabis sativa</i> identifies extensive rearrangements at the <i>THC/CBD acid synthase</i> loci. <i>Genome Research</i> , 2019, 29, 146-156.	2.4	160
1789	Arthropod Genome Sequencing and Assembly Strategies. <i>Methods in Molecular Biology</i> , 2019, 1858, 1-14.	0.4	7
1790	Using BUSCO to Assess Insect Genomic Resources. <i>Methods in Molecular Biology</i> , 2019, 1858, 59-74.	0.4	27
1791	Long Range Sequencing and Validation of Insect Genome Assemblies. <i>Methods in Molecular Biology</i> , 2019, 1858, 33-44.	0.4	3
1792	An important resource for understanding bio-adhesion mechanisms: Cement gland transcriptomes of two goose barnacles, <i>Pollicipes pollicipes</i> and <i>Lepas anatifera</i> (Cirripedia, Thoracica). <i>Marine Genomics</i> , 2019, 45, 16-20.	0.4	11
1793	A high-quality chromosome-level genome assembly of a generalist herbivore, <i>Trichoplusia ni</i> . <i>Molecular Ecology Resources</i> , 2019, 19, 485-496.	2.2	47
1794	Genome sequencing of oomycete isolates from Chile supports the New Zealand origin of <i>Phytophthora kernoviae</i> and makes available the first <i>Nothophytophthora</i> sp. genome. <i>Molecular Plant Pathology</i> , 2019, 20, 423-431.	2.0	16
1795	Integrated Modeling of Structural Genes Using MCuNovo. <i>Methods in Molecular Biology</i> , 2019, 1858, 45-57.	0.4	2
1796	The transcriptome of the marine calanoid copepod <i>Temora longicornis</i> under heat stress and recovery. <i>Marine Environmental Research</i> , 2019, 143, 10-23.	1.1	29
1797	An Improved Genome Assembly for <i>Drosophila navojoa</i> , the Basal Species in the mojavensis Cluster. <i>Journal of Heredity</i> , 2019, 110, 118-123.	1.0	7
1798	Selective colonization ability of human fecal microbes in different mouse gut environments. <i>ISME Journal</i> , 2019, 13, 805-823.	4.4	39
1799	Exploring the genome of Arctic <i>Psychrobacter</i> sp. DAB_AL32B and construction of novel <i>Psychrobacter</i> -specific cloning vectors of an increased carrying capacity. <i>Archives of Microbiology</i> , 2019, 201, 559-569.	1.0	6
1800	Morphological dissection and cellular and transcriptome characterizations of bamboo pith cavity formation reveal a pivotal role of genes related to programmed cell death. <i>Plant Biotechnology Journal</i> , 2019, 17, 982-997.	4.1	30
1801	Identification of Genes Involved in Lipid Biosynthesis through de novo Transcriptome Assembly from <i>Cocos nucifera</i> Developing Endosperm. <i>Plant and Cell Physiology</i> , 2019, 60, 945-960.	1.5	20
1802	Comparative genomics of <i>Rhizoglyphus irregularis</i> , <i>R. Âcerebriforme</i> , <i>R. Âdiaphanus</i> and <i>Gigaspora rosea</i> highlights specific genetic features in Glomeromycotina. <i>New Phytologist</i> , 2019, 222, 1584-1598.	3.5	133
1803	Iso-Seq Allows Genome-Independent Transcriptome Profiling of Grape Berry Development. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 755-767.	0.8	79
1804	Genomic resources for the study of echinoderm development and evolution. <i>Methods in Cell Biology</i> , 2019, 151, 65-88.	0.5	8

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1805	De novo transcriptome assembly for <i>Tracheliastes polycolpus</i> , an invasive ectoparasite of freshwater fish in western Europe. <i>Marine Genomics</i> , 2019, 46, 58-61.	0.4	3
1806	Toxin and Genome Evolution in a <i>Drosophila</i> Defensive Symbiosis. <i>Genome Biology and Evolution</i> , 2019, 11, 253-262.	1.1	14
1807	An Annotated Genome for <i>Haliotis rufescens</i> (Red Abalone) and Resequenced Green, Pink, Pinto, Black, and White Abalone Species. <i>Genome Biology and Evolution</i> , 2019, 11, 431-438.	1.1	41
1808	Genome Sequence of <i>Jaltomata</i> Addresses Rapid Reproductive Trait Evolution and Enhances Comparative Genomics in the Hyper-Diverse Solanaceae. <i>Genome Biology and Evolution</i> , 2019, 11, 335-349.	1.1	17
1809	Comparative Transcriptomics Reveals Patterns of Adaptive Evolution Associated with Depth and Age Within Marine Rockfishes (Sebastes). <i>Journal of Heredity</i> , 2019, 110, 340-350.	1.0	12
1810	Expression of the GAF Sensor, Carbohydrate-Active Enzymes, Elicitors, and RXLRs Differs Markedly Between Two <i>Phytophthora cactorum</i> Isolates. <i>Phytopathology</i> , 2019, 109, 726-735.	1.1	7
1811	Reference Genomes from Distantly Related Species Can Be Used for Discovery of Single Nucleotide Polymorphisms to Inform Conservation Management. <i>Genes</i> , 2019, 10, 9.	1.0	50
1812	Defensin-like peptides in wheat analyzed by whole-transcriptome sequencing: a focus on structural diversity and role in induced resistance. <i>PeerJ</i> , 2019, 7, e6125.	0.9	17
1813	Chromosome-level assembly of the water buffalo genome surpasses human and goat genomes in sequence contiguity. <i>Nature Communications</i> , 2019, 10, 260.	5.8	161
1814	A near-chromosome-scale genome assembly of the gemsbok (<i>Oryx gazella</i>): an iconic antelope of the Kalahari desert. <i>GigaScience</i> , 2019, 8, .	3.3	138
1815	Chromosome level comparative analysis of Brassica genomes. <i>Plant Molecular Biology</i> , 2019, 99, 237-249.	2.0	14
1816	De novo assembly of <i>Vriesea carinata</i> leaf transcriptome to identify candidate cysteine-proteases. <i>Gene</i> , 2019, 691, 96-105.	1.0	1
1817	Stout camphor tree genome fills gaps in understanding of flowering plant genome evolution. <i>Nature Plants</i> , 2019, 5, 63-73.	4.7	124
1818	Repeated Evolution Versus Common Ancestry: Sex Chromosome Evolution in the Haplochromine Cichlid <i>Pseudocrenilabrus philander</i> . <i>Genome Biology and Evolution</i> , 2019, 11, 439-458.	1.1	26
1819	A critical comparison of technologies for a plant genome sequencing project. <i>GigaScience</i> , 2019, 8, .	3.3	41
1820	Ocean warming combined with lower omega-3 nutritional availability impairs the cardio-respiratory function of a marine fish. <i>Journal of Experimental Biology</i> , 2019, 222, .	0.8	10
1821	Domestication and Temperature Modulate Gene Expression Signatures and Growth in the Australasian Snapper <i>Chrysophrys auratus</i> . <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 105-116.	0.8	22
1822	Activation of the Bile Acid Pathway and No Observed Antimicrobial Peptide Sequences in the Skin of a Poison Frog. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 581-589.	0.8	1

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1823	Development of novel microsatellites for population genetic analysis of <i>Phenacoccus solenopsis</i> Tinsley (Hemipeta: Pseudococcidae) based on genomic analysis. <i>International Journal of Biological Macromolecules</i> , 2019, 121, 1135-1144.	3.6	7
1824	Phylotranscriptomic Insights into the Diversification of Endothermic <i>Thunnus</i> Tunas. <i>Molecular Biology and Evolution</i> , 2019, 36, 84-96.	3.5	15
1825	Insights into the Evolution of Shells and Love Darts of Land Snails Revealed from Their Matrix Proteins. <i>Genome Biology and Evolution</i> , 2019, 11, 380-397.	1.1	25
1826	Quantification of gene expression while taking into account RNA alternative splicing. <i>Genomics</i> , 2019, 111, 1517-1528.	1.3	39
1827	Genome and evolution of the arbuscular mycorrhizal fungus <i>Diversispora epigaea</i> (formerly) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50</i>	3.5	88
1828	Whole-genome sequence of the oriental lung fluke <i>Paragonimus westermani</i> . <i>GigaScience</i> , 2019, 8, .	3.3	29
1829	The draft genomes of five agriculturally important African orphan crops. <i>GigaScience</i> , 2019, 8, .	3.3	108
1830	Genome-wide patterns of transposon proliferation in an evolutionary young hybrid fish. <i>Molecular Ecology</i> , 2019, 28, 1491-1505.	2.0	18
1831	First assembly of the genome space of <i>Lolium multiflorum</i> and comparison to other Poaceae genomes. <i>Grassland Science</i> , 2019, 65, 125-134.	0.6	20
1832	Pooled DNA sequencing to identify SNPs associated with a major QTL for bacterial wilt resistance in Italian ryegrass (<i>Lolium multiflorum</i> Lam.). <i>Theoretical and Applied Genetics</i> , 2019, 132, 947-958.	1.8	26
1833	The genome of the jellyfish <i>Aurelia</i> and the evolution of animal complexity. <i>Nature Ecology and Evolution</i> , 2019, 3, 96-104.	3.4	86
1834	Giant tortoise genomes provide insights into longevity and age-related disease. <i>Nature Ecology and Evolution</i> , 2019, 3, 87-95.	3.4	79
1835	Reference genome sequences of two cultivated allotetraploid cottons, <i>Gossypium hirsutum</i> and <i>Gossypium barbadense</i> . <i>Nature Genetics</i> , 2019, 51, 224-229.	9.4	468
1836	SMRT long reads and Direct Label and Stain optical maps allow the generation of a high-quality genome assembly for the European barn swallow (<i>Hirundo rustica rustica</i>). <i>GigaScience</i> , 2019, 8, .	3.3	23
1837	Genome and Transcriptome Sequencing of the Astaxanthin-Producing Green Microalga, <i>Haematococcus pluvialis</i> . <i>Genome Biology and Evolution</i> , 2019, 11, 166-173.	1.1	52
1838	RNAseq-based phylogenetic reconstruction of Taxaceae and Cephalotaxaceae. <i>Cladistics</i> , 2019, 35, 461-468.	1.5	7
1839	<i>Nephromyces</i> Encodes a Urate Metabolism Pathway and Predicted Peroxisomes, Demonstrating That These Are Not Ancient Losses of Apicomplexans. <i>Genome Biology and Evolution</i> , 2019, 11, 41-53.	1.1	20
1840	Phylogenomics of Endogonaceae and evolution of mycorrhizas within Mucoromycota. <i>New Phytologist</i> , 2019, 222, 511-525.	3.5	81

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1841	Insights into the Evolution of the New World Diploid Cottons (<i>Gossypium</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 747 Td (Subgenus <i>peruvianum</i>). <i>Genetics</i> , 2019, 215, 53-71.	1.1	45
1842	Gene Discovery in <i>Gelsemium</i> Highlights Conserved Gene Clusters in Monoterpene Indole Alkaloid Biosynthesis. <i>ChemBioChem</i> , 2019, 20, 83-87.	1.3	66
1843	A full-length transcriptome of <i>Sepia esculenta</i> using a combination of single-molecule long-read (SMRT) and Illumina sequencing. <i>Marine Genomics</i> , 2019, 43, 54-57.	0.4	20
1844	A Roadmap to Domain Based Proteomics. <i>Methods in Molecular Biology</i> , 2019, 1851, 287-300.	0.4	2
1845	Development of Genomic Resources for the Powdery Mildew, <i>Erysiphe pulchra</i> . <i>Plant Disease</i> , 2019, 103, 804-807.	0.7	7
1846	Genome resources for the stem and bark canker pathogens <i>Corinectria fuckeliana</i> , <i>Neonectria hederæ</i> and <i>N. punicea</i> . <i>Plant Disease</i> , 2019, 103, 389-391.	0.7	19
1847	Draft genomes and genomic divergence of two <i>Lepidurus</i> tadpole shrimp species (Crustacea,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 747 Td (Subgenus <i>peruvianum</i>). <i>Genetics</i> , 2019, 215, 22-14.	2.2	14
1848	The proof is in the bulb: glycerol influences key stages of lily development. <i>Plant Journal</i> , 2019, 97, 321-340.	2.8	21
1849	The first transcriptomic resource for the Antarctic scallop <i>Adamussium colbecki</i> . <i>Marine Genomics</i> , 2019, 44, 61-64.	0.4	7
1850	De novo sequencing of the <i>Lavandula angustifolia</i> genome reveals highly duplicated and optimized features for essential oil production. <i>Planta</i> , 2019, 249, 251-256.	1.6	19
1851	A review of methods and databases for metagenomic classification and assembly. <i>Briefings in Bioinformatics</i> , 2019, 20, 1125-1136.	3.2	368
1852	De novo sequencing and initial annotation of the Mongolian gerbil (<i>Meriones unguiculatus</i>) genome. <i>Genomics</i> , 2019, 111, 441-449.	1.3	29
1853	Whole genome sequence analysis of <i>Geitlerinema</i> sp. FC II unveils competitive edge of the strain in marine cultivation system for biofuel production. <i>Genomics</i> , 2019, 111, 465-472.	1.3	5
1854	A comparative in silico linear B-cell epitope prediction and characterization for South American and African <i>Trypanosoma vivax</i> strains. <i>Genomics</i> , 2019, 111, 407-417.	1.3	16
1855	Comprehensive evaluation of non-hybrid genome assembly tools for third-generation PacBio long-read sequence data. <i>Briefings in Bioinformatics</i> , 2019, 20, 866-876.	3.2	86
1856	Whole genome sequence of <i>Auricularia heimuer</i> (Basidiomycota, Fungi), the third most important cultivated mushroom worldwide. <i>Genomics</i> , 2019, 111, 50-58.	1.3	61
1857	275 years of forestry meets genomics in <i>Pinus sylvestris</i> . <i>Evolutionary Applications</i> , 2020, 13, 11-30.	1.5	42
1858	Integrated transcriptome provides resources and insights into the adaptive evolution of colonized brown trout (<i>Salmo trutta fario</i>) in the Tibetan Plateau. <i>Journal of the World Aquaculture Society</i> , 2020, 51, 763-774.	1.2	7

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1859	Sole head transcriptomics reveals a coordinated developmental program during metamorphosis. <i>Genomics</i> , 2020, 112, 592-602.	1.3	10
1860	De novo assembly and annotation of the <i>Ganoderma australe</i> genome. <i>Genomics</i> , 2020, 112, 930-933.	1.3	6
1861	Highly accurate-single chromosomal complete genomes using IonTorrent and MinION sequencing of clinical pathogens. <i>Genomics</i> , 2020, 112, 545-551.	1.3	40
1862	The transcriptome enables the identification of candidate genes behind medicinal value of Drumstick tree (<i>Moringa oleifera</i>). <i>Genomics</i> , 2020, 112, 621-628.	1.3	22
1863	New approaches for metagenome assembly with short reads. <i>Briefings in Bioinformatics</i> , 2020, 21, 584-594.	3.2	140
1864	Microarray-Based Quality Assessment as a Supporting Criterion for <i>de novo</i> Transcriptome Assembly Selection. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, 17, 198-206.	1.9	1
1865	Rapid phenotypic evolution with shallow genomic differentiation during early stages of high elevation adaptation in Eurasian Tree Sparrows. <i>National Science Review</i> , 2020, 7, 113-127.	4.6	36
1866	Draft Genome Sequences of <i>Elsinoë fawcettii</i> and <i>Elsinoë australis</i> Causing Scab Diseases on Citrus. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 135-137.	1.4	13
1867	Comparative Genomic Analysis of the Pheromone Receptor Class 1 Family (V1R) Reveals Extreme Complexity in Mouse Lemurs (Genus, <i>Microcebus</i>) and a Chromosomal Hotspot across Mammals. <i>Genome Biology and Evolution</i> , 2020, 12, 3562-3579.	1.1	12
1868	Patterns of Genomic Differentiation in the <i>Drosophila nasuta</i> Species Complex. <i>Molecular Biology and Evolution</i> , 2020, 37, 208-220.	3.5	26
1869	A high-quality cucumber genome assembly enhances computational comparative genomics. <i>Molecular Genetics and Genomics</i> , 2020, 295, 177-193.	1.0	30
1870	Data, time and money: evaluating the best compromise for inferring molecular phylogenies of non-model animal taxa. <i>Molecular Phylogenetics and Evolution</i> , 2020, 142, 106660.	1.2	13
1871	A chromosome-level genome assembly reveals the genetic basis of cold tolerance in a notorious rice insect pest, <i>Chilo suppressalis</i> . <i>Molecular Ecology Resources</i> , 2020, 20, 268-282.	2.2	51
1872	Comparative genome/transcriptome analysis probes Boraginales' phylogenetic position, WGDs in Boraginales, and key enzyme genes in the alkannin/shikonin core pathway. <i>Molecular Ecology Resources</i> , 2020, 20, 228-241.	2.2	24
1873	The pomegranate (<i>Punica granatum</i> L.) draft genome dissects genetic divergence between soft-seeded and hard-seeded cultivars. <i>Plant Biotechnology Journal</i> , 2020, 18, 955-968.	4.1	70
1874	The Genome Sequence of Five Genotypes of <i>Fusarium oxysporum</i> f. sp. <i>vasinfectum</i> : A Resource for Studies on Fusarium Wilt of Cotton. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 138-140.	1.4	14
1875	Genomic, transcriptomic, and proteomic insights into the symbiosis of deep-sea tubeworm holobionts. <i>ISME Journal</i> , 2020, 14, 135-150.	4.4	41
1876	Genome survey and identification of polymorphic microsatellites provide genomic information and molecular markers for the red crab <i>Charybdis feriatus</i> (Linnaeus, 1758) (Decapoda: Brachyura.) <i>Tj ETQq1 1 0.7843143gBT /Overlock 10</i>		

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1877	Whole-genome sequencing and analysis of the Chinese herbal plant <i>Gelsemium elegans</i> . <i>Acta Pharmaceutica Sinica B</i> , 2020, 10, 374-382.	5.7	29
1878	Comparative de novo assembly and annotation of mantle tissue transcriptomes from the <i>Mytilus edulis</i> species complex (<i>M. edulis</i> , <i>M. galloprovincialis</i> , <i>M. trossulus</i>). <i>Marine Genomics</i> , 2020, 51, 100700.	0.4	11
1879	<i>De novo</i> assembly of a wild pear (<i>Pyrus betuleafolia</i>) genome. <i>Plant Biotechnology Journal</i> , 2020, 18, 581-595.	4.1	72
1880	Phylotranscriptomics resolves phylogeny of the Heliozelidae (Adeloidea: Lepidoptera) and suggests a Late Cretaceous origin in Australia. <i>Systematic Entomology</i> , 2020, 45, 128-143.	1.7	8
1881	New insights into the genomic evolution of cyanobacteria using herbarium exsiccatae. <i>European Journal of Phycology</i> , 2020, 55, 30-38.	0.9	6
1882	Genome-wide analysis sheds light on the high-altitude adaptation of the buff-throated partridge (<i>Tetraophasis szechenyii</i>). <i>Molecular Genetics and Genomics</i> , 2020, 295, 31-46.	1.0	11
1883	Genome assembly provides insights into the genome evolution and flowering regulation of orchardgrass. <i>Plant Biotechnology Journal</i> , 2020, 18, 373-388.	4.1	51
1884	Development of SNVs and indels markers mined out of the first multi-organ transcriptomes from <i>Hypancistrus zebra</i> (Loricariidae), an endangered Amazonian catfish. <i>Genomics</i> , 2020, 112, 971-980.	1.3	3
1885	Population structure and pangenome analysis of <i>Enterobacter bugandensis</i> uncover the presence of blaCTX-M-55, blaNDM-5 and blaIMI-1, along with sophisticated iron acquisition strategies. <i>Genomics</i> , 2020, 112, 1182-1191.	1.3	14
1886	The draft genome of a wild barley genotype reveals its enrichment in genes related to biotic and abiotic stresses compared to cultivated barley. <i>Plant Biotechnology Journal</i> , 2020, 18, 443-456.	4.1	45
1887	<i>Vampirovibrio chlorellavorus</i> draft genome sequence, annotation, and preliminary characterization of pathogenicity determinants. <i>Phycological Research</i> , 2020, 68, 23-29.	0.8	3
1888	The first transcriptomic resource for the flatworm <i>Triaenophorus nodulosus</i> (Cestoda: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 30 100702.	0.4	4
1889	The functional repertoire contained within the native microbiota of the model nematode <i>Caenorhabditis elegans</i> . <i>ISME Journal</i> , 2020, 14, 26-38.	4.4	68
1890	Ancient Adaptive Lateral Gene Transfers in the Symbiotic Opalina "Blastocystis Stramenopile Lineage. <i>Molecular Biology and Evolution</i> , 2020, 37, 651-659.	3.5	7
1891	Chromosome-level genome assembly of the predator <i>Propylea japonica</i> to understand its tolerance to insecticides and high temperatures. <i>Molecular Ecology Resources</i> , 2020, 20, 292-307.	2.2	43
1892	The utility of reptile blood transcriptomes in molecular ecology. <i>Molecular Ecology Resources</i> , 2020, 20, 308-317.	2.2	17
1893	Genomic Resources for Darters (Percidae: Etheostominae) Provide Insight into Postzygotic Barriers Implicated in Speciation. <i>Molecular Biology and Evolution</i> , 2020, 37, 711-729.	3.5	22
1894	Vegetative desiccation tolerance in the resurrection plant <i>Xerophyta humilis</i> has not evolved through reactivation of the seed canonical LAFL regulatory network. <i>Plant Journal</i> , 2020, 101, 1349-1367.	2.8	19

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1895	Molecular mechanisms of acclimation to long-term elevated temperature exposure in marine symbioses. <i>Global Change Biology</i> , 2020, 26, 1271-1284.	4.2	6
1896	<i>Mesostigma viride</i> Genome and Transcriptome Provide Insights into the Origin and Evolution of Streptophyta. <i>Advanced Science</i> , 2020, 7, 1901850.	5.6	40
1897	Heritable temporal gene expression patterns correlate with metabolomic seed content in developing hexaploid oat seed. <i>Plant Biotechnology Journal</i> , 2020, 18, 1211-1222.	4.1	19
1898	Effects of multiple climate change stressors on gene expression in blue rockfish (<i>Sebastes mystinus</i>). <i>Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology</i> , 2020, 239, 110580.	0.8	19
1899	Phylogenomics Identifies an Ancestral Burst of Gene Duplications Predating the Diversification of Aphidomorpha. <i>Molecular Biology and Evolution</i> , 2020, 37, 730-756.	3.5	29
1900	Chromosome-Level Reference Genome of <i>Venturia effusa</i> , Causative Agent of Pecan Scab. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 149-152.	1.4	14
1901	A Comparative Genomic Analysis of the Barley Pathogen <i>Pyrenophora teres</i> f. <i>teres</i> Identifies Subtelomeric Regions as Drivers of Virulence. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 173-188.	1.4	28
1902	Transposons played a major role in the diversification between the closely related almond and peach genomes: results from the almond genome sequence. <i>Plant Journal</i> , 2020, 101, 455-472.	2.8	94
1903	Genome and transcriptome analysis of the latent pathogen <i>Lasiodiplodia theobromae</i> , an emerging threat to the cacao industry. <i>Genome</i> , 2020, 63, 37-52.	0.9	26
1904	The remarkable morphological diversity of leaf shape in sweet potato (<i>Ipomoea batatas</i>): the influence of genetics, environment, and G×E. <i>New Phytologist</i> , 2020, 225, 2183-2195.	3.5	32
1905	The transcriptome of <i>Pinus pinaster</i> under <i>Fusarium circinatum</i> challenge. <i>BMC Genomics</i> , 2020, 21, 28.	1.2	19
1906	Long live the king: chromosome-level assembly of the lion (<i>Panthera leo</i>) using linked-read, Hi-C, and long-read data. <i>BMC Biology</i> , 2020, 18, 3.	1.7	34
1907	Insights into the strategy of micro-environmental adaptation: Transcriptomic analysis of two alvinocaridid shrimps at a hydrothermal vent. <i>PLoS ONE</i> , 2020, 15, e0227587.	1.1	8
1908	Molecular characterization and distribution of the voltage-gated sodium channel, Para, in the brain of the grasshopper and vinegar fly. <i>Journal of Comparative Physiology A: Neuroethology, Sensory, Neural, and Behavioral Physiology</i> , 2020, 206, 289-307.	0.7	6
1909	Eight high-quality genomes reveal pan-genome architecture and ecotype differentiation of <i>Brassica napus</i> . <i>Nature Plants</i> , 2020, 6, 34-45.	4.7	449
1910	An Improved Melon Reference Genome With Single-Molecule Sequencing Uncovers a Recent Burst of Transposable Elements With Potential Impact on Genes. <i>Frontiers in Plant Science</i> , 2019, 10, 1815.	1.7	48
1911	Long-read sequencing reveals genomic structural variations that underlie creation of quality protein maize. <i>Nature Communications</i> , 2020, 11, 17.	5.8	45
1912	Differential Expression in Testis and Liver Transcriptomes from Four Species of <i>Peromyscus</i> (Rodentia: Muridae). <i>Journal of Proteomics</i> , 2020, 23, 100000.	1.1	11

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1913	Chromosome-level genome assembly reveals the unique genome evolution of the swimming crab (<i>Portunus trituberculatus</i>). <i>GigaScience</i> , 2020, 9, .	3.3	44
1914	Draft Genomic Resources for the Brown Rot Fungal Pathogen <i>Monilinia laxa</i> . <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 145-148.	1.4	16
1915	Genomic Sequencing of <i>Phyllosticta citriasiana</i> Provides Insight Into Its Conservation and Diversification With Two Closely Related <i>Phyllosticta</i> Species Associated With Citrus. <i>Frontiers in Microbiology</i> , 2019, 10, 2979.	1.5	15
1916	Comparative genomic and transcriptomic analyses reveal different pathogenicity-related genes among three eucalyptus fungal pathogens. <i>Fungal Genetics and Biology</i> , 2020, 137, 103332.	0.9	9
1917	Extensive chromosomal rearrangements and rapid evolution of novel effector superfamilies contribute to host adaptation and speciation in the basal ascomycetous fungi. <i>Molecular Plant Pathology</i> , 2020, 21, 330-348.	2.0	22
1918	Genome sequence of <i>Pseudomonas aeruginosa</i> PAO1161, a PAO1 derivative with the ICEPae1161 integrative and conjugative element. <i>BMC Genomics</i> , 2020, 21, 14.	1.2	17
1919	Novel genomic resources for shelled pteropods: a draft genome and target capture probes for <i>Limacina bulimoides</i> , tested for cross-species relevance. <i>BMC Genomics</i> , 2020, 21, 11.	1.2	13
1920	Bacterial line of defense in <i>Dirinaria</i> lichen from two different ecosystems: First genomic insights of its mycobiont <i>Dirinaria</i> sp. GBRC AP01. <i>Microbiological Research</i> , 2020, 233, 126407.	2.5	3
1921	An Annotated Draft Genome of the Mountain Hare (<i>Lepus timidus</i>). <i>Genome Biology and Evolution</i> , 2020, 12, 3656-3662.	1.1	13
1922	Whole Genome Sequencing and Assembly of the Asian Honey Bee <i>Apis dorsata</i> . <i>Genome Biology and Evolution</i> , 2020, 12, 3677-3683.	1.1	21
1923	<i>Fusarium virguliforme</i> Transcriptional Plasticity Is Revealed by Host Colonization of Maize versus Soybean. <i>Plant Cell</i> , 2020, 32, 336-351.	3.1	28
1924	Comparative genomics reveals divergent thermal selection in warm- and cold-tolerant marine mussels. <i>Molecular Ecology</i> , 2020, 29, 519-535.	2.0	24
1925	Identification of neuropeptides from eyestalk transcriptome profiling analysis of female oriental river prawn (<i>Macrobrachium nipponense</i>) under hypoxia and reoxygenation conditions. <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 2020, 241, 110392.	0.7	11
1926	Boundary maintenance in the ancestral metazoan Hydra depends on histone acetylation. <i>Developmental Biology</i> , 2020, 458, 200-214.	0.9	4
1927	The fire ant social supergene is characterized by extensive gene and transposable element copy number variation. <i>Molecular Ecology</i> , 2020, 29, 105-120.	2.0	12
1928	Optimization of the culture conditions for production of Polyhydroxyalkanoate and its characterization from a new <i>Bacillus cereus</i> sp. BNPI-92 strain, isolated from plastic waste dumping yard. <i>International Journal of Biological Macromolecules</i> , 2020, 156, 1064-1080.	3.6	15
1929	The Indian cobra reference genome and transcriptome enables comprehensive identification of venom toxins. <i>Nature Genetics</i> , 2020, 52, 106-117.	9.4	139
1930	Genome and population sequencing of a chromosome-level genome assembly of the Chinese tapertail anchovy (<i>Coilia nasus</i>) provides novel insights into migratory adaptation. <i>GigaScience</i> , 2020, 9, .	3.3	26

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1931	Evolutionary superscaffolding and chromosome anchoring to improve Anopheles genome assemblies. BMC Biology, 2020, 18, 1.	1.7	177
1932	Single-molecule real-time (SMRT) sequencing facilitates Tachypleus tridentatus genome annotation. International Journal of Biological Macromolecules, 2020, 147, 89-97.	3.6	14
1933	Characterization of a Yâ€specific duplication/insertion of the antiâ€Mullerian hormone type II receptor gene based on a chromosomeâ€scale genome assembly of yellow perch, <i>Perca flavescens</i>. Molecular Ecology Resources, 2020, 20, 531-543.	2.2	76
1934	A comparative synthesis of transcriptomic analyses reveals major differences between WSSV-susceptible Litopenaeus vannamei and WSSV-refractory Macrobrachium rosenbergii. Developmental and Comparative Immunology, 2020, 104, 103564.	1.0	23
1935	Genome of an iconic Australian bird: Highâ€quality assembly and linkage map of the superb fairyâ€wren (<i>Malurus cyaneus</i>). Molecular Ecology Resources, 2020, 20, 560-578.	2.2	24
1936	Molecular responses to freshwater limitation in the mangrove tree <i>Avicennia germinans</i> (Acanthaceae). Molecular Ecology, 2020, 29, 344-362.	2.0	12
1937	Comparative genomics of six <i>Juglans</i> species reveals diseaseâ€associated gene family contractions. Plant Journal, 2020, 102, 410-423.	2.8	25
1938	Parental origin of the allotetraploid tobacco <i>Nicotiana benthamiana</i>. Plant Journal, 2020, 102, 541-554.	2.8	31
1939	Genomes of early-diverging streptophyte algae shed light on plant terrestrialization. Nature Plants, 2020, 6, 95-106.	4.7	146
1940	Co-option of wing-patterning genes underlies the evolution of the treehopper helmet. Nature Ecology and Evolution, 2020, 4, 250-260.	3.4	38
1941	A High-Quality Reference Genome Assembly of the Saltwater Crocodile, Crocodylus porosus, Reveals Patterns of Selection in Crocodylidae. Genome Biology and Evolution, 2020, 12, 3635-3646.	1.1	15
1942	The water lily genome and the early evolution of flowering plants. Nature, 2020, 577, 79-84.	13.7	238
1943	The Chromosome-Based Rubber Tree Genome Provides New Insights into Spurge Genome Evolution and Rubber Biosynthesis. Molecular Plant, 2020, 13, 336-350.	3.9	73
1944	Early Stage Adaptation of a Mesophilic Green Alga to Antarctica: Systematic Increases in Abundance of Enzymes and LEA Proteins. Molecular Biology and Evolution, 2020, 37, 849-863.	3.5	12
1945	Genomic evidence of population genetic differentiation in deep-sea squat lobster Shinkaia crosnieri (crustacea: Decapoda: Anomura) from Northwestern Pacific hydrothermal vent and cold seep. Deep-Sea Research Part I: Oceanographic Research Papers, 2020, 156, 103188.	0.6	15
1946	Epigenetic patterns within the haplotype phased fig (<i>Ficus carica</i> L.) genome. Plant Journal, 2020, 102, 600-614.	2.8	43
1947	The developmental transcriptome for Lytechinus variegatus exhibits temporally punctuated gene expression changes. Developmental Biology, 2020, 460, 139-154.	0.9	16
1948	The Earth BioGenome project: opportunities and challenges for plant genomics and conservation. Plant Journal, 2020, 102, 222-229.	2.8	35

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1949	Comparison of colonial volvocine algae based on phylotranscriptomic analysis of gene family evolution and natural selection. <i>European Journal of Phycology</i> , 2020, 55, 100-112.	0.9	10
1950	SCGid: a consensus approach to contig filtering and genome prediction from single-cell sequencing libraries of uncultured eukaryotes. <i>Bioinformatics</i> , 2020, 36, 1994-2000.	1.8	2
1951	The Coix Genome Provides Insights into Panicoideae Evolution and Papery Hull Domestication. <i>Molecular Plant</i> , 2020, 13, 309-320.	3.9	28
1952	Evolution and Domestication Footprints Uncovered from the Genomes of Coix. <i>Molecular Plant</i> , 2020, 13, 295-308.	3.9	35
1953	Root transcriptome analysis of <i>Saccharum spontaneum</i> uncovers key genes and pathways in response to low-temperature stress. <i>Environmental and Experimental Botany</i> , 2020, 171, 103935.	2.0	23
1954	De novo transcriptome sequencing of the thecate colonial hydrozoan, <i>Dynamena pumila</i> . <i>Marine Genomics</i> , 2020, 51, 100726.	0.4	4
1955	Long-read sequencing and de novo assembly of the <i>Luffa cylindrica</i> (L.) Roem. genome. <i>Molecular Ecology Resources</i> , 2020, 20, 511-519.	2.2	27
1956	Chromosomal-level assembly of <i>Takifugu obscurus</i> (Abe, 1949) genome using third-generation DNA sequencing and Hi-C analysis. <i>Molecular Ecology Resources</i> , 2020, 20, 520-530.	2.2	46
1957	Gene Expression in the Salivary Gland of <i>Rhipicephalus (Boophilus) microplus</i> Fed on Tick-Susceptible and Tick-Resistant Hosts. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 477.	1.8	12
1958	Draft Genome of a Blister Beetle <i>Mylabris aulica</i> . <i>Frontiers in Genetics</i> , 2020, 10, 1281.	1.1	7
1959	Draft Genomes of Two Artocarpus Plants, Jackfruit (<i>A. heterophyllus</i>) and Breadfruit (<i>A. altilis</i>). <i>Genes</i> , 2020, 11, 27.	1.0	30
1960	The Terrestrial Carnivorous Plant <i>Utricularia reniformis</i> Sheds Light on Environmental and Life-Form Genome Plasticity. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3.	1.8	30
1961	Chromosome-Level Comprehensive Genome of Mangrove Sediment-Derived Fungus <i>Penicillium variable</i> HXQ-H-1. <i>Journal of Fungi (Basel, Switzerland)</i> , 2020, 6, 7.	1.5	6
1962	The draft nuclear genome assembly of <i>Eucalyptus pauciflora</i> : a pipeline for comparing de novo assemblies. <i>GigaScience</i> , 2020, 9, .	3.3	46
1963	Genome Sequence Resource for the Ramie Oomycete Pathogen <i>Phytophthora vexans</i> HF1. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 1270-1273.	1.4	2
1964	Mimicry diversification in <i>Papilio dardanus</i> via a genomic inversion in the regulatory region of <i>engrailed</i> - <i>invected</i> . <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20200443.	1.2	15
1965	Autotransporters Drive Biofilm Formation and Autoaggregation in the Diderm Firmicute <i>Veillonella parvula</i> . <i>Journal of Bacteriology</i> , 2020, 202, .	1.0	22
1966	Genome Sequence of the Human Opportunistic Fungus <i>Arthrocladium fulminans</i> (CBS 136243). <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1817-1821.	0.8	3

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1967	Potential of Platinum Standard Reference Genomes to Exploit Natural Variation in the Wild Relatives of Rice. <i>Frontiers in Plant Science</i> , 2020, 11, 579980.	1.7	15
1968	Aquatic Insects Are Dramatically Underrepresented in Genomic Research. <i>Insects</i> , 2020, 11, 601.	1.0	35
1969	Chromosome-level genome assembly of a parent species of widely cultivated azaleas. <i>Nature Communications</i> , 2020, 11, 5269.	5.8	90
1970	Chromosome-Scale Genome Assembly of <i>Talaromyces rugulosus</i> W13939, a Mycoparasitic Fungus and Promising Biocontrol Agent. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 1446-1450.	1.4	4
1971	The methylome is altered for plants in a high CO ₂ world: Insights into the response of a wild plant population to multigenerational exposure to elevated atmospheric [CO ₂]. <i>Global Change Biology</i> , 2020, 26, 6474-6492.	4.2	13
1972	Reduced stress defence responses contribute to the higher toxicity of a pesticide under warming. <i>Molecular Ecology</i> , 2020, 29, 4735-4748.	2.0	10
1973	Genetic compensation rather than genetic assimilation drives the evolution of plasticity in response to mild warming across latitudes in a damselfly. <i>Molecular Ecology</i> , 2020, 29, 4823-4834.	2.0	17
1974	Development of a relevant strategy using de novo transcriptome assembly method for transcriptome comparisons between Muscovy and common duck species and their reciprocal inter-specific mule and hinny hybrids fed ad libitum and overfed. <i>BMC Genomics</i> , 2020, 21, 687.	1.2	3
1975	A Hu sheep genome with the first ovine Y chromosome reveal introgression history after sheep domestication. <i>Science China Life Sciences</i> , 2021, 64, 1116-1130.	2.3	27
1976	Nanopore MinION Sequencing Reveals Possible Transfer of blaKPC ² Plasmid Across Bacterial Species in Two Healthcare Facilities. <i>Frontiers in Microbiology</i> , 2020, 11, 2007.	1.5	21
1977	The Gut Virome Database Reveals Age-Dependent Patterns of Virome Diversity in the Human Gut. <i>Cell Host and Microbe</i> , 2020, 28, 724-740.e8.	5.1	352
1978	New Lineage of Microbial Predators Adds Complexity to Reconstructing the Evolutionary Origin of Animals. <i>Current Biology</i> , 2020, 30, 4500-4509.e5.	1.8	24
1979	Comparative genomics of Alexander Fleming's original <i>Penicillium</i> isolate (IMI 15378) reveals sequence divergence of penicillin synthesis genes. <i>Scientific Reports</i> , 2020, 10, 15705.	1.6	12
1980	Characterization of mating type genes in heterothallic <i>Neonectria</i> species, with emphasis on <i>N. coccinea</i> , <i>N. ditissima</i> , and <i>N. faginata</i> . <i>Mycologia</i> , 2020, 112, 880-894.	0.8	7
1981	Genome-Wide Analysis of Biosynthetic Gene Cluster Reveals Correlated Gene Loss with Absence of Usnic Acid in Lichen-Forming Fungi. <i>Genome Biology and Evolution</i> , 2020, 12, 1858-1868.	1.1	28
1982	Draft Genome Assembly of the Freshwater Apex Predator Wels Catfish (<i>Silurus glanis</i>) Using Linked-Read Sequencing. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3897-3906.	0.8	9
1983	Haplotype-resolved genome analyses of a heterozygous diploid potato. <i>Nature Genetics</i> , 2020, 52, 1018-1023.	9.4	134
1984	Construction of a chromosome-scale long-read reference genome assembly for potato. <i>GigaScience</i> , 2020, 9, .	3.3	150

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1985	The genomes of a monogenic fly: views of primitive sex chromosomes. <i>Scientific Reports</i> , 2020, 10, 15728.	1.6	6
1986	<i>Chlorella vulgaris</i> and Its Phycosphere in Wastewater: Microalgae-Bacteria Interactions During Nutrient Removal. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 557572.	2.0	34
1987	Differential Gene Expression with an Emphasis on Floral Organ Size Differences in Natural and Synthetic Polyploids of <i>Nicotiana tabacum</i> (Solanaceae). <i>Genes</i> , 2020, 11, 1097.	1.0	15
1988	Polyphyletic origin, intracellular invasion, and meiotic genes in the putatively asexual agamococcidians (Apicomplexa incertae sedis). <i>Scientific Reports</i> , 2020, 10, 15847.	1.6	10
1989	Candidatus <i>Frankia nodulisporulans</i> sp. nov., an <i>Alnus glutinosa</i> -infective <i>Frankia</i> species unable to grow in pure culture and able to sporulate in-plant. <i>Systematic and Applied Microbiology</i> , 2020, 43, 126134.	1.2	17
1990	A Chromosome-Level Genome Assembly of <i>Dendrobium huoshanense</i> Using Long Reads and Hi-C Data. <i>Genome Biology and Evolution</i> , 2020, 12, 2486-2490.	1.1	30
1991	Gene expression response of the alga <i>Fucus virsoides</i> (Fucales, Ochrophyta) to glyphosate solution exposure. <i>Environmental Pollution</i> , 2020, 267, 115483.	3.7	5
1992	IMA Genome - F13. <i>IMA Fungus</i> , 2020, 11, 19.	1.7	13
1993	Comparative eye and liver differentially expressed genes reveal monochromatic vision and cancer resistance in the shortfin mako shark (<i>Isurus oxyrinchus</i>). <i>Genomics</i> , 2020, 112, 4817-4826.	1.3	4
1994	The genome of Chinese flowering cherry (<i>Cerasus serrulata</i>) provides new insights into <i>Cerasus</i> species. <i>Horticulture Research</i> , 2020, 7, 165.	2.9	22
1995	High-quality nuclear genome for <i>Sarcoptes scabiei</i> —A critical resource for a neglected parasite. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008720.	1.3	25
1996	Transcriptome sequencing and screening of genes related to sex determination of <i>Trichosanthes kirilowii</i> Maxim. <i>PLoS ONE</i> , 2020, 15, e0239230.	1.1	9
1997	<i>Oecophyllibacter saccharovorans</i> gen. nov. sp. nov., a bacterial symbiont of the weaver ant <i>Oecophylla smaragdina</i> . <i>Journal of Microbiology</i> , 2020, 58, 988-997.	1.3	14
1998	Evaluation of assembly methods combining long-reads and short-reads to obtain <i>Paenibacillus</i> sp. R4 high-quality complete genome. <i>3 Biotech</i> , 2020, 10, 480.	1.1	1
1999	Transcriptomics of the Rooibos (<i>Aspalathus linearis</i>) Species Complex. <i>BioTech</i> , 2020, 9, 19.	1.3	4
2000	Genomes of the Banyan Tree and Pollinator Wasp Provide Insights into Fig-Wasp Coevolution. <i>Cell</i> , 2020, 183, 875-889.e17.	13.5	71
2001	Origin and adaptation to high altitude of Tibetan semi-wild wheat. <i>Nature Communications</i> , 2020, 11, 5085.	5.8	104
2002	Comparative genomic analyses illuminate the distinct evolution of megabats within Chiroptera. <i>DNA Research</i> , 2020, 27, .	1.5	10

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2003	Factorial estimating assembly base errors using k-mer abundance difference (KAD) between short reads and genome assembled sequences. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa075.	1.5	8
2004	Transcriptome analysis of the growth performance of hybrid mandarin fish after food conversion. <i>PLoS ONE</i> , 2020, 15, e0240308.	1.1	22
2005	From sporadic single genes to a broader transcriptomic approach: Insights into the formation of the biomineralized exoskeleton in decapod crustaceans. <i>Journal of Structural Biology</i> , 2020, 212, 107612.	1.3	4
2006	Draft Genome Sequence of <i>Saccharomyces cerevisiae</i> Strain P-684, Isolated from <i>Prunus verecunda</i> . <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
2007	Large-scale genome sequencing of mycorrhizal fungi provides insights into the early evolution of symbiotic traits. <i>Nature Communications</i> , 2020, 11, 5125.	5.8	258
2008	Genome wide analysis reveals genetic divergence between Goldsinny wrasse populations. <i>BMC Genetics</i> , 2020, 21, 118.	2.7	5
2009	Mating-type locus rearrangements and shifts in thallism states in Citrus-associated <i>Phyllosticta</i> species. <i>Fungal Genetics and Biology</i> , 2020, 144, 103444.	0.9	7
2010	Comparative transcriptome analysis suggests convergent evolution of desiccation tolerance in <i>Selaginella</i> species. <i>BMC Plant Biology</i> , 2020, 20, 468.	1.6	12
2011	Dynamics in Secondary Metabolite Gene Clusters in Otherwise Highly Syntenic and Stable Genomes in the Fungal Genus <i>Botrytis</i> . <i>Genome Biology and Evolution</i> , 2020, 12, 2491-2507.	1.1	22
2012	First Draft Genome Resource for the Tomato Black Leaf Mold Pathogen <i>Pseudocercospora fuligena</i> . <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 1441-1445.	1.4	3
2013	Comparative genomics and community curation further improve gene annotations in the nematode <i>Pristionchus pacificus</i> . <i>BMC Genomics</i> , 2020, 21, 708.	1.2	19
2014	Differential Regulation of Anthocyanins in <i>Cerasus humilis</i> Fruit Color Revealed by Combined Transcriptome and Metabolome Analysis. <i>Forests</i> , 2020, 11, 1065.	0.9	9
2015	Large-Scale Comparative Analyses of Tick Genomes Elucidate Their Genetic Diversity and Vector Capacities. <i>Cell</i> , 2020, 182, 1328-1340.e13.	13.5	145
2016	Identification and characterization of highly active promoters from the fall armyworm, <i>Spodoptera frugiperda</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2020, 126, 103455.	1.2	16
2017	Whole genome sequencing and de novo assembly of three virulent Indian isolates of <i>Leptospira</i> . <i>Infection, Genetics and Evolution</i> , 2020, 85, 104579.	1.0	7
2018	A genome database for a Japanese population of the larvacean <i>Oikopleura dioica</i> . <i>Development Growth and Differentiation</i> , 2020, 62, 450-461.	0.6	13
2019	Species diversity and phylogeography of <i>Cornus kousa</i> (Asian dogwood) captured by genomic and genic microsatellites. <i>Ecology and Evolution</i> , 2020, 10, 8299-8312.	0.8	3
2020	Elucidation of genetic diversity base in <i>Calotropis procera</i> – a potentially emerging new fibre resource. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2020, 18, 159-167.	0.4	5

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2021	Assembly of the threespine stickleback Y chromosome reveals convergent signatures of sex chromosome evolution. <i>Genome Biology</i> , 2020, 21, 177.	3.8	79
2022	Genome Sequence of the Euryhaline Javafish Medaka, <i>Oryzias javanicus</i> : A Small Aquarium Fish Model for Studies on Adaptation to Salinity. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 907-915.	0.8	22
2023	Biological rhythms in the deep-sea hydrothermal mussel <i>Bathymodiolus azoricus</i> . <i>Nature Communications</i> , 2020, 11, 3454.	5.8	30
2024	TandemTools: mapping long reads and assessing/improving assembly quality in extra-long tandem repeats. <i>Bioinformatics</i> , 2020, 36, i75-i83.	1.8	40
2025	The Genome of the Softshell Clam <i>Mya arenaria</i> and the Evolution of Apoptosis. <i>Genome Biology and Evolution</i> , 2020, 12, 1681-1693.	1.1	7
2026	Genomic Analysis of the Only Blind Cichlid Reveals Extensive Inactivation in Eye and Pigment Formation Genes. <i>Genome Biology and Evolution</i> , 2020, 12, 1392-1406.	1.1	14
2027	Chromosome-level de novo assembly of the pig-tailed macaque genome using linked-read sequencing and HiC proximity scaffolding. <i>GigaScience</i> , 2020, 9, .	3.3	6
2028	Draft Genome Sequence Resource for <i>Phyllachora maydis</i> – An Obligate Pathogen That Causes Tar Spot of Corn with Recent Economic Impacts in the United States. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 884-887.	1.4	11
2029	Genomic insights on the contribution of balancing selection and local adaptation to the long-term survival of a widespread living fossil tree, <i>Cercidiphyllum japonicum</i> . <i>New Phytologist</i> , 2020, 228, 1674-1689.	3.5	22
2030	The high-quality genome of diploid strawberry (<i>Fragaria nilgerrensis</i>) provides new insights into anthocyanin accumulation. <i>Plant Biotechnology Journal</i> , 2020, 18, 1908-1924.	4.1	51
2031	Genome analyses provide insights into the evolution and adaptation of the eukaryotic Picophytoplankton <i>Mychonastes homosphaera</i> . <i>BMC Genomics</i> , 2020, 21, 477.	1.2	8
2032	PacBio single molecule long-read sequencing provides insight into the complexity and diversity of the <i>Pinctada fucata martensii</i> transcriptome. <i>BMC Genomics</i> , 2020, 21, 481.	1.2	14
2033	Genomic Analysis of Diverse Members of the Fungal Genus <i>Monosporascus</i> Reveals Novel Lineages, Unique Genome Content and a Potential Bacterial Associate. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2573-2583.	0.8	5
2034	IC4R-2.0: Rice Genome Reannotation Using Massive RNA-seq Data. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 161-172.	3.0	18
2035	Sequencing smart: De novo sequencing and assembly approaches for a non-model mammal. <i>GigaScience</i> , 2020, 9, .	3.3	18
2036	De novo transcriptome assembly and data for the blue-winged teal (<i>Spatula discors</i>). <i>Data in Brief</i> , 2020, 30, 105380.	0.5	2
2037	New insights into the variability of lactic acid production in <i>Lachancea thermotolerans</i> at the phenotypic and genomic level. <i>Microbiological Research</i> , 2020, 238, 126525.	2.5	18
2038	Population genetics of the coral <i>Acropora millepora</i> : Toward genomic prediction of bleaching. <i>Science</i> , 2020, 369, .	6.0	167

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2039	Optimized and affordable high-throughput sequencing workflow for preserved and nonpreserved small zooplankton specimens. <i>Molecular Ecology Resources</i> , 2020, 20, 1632-1646.	2.2	9
2040	Complete Genome Sequence of <i>Methylosinus</i> sp. Strain C49, a Methane-Oxidizing Bacterium Harboring <i>phaABC</i> Genes for Polyhydroxyalkanoate Synthesis. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
2041	Evidence for Dosage Compensation in <i>Coccinia grandis</i> , a Plant with a Highly Heteromorphic XY System. <i>Genes</i> , 2020, 11, 787.	1.0	12
2042	Assessment of ethanol tolerance of <i>Kluyveromyces marxianus</i> CCT 7735 selected by adaptive laboratory evolution. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 7483-7494.	1.7	25
2043	New Draft Genome Sequence of the Ergot Disease Fungus <i>Claviceps paspali</i> . <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	3
2044	Genetic Diversity in Invasive Populations of Argentine Stem Weevil Associated with Adaptation to Biocontrol. <i>Insects</i> , 2020, 11, 441.	1.0	13
2045	Comparative genomics of rice false smut fungi <i>Ustilaginoidea virens</i> Uv-Gvt strain from India reveals genetic diversity and phylogenetic divergence. <i>3 Biotech</i> , 2020, 10, 342.	1.1	10
2046	Multi-omic Directed Discovery of Cellulosomes, Polysaccharide Utilization Loci, and Lignocellulases from an Enriched Rumen Anaerobic Consortium. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	20
2047	First Genome Sequences of Two Multidrug-Resistant <i>Candida haemulonii</i> var. <i>vulnera</i> Isolates From Pediatric Patients With Candidemia. <i>Frontiers in Microbiology</i> , 2020, 11, 1535.	1.5	8
2048	Liver transcriptome resources of four commercially exploited teleost species. <i>Scientific Data</i> , 2020, 7, 214.	2.4	4
2049	Functional shell matrix proteins tentatively identified by asymmetric snail shell morphology. <i>Scientific Reports</i> , 2020, 10, 9768.	1.6	13
2050	Whole genome resequencing of four Italian sweet pepper landraces provides insights on sequence variation in genes of agronomic value. <i>Scientific Reports</i> , 2020, 10, 9189.	1.6	18
2051	Sex in Symbiodiniaceae dinoflagellates: genomic evidence for independent loss of the canonical synaptonemal complex. <i>Scientific Reports</i> , 2020, 10, 9792.	1.6	19
2052	Genome assembly of <i>Chiococca alba</i> uncovers key enzymes involved in the biosynthesis of unusual terpenoids. <i>DNA Research</i> , 2020, 27, .	1.5	10
2053	Genome-enabled discovery of anthraquinone biosynthesis in <i>Senna tora</i> . <i>Nature Communications</i> , 2020, 11, 5875.	5.8	57
2054	Molecular basis of resistance to organophosphate insecticides in the New World screw-worm fly. <i>Parasites and Vectors</i> , 2020, 13, 562.	1.0	6
2055	Transcriptome Analysis and Knockdown of the Juvenile Hormone Esterase Gene Reveal Abnormal Feeding Behavior in the Sugarcane Giant Borer. <i>Frontiers in Physiology</i> , 2020, 11, 588450.	1.3	5
2056	The genomic timeline of cichlid fish diversification across continents. <i>Nature Communications</i> , 2020, 11, 5895.	5.8	41

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2057	Genome Size Versus Genome Assemblies: Are the Genomes Truly Expanded in Polyploid Fungal Symbionts?. <i>Genome Biology and Evolution</i> , 2020, 12, 2384-2390.	1.1	6
2058	Draft Genome of the European Mouflon (<i>Ovis orientalis musimon</i>). <i>Frontiers in Genetics</i> , 2020, 11, 533611.	1.1	3
2059	Temperature Differentially Affects Gene Expression in Antarctic Thraustochytrid <i>Oblongichytrium</i> sp. RT2316-13. <i>Marine Drugs</i> , 2020, 18, 563.	2.2	9
2060	Draft genome assembly and annotation of the masked birch caterpillar, <i>Drepana arcuata</i> (Lepidoptera: Tj ETQq1 1 0.784314 rgBT / Over 0.5	0.5	
2061	Draft genome and transcriptome analyses of halophyte rice <i>Oryza coarctata</i> provide resources for salinity and submergence stress response factors. <i>Physiologia Plantarum</i> , 2021, 173, 1309-1322.	2.6	13
2062	Chromosome-Scale Assembly and Annotation of the Macadamia Genome (<i>Macadamia integrifolia</i>) Tj ETQq1 1 0.784314 rgBT / Over 0.8	0.8	26
2063	Transcriptional Analysis of Metabolic Pathways and Regulatory Mechanisms of Essential Oil Biosynthesis in the Leaves of <i>Cinnamomum camphora</i> (L.) Presl. <i>Frontiers in Genetics</i> , 2020, 11, 598714.	1.1	19
2064	Identification of reference genes for real-time polymerase chain reaction gene expression studies in Nile rats fed Water-Soluble Palm Fruit Extract. <i>Molecular Biology Reports</i> , 2020, 47, 9409-9427.	1.0	2
2065	Positive selection alone is sufficient for whole genome differentiation at the early stage of speciation process in the fall armyworm. <i>BMC Evolutionary Biology</i> , 2020, 20, 152.	3.2	19
2066	The Effect of Iodine-Containing Nano-Micelles, FS-1, on Antibiotic Resistance, Gene Expression and Epigenetic Modifications in the Genome of Multidrug Resistant MRSA Strain <i>Staphylococcus aureus</i> ATCC BAA-39. <i>Frontiers in Microbiology</i> , 2020, 11, 581660.	1.5	9
2067	A high-quality reference genome sequence of <i>Salvia miltiorrhiza</i> provides insights into tanshinone synthesis in its red rhizomes. <i>Plant Genome</i> , 2020, 13, e20041.	1.6	45
2068	The IAG-Switch and Further Transcriptomic Insights Into Sexual Differentiation of a Protandric Shrimp. <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	12
2069	Toll-like signaling pathway in the transcriptome of <i>Littorina littorea</i> . <i>Fish and Shellfish Immunology</i> , 2020, 106, 640-644.	1.6	5
2070	The First Pycnogonid Draft Genome of <i>Nymphon striatum</i> . <i>Frontiers in Ecology and Evolution</i> , 2020, 8, .	1.1	2
2071	Evolution of Biomineralization Genes in the Prismatic Layer of the Pen Shell <i>Atrina pectinata</i> . <i>Journal of Molecular Evolution</i> , 2020, 88, 742-758.	0.8	5
2072	Conservation Genomics of the Threatened Western Spadefoot, <i>Spea hammondi</i> , in Urbanized Southern California. <i>Journal of Heredity</i> , 2020, 111, 613-627.	1.0	7
2073	Characterizing glycosyltransferases by a combination of sequencing platforms applied to the leaf tissues of <i>Stevia rebaudiana</i> . <i>BMC Genomics</i> , 2020, 21, 794.	1.2	14
2074	Genomics and lipidomics analysis of the biotechnologically important oleaginous red yeast <i>Rhodotorula glutinis</i> ZHK provides new insights into its lipid and carotenoid metabolism. <i>BMC Genomics</i> , 2020, 21, 834.	1.2	16

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2081	Accurate assembly of the olive baboon (<i>Papio anubis</i>) genome using long-read and Hi-C data. <i>GigaScience</i> , 2020, 9, .	3.3	18
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2083	Dense sampling of bird diversity increases power of comparative genomics. <i>Nature</i> , 2020, 587, 252-257.	13.7	251
2084	A comparative genomics multitool for scientific discovery and conservation. <i>Nature</i> , 2020, 587, 240-245.	13.7	216
2085	Genomic and transcriptomic variation defines the chromosome-scale assembly of <i>Haemonchus contortus</i> , a model gastrointestinal worm. <i>Communications Biology</i> , 2020, 3, 656.	2.0	91
2086	Massive gene presence-absence variation shapes an open pan-genome in the Mediterranean mussel. <i>Genome Biology</i> , 2020, 21, 275.	3.8	105
2087	Identification and Expression Analysis of Long Non-coding RNA in Large Yellow Croaker (<i>Larimichthys</i>) Tj ETQq0 0 0 rgBT /Overlock 10 TF 1.1 13	1.1	13
2088	Distribution and Evolution of the Bacteriophage WO and Its Antagonism With <i>Wolbachia</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 595629.	1.5	12
2089	Genome of <i>Solanum pimpinellifolium</i> provides insights into structural variants during tomato breeding. <i>Nature Communications</i> , 2020, 11, 5817.	5.8	85
2090	A genome-wide screening for RNAi pathway proteins in Acari. <i>BMC Genomics</i> , 2020, 21, 791.	1.2	12
2091	Genome- and Proteome-Wide Analysis of Lysine Acetylation in <i>Vibrio vulnificus</i> Vv180806 Reveals Its Regulatory Roles in Virulence and Antibiotic Resistance. <i>Frontiers in Microbiology</i> , 2020, 11, 591287.	1.5	11
2092	Genetic Variation and Preliminary Indications of Divergent Niche Adaptation in Cryptic Clade II of <i>Escherichia</i> . <i>Microorganisms</i> , 2020, 8, 1713.	1.6	3

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2094	Genomic analyses of a livestock pest, the New World screwworm, find potential targets for genetic control programs. <i>Communications Biology</i> , 2020, 3, 424.	2.0	26
2095	An evaluation of methodology to determine algal genome completeness. <i>Algal Research</i> , 2020, 51, 102019.	2.4	10
2096	Genome sequence of <i>Acremonium strictum</i> AAJ6 strain isolated from the Cerrado biome in Brazil and CAZymes expression in thermotolerant industrial yeast for ethanol production. <i>Process Biochemistry</i> , 2020, 98, 139-150.	1.8	5
2097	The <i>Acer truncatum</i> genome provides insights into nervonic acid biosynthesis. <i>Plant Journal</i> , 2020, 104, 662-678.	2.8	52
2098	Gut transcriptomic changes during hibernation in the greater horseshoe bat (<i>Rhinolophus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	0.9	4
2099	Pulse magnetization elicits differential gene expression in the central nervous system of the Caribbean spiny lobster, <i>Panulirus argus</i> . <i>Journal of Comparative Physiology A: Neuroethology, Sensory, Neural, and Behavioral Physiology</i> , 2020, 206, 725-742.	0.7	4
2100	The chromosome-level wintersweet (<i>Chimonanthus praecox</i>) genome provides insights into floral scent biosynthesis and flowering in winter. <i>Genome Biology</i> , 2020, 21, 200.	3.8	69
2101	A high-contiguity <i>Brassica nigra</i> genome localizes active centromeres and defines the ancestral <i>Brassica</i> genome. <i>Nature Plants</i> , 2020, 6, 929-941.	4.7	94
2102	Comprehensive chemotaxonomic and genomic profiling of a biosynthetically talented Australian fungus, <i>Aspergillus burnettii</i> sp. nov.. <i>Fungal Genetics and Biology</i> , 2020, 143, 103435.	0.9	19
2103	HASLR: Fast Hybrid Assembly of Long Reads. <i>IScience</i> , 2020, 23, 101389.	1.9	44
2104	The Genome of <i>Microthlaspi erraticum</i> (Brassicaceae) Provides Insights Into the Adaptation to Highly Calcareous Soils. <i>Frontiers in Plant Science</i> , 2020, 11, 943.	1.7	4
2105	Evolutionary network genomics of wood formation in a phylogenetic survey of angiosperm forest trees. <i>New Phytologist</i> , 2020, 228, 1811-1823.	3.5	8
2106	Draft Genome Sequence of <i>Fusarium oxysporum</i> f. sp. <i>albedinis</i> Strain Foa 133, the Causal Agent of Bayoud Disease on Date Palm. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	9
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2108	Transcriptome analysis of <i>Paris polyphylla</i> var. <i>yunnanensis</i> illuminates the biosynthesis and accumulation of steroidal saponins in rhizomes and leaves. <i>Phytochemistry</i> , 2020, 178, 112460.	1.4	16
2109	Insights into the evolution of symbiosis gene copy number and distribution from a chromosome-scale <i>Lotus japonicus</i> genome sequence. <i>DNA Research</i> , 2020, 27, .	1.5	35
2110	Reference Genome Assembly for Australian <i>Ascochyta rabiei</i> Isolate ArME14. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2131-2140.	0.8	15

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2112	Pathogenic Adaptations Revealed by Comparative Genome Analyses of Two <i>Colletotrichum</i> spp., the Causal Agent of Anthracnose in Rubber Tree. <i>Frontiers in Microbiology</i> , 2020, 11, 1484.	1.5	9
2113	Improved Reference Genome for <i>Cyclotella cryptica</i> CCMP332, a Model for Cell Wall Morphogenesis, Salinity Adaptation, and Lipid Production in Diatoms (Bacillariophyta). <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2965-2974.	0.8	14
2114	Epigenetic Regulation of <i>Verticillium dahliae</i> Virulence: Does DNA Methylation Level Play A Role?. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5197.	1.8	5
2115	A tree frog (<i>Boana pugnax</i>) dataset of skin transcriptome for the identification of biomolecules with potential antimicrobial activities. <i>Data in Brief</i> , 2020, 32, 106084.	0.5	3
2116	Draft Genome Sequence of <i>Simplicillium aogashimaense</i> 72-15.1, a Putative Endophyte of <i>Brachiaria brizantha</i> . <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	4
2117	Chromosome-Level Assembly of <i>Drosophila bifasciata</i> Reveals Important Karyotypic Transition of the X Chromosome. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 891-897.	0.8	12
2118	Beaver and Naked Mole Rat Genomes Reveal Common Paths to Longevity. <i>Cell Reports</i> , 2020, 32, 107949.	2.9	26
2119	Dataset of de novo assembly and functional annotation of the transcriptomes of three native oleaginous microalgae from the Peruvian Amazon. <i>Data in Brief</i> , 2020, 31, 105917.	0.5	2
2120	Cultivar-specific transcriptome and pan-transcriptome reconstruction of tetraploid potato. <i>Scientific Data</i> , 2020, 7, 249.	2.4	27
2121	Draft Genome Sequence of <i>Clostridium cochlearium</i> Strain AGROS13, Isolated from a Sheep Dairy Farm in New Zealand. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
2122	Genome-Wide Analysis Reveals Genetic Potential for Aromatic Compounds Biodegradation of <i>Spingopyxis</i> . <i>BioMed Research International</i> , 2020, 2020, 1-12.	0.9	13
2123	Evaluating metagenomics tools for genome binning with real metagenomic datasets and CAMI datasets. <i>BMC Bioinformatics</i> , 2020, 21, 334.	1.2	53
2124	Genomic architecture of endogenous ichnoviruses reveals distinct evolutionary pathways leading to virus domestication in parasitic wasps. <i>BMC Biology</i> , 2020, 18, 89.	1.7	24
2125	The genome of the marine monogonont rotifer <i>Brachionus rotundiformis</i> and insight into species-specific detoxification components in <i>Brachionus</i> spp.. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2020, 36, 100714.	0.4	7
2126	Differential Expression of Fungal Genes Determines the Lifestyle of <i>Plectosphaerella</i> Strains During <i>Arabidopsis thaliana</i> Colonization. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 1299-1314.	1.4	9
2127	Spatio-temporal patterns in the gene expression of the calanoid copepod <i>Temora longicornis</i> in the Belgian part of the North Sea. <i>Marine Environmental Research</i> , 2020, 160, 105037.	1.1	8
2128	Full-length transcriptome sequences of ridgetail white prawn <i>Exopalaemon carinicauda</i> provide insight into gene expression dynamics during thermal stress. <i>Science of the Total Environment</i> , 2020, 747, 141238.	3.9	13

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2130	Genome sequencing of four culinary herbs reveals terpenoid genes underlying chemodiversity in the Nepetoideae. DNA Research, 2020, 27, .	1.5	18
2131	Enjoying the warming Mediterranean: Transcriptomic responses to temperature changes of a thermophilous keystone species in benthic communities. Molecular Ecology, 2020, 29, 3299-3315.	2.0	11
2132	Whole-genome <i>de novo</i> assemblies reveal extensive structural variations and dynamic organelle-to-nucleus DNA transfers in African and Asian rice. Plant Journal, 2020, 104, 596-612.	2.8	19
2133	Comparative gut transcriptome analysis of <i>Diatraea saccharalis</i> in response to the dietary source. PLoS ONE, 2020, 15, e0235575.	1.1	7
2134	Transcriptome Analysis of <i>Pistacia vera</i> Inflorescence Buds in Bearing and Non-Bearing Shoots Reveals the Molecular Mechanism Causing Premature Flower Bud Abscission. Genes, 2020, 11, 851.	1.0	9
2135	Illuminating the impact of diel vertical migration on visual gene expression in deep-sea shrimp. Molecular Ecology, 2020, 29, 3494-3510.	2.0	14
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2137	Comparative Genome Analysis Reveals <i>Cyanidiococcus</i> gen. nov., A New Extremophilic Red Algal Genus Sister to <i>Cyanidioschyzon</i> (Cyanidioschyzonaceae, Rhodophyta). Journal of Phycology, 2020, 56, 1428-1442.	1.0	22
2138	A reference genome assembly and adaptive trait analysis of <i>Castanea mollissima</i> 'Vanuxem', a source of resistance to chestnut blight in restoration breeding. Tree Genetics and Genomes, 2020, 16, 1.	0.6	14
2139	Response of gut microbiota and immune function to hypoosmotic stress in the yellowfin seabream (<i>Acanthopagrus latus</i>). Science of the Total Environment, 2020, 745, 140976.	3.9	23
2140	Peculiar genomic traits in the stress-adapted cryptoendolithic Antarctic fungus <i>Friedmanniomyces endolithicus</i> . Fungal Biology, 2020, 124, 458-467.	1.1	23
2141	A Chromosome-Level Genome Assembly of Garlic (<i>Allium sativum</i>) Provides Insights into Genome Evolution and Allicin Biosynthesis. Molecular Plant, 2020, 13, 1328-1339.	3.9	89
2142	Tracing animal genomic evolution with the chromosomal-level assembly of the freshwater sponge <i>Ephydatia muelleri</i> . Nature Communications, 2020, 11, 3676.	5.8	72
2143	European maize genomes highlight intraspecies variation in repeat and gene content. Nature Genetics, 2020, 52, 950-957.	9.4	84
2144	Population Genomic Analyses of the Sea Urchin <i>Echinometra</i> sp. EZ across an Extreme Environmental Gradient. Genome Biology and Evolution, 2020, 12, 1819-1829.	1.1	8
2145	<i>Pyropia yezoensis</i> genome reveals diverse mechanisms of carbon acquisition in the intertidal environment. Nature Communications, 2020, 11, 4028.	5.8	49
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2148	<i>De Novo</i> Assembly of the Northern Cardinal (<i>Cardinalis cardinalis</i>) Genome Reveals Candidate Regulatory Regions for Sexually Dichromatic Red Plumage Coloration. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3541-3548.	0.8	9
2149	Genomic Evidence for Sensorial Adaptations to a Nocturnal Predatory Lifestyle in Owls. <i>Genome Biology and Evolution</i> , 2020, 12, 1895-1908.	1.1	9
2150	Hybrid Genome Assembly and Evidence-Based Annotation of the Egg Parasitoid and Biological Control Agent <i>Trichogramma brassicae</i>. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3533-3540.	0.8	14
2151	Draft Genome Sequence of <i>Pseudomonas nitritolerans</i> Strain AGROB37, Isolated from a Sheep Dairy Farm in New Zealand. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	0
2152	“Mind the Gap” Hi-C Technology Boosts Contiguity of the Globe Artichoke Genome in Low-Recombination Regions. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3557-3564.	0.8	12
2153	De novo biosynthesis of simple aromatic compounds by an arthropod (<i>Archezogozetes</i> Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 502 Td (1.2	4
2154	The mechanism of potato resistance to <i>Globodera rostochiensis</i> : comparison of root transcriptomes of resistant and susceptible <i>Solanum phureja</i> genotypes. <i>BMC Plant Biology</i> , 2020, 20, 350.	1.6	5
2155	Genome-enabled insights into the biology of thrips as crop pests. <i>BMC Biology</i> , 2020, 18, 142.	1.7	54
2156	Genome Sequencing of <i>Paecilomyces Penicillatus</i> Provides Insights into Its Phylogenetic Placement and Mycoparasitism Mechanisms on Morel Mushrooms. <i>Pathogens</i> , 2020, 9, 834.	1.2	19
2157	Transgenerational inheritance of chemical-induced signature: A case study with simvastatin. <i>Environment International</i> , 2020, 144, 106020.	4.8	13
2158	De novo transcriptome assembly from the gonads of a scleractinian coral, <i>Euphyllia ancora</i> : molecular mechanisms underlying scleractinian gametogenesis. <i>BMC Genomics</i> , 2020, 21, 732.	1.2	14
2159	Low-temperature effects on docosahexaenoic acid biosynthesis in <i>Schizochytrium</i> sp. TIO01 and its proposed underlying mechanism. <i>Biotechnology for Biofuels</i> , 2020, 13, 172.	6.2	25
2160	Resolution of polycistronic RNA by SL2<i>trans</i>-splicing is a widely conserved nematode trait. <i>Rna</i> , 2020, 26, 1891-1904.	1.6	3
2161	Long-Read Genome Sequencing and Assembly of <i>Leptopilina bouvardi</i>: A Specialist <i>Drosophila</i> Parasitoid. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1485-1494.	0.8	3
2162	Genome Sequence of the Banana Aphid, <i>Pentalonia nigronervosa</i> Coquerel (Hemiptera: Aphididae) and Its Symbionts. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 4315-4321.	0.8	18
2163	Genomic and Transcriptomic Analyses of Bioluminescence Genes in the Enope Squid <i>Watasenia scintillans</i> . <i>Marine Biotechnology</i> , 2020, 22, 760-771.	1.1	3
2164	De novo Genome Assembly, Annotation, and SNP Identification of an Endangered Rockcress, <i>Boechera fecunda</i> . <i>Frontiers in Ecology and Evolution</i> , 2020, 8, .	1.1	3

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2166	An improved draft genome sequence of hybrid <i>Populus alba</i> – <i>Populus glandulosa</i> . <i>Journal of Forestry Research</i> , 2021, 32, 1663-1672.	1.7	15
2167	Genome sequencing, assembly, and annotation of the self-flocculating microalga <i>Scenedesmus obliquus</i> AS-6-11. <i>BMC Genomics</i> , 2020, 21, 743.	1.2	15
2168	Most Cephalaspidea have a shell, but transcriptomes can provide them with a backbone (Gastropoda: <i>Tj ETQq1 1 0.784314 ggBT / Overl</i>)	1.2	15
2169	Genome biology of the paleotetraploid perennial biomass crop <i>Miscanthus</i> . <i>Nature Communications</i> , 2020, 11, 5442.	5.8	67
2170	Contrasting signatures of genomic divergence during sympatric speciation. <i>Nature</i> , 2020, 588, 106-111.	13.7	115
2171	African Arowana Genome Provides Insights on Ancient Teleost Evolution. <i>IScience</i> , 2020, 23, 101662.	1.9	3
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2173	Genomics and Proteomics Analyses Revealed Novel Candidate Pesticidal Proteins in a Lepidopteran-Toxic <i>Bacillus thuringiensis</i> Strain. <i>Toxins</i> , 2020, 12, 673.	1.5	7
2174	Draft genome of <i>Bugula neritina</i> , a colonial animal packing powerful symbionts and potential medicines. <i>Scientific Data</i> , 2020, 7, 356.	2.4	6
2175	Raw transcriptomics data to gene specific SSRs: a validated free bioinformatics workflow for biologists. <i>Scientific Reports</i> , 2020, 10, 18236.	1.6	8
2176	Molecular insights into the powerful mucus-based adhesion of limpets (<i>Patella vulgata</i> L.). <i>Open Biology</i> , 2020, 10, 200019.	1.5	23
2177	Genetic diversity, demographic history and neo-sex chromosomes in the Critically Endangered Raso lark. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20192613.	1.2	23
2178	Genome structure and content of the rice root-knot nematode (<i>Meloidogyne graminicola</i>). <i>Ecology and Evolution</i> , 2020, 10, 11006-11021.	0.8	27
2179	Insights into oleaginous phenotype of the yeast <i>Papiliotrema laurentii</i> . <i>Fungal Genetics and Biology</i> , 2020, 144, 103456.	0.9	5
2180	Transcriptomic changes across vitellogenesis in the black tiger prawn (<i>Penaeus monodon</i>), neuropeptides and G protein-coupled receptors repertoire curation. <i>General and Comparative Endocrinology</i> , 2020, 298, 113585.	0.8	15
2181	Formation and diversification of a paradigm biosynthetic gene cluster in plants. <i>Nature Communications</i> , 2020, 11, 5354.	5.8	50
2182	Draft Genome Sequences of Four <i>Aspergillus</i> Section <i>Fumigati</i> Clinical Strains. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	4

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2183	Draft Genome Sequence of Glycoside Hydrolase-Producing <i>Trichoderma asperellum</i> Strain IC-1. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	3
2184	Fruit Development in <i>Ficus carica</i> L.: Morphological and Genetic Approaches to Fig Buds for an Evolution From Monoecy Toward Dioecy. <i>Frontiers in Plant Science</i> , 2020, 11, 1208.	1.7	15
2185	The yellow mealworm (<i>Tenebrio molitor</i>) genome: a resource for the emerging insects as food and feed industry. <i>Journal of Insects As Food and Feed</i> , 2020, 6, 445-455.	2.1	18
2186	Genetic Adaptations of an Island Pit-Viper to a Unique Sedentary Life with Extreme Seasonal Food Availability. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1639-1646.	0.8	3
2187	Domestication modulates the expression of genes involved in neurogenesis in high-quality eggs of <i>Sander lucioperca</i> . <i>Molecular Reproduction and Development</i> , 2020, 87, 934-951.	1.0	10
2188	Nucleotide diversity of functionally different groups of immune response genes in Old World camels based on newly annotated and reference-guided assemblies. <i>BMC Genomics</i> , 2020, 21, 606.	1.2	15
2189	Genome-wide patterns of divergence and introgression after secondary contact between <i>Pungitius</i> sticklebacks. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190548.	1.8	32
2190	Genome Sequencing of <i>Musa acuminata</i> Dwarf Cavendish Reveals a Duplication of a Large Segment of Chromosome 2. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 37-42.	0.8	10
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2204	Long-read only assembly of <i>Drechmeria coniospora</i> genomes reveals widespread chromosome plasticity and illustrates the limitations of current nanopore methods. <i>GigaScience</i> , 2020, 9, .	3.3	11
2205	Transcriptome of the Southern Muriqui <i>Brachyteles arachnoides</i> (Primates:Platyrrhini), a Critically Endangered New World Monkey: Evidence of Adaptive Evolution. <i>Frontiers in Genetics</i> , 2020, 11, 831.	1.1	1
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2216	Regional sequence expansion or collapse in heterozygous genome assemblies. <i>PLoS Computational Biology</i> , 2020, 16, e1008104.	1.5	31
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2218	Comparative transcriptional analysis revealed genes related to short winter-dormancy regulation in <i>Camellia sinensis</i> . <i>Plant Growth Regulation</i> , 2020, 92, 401-415.	1.8	8

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2220	Wireworm (Coleoptera: Elateridae) genomic analysis reveals putative cryptic species, population structure, and adaptation to pest control. <i>Communications Biology</i> , 2020, 3, 489.	2.0	21
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2225	Chromosome Genome Assembly of the Leopard Coral Grouper (<i>Plectropomus leopardus</i>) With Nanopore and Hi-C Sequencing Data. <i>Frontiers in Genetics</i> , 2020, 11, 876.	1.1	9
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2238	TGS-GapCloser: A fast and accurate gap closer for large genomes with low coverage of error-prone long reads. <i>GigaScience</i> , 2020, 9, .	3.3	156
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2242	Signaling pathways in the coral polyp bail-out response. <i>Coral Reefs</i> , 2020, 39, 1535-1548.	0.9	15
2243	The chromosome-level draft genome of <i>Dalbergia odorifera</i> . <i>GigaScience</i> , 2020, 9, .	3.3	21
2244	Hybrid transcriptome sequencing approach improved assembly and gene annotation in <i>Cynara cardunculus</i> (L.). <i>BMC Genomics</i> , 2020, 21, 317.	1.2	18
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2246	A haplotype-resolved, <i>de novo</i> genome assembly for the wood tiger moth (<i>Arctia</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	3.3	20
2247	Genome sequencing and population genomics modeling provide insights into the local adaptation of weeping forsythia. <i>Horticulture Research</i> , 2020, 7, 130.	2.9	33
2248	De novo transcriptome assembly, functional annotation, and expression profiling of rye (<i>Secale</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	1.6	16
2249	Complete Genome Assembly of a Multidrug-Resistant New Delhi Metallo- β -Lactamase 1 (NDM-1)-Producing <i>Escherichia coli</i> Human Isolate from a New Zealand Hospital. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
2250	Genomic and transcriptomic insights into <i>Raffaella lauricola</i> pathogenesis. <i>BMC Genomics</i> , 2020, 21, 570.	1.2	6
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2254	Molecular insights into the mechanisms of susceptibility of <i>Labeo rohita</i> against oomycete <i>Aphanomyces invadans</i> . <i>Scientific Reports</i> , 2020, 10, 19531.	1.6	11

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2259	Metabolic Contributions of an Alphaproteobacterial Endosymbiont in the Apicomplexan <i>Cardiosporidium cionae</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 580719.	1.5	8
2260	Genomics Reveals Widespread Ecological Speciation in Flightless Insects. <i>Systematic Biology</i> , 2021, 70, 863-876.	2.7	18
2261	Complete Genome Sequences of Two Strains of <i>Francisella tularensis</i> subsp. <i>holarctica</i> bv. <i>japonica</i> . <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
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2268	Differential Gene Expression Analysis of Wheat Breeding Lines Reveal Molecular Insights in Yellow Rust Resistance under Field Conditions. <i>Agronomy</i> , 2020, 10, 1888.	1.3	8
2269	Pick Your Poison: Molecular Evolution of Venom Proteins in Asilidae (Insecta: Diptera). <i>Toxins</i> , 2020, 12, 738.	1.5	2
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2272	Full-length transcriptome of anadromous <i>Coilia nasus</i> using single molecule real-time (SMRT) sequencing. <i>Aquaculture and Fisheries</i> , 2022, 7, 420-426.	1.2	3

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2276	Chromosome-level draft genome of a diploid plum (<i>Prunus salicina</i>). <i>GigaScience</i> , 2020, 9, .	3.3	39
2277	Moose genomes reveal past glacial demography and the origin of modern lineages. <i>BMC Genomics</i> , 2020, 21, 854.	1.2	23
2278	First De Novo Transcriptome of the Copepod <i>Rhincalanus gigas</i> from Antarctic Waters. <i>Biology</i> , 2020, 9, 410.	1.3	6
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2281	Genomic differences between the new <i>Fusarium oxysporum</i> f. sp. <i>apii</i> (Foa) race 4 on celery, the less virulent Foa races 2 and 3, and the avirulent on celery f. sp. <i>coriandrii</i> . <i>BMC Genomics</i> , 2020, 21, 730.	1.2	12
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2284	Comparative Genomic Analysis of <i>Dactylonectria torresensis</i> Strains from Grapevine, Soil and Weed Highlights Potential Mechanisms in Pathogenicity and Endophytic Lifestyle. <i>Journal of Fungi (Basel)</i> , 2020, 6, 1014.	1.0	1
2285	Integration analysis of PacBio SMRT- and Illumina RNA-seq reveals candidate genes and pathway involved in selenium metabolism in hyperaccumulator <i>Cardamine violifolia</i> . <i>BMC Plant Biology</i> , 2020, 20, 492.	1.6	25
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2287	Yeast communities associated with cacti in Brazil and the description of <i>Kluyveromyces starmeri</i> sp. nov. based on phylogenomic analyses. <i>Yeast</i> , 2020, 37, 625-637.	0.8	6
2288	Gene Sequences of Potential Targets of Insecticidal PF2 Lectin Identified from the Larval De Novo Transcriptome of the Mexican Bean Weevil (<i>Zabrotes subfasciatus</i> ; Boheman 1833). <i>Insects</i> , 2020, 11, 736.	1.0	3
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2292	Genome Sequence of <i>Oenococcus oeni</i> OE37, an Autochthonous Strain Isolated from an Italian White Wine. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	2
2293	A phylogenomic study of Steganinae fruit flies (Diptera: Drosophilidae): strong gene tree heterogeneity and evidence for monophyly. <i>BMC Evolutionary Biology</i> , 2020, 20, 141.	3.2	4
2294	Complete Genome Sequence of <i>Bacillus</i> sp. Strain KH172YL63, Isolated from Deep-Sea Sediment. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
2295	Genome Sequence of <i>Vibrio cholerae</i> Strain RFB16, Isolated from North Park Lake in Allegheny County, Pennsylvania. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	6
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2297	Nanopore sequencing and the Shasta toolkit enable efficient de novo assembly of eleven human genomes. <i>Nature Biotechnology</i> , 2020, 38, 1044-1053.	9.4	344
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2299	Genome Sequence Resources of <i>Colletotrichum truncatum</i> , <i>C. plurivorum</i> , <i>C. musicola</i> , and <i>C. sojae</i> : Four Species Pathogenic to Soybean (<i>Glycine max</i>). <i>Phytopathology</i> , 2020, 110, 1497-1499.	1.1	12
2300	Draft Genome Sequence of the Globally Distributed Cockroach-Infecting Fungus <i>Herpomyces periplanetae</i> Strain D. Haelew. 1187d. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
2301	Draft Genome Sequence of the Strawberry Anthracnose Pathogen <i>Colletotrichum fructicola</i> . <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	4
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2303	A high-quality reference genome of wild <i>Cannabis sativa</i> . <i>Horticulture Research</i> , 2020, 7, 73.	2.9	73
2304	Genomes of the Venus Flytrap and Close Relatives Unveil the Roots of Plant Carnivory. <i>Current Biology</i> , 2020, 30, 2312-2320.e5.	1.8	60
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2307	Transcriptomes shed light on transgenerational and developmental effects of ocean warming on embryos of the sea urchin <i>Strongylocentrotus intermedius</i> . <i>Scientific Reports</i> , 2020, 10, 7931.	1.6	13
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2310	The draft genome sequence of an upland wild rice species, <i>Oryza granulata</i> . <i>Scientific Data</i> , 2020, 7, 131.	2.4	21
2311	The genome of Mekong tiger perch (<i>Datnioides undecimradiatus</i>) provides insights into the phylogenetic position of Lobotiformes and biological conservation. <i>Scientific Reports</i> , 2020, 10, 8164.	1.6	3
2312	The Evolution of Human Cancer Gene Duplications across Mammals. <i>Molecular Biology and Evolution</i> , 2020, 37, 2875-2886.	3.5	31
2313	Linked-read sequencing enables haplotype-resolved resequencing at population scale. <i>Molecular Ecology Resources</i> , 2020, 20, 1311-1322.	2.2	18
2314	Improved Genome Assembly and Annotation of the Soybean Aphid (<i>Aphis glycines</i> Matsumura). <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 899-906.	0.8	22
2315	A Highly Contiguous Genome for the Golden-Fronted Woodpecker (<i>Melanerpes aurifrons</i>) via Hybrid Oxford Nanopore and Short Read Assembly. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1829-1836.	0.8	9
2316	Multimics-based characterization of specialized metabolites biosynthesis in <i>Cornus Officinalis</i> . <i>DNA Research</i> , 2020, 27, .	1.5	8
2317	The Genome of <i>Peronospora belbahrii</i> Reveals High Heterozygosity, a Low Number of Canonical Effectors, and TC-Rich Promoters. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 742-753.	1.4	15
2318	Chromosome-level assembly of the horseshoe crab genome provides insights into its genome evolution. <i>Nature Communications</i> , 2020, 11, 2322.	5.8	57
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2320	Genome Sequence Data of the Soybean Pathogen <i>Stagonosporopsis vannaccii</i> : A Resource for Studies on Didymellaceae Evolution. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 1022-1024.	1.4	1
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2322	A de novo chromosome-level genome assembly of <i>Coregonus</i> sp. <i>Balchen</i> : One representative of the Swiss Alpine whitefish radiation. <i>Molecular Ecology Resources</i> , 2020, 20, 1093-1109.	2.2	29
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2326	Transcriptome profiling of spike provides expression features of genes related to terpene biosynthesis in lavender. <i>Scientific Reports</i> , 2020, 10, 6933.	1.6	9

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2331	Active Notch signaling is required for arm regeneration in a brittle star. <i>PLoS ONE</i> , 2020, 15, e0232981.	1.1	16
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2342	Natural hybridization reveals incompatible alleles that cause melanoma in swordtail fish. <i>Science</i> , 2020, 368, 731-736.	6.0	86
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2437	Genomic Signature of Shifts in Selection in a Subalpine Ant and Its Physiological Adaptations. <i>Molecular Biology and Evolution</i> , 2020, 37, 2211-2227.	3.5	14
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2453	Whole Genome Analysis Revealed the Genes Responsible for Citreoviridin Biosynthesis in <i>Penicillium citreonigrum</i> . <i>Toxins</i> , 2020, 12, 125.	1.5	2
2454	Chromosome-level genome assembly and annotation of the loquat (<i>Eriobotrya japonica</i>) genome. <i>GigaScience</i> , 2020, 9, .	3.3	43
2455	The genome of the harpacticoid copepod <i>Tigriopus japonicus</i> : Potential for its use in marine molecular ecotoxicology. <i>Aquatic Toxicology</i> , 2020, 222, 105462.	1.9	27
2456	A well-resolved transcriptomic phylogeny of the mite harvestman family Pettalidae (Arachnida). <i>Tj ETQq1 1 0.784314 rgBT /Overlock</i> 2020, 47, 1345-1361.	1.4	20
2457	Assembly and analysis of the whole genome of <i>Arthroderma uncinatum</i> strain T10, compared with <i>Microsporium canis</i> and <i>Trichophyton rubrum</i> . <i>Mycoses</i> , 2020, 63, 683-693.	1.8	6
2458	Isopod holobionts as promising models for lignocellulose degradation. <i>Biotechnology for Biofuels</i> , 2020, 13, 49.	6.2	23
2459	A Partially Phase-Separated Genome Sequence Assembly of the <i>Vitis</i> Rootstock 'Bârner'™ (<i>Vitis riparia</i> L.) <i>Tj ETQq0 0 0 rgBT /Overlock</i> Science, 2020, 11, 156.	1.7	6
2460	Improved hybrid <i>de novo</i> genome assembly and annotation of African wild rice, <i>Oryza longistaminata</i> , from Illumina and PacBio sequencing reads. <i>Plant Genome</i> , 2020, 13, e20001.	1.6	15
2461	First draft genome for the sand-hopper <i>Trinorchestia longiramus</i> . <i>Scientific Data</i> , 2020, 7, 85.	2.4	8
2462	Phylogenetic relationship between Australian <i>Fusarium oxysporum</i> isolates and resolving the species complex using the multispecies coalescent model. <i>BMC Genomics</i> , 2020, 21, 248.	1.2	25
2463	Chromosome-level analysis of the <i>Crassostrea hongkongensis</i> genome reveals extensive duplication of immune-related genes in bivalves. <i>Molecular Ecology Resources</i> , 2020, 20, 980-994.	2.2	45
2464	Genome Sequence of the Chestnut Blight Fungus <i>Cryphonectria parasitica</i> EP155: A Fundamental Resource for an Archetypical Invasive Plant Pathogen. <i>Phytopathology</i> , 2020, 110, 1180-1188.	1.1	34
2465	Inferring Tunicate Relationships and the Evolution of the Tunicate Hox Cluster with the Genome of <i>Corella inflata</i> . <i>Genome Biology and Evolution</i> , 2020, 12, 948-964.	1.1	12
2466	Draft Genome Resource for the Ex-types of <i>Phytophthora ramorum</i> , <i>P. kernoviae</i> , and <i>P. melonis</i> , Species of Regulatory Concern, Using Ultra-Long Read MinION Nanopore Sequencing. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 794-797.	1.4	8
2467	Pleiotropy facilitates local adaptation to distant optima in common ragweed (<i>Ambrosia</i>) <i>Tj ETQq0 0 0 rgBT /Overlock_10 Tf 50_182 Td (a</i>	1.5	30
2468	Genome sequence of the fungus <i>Pycnoporus sanguineus</i> , which produces cinnabarinic acid and pH- and thermo- stable laccases. <i>Gene</i> , 2020, 742, 144586.	1.0	8
2469	High-quality genome assembly and transcriptome of <i>Ancherythroculter nigrocauda</i> , an endemic Chinese cyprinid species. <i>Molecular Ecology Resources</i> , 2020, 20, 882-891.	2.2	11
2470	Chromosome-level genome assembly of the greenhouse whitefly (<i>Trialeurodes vaporariorum</i>) <i>Tj ETQq1 1 0,784314 rgBT /Overlock</i>	2.2	21

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2472	A Giant Genome for a Giant Crayfish (<i>Cherax quadricarinatus</i>) With Insights Into <i>cox1</i> Pseudogenes in Decapod Genomes. <i>Frontiers in Genetics</i> , 2020, 11, 201.	1.1	23
2473	Transcriptomic Insights into Mechanisms of Early Seed Maturation in the Garden Pea (<i>Pisum sativum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.8	14
2474	Dataset for de novo transcriptome assembly of the African bullfrog <i>Pyxicephalus adspersus</i> . <i>Data in Brief</i> , 2020, 30, 105388.	0.5	2
2475	Genome Sequence and Comparative Analysis of <i>Colletotrichum gloeosporioides</i> Isolated from <i>Liriodendron</i> Leaves. <i>Phytopathology</i> , 2020, 110, 1260-1269.	1.1	13
2476	Gene correlation networks reveal the transcriptomic response to elevated nitrogen in a photosynthetic sponge. <i>Molecular Ecology</i> , 2020, 29, 1452-1462.	2.0	4
2477	A Chromosome-Scale Assembly of the Asian Honeybee <i>Apis cerana</i> Genome. <i>Frontiers in Genetics</i> , 2020, 11, 279.	1.1	13
2478	The chromosome-scale assembly of the willow genome provides insight into Salicaceae genome evolution. <i>Horticulture Research</i> , 2020, 7, 45.	2.9	35
2479	A high-quality genome provides insights into the new taxonomic status and genomic characteristics of <i>Cladopus chinensis</i> (Podostemaceae). <i>Horticulture Research</i> , 2020, 7, 46.	2.9	11
2480	The <i>Litsea</i> genome and the evolution of the laurel family. <i>Nature Communications</i> , 2020, 11, 1675.	5.8	80
2481	Water lily (<i>Nymphaea thermarum</i>) genome reveals variable genomic signatures of ancient vascular cambium losses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 8649-8656.	3.3	33
2482	An improved de novo genome assembly of the common marmoset genome yields improved contiguity and increased mapping rates of sequence data. <i>BMC Genomics</i> , 2020, 21, 243.	1.2	9
2483	Genome-wide characterization of simple sequence repeats in <i>Palmae</i> genomes. <i>Genes and Genomics</i> , 2020, 42, 597-608.	0.5	8
2484	Comparison of transcriptomes from two chemosensory organs in four decapod crustaceans reveals hundreds of candidate chemoreceptor proteins. <i>PLoS ONE</i> , 2020, 15, e0230266.	1.1	38
2485	Chromosomal assembly and analyses of genome-wide recombination rates in the forest pathogenic fungus <i>Armillaria ostoyae</i> . <i>Heredity</i> , 2020, 124, 699-713.	1.2	17
2486	Horizontal transfer and evolution of transposable elements in vertebrates. <i>Nature Communications</i> , 2020, 11, 1362.	5.8	58
2487	<i>Anthoceros</i> genomes illuminate the origin of land plants and the unique biology of hornworts. <i>Nature Plants</i> , 2020, 6, 259-272.	4.7	225
2488	Genome assembly of six polyploid potato genomes. <i>Scientific Data</i> , 2020, 7, 88.	2.4	30

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2490	Light organ photosensitivity in deep-sea shrimp may suggest a novel role in counterillumination. <i>Scientific Reports</i> , 2020, 10, 4485.	1.6	14
2491	What Is in <i>Umbilicaria pustulata</i> ? A Metagenomic Approach to Reconstruct the Holo-Genome of a Lichen. <i>Genome Biology and Evolution</i> , 2020, 12, 309-324.	1.1	37
2492	Multiple Genetic Trajectories to Extreme Abiotic Stress Adaptation in Arctic Brassicaceae. <i>Molecular Biology and Evolution</i> , 2020, 37, 2052-2068.	3.5	28
2493	Survival in the Tropics despite isolation, inbreeding and asexual reproduction: insights from the genome of the world's southernmost poplar (<i>Populus ilicifolia</i>). <i>Plant Journal</i> , 2020, 103, 430-442.	2.8	23
2494	Phylogeny of teleost connexins reveals highly inconsistent intra- and interspecies use of nomenclature and misassemblies in recent teleost chromosome assemblies. <i>BMC Genomics</i> , 2020, 21, 223.	1.2	8
2495	GenomeQC: a quality assessment tool for genome assemblies and gene structure annotations. <i>BMC Genomics</i> , 2020, 21, 193.	1.2	52
2496	New genome assemblies reveal patterns of domestication and adaptation across <i>Brettanomyces</i> (Dekkera) species. <i>BMC Genomics</i> , 2020, 21, 194.	1.2	21
2497	The draft nuclear genome sequence and predicted mitochondrial proteome of <i>Andalucia godoyi</i> , a protist with the most gene-rich and bacteria-like mitochondrial genome. <i>BMC Biology</i> , 2020, 18, 22.	1.7	43
2498	Evolution of metabolic capabilities and molecular features of diplomonads, kinetoplastids, and euglenids. <i>BMC Biology</i> , 2020, 18, 23.	1.7	48
2499	Benchmarking hybrid assemblies of <i>Giardia</i> and prediction of widespread intra-isolate structural variation. <i>Parasites and Vectors</i> , 2020, 13, 108.	1.0	8
2500	Animal, Fungi, and Plant Genome Sequences Harbor Different Non-Canonical Splice Sites. <i>Cells</i> , 2020, 9, 458.	1.8	28
2501	Genome survey and development of polymorphic microsatellite loci for <i>Sillago sihama</i> based on Illumina sequencing technology. <i>Molecular Biology Reports</i> , 2020, 47, 3011-3017.	1.0	13
2502	Comparative and population genomics approaches reveal the basis of adaptation to deserts in a small rodent. <i>Molecular Ecology</i> , 2020, 29, 1300-1314.	2.0	39
2503	First Genome of the Brown Alga <i>Undaria pinnatifida</i> : Chromosome-Level Assembly Using PacBio and Hi-C Technologies. <i>Frontiers in Genetics</i> , 2020, 11, 140.	1.1	39
2504	Molecular mechanisms underlying milk production and viviparity in the cockroach, <i>Diploptera punctata</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2020, 120, 103333.	1.2	7
2505	A comprehensive non-redundant reference transcriptome for the Atlantic silverside <i>Menidia menidia</i> . <i>Marine Genomics</i> , 2020, 53, 100738.	0.4	6
2506	Draft genome assemblies using sequencing reads from Oxford Nanopore Technology and Illumina platforms for four species of North American <i>Fundulus</i> killifish. <i>GigaScience</i> , 2020, 9, .	3.3	15

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2508	Characterisation of the <i>Pseudomonas savastanoi</i> pv. <i>phaseolicola</i> population found in Eastern Australia associated with halo blight disease in <i>Vigna radiata</i> . <i>Australasian Plant Pathology</i> , 2020, 49, 515-524.	0.5	3
2509	Benchmarking of long-read correction methods. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa037.	1.5	75
2510	Chromosome-level genome assembly of the East Asian common octopus (<i>Octopus sinensis</i>) using PacBio sequencing and Hi-C technology. <i>Molecular Ecology Resources</i> , 2020, 20, 1572-1582.	2.2	28
2511	Interactive Gene Expression Patterns of Susceptible and Resistant <i>Lens ervoides</i> Recombinant Inbred Lines and the Necrotroph <i>Ascochyta lentis</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 1259.	1.5	1
2512	Draft Genome Sequence of the Astaxanthin-Producing Microalga <i>Haematococcus lacustris</i> Strain NIES-144. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	7
2513	What Is Metagenomics Teaching Us, and What Is Missed?. <i>Annual Review of Microbiology</i> , 2020, 74, 117-135.	2.9	54
2514	An efficient single-cell transcriptomics workflow for microbial eukaryotes benchmarked on <i>Giardia intestinalis</i> cells. <i>BMC Genomics</i> , 2020, 21, 448.	1.2	8
2515	Measuring Genome Sizes Using Read-Depth, k-mers, and Flow Cytometry: Methodological Comparisons in Beetles (Coleoptera). <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3047-3060.	0.8	78
2516	Degradative Capacity of Two Strains of <i>Rhodonia placenta</i> : From Phenotype to Genotype. <i>Frontiers in Microbiology</i> , 2020, 11, 1338.	1.5	9
2517	Adaptation to Extreme Antarctic Environments Revealed by the Genome of a Sea Ice Green Alga. <i>Current Biology</i> , 2020, 30, 3330-3341.e7.	1.8	48
2518	The Genomes of the Allohexaploid <i>Echinochloa crus-galli</i> and Its Progenitors Provide Insights into Polyploidization-Driven Adaptation. <i>Molecular Plant</i> , 2020, 13, 1298-1310.	3.9	47
2519	Fulvic acid increases forage legume growth inducing preferential up-regulation of nodulation and signalling-related genes. <i>Journal of Experimental Botany</i> , 2020, 71, 5689-5704.	2.4	19
2520	The Importance of Genomics for Deciphering the Invasion Success of the Seagrass <i>Halophila stipulacea</i> in the Changing Mediterranean Sea. <i>Diversity</i> , 2020, 12, 263.	0.7	6
2521	A chromosome-scale reference genome of <i>Aquilegia oxysepala</i> var. <i>kansuensis</i> . <i>Horticulture Research</i> , 2020, 7, 113.	2.9	20
2522	Genetic structure and insecticide resistance characteristics of fall armyworm populations invading China. <i>Molecular Ecology Resources</i> , 2020, 20, 1682-1696.	2.2	116
2523	Whole-genome, transcriptome, and methylome analyses provide insights into the evolution of platycoside biosynthesis in <i>Platycodon grandiflorus</i> , a medicinal plant. <i>Horticulture Research</i> , 2020, 7, 112.	2.9	38
2524	Toward a more holistic method of genome assembly assessment. <i>BMC Bioinformatics</i> , 2020, 21, 249.	1.2	20

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2526	Genome comparisons suggest an association between <i>Ceratocystis</i> host adaptations and effector clusters in unique transposable element families. <i>Fungal Genetics and Biology</i> , 2020, 143, 103433.	0.9	9
2527	Discovery and population genomics of structural variation in a songbird genus. <i>Nature Communications</i> , 2020, 11, 3403.	5.8	83
2528	Mandarin fish (<i>Siniperca</i>) genomes provide insights into innate predatory feeding. <i>Communications Biology</i> , 2020, 3, 361.	2.0	33
2529	Molecular adaptation and convergent evolution of frugivory in Old World and neotropical fruit bats. <i>Molecular Ecology</i> , 2020, 29, 4366-4381.	2.0	32
2530	Metagenomic dataset on lichen <i>Dirinaria</i> sp. from the Great Rann of Kutch and tropical moist deciduous Dang forest of Gujarat. <i>Data in Brief</i> , 2020, 30, 105504.	0.5	1
2531	Complete Genome Sequence of <i>Phytobacter diazotrophicus</i> Strain UAEU22, a Plant Growth-Promoting Bacterium Isolated from the Date Palm Rhizosphere. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	4
2532	Population genomics of <i>Vibrionaceae</i> isolated from an endangered oasis reveals local adaptation after an environmental perturbation. <i>BMC Genomics</i> , 2020, 21, 418.	1.2	6
2533	The genome, transcriptome, and proteome of the fish parasite <i>Pomphorhynchus laevis</i> (<i>Acanthocephala</i>). <i>PLoS ONE</i> , 2020, 15, e0232973.	1.1	19
2534	Interspecific Gene Flow and the Evolution of Specialization in Black and White Rhinoceros. <i>Molecular Biology and Evolution</i> , 2020, 37, 3105-3117.	3.5	20
2535	Genotyping-Guided Discovery of Persiamycin A From Sponge-Associated Halophilic <i>Streptomonospora</i> sp. PA3. <i>Frontiers in Microbiology</i> , 2020, 11, 1237.	1.5	15
2536	CCPRD: A Novel Analytical Framework for the Comprehensive Proteomic Reference Database Construction of NonModel Organisms. <i>ACS Omega</i> , 2020, 5, 15370-15384.	1.6	7
2537	Chromosome-level genome assembly of Tarim red deer, <i>Cervus elaphus yarkandensis</i> . <i>Scientific Data</i> , 2020, 7, 187.	2.4	10
2538	Chromosome-Scale Genome Assembly of <i>Fusarium oxysporum</i> Strain Fo47, a Fungal Endophyte and Biocontrol Agent. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 1108-1111.	1.4	29
2539	Evolutionary History of the <i>Marchantia polymorpha</i> Complex. <i>Frontiers in Plant Science</i> , 2020, 11, 829.	1.7	15
2540	A genome-wide survey of copy number variations reveals an asymmetric evolution of duplicated genes in rice. <i>BMC Biology</i> , 2020, 18, 73.	1.7	7
2541	De Novo Genome Assemblies for Three North American Bumble Bee Species: <i>Bombus bifarius</i> , <i>Bombus vancouverensis</i> , and <i>Bombus vosnesenskii</i> . <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2585-2592.	0.8	18
2542	Near-chromosome level genome assembly of the fruit pest <i>Drosophila suzukii</i> using long-read sequencing. <i>Scientific Reports</i> , 2020, 10, 11227.	1.6	42

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2544	Complete genome sequence and epigenetic profile of <i>Bacillus velezensis</i> UCMB5140 used for plant and crop protection in comparison with other plant-associated <i>Bacillus</i> strains. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 7643-7656.	1.7	10
2545	Comprehensive temporal reprogramming ensures dynamicity of transcriptomic profile for adaptive response in <i>Taxus contorta</i> . <i>Molecular Genetics and Genomics</i> , 2020, 295, 1401-1414.	1.0	8
2546	Cartilaginous fishes offer unique insights into the evolution of the nuclear receptor gene repertoire in gnathostomes. <i>General and Comparative Endocrinology</i> , 2020, 295, 113527.	0.8	22
2547	Metabolic Reconfiguration in <i>C.Âlegans</i> Suggests a Pathway for Widespread Sterol Auxotrophy in the Animal Kingdom. <i>Current Biology</i> , 2020, 30, 3031-3038.e7.	1.8	20
2548	A novel cyanobacterial geosmin producer, revising GeoA distribution and dispersion patterns in Bacteria. <i>Scientific Reports</i> , 2020, 10, 8679.	1.6	17
2549	Complete Genome Sequence of <i>Bifidobacterium longum</i> Strain Jih1, Isolated from Human Feces. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
2550	Draft Genome Sequences of Three Isolates of <i>Golubevia</i> sp. Basidiomycete Fungi Isolated from Powdery Mildew Pustules. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	2
2551	Comparison of spleen transcriptomes of two wild rodent species reveals differences in the immune response against <i>Borrelia afzelii</i> . <i>Ecology and Evolution</i> , 2020, 10, 6421-6434.	0.8	5
2552	Identification and functional study of oleoresin terpenoid biosynthesis-related genes in masson pine (<i>Pinus massoniana</i> L.) based on transcriptome analysis. <i>Tree Genetics and Genomes</i> , 2020, 16, 1.	0.6	13
2553	Pathogenic Allodiploid Hybrids of <i>Aspergillus</i> Fungi. <i>Current Biology</i> , 2020, 30, 2495-2507.e7.	1.8	39
2554	New genomic resources for three exploited Mediterranean fishes. <i>Genomics</i> , 2020, 112, 4297-4303.	1.3	8
2555	Signatures of adaptation to a monocot host in the plantâ€parasitic cyst nematode <i>Heterodera sacchari</i> . <i>Plant Journal</i> , 2020, 103, 1263-1274.	2.8	9
2556	Genome-scale data reveal the role of hybridization in lichen-forming fungi. <i>Scientific Reports</i> , 2020, 10, 1497.	1.6	26
2557	Nanopore sequencing-based genome assembly and evolutionary genomics of circum-basmati rice. <i>Genome Biology</i> , 2020, 21, 21.	3.8	73
2558	High-Quality Genome Assembly of <i>Eriocheir japonica sinensis</i> Reveals Its Unique Genome Evolution. <i>Frontiers in Genetics</i> , 2019, 10, 1340.	1.1	32
2559	The Genome Assembly and Annotation of the Southern Elephant Seal <i>Mirounga leonina</i> . <i>Genes</i> , 2020, 11, 160.	1.0	3
2560	Complete transcriptome assembly and annotation of a critically important amphipod species in freshwater ecotoxicological risk assessment: <i>Gammarus fossarum</i> . <i>Environment International</i> , 2020, 137, 105319.	4.8	8

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2561	Improved genome assembly provides new insights into genome evolution in a desert poplar (<i>Populus euphratica</i>). <i>Molecular Ecology Resources</i> , 2020, 20, 781-794.	2.2	45
2562	Comparative transcriptome profiling provides insights into plant salt tolerance in seashore paspalum (<i>Paspalum vaginatum</i>). <i>BMC Genomics</i> , 2020, 21, 131.	1.2	26
2563	Analysis of Alternative Splicing and Alternative Polyadenylation in <i>Populus alba</i> var. <i>pyramidalis</i> by Single-Molecular Long-Read Sequencing. <i>Frontiers in Genetics</i> , 2020, 11, 48.	1.1	19
2564	De Novo Transcriptomic Resources in the Brain of <i>Vespa velutina</i> for Invasion Control. <i>Insects</i> , 2020, 11, 101.	1.0	2
2565	The hornwort genome and early land plant evolution. <i>Nature Plants</i> , 2020, 6, 107-118.	4.7	203
2566	Characterization of Growth Morphology and Pathology, and Draft Genome Sequencing of <i>Botrytis fabae</i> , the Causal Organism of Chocolate Spot of Faba Bean (<i>Vicia faba</i> L.). <i>Frontiers in Microbiology</i> , 2020, 11, 217.	1.5	9
2567	Insights on the genetic repertoire of the coral <i>Mussismilia braziliensis</i> endosymbiont Symbiodinium. <i>Symbiosis</i> , 2020, 80, 183-193.	1.2	7
2568	Transcriptome analyses reveal the synergistic effects of feeding and eyestalk ablation on ovarian maturation in black tiger shrimp. <i>Scientific Reports</i> , 2020, 10, 3239.	1.6	16
2569	Streamlining universal single-copy orthologue and ultraconserved element design: A case study in <i>Collembola</i> . <i>Molecular Ecology Resources</i> , 2020, 20, 706-717.	2.2	10
2570	De novo transcriptome assembly and sex-biased gene expression in the gonads of Amur catfish (<i>Silurus</i>) Tj ETQq1 1.0.784314.rgBT / Qve 1.3 17	1.3	17
2571	Chromosomal-level assembly of <i>Juglans sigillata</i> genome using Nanopore, BioNano, and Hi-C analysis. <i>GigaScience</i> , 2020, 9, .	3.3	33
2572	Draft Genome Resource for <i>Macrophomina phaseolina</i> Associated With Charcoal Rot in Sorghum. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 724-726.	1.4	11
2573	A comparative genomics study of 23 <i>Aspergillus</i> species from section Flavi. <i>Nature Communications</i> , 2020, 11, 1106.	5.8	125
2574	The sequence and de novo assembly of the wild yak genome. <i>Scientific Data</i> , 2020, 7, 66.	2.4	16
2575	Genomic consequences of population decline in critically endangered pangolins and their demographic histories. <i>National Science Review</i> , 2020, 7, 798-814.	4.6	45
2576	Whole genome sequencing and comparative genomic analysis of oleaginous red yeast <i>Sporobolomyces pararoseus</i> NGR identifies candidate genes for biotechnological potential and ballistospores-shooting. <i>BMC Genomics</i> , 2020, 21, 181.	1.2	9
2577	Whole-chromosome hitchhiking driven by a male-killing endosymbiont. <i>PLoS Biology</i> , 2020, 18, e3000610.	2.6	44
2578	Transcriptomic characterisation of neuropeptides and their putative cognate G protein-coupled receptors during late embryo and stage-1 juvenile development of the Aotearoa-New Zealand crayfish, <i>Paranephrops zealandicus</i> . <i>General and Comparative Endocrinology</i> , 2020, 292, 113443.	0.8	7

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2579	New genome assembly of the barn owl (<i>Tyto alba alba</i>). Ecology and Evolution, 2020, 10, 2284-2298.	0.8	11
2580	Specialized bacteriome uncovered in the coralloid roots of the epiphytic gymnosperm, <i>Zamia pseudoparasitica</i> . Environmental DNA, 2020, 2, 418-428.	3.1	22
2581	Using genetic markers to identify the origin of illegally traded agarwood-producing <i>Aquilaria sinensis</i> trees. Global Ecology and Conservation, 2020, 22, e00958.	1.0	5
2582	Soybean aphid biotype 1 genome: Insights into the invasive biology and adaptive evolution of a major agricultural pest. Insect Biochemistry and Molecular Biology, 2020, 120, 103334.	1.2	15
2583	An ancestral signalling pathway is conserved in intracellular symbioses-forming plant lineages. Nature Plants, 2020, 6, 280-289.	4.7	150
2584	Genome sequence of the agarwood tree <i>Aquilaria sinensis</i> (Lour.) Spreng: the first chromosome-level draft genome in the Thymelaeaceae family. GigaScience, 2020, 9, .	3.3	34
2585	Genome Resource for Two <i>Stemphylium vesicarium</i> Isolates Causing Stemphylium Leaf Blight of Onion in New York. Molecular Plant-Microbe Interactions, 2020, 33, 562-564.	1.4	8
2586	Thirty complete <i>Streptomyces</i> genome sequences for mining novel secondary metabolite biosynthetic gene clusters. Scientific Data, 2020, 7, 55.	2.4	67
2587	The draft genome of mandrill (<i>Mandrillus sphinx</i>): An Old World monkey. Scientific Reports, 2020, 10, 2431.	1.6	3
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2779	An Unbiased Molecular Approach Using 3â€²-UTRs Resolves the Avian Family-Level Tree of Life. <i>Molecular Biology and Evolution</i> , 2021, 38, 108-127.	3.5	99
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2791	Chromosome-level genome assembly of <i>Paralithodes platypus</i> provides insights into evolution and adaptation of king crabs. <i>Molecular Ecology Resources</i> , 2021, 21, 511-525.	2.2	14
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2794	Genome Resources for Seven Fungal Isolates That Cause Dollar Spot Disease in Turfgrass, Including <i>Clariireedia jacksonii</i> and <i>C. monteithiana</i> . <i>Plant Disease</i> , 2021, 105, 691-694.	0.7	6

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2796	The celery genome sequence reveals sequential paleopolyploidizations, karyotype evolution and resistance gene reduction in apiaceae. <i>Plant Biotechnology Journal</i> , 2021, 19, 731-744.	4.1	62
2797	Genome Resource for Peanut Web Blotch Causal Agent <i>Peyronellaea arachidicola</i> Strain YY187. <i>Plant Disease</i> , 2021, 105, 1177-1178.	0.7	10
2798	A chromosome-level genome assembly of rice leaffolder, <i>Cnaphalocrocis medinalis</i> . <i>Molecular Ecology Resources</i> , 2021, 21, 561-572.	2.2	15
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2807	Expression profiles of neotropical termites reveal microbiota-associated, caste-biased genes and biotechnological targets. <i>Insect Molecular Biology</i> , 2021, 30, 152-164.	1.0	1
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2815	Genome Sequence Resource of <i>Bacillus velezensis</i> EB14, a Native Endophytic Bacterial Strain with Biocontrol Potential Against the Poplar Stem Canker Causative Pathogen, <i>Sphaerulina musiva</i> . <i>Phytopathology</i> , 2021, 111, 890-892.	1.1	2
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2825	Conservative route to genome compaction in a miniature annelid. <i>Nature Ecology and Evolution</i> , 2021, 5, 231-242.	3.4	51
2826	A potential endogenous gibberellin-mediated signaling cascade regulated floral transition in <i>Magnolia soulangeana</i> 'Changchun'. <i>Molecular Genetics and Genomics</i> , 2021, 296, 207-222.	1.0	9
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2828	Draft Genome Sequence Resource of the Citrus Stem-End Rot Fungal Pathogen <i>Lasiodiplodia theobromae</i> CITRA15. <i>Phytopathology</i> , 2021, 111, 761-764.	1.1	9
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2830	Limits to the cellular control of sequestered cryptophyte prey in the marine ciliate <i>Mesodinium rubrum</i> . <i>ISME Journal</i> , 2021, 15, 1056-1072.	4.4	15
2831	Chromosome-level genome assembly of the aphid parasitoid <i>Aphidius gifuensis</i> using Oxford Nanopore sequencing and Hi-C technology. <i>Molecular Ecology Resources</i> , 2021, 21, 941-954.	2.2	10

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2851	Desert truffle genomes reveal their reproductive modes and new insights into plant–fungal interaction and ectendomycorrhizal lifestyle. <i>New Phytologist</i> , 2021, 229, 2917-2932.	3.5	19
2852	A chromosome-level genome assembly provides insights into ascorbic acid accumulation and fruit softening in guava (<i>Psidium guajava</i>). <i>Plant Biotechnology Journal</i> , 2021, 19, 717-730.	4.1	52
2853	Identifying conserved polychaete molecular markers of metal exposure: Comparative analyses using the <i>Alitta virens</i> (Annelida, Lophotrochozoa) transcriptome. <i>Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology</i> , 2021, 240, 108913.	1.3	3
2854	Chromosome-level genome of the peach fruit moth <i>Carposina sasakii</i> (Lepidoptera: Carposinidae) provides a resource for evolutionary studies on moths. <i>Molecular Ecology Resources</i> , 2021, 21, 834-848.	2.2	25
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2856	Phylogenomic inference of the interrelationships of Lake Baikal sponges. <i>Systematics and Biodiversity</i> , 2021, 19, 209-217.	0.5	4
2857	Canonical correlations reveal adaptive loci and phenotypic responses to climate in perennial ryegrass. <i>Molecular Ecology Resources</i> , 2021, 21, 849-870.	2.2	20
2858	Expression dynamics of dehydration tolerance in the tropical plant <i>Marchantia inflexa</i> . <i>Plant Journal</i> , 2021, 105, 209-222.	2.8	8
2859	Putative Effector Genes Distinguish Two Pathogenicity Groups of <i>Fusarium oxysporum</i> f. sp. <i>spinaciae</i> . <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 141-156.	1.4	14
2860	Life and Death of Selfish Genes: Comparative Genomics Reveals the Dynamic Evolution of Cytoplasmic Incompatibility. <i>Molecular Biology and Evolution</i> , 2021, 38, 2-15.	3.5	72
2861	Eighteen Coral Genomes Reveal the Evolutionary Origin of <i>Acropora</i> Strategies to Accommodate Environmental Changes. <i>Molecular Biology and Evolution</i> , 2021, 38, 16-30.	3.5	75
2862	Genome Resources of Four Distinct Pathogenic Races Within <i>Fusarium oxysporum</i> f. sp. <i>vasinfectum</i> that Cause Vascular Wilt Disease of Cotton. <i>Phytopathology</i> , 2021, 111, 593-596.	1.1	7
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2864	The genome of <i>Cleistogenes songorica</i> provides a blueprint for functional dissection of dimorphic flower differentiation and drought adaptability. <i>Plant Biotechnology Journal</i> , 2021, 19, 532-547.	4.1	21
2865	The chromosome-level reference genome assembly for <i>Panax notoginseng</i> and insights into ginsenoside biosynthesis. <i>Plant Communications</i> , 2021, 2, 100113.	3.6	54
2866	Genomic Sequence Resource of <i>Alternaria alternata</i> Strain B3 Causing Leaf Blight on <i>Ophiopogon japonicus</i> . <i>Plant Disease</i> , 2021, 105, 684-687.	0.7	7
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2869	Chromosome-level de novo genome assembly of <i>Sarcophaga peregrina</i> provides insights into the evolutionary adaptation of flesh flies. <i>Molecular Ecology Resources</i> , 2021, 21, 251-262.	2.2	16
2870	Suppression of wheat blast resistance by an effector of <i>Pyricularia oryzae</i> is counteracted by a host specificity resistance gene in wheat. <i>New Phytologist</i> , 2021, 229, 488-500.	3.5	13
2871	Next Generation Sequencing: Transcriptomics. , 2021, , 1-11.		0
2872	Detection of genes positively selected in Cuban Anolis lizards that naturally inhabit hot and open areas and currently thrive in urban areas. <i>Ecology and Evolution</i> , 2021, 11, 1719-1728.	0.8	7
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2878	Identifying a melanogenesis-related candidate gene by a high-quality genome assembly and population diversity analysis in <i>Hypsizygus marmoreus</i> . <i>Journal of Genetics and Genomics</i> , 2021, 48, 75-87.	1.7	14
2879	Genomes reveal selective sweeps in kiang and donkey for high-altitude adaptation. <i>Zoological Research</i> , 2021, 42, 450-460.	0.9	9
2880	Sequencing, Assembly, and Annotation of the Alfalfa Genome. <i>Compendium of Plant Genomes</i> , 2021, , 87-109.	0.3	0
2881	The assembled and annotated genome of the pigeon louse <i>Columbicola columbae</i> , a model ectoparasite. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	18
2882	The utility of <i>Escherichia coli</i> as a contamination indicator for rural drinking water: Evidence from whole genome sequencing. <i>PLoS ONE</i> , 2021, 16, e0245910.	1.1	28
2883	De novo genome assembly of the potent medicinal plant <i>Rehmannia glutinosa</i> using nanopore technology. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 3954-3963.	1.9	26
2884	The Tiger Rattlesnake genome reveals a complex genotype underlying a simple venom phenotype. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	43
2885	Patterns of genetic variation in a prairie wildflower, <i>Silphium integrifolium</i> , suggest a non-prairie origin and locally adaptive variation. <i>American Journal of Botany</i> , 2021, 108, 145-158.	0.8	9
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2898	Genome-wide signatures of mammalian skin covering evolution. <i>Science China Life Sciences</i> , 2021, 64, 1765-1780.	2.3	5
2900	Know your enemy – transcriptome of myxozoan <i>Tetracapsuloides bryosalmonae</i> reveals potential drug targets against proliferative kidney disease in salmonids. <i>Parasitology</i> , 2021, 148, 726-739.	0.7	9
2901	The Chromosome-Scale Genome Resource for Two Endophytic <i>Fusarium</i> species, <i>F. culmorum</i> and <i>F. pseudograminearum</i> . <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 703-706.	1.4	5
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2903	Ethanol production process driving changes on industrial strains. <i>FEMS Yeast Research</i> , 2021, 21, .	1.1	10
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2907	Draft Genome Sequence of NYR20, a Red Pigment-Secreting Mutant of <i>Saccharomyces cerevisiae</i> . <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	0
2908	Draft Genome Sequence of the Phosphate-Solubilizing Rhizobacterium <i>Burkholderia pseudomultivorans</i> Strain MPSB1, Isolated from a Copper Mined-Out Site. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	0
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2925	Draft genome sequences of three filamentous cyanobacteria isolated from brackish habitats. <i>Journal of Genomics</i> , 2021, 9, 20-25.	0.6	3
2926	A Chromosome-Scale Quinoa Reference Genome Assembly. <i>Compendium of Plant Genomes</i> , 2021, , 65-80.	0.3	0
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2930	Draft Genome Sequence of <i>Pseudomonas saudiphocaensis</i> Strain AGROB56, Isolated from a Dairy Farm in New Zealand. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	1

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2934	Chromosome-scale genome assembly of brown-spotted flathead <i>Platycephalus</i> sp.1 provides insights into demersal adaptation in flathead fish. <i>Zoological Research</i> , 2021, 42, 660-665.	0.9	2
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2942	The complete genome sequence of <i>Hafnia alvei</i> A23BA; a potential antibiotic-producing rhizobacterium. <i>BMC Research Notes</i> , 2021, 14, 8.	0.6	3
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2944	Chemoreceptor Diversity in Apoid Wasps and Its Reduction during the Evolution of the Pollen-Collecting Lifestyle of Bees (Hymenoptera: Apoidea). <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	11
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2974	The "Tommy Atkins" mango genome reveals candidate genes for fruit quality. <i>BMC Plant Biology</i> , 2021, 21, 108.	1.6	28
2975	Metabolic Potential, Ecology and Presence of Associated Bacteria Is Reflected in Genomic Diversity of Mucromycotina. <i>Frontiers in Microbiology</i> , 2021, 12, 636986.	1.5	11
2977	The <i>Mastigamoeba balamuthi</i> Genome and the Nature of the Free-Living Ancestor of <i>Entamoeba</i> . <i>Molecular Biology and Evolution</i> , 2021, 38, 2240-2259.	3.5	14
2978	Genome Assembly of the Canadian two-row Malting Barley cultivar AAC Synergy. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	6
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2984	Evolutionary dynamics of transposable elements in bdelloid rotifers. <i>ELife</i> , 2021, 10, .	2.8	26
2985	Gene family amplification facilitates adaptation in freshwater unionid bivalve <i>Megaloniais nervosa</i> . <i>Molecular Ecology</i> , 2021, 30, 1155-1173.	2.0	19
2986	A chromosome-level genome assembly for the tertiary relict plant <i>Tetracentron sinense</i> oliv. (trochodendraceae). <i>Molecular Ecology Resources</i> , 2021, 21, 1186-1199.	2.2	12
2987	Genome assembly and population genomic analysis provide insights into the evolution of modern sweet corn. <i>Nature Communications</i> , 2021, 12, 1227.	5.8	37
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2992	A Chromosome-Level Genome Assembly of the Dark Sleeper <i>Odontobutis potamophila</i> . <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	7
2993	Analyses of transcriptomes and the first complete genome of <i>Leucocalocybe mongolica</i> provide new insights into phylogenetic relationships and conservation. <i>Scientific Reports</i> , 2021, 11, 2930.	1.6	7
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2999	<i>Helicobacter pylori</i> type 4 secretion systems as gastroduodenal disease markers. <i>Scientific Reports</i> , 2021, 11, 4584.	1.6	9
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3007	Near-Chromosome-Level Genome Assembly of the Dark Septate Endophyte <i>Laburnicola rhizohalophila</i> : A Model for Investigating Root-Fungus Symbiosis. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	6
3008	A highly contiguous reference genome assembly for <i>Colletotrichum falcatum</i> pathotype Cf08 causing red rot disease in sugarcane. <i>3 Biotech</i> , 2021, 11, 148.	1.1	0
3009	Comparative genomics of <i>Flavobacterium columnare</i> unveils novel insights in virulence and antimicrobial resistance mechanisms. <i>Veterinary Research</i> , 2021, 52, 18.	1.1	5
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3011	The genome of <i>Tripterygium wilfordii</i> and characterization of the celastrol biosynthesis pathway. <i>GigaByte</i> , 0, 2021, 1-32.	0.0	3
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3014	Insight of transcriptional regulators reveals the tolerance mechanism of carpet-grass (<i>Axonopus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 11	1.6	5
3016	De Novo Whole-Genome Assembly of the Swede Midge (<i>Contarinia nasturtii</i>), a Specialist of Brassicaceae, Using Linked-Read Sequencing. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	6
3017	Comparative analysis of <i>Phytophthora</i> genomes reveals oomycete pathogenesis in crops. <i>Heliyon</i> , 2021, 7, e06317.	1.4	3
3018	Evolution of genome structure in the <i>Drosophila simulans</i> species complex. <i>Genome Research</i> , 2021, 31, 380-396.	2.4	55
3019	Genome sequences of <i>Tropheus moorii</i> and <i>Petrochromis trewavasae</i> , two eco-morphologically divergent cichlid fishes endemic to Lake Tanganyika. <i>Scientific Reports</i> , 2021, 11, 4309.	1.6	4
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3021	Genome sequence and evolution of <i>Betula platyphylla</i> . <i>Horticulture Research</i> , 2021, 8, 37.	2.9	53
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3032	Protein Complexes Form a Basis for Complex Hybrid Incompatibility. <i>Frontiers in Genetics</i> , 2021, 12, 609766.	1.1	13
3033	Accurate haplotype-resolved assembly reveals the origin of structural variants for human trios. <i>Bioinformatics</i> , 2021, 37, 2095-2102.	1.8	4

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3034	A draft phased assembly of the diploid Cascade hop (<i>Humulus lupulus</i>) genome. <i>Plant Genome</i> , 2021, 14, e20072.	1.6	25
3035	A new <i>Cannabis</i> genome assembly associates elevated cannabidiol (CBD) with hemp introgressed into marijuana. <i>New Phytologist</i> , 2021, 230, 1665-1679.	3.5	87
3036	Recent Evolutionary History of Tigers Highlights Contrasting Roles of Genetic Drift and Selection. <i>Molecular Biology and Evolution</i> , 2021, 38, 2366-2379.	3.5	35
3037	A chromosome-level assembly of the harlequin ladybird <i>Harmonia axyridis</i> as a genomic resource to study beetle and invasion biology. <i>Molecular Ecology Resources</i> , 2021, 21, 1318-1332.	2.2	17
3039	De novo assembly and characterization of the first draft genome of quince (<i>Cydonia oblonga</i> Mill.). <i>Scientific Reports</i> , 2021, 11, 3818.	1.6	10
3040	Digital RNA-seq transcriptome plus tissue anatomy analyses reveal the developmental mechanism of the calabash-shaped root in <i>Tetrastigma hemsleyanum</i> . <i>Tree Physiology</i> , 2021, 41, 1729-1748.	1.4	5
3041	<i>Streptomyces</i> sp. M54: an actinobacteria associated with a neotropical social wasp with high potential for antibiotic production. <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 379-398.	0.7	9
3043	Characterization of a pericentric inversion in plateau fence lizards (<i>Sceloporus tristichus</i>): evidence from chromosome-scale genomes. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	8
3044	Genomic Resource Development for <i>Hydrangea</i> (<i>Hydrangea macrophylla</i> (Thunb.) Ser.)'A Transcriptome Assembly and a High-Density Genetic Linkage Map. <i>Horticulturae</i> , 2021, 7, 25.	1.2	6
3045	Complete Genome Sequence of <i>Sphingomonas paucimobilis</i> Strain Kira, Isolated from Human Neuroblastoma SH-SY5Y Cell Cultures Supplemented with Retinoic Acid. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	2
3047	Integrated Full-Length Transcriptome and RNA-Seq to Identify Immune System Genes from the Skin of Sperm Whale (<i>Physeter macrocephalus</i>). <i>Genes</i> , 2021, 12, 233.	1.0	4
3049	Draft Genome Sequence of <i>Halomonas</i> sp. Strain KAO, a Halophilic Mn(II)-Oxidizing Bacterium. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	2
3051	The Genome of Banana Leaf Blight Pathogen <i>Fusarium sacchari</i> str. FS66 Harbors Widespread Gene Transfer From <i>Fusarium oxysporum</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 629859.	1.7	5
3052	Reference-based QUantification Of gene Dispensability (QUOD). <i>Plant Methods</i> , 2021, 17, 18.	1.9	3
3053	<i>Novakomyces olei</i> sp. nov., the First Member of a Novel Taphrinomycotina Lineage. <i>Microorganisms</i> , 2021, 9, 301.	1.6	3
3055	Genome sequencing and annotation and phylogenomic analysis of the medicinal mushroom <i>Amauroderma rugosum</i> , a traditional medicinal species in the family Ganodermataceae. <i>Mycologia</i> , 2021, 113, 268-277.	0.8	7
3057	Genome Sequence of <i>Fusarium oxysporum</i> f. sp. <i>conglutinans</i> , the Etiological Agent of Cabbage Fusarium Wilt. <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 210-213.	1.4	5
3058	Sociality sculpts similar patterns of molecular evolution in two independently evolved lineages of eusocial bees. <i>Communications Biology</i> , 2021, 4, 253.	2.0	20

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3060	Determinants of genome-wide distribution and evolution of uORFs in eukaryotes. <i>Nature Communications</i> , 2021, 12, 1076.	5.8	37
3061	Chromosome-Level Genome Assembly of the American Cranberry (<i>Vaccinium macrocarpon</i> Ait.) and Its Wild Relative <i>Vaccinium microcarpum</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 633310.	1.7	29
3062	Genomic and functional analyses of fungal and bacterial consortia that enable lignocellulose breakdown in goat gut microbiomes. <i>Nature Microbiology</i> , 2021, 6, 499-511.	5.9	116
3063	Taxonomic Sampling and Rare Genomic Changes Overcome Long-Branch Attraction in the Phylogenetic Placement of Pseudoscorpions. <i>Molecular Biology and Evolution</i> , 2021, 38, 2446-2467.	3.5	53
3064	Draft Genome Sequence of <i>Streptococcus agalactiae</i> TA B490, a Multidrug-Resistant Strain Isolated from Bovine Mastitis in Argentina. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	3
3065	Complete Genome Sequence of <i>Klebsiella pneumoniae</i> Strain ATCC 43816. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	11
3066	Population Genomic Analysis of <i>Listeria monocytogenes</i> From Food Reveals Substrate-Specific Genome Variation. <i>Frontiers in Microbiology</i> , 2021, 12, 620033.	1.5	6
3067	A large genome with chromosome-scale assembly sheds light on the evolutionary success of a true toad (<i>Bufo gargarizans</i>). <i>Molecular Ecology Resources</i> , 2021, 21, 1256-1273.	2.2	32
3068	Pharaoh Cuttlefish, <i>Sepia pharaonis</i> , Genome Reveals Unique Reflectin Camouflage Gene Set. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	10
3069	Function of the pseudo phosphotransfer proteins has diverged between rice and <i>Arabidopsis</i> . <i>Plant Journal</i> , 2021, 106, 159-173.	2.8	7
3070	Sublethal Exposure Effects of the Neonicotinoid Clothianidin Strongly Modify the Brain Transcriptome and Proteome in the Male Moth <i>Agrotis ipsilon</i> . <i>Insects</i> , 2021, 12, 152.	1.0	4
3071	<i>Trichoderma reesei</i> Rad51 tolerates mismatches in hybrid meiosis with diverse genome sequences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	8
3072	A de novo Transcriptome Assembly of the European Flounder (<i>Platichthys flesus</i>): The Preselection of Transcripts Encoding Active Forms of Enzymes. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	5
3073	A taxonomic revision of the genus <i>Phrynoglossus</i> in Indochina with the description of a new species and comments on the classification within <i>Occidozyginae</i> (Amphibia, Anura, <i>Dicroglossidae</i>). <i>Vertebrate Zoology</i> , 0, 71, 1-26.	2.0	8
3074	Insights into triterpene synthesis and unsaturated fatty-acid accumulation provided by chromosomal-level genome analysis of <i>Akebia trifoliata</i> subsp. <i>australis</i> . <i>Horticulture Research</i> , 2021, 8, 33.	2.9	23
3075	Topologically associating domains and their role in the evolution of genome structure and function in <i>Drosophila</i> . <i>Genome Research</i> , 2021, 31, 397-410.	2.4	36
3076	Genetics of nodulation in <i>Aeschynomene evenia</i> uncovers mechanisms of the rhizobium-legume symbiosis. <i>Nature Communications</i> , 2021, 12, 829.	5.8	38

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3078	Bacteria and Metabolic Potential in Karst Caves Revealed by Intensive Bacterial Cultivation and Genome Assembly. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	12
3079	New alignment-based sequence extraction software (ALiBaSeq) and its utility for deep level phylogenetics. <i>PeerJ</i> , 2021, 9, e11019.	0.9	12
3081	A high-quality genome assembly highlights rye genomic characteristics and agronomically important genes. <i>Nature Genetics</i> , 2021, 53, 574-584.	9.4	164
3082	Secretomic insight into the biomass hydrolysis potential of the phytopathogenic fungus <i>Chrysoporthe cubensis</i> . <i>Journal of Proteomics</i> , 2021, 236, 104121.	1.2	8
3083	Characterization of multidrug-resistant <i>Acinetobacter baumannii</i> strain ATCC BAA1605 using whole-genome sequencing. <i>BMC Research Notes</i> , 2021, 14, 83.	0.6	8
3084	Antennal Transcriptome Analysis and Identification of Candidate Chemosensory Genes of the Harlequin Ladybird Beetle, <i>Harmonia axyridis</i> (Pallas) (Coleoptera: Coccinellidae). <i>Insects</i> , 2021, 12, 209.	1.0	12
3085	The first genomic resources for <i>Phymatotrichopsis omnivora</i> , a soil-borne peizizomycete pathogen with a broad host range. <i>Phytopathology</i> , 2021, , PHYTO01210014A.	1.1	3
3086	Improving the quality of barley transcriptome <i>de novo</i> assembling by using a hybrid approach for lines with varying spike and stem coloration. <i>Vavilovskii Zhurnal Genetiki I Seleksii</i> , 2021, 25, 30-38.	0.4	1
3087	A study of the heterochronic sense/antisense RNA representation in florets of sexual and apomictic <i>Paspalum notatum</i> . <i>BMC Genomics</i> , 2021, 22, 185.	1.2	6
3088	Deciphering the transcriptomic regulation of heat stress responses in <i>Nothofagus pumilio</i> . <i>PLoS ONE</i> , 2021, 16, e0246615.	1.1	6
3089	The completed genome sequence of the pathogenic ascomycete fungus <i>Penicillium digitatum</i> . <i>Genomics</i> , 2021, 113, 439-446.	1.3	10
3090	A coffee berry borer (<i>Hypothenemus hampei</i>) genome assembly reveals a reduced chemosensory receptor gene repertoire and male-specific genome sequences. <i>Scientific Reports</i> , 2021, 11, 4900.	1.6	8
3091	Transcriptional Changes in Potato Sprouts upon Interaction with <i>Rhizoctonia solani</i> Indicate Pathogen-Induced Interference in the Defence Pathways of Potato. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3094.	1.8	14
3092	Long-read sequencing and <i>de novo</i> genome assemblies reveal complex chromosome end structures caused by telomere dysfunction at the single nucleotide level. <i>Nucleic Acids Research</i> , 2021, 49, 3338-3353.	6.5	12
3093	Telomere-to-telomere assembly of the genome of an individual <i>Oikopleura dioica</i> from Okinawa using Nanopore-based sequencing. <i>BMC Genomics</i> , 2021, 22, 222.	1.2	18
3094	De novo transcriptome reveals blood coagulation/antithrombin factors and infection mechanisms in <i>Angiostrongylus cantonensis</i> adult worms. <i>Parasitology</i> , 2021, 148, 857-870.	0.7	0
3095	Multi-omics reveal the pathways involved in induced defensive colony formation of <i>Tetradesmus obliquus</i> in response to <i>Daphnia</i> grazing cues. <i>Limnology and Oceanography</i> , 2021, 66, 1819-1831.	1.6	11

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3097	Transcriptome profiling of <i>Lymnaea stagnalis</i> (Gastropoda) for ecoimmunological research. <i>BMC Genomics</i> , 2021, 22, 144.	1.2	22
3098	Inferring the Genetic Basis of Sex Determination from the Genome of a Dioecious Nightshade. <i>Molecular Biology and Evolution</i> , 2021, 38, 2946-2957.	3.5	2
3099	Chromosomal-Level Genome Assembly of the Painted Sea Urchin <i>Lytechinus pictus</i> : A Genetically Enabled Model System for Cell Biology and Embryonic Development. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	15
3100	A De Novo Transcriptome Assembly of <i>Ceratopteris richardii</i> Provides Insights into the Evolutionary Dynamics of Complex Gene Families in Land Plants. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	34
3102	Genome sequence and genetic diversity analysis of an under-domesticated orphan crop, white fonio (<i>Digitaria exilis</i>). <i>GigaScience</i> , 2021, 10, .	3.3	23
3103	A chromosome-level assembly of the black tiger shrimp (<i>Penaeus monodon</i>) genome facilitates the identification of growth-associated genes. <i>Molecular Ecology Resources</i> , 2021, 21, 1620-1640.	2.2	43
3104	A towering genome: Experimentally validated adaptations to high blood pressure and extreme stature in the giraffe. <i>Science Advances</i> , 2021, 7, .	4.7	31
3105	Assessing genome assembly quality prior to downstream analysis: N50 versus BUSCO. <i>Molecular Ecology Resources</i> , 2021, 21, 1416-1421.	2.2	28
3106	Genomic insights into the host specific adaptation of the <i>Pneumocystis</i> genus. <i>Communications Biology</i> , 2021, 4, 305.	2.0	23
3107	<i>Datura</i> genome reveals duplications of psychoactive alkaloid biosynthetic genes and high mutation rate following tissue culture. <i>BMC Genomics</i> , 2021, 22, 201.	1.2	8
3108	Genomic analysis of <i>Medicago ruthenica</i> provides insights into its tolerance to abiotic stress and demographic history. <i>Molecular Ecology Resources</i> , 2021, 21, 1641-1657.	2.2	17
3110	Most Genomic Loci Misrepresent the Phylogeny of an Avian Radiation Because of Ancient Gene Flow. <i>Systematic Biology</i> , 2021, 70, 961-975.	2.7	45
3111	A Revised and Improved Version of the Northern Wheatear (<i>Oenanthe oenanthe</i>) Transcriptome. <i>Diversity</i> , 2021, 13, 151.	0.7	5
3113	Transcriptomic Responses of Four Pelagophytes to Nutrient (N, P) and Light Stress. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	3
3114	A new symbiotic lineage related to <i>Neisseria</i> and <i>Snodgrassella</i> arises from the dynamic and diverse microbiomes in sucking lice. <i>Molecular Ecology</i> , 2021, 30, 2178-2196.	2.0	16
3117	Molecular mechanisms of local adaptation for salt tolerance in a treefrog. <i>Molecular Ecology</i> , 2021, 30, 2065-2086.	2.0	18
3119	RNA-seq analysis and gene expression dynamics in the salivary glands of the argasid tick <i>Ornithodoros erraticus</i> along the trophogonic cycle. <i>Parasites and Vectors</i> , 2021, 14, 170.	1.0	14

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3122	Primary Metabolism co-Opted for Defensive Chemical Production in the Carabid Beetle, <i>Harpalus pensylvanicus</i> . <i>Journal of Chemical Ecology</i> , 2021, 47, 334-349.	0.9	0
3123	Genomics and transcriptomics of the green mussel explain the durability of its byssus. <i>Scientific Reports</i> , 2021, 11, 5992.	1.6	14
3124	Deeply Altered Genome Architecture in the Endoparasitic Flowering Plant <i>Sapria himalayana</i> Griff. (<i>Rafflesiaceae</i>). <i>Current Biology</i> , 2021, 31, 1002-1011.e9.	1.8	63
3125	A chromosome-level genome assembly for the Pacific oyster <i>Crassostrea gigas</i> . <i>GigaScience</i> , 2021, 10, .	3.3	88
3126	Complete genome sequence of <i>Escherichia coli</i> K_EC180, a bacterium producing shiga-like toxin isolated from swine feces. <i>Journal of Animal Science and Technology</i> , 2021, 63, 461-464.	0.8	1
3127	Genomic region associated with pod color variation in pea (<i>Pisum sativum</i>). <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	9
3128	The Crown Pearl: a draft genome assembly of the European freshwater pearl mussel <i>Margaritifera margaritifera</i> (Linnaeus, 1758). <i>DNA Research</i> , 2021, 28, .	1.5	15
3129	Comparative transcriptome analysis of the newly discovered insect vector of the pine wood nematode in China, revealing putative genes related to host plant adaptation. <i>BMC Genomics</i> , 2021, 22, 189.	1.2	14
3131	Chromosome-scale assembly of the genome of <i>Salix dunnii</i> reveals a male heterogametic sex determination system on chromosome 7. <i>Molecular Ecology Resources</i> , 2021, 21, 1966-1982.	2.2	28
3132	A Survey of Transposon Landscapes in the Putative Ancient Asexual Ostracod <i>Darwinula stevensoni</i> . <i>Genes</i> , 2021, 12, 401.	1.0	4
3133	A Hybrid Genome Assembly Resource for <i>Podospheera xanthii</i> , the Main Causal Agent of Powdery Mildew Disease in Cucurbits. <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 319-324.	1.4	14
3134	Chromosome-length genome assembly and structural variations of the primal Basenji dog (<i>Canis lupus</i>). <i>Overlock</i> 10	1.2	22
3135	High-Resolution Transcriptome Atlas and Improved Genome Assembly of Common Buckwheat, <i>Fagopyrum esculentum</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 612382.	1.7	17
3136	A single QTL with large effect is associated with female functional virginity in an asexual parasitoid wasp. <i>Molecular Ecology</i> , 2021, 30, 1979-1992.	2.0	9
3137	Comparing de novo transcriptome assembly tools in di- and autotetraploid non-model plant species. <i>BMC Bioinformatics</i> , 2021, 22, 146.	1.2	14
3138	Genomes of 12 fig wasps provide insights into the adaptation of pollinators to fig syconia. <i>Journal of Genetics and Genomics</i> , 2021, 48, 225-236.	1.7	6
3139	Full length sequencing reveals novel transcripts of detoxification genes along with related alternative splicing events and lncRNAs in <i>Phyllotreta striolata</i> . <i>PLoS ONE</i> , 2021, 16, e0248749.	1.1	5

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3142	Complex evolutionary history of two ecologically significant grass genera, <i>Themeda</i> and <i>Heteropogon</i> (Poaceae: Panicoideae: Andropogoneae). Botanical Journal of the Linnean Society, 2021, 196, 437-455.	0.8	10
3143	gapseq: informed prediction of bacterial metabolic pathways and reconstruction of accurate metabolic models. Genome Biology, 2021, 22, 81.	3.8	103
3144	A multi-omic characterization of temperature stress in a halotolerant <i>Scenedesmus</i> strain for algal biotechnology. Communications Biology, 2021, 4, 333.	2.0	22
3145	Chromosome-level genome of <i>Poropuntius huangchuchieni</i> provides a diploid progenitor-like reference genome for the allotetraploid <i>Cyprinus carpio</i> . Molecular Ecology Resources, 2021, 21, 1658-1669.	2.2	13
3146	Stretch-activated ion channels identified in the touch-sensitive structures of carnivorous Droseraceae plants. ELife, 2021, 10, .	2.8	43
3147	Genome Assembly : A Review. , 2021, , .		1
3148	A chromosome level genome assembly of <i>Propiloscerus akamusi</i> to understand its response to heavy metal exposure. Molecular Ecology Resources, 2021, 21, 1996-2012.	2.2	11
3149	De novo transcriptome assemblies of <i>Epicauta tibialis</i> provide insights into the sexual dimorphism in the production of cantharidin. Archives of Insect Biochemistry and Physiology, 2021, 106, e21784.	0.6	3
3150	Full-Length Transcriptome Sequencing and Comparative Transcriptome Analysis to Evaluate Drought and Salt Stress in <i>Iris lactea</i> var. <i>chinensis</i> . Genes, 2021, 12, 434.	1.0	14
3155	Engineered yeast genomes accurately assembled from pure and mixed samples. Nature Communications, 2021, 12, 1485.	5.8	11
3156	A Tale of Two Transcriptomic Responses in Agricultural Pests via Host Defenses and Viral Replication. International Journal of Molecular Sciences, 2021, 22, 3568.	1.8	8
3157	Shifts in morphology, gene expression, and selection underlie web loss in Hawaiian Tetragnatha spiders. BMC Ecology and Evolution, 2021, 21, 48.	0.7	6
3158	Rapid selection response to ethanol in <i>Saccharomyces eubayanus</i> emulates the domestication process under brewing conditions. Microbial Biotechnology, 2022, 15, 967-984.	2.0	9
3159	The community-curated <i>Pristionchus pacificus</i> genome facilitates automated gene annotation improvement in related nematodes. BMC Genomics, 2021, 22, 216.	1.2	11
3160	A first insight into the genome of <i>Prototheca wickerhamii</i> , a major causative agent of human protothecosis. BMC Genomics, 2021, 22, 168.	1.2	9
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3162	Characterization of Pre-mRNA Splicing and Spliceosomal Machinery in <i>Porphyridium purpureum</i> and Evolutionary Implications for Red Algae. <i>Journal of Eukaryotic Microbiology</i> , 2021, 68, e12844.	0.8	5
3163	Biosynthesis of the Sex Pheromone Component (E,Z)-7,9-Dodecadienyl Acetate in the European Grapevine Moth, <i>Lobesia botrana</i> , Involving Δ^{11} Desaturation and an Elusive Δ^7 Desaturase. <i>Journal of Chemical Ecology</i> , 2021, 47, 248-264.	0.9	8
3164	Accurate and sensitive detection of microbial eukaryotes from whole metagenome shotgun sequencing. <i>Microbiome</i> , 2021, 9, 58.	4.9	60
3166	Limited Evidence for Parallel Evolution Among Desert-Adapted <i>Peromyscus</i> Deer Mice. <i>Journal of Heredity</i> , 2021, 112, 286-302.	1.0	14
3167	Tracing the genetic footprints of vertebrate landing in non-teleost ray-finned fishes. <i>Cell</i> , 2021, 184, 1377-1391.e14.	13.5	66
3168	Signal, bias, and the role of transcriptome assembly quality in phylogenomic inference. <i>Bmc Ecology and Evolution</i> , 2021, 21, 43.	0.7	8
3169	Comparative genome analyses suggest a hemibiotrophic lifestyle and virulence differences for the beech bark disease fungal pathogens <i>Neonectria faginata</i> and <i>Neonectria coccinea</i> . <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	2
3170	Comparative Genomics of <i>Xanthomonas euroxanthea</i> and <i>Xanthomonas arboricola</i> pv. <i>juglandis</i> Strains Isolated from a Single Walnut Host Tree. <i>Microorganisms</i> , 2021, 9, 624.	1.6	10
3171	Chromosome-level reference genome of the soursop (<i>Annona muricata</i>): A new resource for Magnoliid research and tropical pomology. <i>Molecular Ecology Resources</i> , 2021, 21, 1608-1619.	2.2	18
3172	The <i>Corylus mandshurica</i> genome provides insights into the evolution of Betulaceae genomes and hazelnut breeding. <i>Horticulture Research</i> , 2021, 8, 54.	2.9	20
3173	Transcriptome of <i>Aquilaria malaccensis</i> containing agarwood formed naturally and induced artificially. <i>BMC Research Notes</i> , 2021, 14, 117.	0.6	3
3175	Comparative Analysis of Annotation Pipelines Using the First Japanese White-Eye (<i>Zosterops</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 187 T	1.1	3
3176	Chromosome-level genome assemblies of the malaria vectors <i>Anopheles coluzzii</i> and <i>Anopheles arabiensis</i> . <i>GigaScience</i> , 2021, 10, .	3.3	12
3177	Genome Sequence of the Black Yeast-Like Strain <i>Aureobasidium pullulans</i> var. <i>aubasidani</i> CBS 100524. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	3
3178	Genomes of the willow-galling sawflies <i>Euura lappo</i> and <i>Eupontania aestiva</i> (Hymenoptera:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 187 T	0.8	3
3181	Genome Assembly of Salicaceae <i>Populus deltoides</i> (Eastern Cottonwood) Δ^{69} Based on Nanopore Sequencing and Hi-C Technologies. <i>Journal of Heredity</i> , 2021, 112, 303-310.	1.0	13
3182	Chromosome-scale genome assembly of <i>Cucumis hystrix</i> a wild species interspecifically cross-compatible with cultivated cucumber. <i>Horticulture Research</i> , 2021, 8, 40.	2.9	18
3183	A bird-like genome from a frog: Mechanisms of genome size reduction in the ornate burrowing frog, <i>Platyplectrum ornatum</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	26

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3184	Evolution of mammalian longevity: age-related increase in autophagy in bats compared to other mammals. <i>Aging</i> , 2021, 13, 7998-8025.	1.4	16
3185	Transcriptomic analysis provides insights into candidate genes and molecular pathways involved in growth of Manila clam <i>Ruditapes philippinarum</i> . <i>Functional and Integrative Genomics</i> , 2021, 21, 341-353.	1.4	13
3186	Complete Genome Sequences of Three Uropathogenic <i>Klebsiella quasipneumoniae</i> Strains Isolated from Postmenopausal Women with Recurrent Urinary Tract Infection. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	4
3187	Hunting the eagle killer: A cyanobacterial neurotoxin causes vacuolar myelinopathy. <i>Science</i> , 2021, 371, .	6.0	96
3188	Long-read sequence assembly: a technical evaluation in barley. <i>Plant Cell</i> , 2021, 33, 1888-1906.	3.1	180
3189	Phylogenomics of Plant-Associated Botryosphaeriaceae Species. <i>Frontiers in Microbiology</i> , 2021, 12, 652802.	1.5	28
3191	IMA genome - F14. <i>IMA Fungus</i> , 2021, 12, 5.	1.7	5
3192	Probing the <i>Rhipicephalus bursa</i> Sialomes in Potential Anti-Tick Vaccine Candidates: A Reverse Vaccinology Approach. <i>Biomedicines</i> , 2021, 9, 363.	1.4	10
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3199	Nutrient-driven genome evolution revealed by comparative genomics of chryomonad flagellates. <i>Communications Biology</i> , 2021, 4, 328.	2.0	7
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3357	Genomic Resources for the North American Water Vole (<i>Microtus richardsoni</i>) and the Montane Vole (<i>Microtus montanus</i>). <i>GigaByte</i> , 0, 2021, 1-13.	0.0	1
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3370	Conserved noncoding sequences provide insights into regulatory sequence and loss of gene expression in maize. <i>Genome Research</i> , 2021, 31, 1245-1257.	2.4	29

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3372	Mobile genetic elements mediate the mixotrophic evolution of novel <i>Alicyclobacillus</i> species for acid mine drainage adaptation. <i>Environmental Microbiology</i> , 2021, 23, 3896-3912.	1.8	12
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3376	De novo genome assembly and analysis unveil biosynthetic and metabolic potentials of <i>Pseudomonas fragi</i> A13BB. <i>BMC Genomic Data</i> , 2021, 22, 15.	0.7	3
3377	Evolution of the "world's only alpine parrot": Genomic adaptation or phenotypic plasticity, behaviour and ecology?. <i>Molecular Ecology</i> , 2021, 30, 6370-6386.	2.0	11
3378	The Assembled and Annotated Genome of the Fairy-Ring Fungus <i>Marasmius oreades</i> . <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	13
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3387	Species and population specific gene expression in blood transcriptomes of marine turtles. <i>BMC Genomics</i> , 2021, 22, 346.	1.2	9
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3389	Full-length transcriptome sequencing and identification and immune response of TRIM genes in Dabry's sturgeon (<i>Acipenser dabryanus</i>). <i>Aquaculture</i> , 2021, 538, 736599.	1.7	8
3390	Chromosome-scale assembly of the <i>Sparassis latifolia</i> genome obtained using long-read and Hi-C sequencing. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	4
3391	Detection of alternative splicing in western corn rootworm (<i>Diabrotica virgifera</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 107 Td (<sc>RNA-seq and <sc>PacBio Iso-seq). <i>Insect Molecular Biology</i> , 2021, 30, 436-445.	1.0	6
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3406	Genetic basis of high aroma and stress tolerance in the oolong tea cultivar genome. <i>Horticulture Research</i> , 2021, 8, 107.	2.9	80
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3409	Antifungal mechanism of <i>Bacillus amyloliquefaciens</i> strain GKT04 against <i>Fusarium</i> wilt revealed using genomic and transcriptomic analyses. <i>MicrobiologyOpen</i> , 2021, 10, e1192.	1.2	13
3410	Transitions in symbiosis: evidence for environmental acquisition and social transmission within a clade of heritable symbionts. <i>ISME Journal</i> , 2021, 15, 2956-2968.	4.4	26
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3427	Population genomics and phylogeography of the boll weevil, <i>Anthonomus grandis</i> Boheman (Coleoptera: Curculionidae), in the United States, northern Mexico, and Argentina. <i>Evolutionary Applications</i> , 2021, 14, 1778-1793.	1.5	10
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3430	A novel family of secreted insect proteins linked to plant gall development. <i>Current Biology</i> , 2021, 31, 1836-1849.e12.	1.8	37
3431	Polyploidy underlies co-option and diversification of biosynthetic triterpene pathways in the apple tribe. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	37
3433	The genome sequence of the European golden eagle, <i>Aquila chrysaetos chrysaetos</i> Linnaeus 1758. <i>Wellcome Open Research</i> , 2021, 6, 112.	0.9	3
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3441	First draft genome assembly of the desert locust, <i>Schistocerca gregaria</i> . <i>F1000Research</i> , 2020, 9, 775.	0.8	24
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3448	Single-cell transcriptome profiling of buffelgrass (<i>Cenchrus ciliaris</i>) eggs unveils apomictic parthenogenesis signatures. <i>Scientific Reports</i> , 2021, 11, 9880.	1.6	5
3449	The domestication of <i>Cucurbita argyrosperma</i> as revealed by the genome of its wild relative. <i>Horticulture Research</i> , 2021, 8, 109.	2.9	21
3450	Whole genome sequencing of a snailfish from the Yap Trench (~7,000 m) clarifies the molecular mechanisms underlying adaptation to the deep sea. <i>PLoS Genetics</i> , 2021, 17, e1009530.	1.5	26
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3458	Transcriptome analysis unravels RNAi pathways genes and putative expansion of CYP450 gene family in cotton leafhopper <i>Amrasca biguttula</i> (Ishida). <i>Molecular Biology Reports</i> , 2021, 48, 4383-4396.	1.0	3
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3461	Population-scale peach genome analyses unravel selection patterns and biochemical basis underlying fruit flavor. <i>Nature Communications</i> , 2021, 12, 3604.	5.8	31
3463	The chromosome-level reference genome of <i>Coptis chinensis</i> provides insights into genomic evolution and berberine biosynthesis. <i>Horticulture Research</i> , 2021, 8, 121.	2.9	25
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3468	Genomic analysis of <i>Neisseria elongata</i> isolate from a patient with infective endocarditis. <i>FEBS Open Bio</i> , 2021, 11, 1987-1996.	1.0	1
3469	Chromosome-level genome assembly of the blue crab, <i>Callinectes sapidus</i> . <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	10
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3473	Gapless indica rice genome reveals synergistic contributions of active transposable elements and segmental duplications to rice genome evolution. <i>Molecular Plant</i> , 2021, 14, 1745-1756.	3.9	50
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3475	Chromosome-Scale Assembly of the Complete Genome Sequence of <i>Leishmania</i> (<i>Mundinia</i>) Tj ETQq1 1 0.784314 rgBT e0005821.	0.3	5
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3477	To hum or not to hum: Neural transcriptome signature of male courtship vocalization in a teleost fish. <i>Genes, Brain and Behavior</i> , 2021, 20, e12740.	1.1	2
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3479	A Combined Morphological and Molecular Evolutionary Analysis of Karst-Environment Adaptation for the Genus <i>Urophysa</i> (Ranunculaceae). <i>Frontiers in Plant Science</i> , 2021, 12, 667988.	1.7	2
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3481	Toward genomic selection in <i>Pinus taeda</i> : Integrating resources to support array design in a complex conifer genome. <i>Applications in Plant Sciences</i> , 2021, 9, e11439.	0.8	19
3482	The genome sequence of the European water vole, <i>Arvicola amphibius</i> Linnaeus 1758. <i>Wellcome Open Research</i> , 0, 6, 162.	0.9	1
3483	Wolfberry genomes and the evolution of <i>Lycium</i> (Solanaceae). <i>Communications Biology</i> , 2021, 4, 671.	2.0	40

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3485	Chromosomal-scale de novo genome assemblies of <i>Cynomolgus</i> Macaque and Common Marmoset. <i>Scientific Data</i> , 2021, 8, 159.	2.4	9
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3487	Whole genome data from <i>Curtobacterium flaccumfaciens</i> pv. <i>flaccumfaciens</i> strains associated with tan spot of mungbean and soybean reveal diverse plasmid profiles. <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 1216-1222.	1.4	7
3488	A de novo transcriptional atlas in <i>Danaus plexippus</i> reveals variability in dosage compensation across tissues. <i>Communications Biology</i> , 2021, 4, 791.	2.0	9
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3490	Identification of Key Metabolic Pathways and Biomarkers Underlying Flowering Time of Guar (<i>Cyamopsis tetragonoloba</i> (L.) Taub.) via Integrated Transcriptome-Metabolome Analysis. <i>Genes</i> , 2021, 12, 952.	1.0	5
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3493	Long-read RNA sequencing reveals widespread sex-specific alternative splicing in threespine stickleback fish. <i>Genome Research</i> , 2021, 31, 1486-1497.	2.4	23
3494	Transcriptome-Wide Identification and Quantification of Caffeoylquinic Acid Biosynthesis Pathway and Prediction of Its Putative BAHDs Gene Complex in <i>A. spathulifolius</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 6333.	1.8	4
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3499	Response to selection for parasitism of a suboptimal, low-preference host in an aphid parasitoid. <i>Evolutionary Applications</i> , 2021, 14, 2012-2024.	1.5	8
3500	Isolating the Role of Corticosterone in the Hypothalamic-Pituitary-Gonadal Transcriptomic Stress Response. <i>Frontiers in Endocrinology</i> , 2021, 12, 632060.	1.5	11
3501	Brain transcriptomic responses of Yarrow's spiny lizard, <i>Sceloporus jarrovii</i> , to conspecific visual or chemical signals. <i>Genes, Brain and Behavior</i> , 2021, 20, e12753.	1.1	0

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3503	Population genomics of apricots unravels domestication history and adaptive events. <i>Nature Communications</i> , 2021, 12, 3956.	5.8	45
3504	Overcoming uncollapsed haplotypes in long-read assemblies of non-model organisms. <i>BMC Bioinformatics</i> , 2021, 22, 303.	1.2	32
3505	Molecular Evolution of Phototransduction Pathway Genes in Nocturnal and Diurnal Fireflies (Coleoptera: Lampyridae). <i>Insects</i> , 2021, 12, 561.	1.0	3
3506	Genetic and behavioral adaptation of <i>Candida parapsilosis</i> to the microbiome of hospitalized infants revealed by in situ genomics, transcriptomics, and proteomics. <i>Microbiome</i> , 2021, 9, 142.	4.9	14
3508	Cellular Reprogramming and Immortality: Expression Profiling Reveals Putative Genes Involved in <i>Turritopsis dohrnii</i> Life Cycle Reversal. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	3
3509	The Genome Assembly and Annotation of the Apollo Butterfly <i>Parnassius apollo</i> , a Flagship Species for Conservation Biology. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	19
3510	Tightening the girdle: phylotranscriptomics of Polyplacophora. <i>Journal of Molluscan Studies</i> , 2021, 87, .	0.4	6
3511	Genome and Evolutionary Analysis of <i>Nosema ceranae</i> : A Microsporidian Parasite of Honey Bees. <i>Frontiers in Microbiology</i> , 2021, 12, 645353.	1.5	12
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3521	Museomics Dissects the Genetic Basis for Adaptive Seasonal Coloration in the Least Weasel. <i>Molecular Biology and Evolution</i> , 2021, 38, 4388-4402.	3.5	8
3522	Wide Distribution and Specific Resistance Pattern to Third-Generation Cephalosporins of <i>Enterobacter cloacae</i> Complex Members in Humans and in the Environment in Guadeloupe (French) Tj ETQq1 1 0.784314 rg88 /Overl		
3523	The Pleistocene species pump past its prime: Evidence from European butterfly sister species. <i>Molecular Ecology</i> , 2021, 30, 3575-3589.	2.0	35
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3526	High-Quality Genome Reconstruction of <i>Candida albicans</i> CHN1 Using Nanopore and Illumina Sequencing and Hybrid Assembly. <i>Microbiology Resource Announcements</i> , 2021, 10, e0029921.	0.3	3
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3564	Chromosome-scale genome assembly of areca palm (<i>Areca catechu</i>). <i>Molecular Ecology Resources</i> , 2021, 21, 2504-2519.	2.2	20
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3665	Genome design of hybrid potato. <i>Cell</i> , 2021, 184, 3873-3883.e12.	13.5	112
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3689	Draft Genome Resources for Brassicaceae Pathogens <i>Fusarium oxysporum</i> f. sp. <i>raphani</i> and <i>Fusarium oxysporum</i> f. sp. <i>rapae</i> . <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 1316-1319.	1.4	6
3690	Complete Genome Sequence of <i>Effusibacillus</i> sp. Strain skT53, Isolated from Farm Soil. <i>Microbiology Resource Announcements</i> , 2021, 10, e0048121.	0.3	0
3691	The mitochondrial genome of the grape powdery mildew pathogen <i>Erysiphe necator</i> is intron rich and exhibits a distinct gene organization. <i>Scientific Reports</i> , 2021, 11, 13924.	1.6	7
3692	RNA-Seq reveals divergent gene expression between larvae with contrasting trophic modes in the poecilogonous polychaete <i>Boccardia wellingtonensis</i> . <i>Scientific Reports</i> , 2021, 11, 14997.	1.6	2

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3693	Genome sequences and in silico effector mining of <i>Corynespora cassiicola</i> CC_29 and <i>Corynespora olivacea</i> CBS 114450. <i>Archives of Microbiology</i> , 2021, 203, 5257-5265.	1.0	6
3694	Genome assembly of <i>Vitis rotundifolia</i> Michx. using third-generation sequencing (Oxford Nanopore) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 502	0.1	0
3695	Deep Ancestral Introgression Shapes Evolutionary History of Dragonflies and Damselflies. <i>Systematic Biology</i> , 2022, 71, 526-546.	2.7	32
3696	Chromosome-level genome assembly and population genetic analysis of a critically endangered rhododendron provide insights into its conservation. <i>Plant Journal</i> , 2021, 107, 1533-1545.	2.8	35
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3701	Six de novo assemblies from pathogenic and non-pathogenic strains of <i>Fusarium oxysporum</i> f. sp. <i>niveum</i> . <i>PhytoFrontiers</i> , 0, , .	0.8	2
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3703	TransPI: A balancing act between transcriptome assemblers. <i>Peer Community in Genomics</i> , 0, , .	0.0	0
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3706	Global patterns in genomic diversity underpinning the evolution of insecticide resistance in the aphid crop pest <i>Myzus persicae</i> . <i>Communications Biology</i> , 2021, 4, 847.	2.0	55
3707	Improved draft reference genome for the Glassy-winged Sharpshooter (<i>Homalodisca</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 502	0.8	9
3708	De novo genome assembly of the marine teleost, bluefin trevally (<i>Caranx melampygus</i>). <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	2
3709	Chromosome-scale assembly of wild barley accession 'OUH602'. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	14
3711	A reference-grade genome identifies salt-tolerance genes from the salt-secreting mangrove species <i>Avicennia marina</i> . <i>Communications Biology</i> , 2021, 4, 851.	2.0	32
3712	The Dynamics of Flower Development in <i>Castanea sativa</i> Mill.. <i>Plants</i> , 2021, 10, 1538.	1.6	4

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3727	<i>Chitinophaga oryzae</i> sp. nov., an epiphytic bacterium isolated from rice root surfaces. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	8
3728	BUSCO Update: Novel and Streamlined Workflows along with Broader and Deeper Phylogenetic Coverage for Scoring of Eukaryotic, Prokaryotic, and Viral Genomes. <i>Molecular Biology and Evolution</i> , 2021, 38, 4647-4654.	3.5	1,968
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3731	Evaluation of a high-throughput, cost-effective Illumina library preparation kit. <i>Scientific Reports</i> , 2021, 11, 15925.	1.6	6
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3733	Genome Analysis of <i>Streptomyces nojiriensis</i> JCM 3382 and Distribution of Gene Clusters for Three Antibiotics and an Azasugar across the Genus <i>Streptomyces</i> . <i>Microorganisms</i> , 2021, 9, 1802.	1.6	5
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3736	Chromosome-level genome assembly of <i>Welwitschia mirabilis</i> , a unique Namib Desert species. <i>Molecular Ecology Resources</i> , 2022, 22, 391-403.	2.2	1
3737	De novo transcriptome assembly data of the marine bioluminescent dinoflagellate <i>Pyrocystis lunula</i> . <i>Data in Brief</i> , 2021, 37, 107254.	0.5	3
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3750	Haplotype-resolved genome of diploid ginger (<i>Zingiber officinale</i>) and its unique gingerol biosynthetic pathway. <i>Horticulture Research</i> , 2021, 8, 189.	2.9	53
3751	Analysis of meiosis in <i>Pristionchus pacificus</i> reveals plasticity in homolog pairing and synapsis in the nematode lineage. <i>ELife</i> , 2021, 10, .	2.8	21
3752	Chromosome-Level Genome Assembly of Chinese Sucker (<i>Myxocyprinus asiaticus</i>) Reveals Strongly Conserved Synteny Following a Catostomid-Specific Whole-Genome Duplication. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	12
3753	Comparative Whole-Genome Sequence Analyses of <i>Fusarium</i> Wilt Pathogen (Foc R1, STR4 and TR4) Infecting Cavendish (AAA) Bananas in India, with a Special Emphasis on Pathogenicity Mechanisms. <i>Journal of Fungi</i> (Basel, Switzerland), 2021, 7, 717.	1.5	9

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3759	Quinoa genome assembly employing genomic variation for guided scaffolding. <i>Theoretical and Applied Genetics</i> , 2021, 134, 3577-3594.	1.8	4
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3761	Chitosan Oligosaccharide Production Potential of <i>Mitsuaria</i> sp. C4 and Its Whole-Genome Sequencing. <i>Frontiers in Microbiology</i> , 2021, 12, 695571.	1.5	3
3762	Haplotype-resolved genome assembly and allele-specific gene expression in cultivated ginger. <i>Horticulture Research</i> , 2021, 8, 188.	2.9	31
3763	Timing the evolution of antioxidant enzymes in cyanobacteria. <i>Nature Communications</i> , 2021, 12, 4742.	5.8	57
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3765	Chromosome-Scale Genome Sequence of <i>Alternaria alternata</i> Causing Alternaria Brown Spot of Citrus. <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 726-732.	1.4	15
3767	A high-quality draft genome for <i>Melaleuca alternifolia</i> (tea tree): a new platform for evolutionary genomics of myrtaceous terpene-rich species. <i>GigaByte</i> , 0, 2021, 1-15.	0.0	11
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3776	<i>Aspergillus</i> sp. A31 and <i>Curvularia geniculata</i> P1 mitigate mercury toxicity to <i>Oryza sativa</i> L. <i>Archives of Microbiology</i> , 2021, 203, 5345-5361.	1.0	6
3777	Transcriptomes of <i>Saussurea</i> (Asteraceae) Provide Insights into High-Altitude Adaptation. <i>Plants</i> , 2021, 10, 1715.	1.6	11
3778	The Bacterial Diversity Lurking in Protist Cell Cultures. <i>American Museum Novitates</i> , 2021, 2021, .	0.2	2
3779	Genetic response to nitrogen starvation in the aggressive <i>Eucalyptus</i> foliar pathogen <i>Teratosphaeria destructans</i> . <i>Current Genetics</i> , 2021, 67, 981-990.	0.8	2
3780	Apicidin biosynthesis is linked to accessory chromosomes in <i>Fusarium poae</i> isolates. <i>BMC Genomics</i> , 2021, 22, 591.	1.2	7
3781	Signals of Positive Selection in Sea Slug Transcriptomes. <i>Biological Bulletin</i> , 2021, 241, 55-64.	0.7	0
3783	AQPX-cluster aquaporins and aquaglyceroporins are asymmetrically distributed in trypanosomes. <i>Communications Biology</i> , 2021, 4, 953.	2.0	4
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3788	Can functional genomic diversity provide novel insights into mechanisms of community assembly? A pilot study from an invaded alpine streambed. <i>Ecology and Evolution</i> , 2021, 11, 12075-12091.	0.8	0
3789	Mimopidae is the sister group to all other scolopendromorph centipedes (Chilopoda.) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 347 Td (Sc</i> <i>591-598.</i>	0.7	4
3791	Phylogenomic Analysis of Velvet Worms (Onychophora) Uncovers an Evolutionary Radiation in the Neotropics. <i>Molecular Biology and Evolution</i> , 2021, 38, 5391-5404.	3.5	10
3792	High-quality draft genome sequence data of six <i>Lactiplantibacillus plantarum</i> subsp. <i>argentoratensis</i> strains isolated from various Greek wheat sourdoughs. <i>Data in Brief</i> , 2021, 37, 107172.	0.5	4
3793	The <i>Cardamine enshiensis</i> genome reveals whole genome duplication and insight into selenium hyperaccumulation and tolerance. <i>Cell Discovery</i> , 2021, 7, 62.	3.1	15
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3801	The Bipartite Structure of the First Genome of <i>Ampelomyces quisqualis</i> , a Common Hyperparasite and Biocontrol Agent of Powdery Mildews, May Point to Its Evolutionary Origin from Plant Pathogenic Fungi. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	4
3804	New high-quality peach (<i>Prunus persica</i> L. Batsch) genome assembly to analyze the molecular evolutionary mechanism of volatile compounds in peach fruits. <i>Plant Journal</i> , 2021, 108, 281-295.	2.8	31
3805	The chromosome-scale reference genome of <i>Rubus chingii</i> Hu provides insight into the biosynthetic pathway of hydrolyzable tannins. <i>Plant Journal</i> , 2021, 107, 1466-1477.	2.8	26
3806	Genome Sequence of <i>Rhizoctonia solani</i> Anastomosis Group 4 Strain Rhs4ca, a Widespread Pathomycete in Field Crops. <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 826-829.	1.4	12
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3811	De novo assembly, annotation, and comparative analysis of 26 diverse maize genomes. <i>Science</i> , 2021, 373, 655-662.	6.0	282
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3813	Genomic investigation of colour polymorphism and phylogeographic variation among populations of black-headed bulbul (<i>Brachypodius atriceps</i>) in insular southeast Asia. <i>Molecular Ecology</i> , 2021, 30, 4757-4770.	2.0	4
3814	Transcriptome-wide SNPs for <i>Botrychium lunaria</i> ferns enable fine-grained analysis of ploidy and population structure. <i>Molecular Ecology Resources</i> , 2022, 22, 254-271.	2.2	3
3815	Genome Analysis of <i>Phytophthora nicotianae</i> JM01 Provides Insights into Its Pathogenicity Mechanisms. <i>Plants</i> , 2021, 10, 1620.	1.6	4
3816	Transcriptomic Analysis of Salivary Glands of <i>Ornithodoros brasiliensis</i> Aragão, 1923, the Agent of a Neotropical Tick-Toxicosis Syndrome in Humans. <i>Frontiers in Physiology</i> , 2021, 12, 725635.	1.3	4
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3821	Insights into the Host Specificity of a New Oomycete Root Pathogen, <i>Pythium brassicum</i> P1: Whole Genome Sequencing and Comparative Analysis Reveals Contracted Regulation of Metabolism, Protein Families, and Distinct Pathogenicity Repertoire. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9002.	1.8	3

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3826	Improved <i>Gossypium raimondii</i> genome using a Hi-C-based proximity-guided assembly. <i>Journal of Cotton Research</i> , 2021, 4, .	1.0	0
3827	Sequencing and de Novo Assembly of Abaca (<i>Musa textilis</i> NÅ©e) var. Abuab Genome. <i>Genes</i> , 2021, 12, 1202.	1.0	9
3828	Antibiotic Biosynthesis Pathways from Endophytic <i>Streptomyces</i> SUK 48 through Metabolomics and Genomics Approaches. <i>Antibiotics</i> , 2021, 10, 969.	1.5	4
3829	The Easter Egg Weevil (<i>Pachyrhynchus</i>) genome reveals syntenic patterns in Coleoptera across 200 million years of evolution. <i>PLoS Genetics</i> , 2021, 17, e1009745.	1.5	14
3830	Genome Sequence Resource of <i>Phomopsis longicolla</i> YC2-1, a Fungal Pathogen Causing Phomopsis Stem Blight in Soybean. <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 842-844.	1.4	6
3832	High-quality evergreen azalea genome reveals tandem duplication-facilitated low-altitude adaptability and floral scent evolution. <i>Plant Biotechnology Journal</i> , 2021, 19, 2544-2560.	4.1	35
3833	Phylogenomics of a new fungal phylum reveals multiple waves of reductive evolution across Holomycota. <i>Nature Communications</i> , 2021, 12, 4973.	5.8	48
3834	Concerted genomic and epigenomic changes accompany stabilization of <i>Arabidopsis</i> allopolyploids. <i>Nature Ecology and Evolution</i> , 2021, 5, 1382-1393.	3.4	41
3835	Whole-genome assembly and annotation of northern wild rice, <i>Zizania palustris</i> L., supports a whole-genome duplication in the <i>Zizania</i> genus. <i>Plant Journal</i> , 2021, 107, 1802-1818.	2.8	7
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3838	Genome Sequence of <i>Venturia carpophila</i> , the Causal Agent of Peach Scab. <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, MPMI-11-20-0321.	1.4	6
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3840	Iso-seq analysis and functional annotation of the Santa Fe cave crayfish (<i>Procambarus erythropterus</i>) transcriptome. <i>Marine Genomics</i> , 2021, 58, 100842.	0.4	2
3843	Virulence Traits and Population Genomics of the Black Yeast <i>Aureobasidium melanogenum</i> . <i>Journal of Fungi</i> (Basel, Switzerland), 2021, 7, 665.	1.5	8

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3845	Decontamination, pooling and dereplication of the 678 samples of the Marine Microbial Eukaryote Transcriptome Sequencing Project. <i>BMC Research Notes</i> , 2021, 14, 306.	0.6	13
3850	Environmental stress leads to genome streamlining in a widely distributed species of soil bacteria. <i>ISME Journal</i> , 2022, 16, 423-434.	4.4	36
3852	Modelling of gene loss propensity in the pangenomes of three <i>Brassica</i> species suggests different mechanisms between polyploids and diploids. <i>Plant Biotechnology Journal</i> , 2021, 19, 2488-2500.	4.1	44
3853	Long-Read Genome Sequence Resources of <i>Xanthomonas citri</i> pv. <i>punicae</i> Strain Bagalkot Causing Pomegranate Bacterial Blight. <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 874-877.	1.4	5
3854	Whole-Genome Sequence Resource of <i>Calonectria ilicicola</i> , the Casual Pathogen of Soybean Red Crown Rot. <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 848-851.	1.4	7
3855	De novo transcriptome characterization of <i>Iris atropurpurea</i> (the Royal Iris) and phylogenetic analysis of MADS-box and R2R3-MYB gene families. <i>Scientific Reports</i> , 2021, 11, 16246.	1.6	7
3856	The whale shark genome reveals patterns of vertebrate gene family evolution. <i>ELife</i> , 2021, 10, .	2.8	19
3857	A chromosome-scale genome assembly and karyotype of the ctenophore <i>Hormiphora californensis</i> . <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	18
3858	The genome of <i>Cymbidium sinense</i> revealed the evolution of orchid traits. <i>Plant Biotechnology Journal</i> , 2021, 19, 2501-2516.	4.1	46
3859	A Y-linked anti-M β 1/4llergian hormone type-II receptor is the sex-determining gene in ayu, <i>Plecoglossus altivelis</i> . <i>PLoS Genetics</i> , 2021, 17, e1009705.	1.5	25
3860	Chromosome-scale assembly and evolution of the tetraploid <i>Salvia splendens</i> (Lamiaceae) genome. <i>Horticulture Research</i> , 2021, 8, 177.	2.9	27
3861	A chromosome-level genome assembly of the striped catfish (<i>Pangasianodon hypophthalmus</i>). <i>Genomics</i> , 2021, 113, 3349-3356.	1.3	18
3862	A near complete genome for goat genetic and genomic research. <i>Genetics Selection Evolution</i> , 2021, 53, 74.	1.2	16
3863	Chromosome-scale genome assembly and population genomics provide insights into the adaptation, domestication, and flavonoid metabolism of Chinese plum. <i>Plant Journal</i> , 2021, 108, 1174-1192.	2.8	16
3864	Chromosome-scale assembly of the <i>Dendrobium chrysotoxum</i> genome enhances the understanding of orchid evolution. <i>Horticulture Research</i> , 2021, 8, 183.	2.9	41
3867	Chromosome-scale assembly and whole-genome sequencing of 266 giant panda roundworms provide insights into their evolution, adaptation and potential drug targets. <i>Molecular Ecology Resources</i> , 2022, 22, 768-785.	2.2	6
3869	Performance and competitiveness of red vs. green phenotypes of a cyanobacterium grown under artificial lake browning. <i>Algae</i> , 2021, 36, 195-206.	0.9	7
3870	Incipient diploidization of the medicinal plant <i>Perilla</i> within 10,000 years. <i>Nature Communications</i> , 2021, 12, 5508.	5.8	35

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3871	Improved Whole-Genome Sequence of <i>Fusarium meridionale</i> , the Fungal Pathogen Causing Fusarium Head Blight in Rice. <i>Molecular Plant-Microbe Interactions</i> , 2022, 35, 85-89.	1.4	1
3873	Genome-Wide Transcriptional Changes of <i>Rhodosporidium kratochvilovae</i> at Low Temperature. <i>Frontiers in Microbiology</i> , 2021, 12, 727105.	1.5	5
3874	Quorum sensing disruption regulates hydrolytic enzyme and biofilm production in estuarine bacteria. <i>Environmental Microbiology</i> , 2021, 23, 7183-7200.	1.8	8
3875	High-Quality Genome Resource of <i>Clonostachys rosea</i> Strain CanS41 by Oxford Nanopore Long-Read Sequencing. <i>Plant Disease</i> , 2021, 105, 2231-2234.	0.7	8
3876	The Response of Airborne Mycobiome to Dust Storms in the Eastern Mediterranean. <i>Journal of Fungi</i> (Basel, Switzerland), 2021, 7, 802.	1.5	6
3877	The genomic basis of army ant chemosensory adaptations. <i>Molecular Ecology</i> , 2021, 30, 6627-6641.	2.0	9
3878	Host-symbiont transcriptomic changes during natural bleaching and recovery in the leaf coral <i>Pavona decussata</i> . <i>Science of the Total Environment</i> , 2022, 806, 150656.	3.9	10
3880	Whole-Genome and Transcriptome Sequencing of <i>Phlebopus portentosus</i> Reveals Its Associated Ectomycorrhizal Niche and Conserved Pathways Involved in Fruiting Body Development. <i>Frontiers in Microbiology</i> , 2021, 12, 732458.	1.5	8
3881	In-depth Phylogenomic Analysis of Arbuscular Mycorrhizal Fungi Based on a Comprehensive Set of de novo Genome Assemblies. <i>Frontiers in Fungal Biology</i> , 2021, 2, .	0.9	15
3882	High-Quality Genome of the Medicinal Plant <i>Strobilanthes cusia</i> Provides Insights Into the Biosynthesis of Indole Alkaloids. <i>Frontiers in Plant Science</i> , 2021, 12, 742420.	1.7	10
3883	High quality haplotype-resolved genome assemblies of <i>Populus tomentosa</i> Carr., a stabilized interspecific hybrid species widespread in Asia. <i>Molecular Ecology Resources</i> , 2022, 22, 786-802.	2.2	19
3884	MOSGA 2: Comparative genomics and validation tools. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 5504-5509.	1.9	4
3885	Introgression among North American wild grapes (<i>Vitis</i>) fuels biotic and abiotic adaptation. <i>Genome Biology</i> , 2021, 22, 254.	3.8	25
3886	Haploid Genome Analysis Reveals a Tandem Cluster of Four HSP20 Genes Involved in the High-Temperature Adaptation of <i>Coriopsis trogii</i> . <i>Microbiology Spectrum</i> , 2021, 9, e0028721.	1.2	7
3887	Understanding molt control switches: Transcriptomic and expression analysis of the genes involved in ecdysteroidogenesis and cholesterol uptake pathways in the Y-organ of the blue crab, <i>Callinectes sapidus</i> . <i>PLoS ONE</i> , 2021, 16, e0256735.	1.1	8
3888	The genome of a nonphotosynthetic diatom provides insights into the metabolic shift to heterotrophy and constraints on the loss of photosynthesis. <i>New Phytologist</i> , 2021, 232, 1750-1764.	3.5	7
3890	Chromosome-Scale Assembly of the Complete Genome Sequence of <i>Leishmania</i> (<i>Mundinia</i>) <i>orientalis</i> , Isolate LSCM4, Strain LV768. <i>Microbiology Resource Announcements</i> , 2021, 10, e0057421.	0.3	5
3891	Chromosome-level genome assembly of the mirid predator <i>Cyrtorhinus lividipennis</i> Reuter (Hemiptera: Miridae), an important natural enemy in the rice ecosystem. <i>Molecular Ecology Resources</i> , 2022, 22, 1086-1099.	2.2	7

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3892	The genome sequence of the small tortoiseshell butterfly, <i>Aglais urticae</i> (Linnaeus, 1758). Wellcome Open Research, 0, 6, 233.	0.9	4
3893	Relaxed selection on male mitochondrial genes in DUI bivalves eases the need for mitonuclear coevolution. <i>Journal of Evolutionary Biology</i> , 2021, 34, 1722-1736.	0.8	10
3894	Whole-genome assembly of <i>Ganoderma leucocontextum</i> (Ganodermataceae, Fungi) discovered from the Tibetan Plateau of China. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	11
3896	The Arabinogalactan Protein Family of <i>Centaurium erythraea</i> Rafn. <i>Plants</i> , 2021, 10, 1870.	1.6	3
3898	Complete genome sequence of the biocontrol yeast <i>Papiliotrema terrestris</i> strain LS28. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	5
3899	The genome sequence of the poplar hawk-moth, <i>Laothoe populi</i> (Linnaeus, 1758). Wellcome Open Research, 0, 6, 237.	0.9	2
3900	Genome of <i>Ganoderma</i> Species Provides Insights Into the Evolution, Conifers Substrate Utilization, and Terpene Synthesis for <i>Ganoderma tsugae</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 724451.	1.5	13
3901	Comparative Genomics Sheds Light on the Convergent Evolution of Miniaturized Wasps. <i>Molecular Biology and Evolution</i> , 2021, 38, 5539-5554.	3.5	11
3903	Chromosome-Scale Genome Assembly and Transcriptome Assembly of Kawakawa <i>Euthynnus affinis</i> ; A Tuna-Like Species. <i>Frontiers in Genetics</i> , 2021, 12, 739781.	1.1	3
3904	An Improved Assembly of the <i>Albugo candida</i> Ac2V Genome Reveals the Expansion of the CCG Class of Effectors. <i>Molecular Plant-Microbe Interactions</i> , 2022, 35, 39-48.	1.4	6
3905	Complete Genome Sequence of <i>Amycolatopsis</i> sp. CA-230715, Encoding a 35-Module Type I Polyketide Synthase. <i>Microbiology Resource Announcements</i> , 2021, 10, e0080521.	0.3	1
3906	Phenotypic and genomic adaptations to the extremely high elevation in plateau zokor (<i>Myospalax</i>) Tj ETQq1 1 0,784314 rgBT / Overl	2.0	13
3907	Elucidating gene expression adaptation of phylogenetically divergent coral holobionts under heat stress. <i>Nature Communications</i> , 2021, 12, 5731.	5.8	29
3908	The genome sequence of the snout, <i>Hypena proboscidalis</i> (Linnaeus, 1758). Wellcome Open Research, 0, 6, 236.	0.9	0
3909	Near-Complete Genome Assembly of the Grapevine Crown Gall Pathogen <i>Allorhizobium vitis</i> Strain K377. <i>Microbiology Resource Announcements</i> , 2021, 10, e0135920.	0.3	2
3910	The <i>Euscaphis japonica</i> genome and the evolution of malvids. <i>Plant Journal</i> , 2021, 108, 1382-1399.	2.8	6
3911	Haplotype divergence supports long-term asexuality in the oribatid mite <i>Oppiella nova</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	23
3912	A high-quality chromosome-scale assembly of the centipedegrass [<i>Eremochloa ophiuroides</i> (Munro) Hack.] genome provides insights into chromosomal structural evolution and prostrate growth habit. <i>Horticulture Research</i> , 2021, 8, 201.	2.9	8

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3915	Genome Mining and Molecular Networking-Based Metabolomics of the Marine Facultative <i>Aspergillus</i> sp. MEXU 27854. <i>Molecules</i> , 2021, 26, 5362.	1.7	4
3919	A high-quality genome assembly of <i>Jasminum sambac</i> provides insight into floral trait formation and Oleaceae genome evolution. <i>Molecular Ecology Resources</i> , 2022, 22, 724-739.	2.2	18
3920	A chromosome-level reference genome of red swamp crayfish <i>Procambarus clarkii</i> provides insights into the gene families regarding growth or development in crustaceans. <i>Genomics</i> , 2021, 113, 3274-3284.	1.3	20
3921	Genome sequencing of the neotype strain CBS 554.65 reveals the MAT1-2 locus of <i>Aspergillus niger</i> . <i>BMC Genomics</i> , 2021, 22, 679.	1.2	5
3922	Up-regulation of apoptotic- and cell survival-related gene pathways following exposures of western corn rootworm to <i>B. thuringiensis</i> crystalline pesticidal proteins in transgenic maize roots. <i>BMC Genomics</i> , 2021, 22, 639.	1.2	4
3923	<i>Zanthoxylum</i> -specific whole genome duplication and recent activity of transposable elements in the highly repetitive paleotetraploid <i>Z. bungeanum</i> genome. <i>Horticulture Research</i> , 2021, 8, 205.	2.9	19
3925	The chromosome-scale genome of <i>Magnolia officinalis</i> provides insight into the evolutionary position of magnoliids. <i>IScience</i> , 2021, 24, 102997.	1.9	14
3926	A Chromosome-Level Genome Assembly of the Reed Warbler (<i>Acrocephalus scirpaceus</i>). <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	4
3927	Transcriptome analysis reveals the molecular mechanisms of response to an emergent yellow-flower disease in green Chinese prickly ash (<i>Zanthoxylum schinifolium</i>). <i>Scientific Reports</i> , 2021, 11, 18886.	1.6	2
3928	Chromosome-scale assembly reveals asymmetric paleo-subgenome evolution and targets for the acceleration of fungal resistance breeding in the nut crop, pecan. <i>Plant Communications</i> , 2021, 2, 100247.	3.6	10
3930	A high-quality chromosome-level genome of wild <i>Rosa rugosa</i> . <i>DNA Research</i> , 2021, 28, .	1.5	10
3931	DisoLipPred: accurate prediction of disordered lipid-binding residues in protein sequences with deep recurrent networks and transfer learning. <i>Bioinformatics</i> , 2021, 38, 115-124.	1.8	31
3932	Remarkable Metabolic Reconfiguration due to N Deficiency and an Ammonium-to-Nitrate Shift in the Free-Living <i>Effrenium voratum</i> (Symbiodiniaceae). <i>Journal of Geophysical Research G: Biogeosciences</i> , 2021, 126, e2020JG006172.	1.3	2
3933	Draft genome sequence, annotation and SSR mining data of <i>Oryctes rhinoceros</i> Linn. (Coleoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50,5	0.5	2
3935	Draft Genome Sequence of the Yeast <i>Ogataea degrootiae</i> Strain UCD465, Isolated from Soil in Ireland. <i>Microbiology Resource Announcements</i> , 2021, 10, e0073621.	0.3	2
3936	Hidden Historical Habitat-Linked Population Divergence and Contemporary Gene Flow of a Deep-Sea Patellogastropod <i>Limpet</i> . <i>Molecular Biology and Evolution</i> , 2021, 38, 5640-5654.	3.5	12
3938	Hypoosmotic stress induced functional alternations of intestinal barrier integrity, inflammatory reactions, and neurotransmission along gut-brain axis in the yellowfin seabream (<i>Acanthopagrus</i>) Tj ETQq1 1 0.784614 rgBT /Overlock 10 Tf 50,5	0.5	2

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3939	Draft Genome Sequence of <i>Enterobacter oligotrophicus</i> , Isolated from the Microbiome of a Lizard in the Caribbean. <i>Microbiology Resource Announcements</i> , 2021, 10, e0060221.	0.3	1
3940	Phylogenomic approach reveals strong signatures of introgression in the rapid diversification of neotropical true fruit flies (<i>Anastrepha</i> : Tephritidae). <i>Molecular Phylogenetics and Evolution</i> , 2021, 162, 107200.	1.2	8
3941	Improving the genome assembly of rabbits with long-read sequencing. <i>Genomics</i> , 2021, 113, 3216-3223.	1.3	7
3943	Genome Sequence Resource for <i>Stagonosporopsis cucurbitacearum</i> , a Cause of Gummy Stem Blight Disease of Watermelon. <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 977-980.	1.4	3
3944	Genomic insights into the origin, domestication and diversification of <i>Brassica juncea</i> . <i>Nature Genetics</i> , 2021, 53, 1392-1402.	9.4	66
3945	Avian Neo-Sex Chromosomes Reveal Dynamics of Recombination Suppression and W Degeneration. <i>Molecular Biology and Evolution</i> , 2021, 38, 5275-5291.	3.5	25
3947	Transcriptional changes revealed water acidification leads to the immune response and ovary maturation delay in the Chinese mitten crab <i>Eriocheir sinensis</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2021, 39, 100868.	0.4	5
3948	Rapid Macrosatellite Evolution Promotes X-Linked Hybrid Male Sterility in a Feline Interspecies Cross. <i>Molecular Biology and Evolution</i> , 2021, 38, 5588-5609.	3.5	8
3949	Annelid genomes: <i>Enchytraeus crypticus</i> , a soil model for the innate (and primed) immune system. <i>Lab Animal</i> , 2021, 50, 285-294.	0.2	11
3950	<i>De novo</i> genome assembly and <i>in natura</i> epigenomics reveal salinity-induced DNA methylation in the mangrove tree <i>Bruguiera gymnorhiza</i> . <i>New Phytologist</i> , 2022, 233, 2094-2110.	3.5	25
3951	Unveiling the transcriptomic complexity of <i>Miscanthus sinensis</i> using a combination of PacBio long read- and Illumina short read sequencing platforms. <i>BMC Genomics</i> , 2021, 22, 690.	1.2	2
3952	Different ways to play it cool: Transcriptomic analysis sheds light on different activity patterns of three amphipod species under long-term cold exposure. <i>Molecular Ecology</i> , 2021, 30, 5735-5751.	2.0	11
3953	Comparative analysis reveals within-population genome size variation in a rotifer is driven by large genomic elements with highly abundant satellite DNA repeat elements. <i>BMC Biology</i> , 2021, 19, 206.	1.7	8
3955	De Novo Transcriptome Assembly, Functional Annotation, and Transcriptome Dynamics Analyses Reveal Stress Tolerance Genes in Mangrove Tree (<i>Bruguiera gymnorhiza</i>). <i>International Journal of Molecular Sciences</i> , 2021, 22, 9874.	1.8	3
3956	Whole-genome sequencing of brown-marbled grouper (<i>Epinephelus fuscoguttatus</i>) provides insights into adaptive evolution and growth differences. <i>Molecular Ecology Resources</i> , 2022, 22, 711-723.	2.2	16
3957	Insights into the Lignocellulose-Degrading Enzyme System of <i>Humicola grisea</i> var. <i>thermoidea</i> Based on Genome and Transcriptome Analysis. <i>Microbiology Spectrum</i> , 2021, 9, e0108821.	1.2	12
3958	First draft genome assemblies of <i>Pleochaeta shiraiana</i> and <i>Phyllactinia moricola</i> , two tree-parasitic powdery mildew fungi with hemiendophytic mycelia. <i>Phytopathology</i> , 2021, , .	1.1	3
3959	Comparative analysis of draft genome assemblies developed from whole genome sequences of two <i>Hyaloperonospora brassicae</i> isolate samples differing in field virulence on <i>Brassica napus</i> . <i>Biotechnology Reports (Amsterdam, Netherlands)</i> , 2021, 31, e00653.	2.1	3

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3962	<scp>PANNZER</scp>â€”A practical tool for protein function prediction. <i>Protein Science</i> , 2022, 31, 118-128.	3.1	55
3963	The genome sequence of the large tortoiseshell, <i>Nymphalis polychloros</i> (Linnaeus, 1758). <i>Wellcome Open Research</i> , 2021, 6, 238.	0.9	3
3965	Whole-Genome Sequencing and Genome-Wide Studies of Spiny Head Croaker (<i>Collichthys lucidus</i>) Reveals Potential Insights for Well-Developed Otoliths in the Family Sciaenidae. <i>Frontiers in Genetics</i> , 2021, 12, 730255.	1.1	0
3966	Insights into angiosperm evolution, floral development and chemical biosynthesis from the <i>Aristolochia fimbriata</i> genome. <i>Nature Plants</i> , 2021, 7, 1239-1253.	4.7	51
3967	Genomic Resources to Guide Improvement of the Shea Tree. <i>Frontiers in Plant Science</i> , 2021, 12, 720670.	1.7	11
3968	Fine-scale morphological, genomic, reproductive, and symbiont differences delimit the Caribbean octocorals <i>Plexaura homomalla</i> and <i>P. kenthali</i> . <i>Coral Reefs</i> , 2022, 41, 635-653.	0.9	1
3969	Multi-tissue transcriptome analysis of two <i>Begonia</i> species reveals dynamic patterns of evolution in the chalcone synthase gene family. <i>Scientific Reports</i> , 2021, 11, 17773.	1.6	6
3970	High contiguity de novo genome assembly and DNA modification analyses for the fungus fly, <i>Sciara coprophila</i> , using single-molecule sequencing. <i>BMC Genomics</i> , 2021, 22, 643.	1.2	17
3971	De novo Assembly, Annotation, and Analysis of Transcriptome Data of the Ladakh Ground Skink Provide Genetic Information on High-Altitude Adaptation. <i>Genes</i> , 2021, 12, 1423.	1.0	0
3972	Investigating Sources of Conflict in Deep Phylogenomics of Vetigastropod Snails. <i>Systematic Biology</i> , 2022, 71, 1009-1022.	2.7	10
3973	The genome sequence of the common wasp, <i>Vespula vulgaris</i> (Linnaeus, 1758). <i>Wellcome Open Research</i> , 0, 6, 232.	0.9	4
3974	Culture and genome-based analysis of four soil <i>Clostridium</i> isolates reveal their potential for antimicrobial production. <i>BMC Genomics</i> , 2021, 22, 686.	1.2	4
3975	Chromosome-Scale Assembly of the Complete Genome Sequence of <i>Leishmania (Mundinia) enriettii</i> , Isolate CUR178, Strain LV763. <i>Microbiology Resource Announcements</i> , 2021, 10, e0057521.	0.3	2
3976	The genome sequence of the yellow-tail moth, <i>Euproctis similis</i> (Fuessly, 1775). <i>Wellcome Open Research</i> , 2021, 6, 227.	0.9	0
3977	Effect of food source availability in the salivary gland transcriptome of the unique burying beetle <i>Nicrophorus pustulatus</i> (Coleoptera: Silphidae). <i>PLoS ONE</i> , 2021, 16, e0255660.	1.1	0
3978	Low-Coverage Whole Genomes Reveal the Higher Phylogeny of Green Lacewings. <i>Insects</i> , 2021, 12, 857.	1.0	4
3979	The genome sequence of the common red soldier beetle, <i>Rhagonycha fulva</i> (Scopoli, 1763). <i>Wellcome Open Research</i> , 0, 6, 243.	0.9	1

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3981	The genome of the naturally evolved obesity-prone Ossabaw miniature pig. <i>Science</i> , 2021, 24, 103081.	1.9	9
3982	Development of Genome-Wide Functional Markers Using Draft Genome Assembly of Guava (<i>Psidium</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 708332.	1.7	8
3983	A draft genome assembly for the eastern fox squirrel, <i>Sciurus niger</i> . <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	0
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3985	De Novo Genome Assembly of the Electric Fish <i>Brachyhypopomus occidentalis</i> (Hypopomidae,) Tj ETQq1 1 0,784314 rgBT /Over	1.1	8
3987	<i>Aegilops tauschii</i> genome assembly Aet v5.0 features greater sequence contiguity and improved annotation. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	19
3988	The first chromosome-level genome assembly of a green lacewing <i>Chrysopa pallens</i> and its implication for biological control. <i>Molecular Ecology Resources</i> , 2022, 22, 755-767.	2.2	7
3989	Comparative genomics provides insights into the aquatic adaptations of mammals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	43
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3991	Chromosome-Scale Assembly of the Complete Genome Sequence of <i>Leishmania (Mundinia)</i> sp. Ghana, Isolate GH5, Strain LV757. <i>Microbiology Resource Announcements</i> , 2021, 10, e0059121.	0.3	0
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3993	The genome of the minute marine rotifer <i>Proales similis</i> : Genome-wide identification of 401 G protein-coupled receptor (GPCR) genes. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2021, 39, 100861.	0.4	6
3994	Rambutan genome revealed gene networks for spine formation and aril development. <i>Plant Journal</i> , 2021, 108, 1037-1052.	2.8	7
3996	Pan-Genome of the Genus <i>Streptomyces</i> and Prioritization of Biosynthetic Gene Clusters With Potential to Produce Antibiotic Compounds. <i>Frontiers in Microbiology</i> , 2021, 12, 677558.	1.5	21
3997	<i>Pseudonocardia abyssalis</i> sp. nov. and <i>Pseudonocardia oceani</i> sp. nov., two novel actinomycetes isolated from the deep Southern Ocean. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	11
3998	Draft Genome Sequence of the Environmental Fungus <i>Scedosporium dehoogii</i> . <i>Mycopathologia</i> , 2021, 186, 889-892.	1.3	1
4000	Raspberry ketone diet supplement reduces attraction of sterile male Queensland fruit fly to cuelure by altering expression of chemoreceptor genes. <i>Scientific Reports</i> , 2021, 11, 17632.	1.6	2

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4004	Genomic basis of high-altitude adaptation in Tibetan <i>Prunus</i> fruit trees. <i>Current Biology</i> , 2021, 31, 3848-3860.e8.	1.8	41
4005	A population-level invasion by transposable elements triggers genome expansion in a fungal pathogen. <i>ELife</i> , 2021, 10, .	2.8	49
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4121	Chromosomal genome of <i>Triplophysa bleekeri</i> provides insights into its evolution and environmental adaptation. <i>GigaScience</i> , 2020, 9, .	3.3	19
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4134	<i>Paraburkholderia solitsugae</i> sp. nov. and <i>Paraburkholderia elongata</i> sp. nov., phenolic acid-degrading bacteria isolated from forest soil and emended description of <i>Paraburkholderia madseniana</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 5093-5105.	0.8	19
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4138	Complete genome of a unicellular parasite (<i>Antonospora locustae</i>) and transcriptional interactions with its host locust. <i>Microbial Genomics</i> , 2020, 6, .	1.0	4
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4505	A chromosome-scale genome assembly of <i>Antheraea pernyi</i> (Saturniidae, Lepidoptera). <i>Molecular Ecology Resources</i> , 2020, 20, 1372-1383.	2.2	20
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4511	Draft Genome Sequence of the Yeast <i>Rhodotorula</i> sp. Strain CCFEE 5036, Isolated from McMurdo Dry Valleys, Antarctica. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	7
4512	<i>Salmonella enterica</i> subsp. <i>arizonae</i> Isolated from a Canine Clinical Case of Prostatitis. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	2
4513	Draft Genome Sequence of <i>Lactobacillus plantarum</i> IYO1511, Isolated from Ishizuchi-Kurocha. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	7
4514	Draft Genome Sequence of <i>Clostridium senegalense</i> Strain AGRFS4, Isolated from a Dairy Farm in New Zealand. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
4515	Draft Genome Sequence of a <i>Cladosporium</i> Species Isolated from the Mesophotic Ascidian <i>Didemnum maculosum</i> . <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	4
4516	Draft Genome Sequence of <i>Massilia</i> sp. Strain ONC3, a Novel Bacterial Species of the <i>Oxalobacteraceae</i> Family Isolated from Garden Soil. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	9
4517	MiSeq Sequencing of <i>Salmonella enterica</i> subsp. <i>houtenae</i> Isolates from a Dog Treated for Hind-Limb Paresis. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	3

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4519	Complete Genome Sequence of <i>Paenibacillus</i> sp. Strain E222, a Bacterial Symbiont of an <i>Epichloa</i> Fungal Endophyte of Ryegrass. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	6
4520	Draft Genome Sequence of <i>Clostridium cadaveris</i> Strain AGRFS2.2, Isolated from a Bovine Dairy Farm in New Zealand. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	2
4521	Draft Genome Sequence of <i>Naganishia liquefaciens</i> Strain N6, Isolated from the Japan Trench. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	7
4522	Draft Genome Sequence of <i>Duganella</i> sp. Strain DN04, Isolated from Cultivated Soil. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	2
4523	Draft Genome Sequence of the Griseofulvin-Producing Fungus <i>Xylaria flabelliformis</i> Strain G536. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	14
4524	Complete Genome Sequences of Walnut-Associated <i>Xanthomonas euroxanthea</i> Strains CPBF 367 and CPBF 426 Obtained by Illumina/Nanopore Hybrid Assembly. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	5
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4526	Revised Transcriptome-Based Gene Annotation for <i>Aspergillus flavus</i> Strain NRRL 3357. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	5
4527	Transcriptome analysis of <i>Anastrepha fraterculus</i> sp. 1 males, females, and embryos: insights into development, courtship, and reproduction. <i>BMC Genetics</i> , 2020, 21, 136.	2.7	3
4528	Coexpression and Transcriptome analyses identify active Apomixis-related genes in <i>Paspalum notatum</i> leaves. <i>BMC Genomics</i> , 2020, 21, 78.	1.2	12
4531	Transcriptome of pleuropodia from locust embryos supports that these organs produce enzymes enabling the larva to hatch. <i>Frontiers in Zoology</i> , 2020, 17, 4.	0.9	7
4532	Gamete binning: chromosome-level and haplotype-resolved genome assembly enabled by high-throughput single-cell sequencing of gamete genomes. <i>Genome Biology</i> , 2020, 21, 306.	3.8	44
4533	Thiocyanate Degradation by a Highly Enriched Culture of the Neutrophilic Halophile <i>Halobacter</i> sp. Strain FOKN1 from Activated Sludge and Genomic Insights into Thiocyanate Metabolism. <i>Microbes and Environments</i> , 2019, 34, 402-412.	0.7	11
4534	Draft genomes of two Australian strains of the plant pathogen, <i>Phytophthora cinnamomi</i> . <i>F1000Research</i> , 2017, 6, 1972.	0.8	10
4535	Draft genomes of two Australian strains of the plant pathogen, <i>Phytophthora cinnamomi</i> . <i>F1000Research</i> , 2017, 6, 1972.	0.8	7
4536	A draft genome sequence for the <i>Ixodes scapularis</i> cell line, ISE6. <i>F1000Research</i> , 2018, 7, 297.	0.8	49
4537	First draft genome assembly of the Argane tree (<i>Argania spinosa</i>). <i>F1000Research</i> , 2018, 7, 1310.	0.8	7

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4539	Do you cov me? Effect of coverage reduction on metagenome shotgun sequencing studies. <i>F1000Research</i> , 2018, 7, 1767.	0.8	16
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4551	Evolution of the Tetrapyrrole Biosynthetic Pathway in Secondary Algae: Conservation, Redundancy and Replacement. <i>PLoS ONE</i> , 2016, 11, e0166338.	1.1	33
4552	Doubled Haploid "CUDH2107" as a Reference for Bulb Onion (<i>Allium cepa</i> L.) Research: Development of a Transcriptome Catalogue and Identification of Transcripts Associated with Male Fertility. <i>PLoS ONE</i> , 2016, 11, e0166568.	1.1	14
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4559	Multi-tissue RNA-seq and transcriptome characterisation of the spiny dogfish shark (<i>Squalus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 osmoregulation. PLoS ONE, 2017, 12, e0182756.	1.1	22
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4574	Independent Whole-Genome Duplications Define the Architecture of the Genomes of the Devastating West African Cacao Black Pod Pathogen <i>Phytophthora megakarya</i> and Its Close Relative <i>Phytophthora palmivora</i> . G3: Genes, Genomes, Genetics, 2020, 10, 2241-2255.	0.8	18

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4583	The draft genome of <i>Ditylenchus dipsaci</i> . Journal of Nematology, 2019, 51, 1-3.	0.4	8
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4603	Draft genome of the aquatic moss <i>Fontinalis antipyretica</i> (Fontinalaceae, Bryophyta). <i>GigaByte</i> , 0, 2020, 1-9.	0.0	12
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4613	Genome streamlining in a minute herbivore that manipulates its host plant. <i>ELife</i> , 2020, 9, .	2.8	33
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4623	Expression differences in <i>Aphidius ervi</i> (Hymenoptera: Braconidae) females reared on different aphid host species. <i>PeerJ</i> , 2017, 5, e3640.	0.9	11
4624	A practical guide to build <i>de-novo</i> assemblies for single tissues of non-model organisms: the example of a Neotropical frog. <i>PeerJ</i> , 2017, 5, e3702.	0.9	16
4625	Candidate genes for shell colour polymorphism in <i>Cepaea nemoralis</i> . <i>PeerJ</i> , 2017, 5, e3715.	0.9	22
4626	Transcriptome sequencing reveals high isoform diversity in the ant <i>Formica exsecta</i> . <i>PeerJ</i> , 2017, 5, e3998.	0.9	7
4627	Comparative genomic analysis of a new tellurite-resistant <i>Psychrobacter</i> strain isolated from the Antarctic Peninsula. <i>PeerJ</i> , 2018, 6, e4402.	0.9	30
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4631	Genome analysis of the ubiquitous boxwood pathogen <i>Pseudonectria foliicola</i> . PeerJ, 2018, 6, e5401.	0.9	18
4632	The Oyster River Protocol: a multi-assembler and kmer approach for de novo transcriptome assembly. PeerJ, 2018, 6, e5428.	0.9	85
4633	A bioinformatics approach to identifying <i>Wolbachia</i> infections in arthropods. PeerJ, 2018, 6, e5486.	0.9	41
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4635	Genes of the pig, <i>Sus scrofa</i> , reconstructed with EvidentialGene. PeerJ, 2019, 7, e6374.	0.9	40
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4637	TarSynFlow, a workflow for bacterial genome comparisons that revealed genes putatively involved in the probiotic character of <i>Shewanella putrefaciens</i> strain Pdp11. PeerJ, 2019, 7, e6526.	0.9	3
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4645	A de novo assembly of the sweet cherry (<i>Prunus avium</i> cv. Tieton) genome using linked-read sequencing technology. PeerJ, 2020, 8, e9114.	0.9	8
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4648	Chromosome Level Genome Assembly and Annotation of Highly Invasive Japanese Stiltgrass (<i>Microstegium vimineum</i>). <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	4
4651	<i>Gemmata palustris</i> sp. nov., a Novel Planctomycete from a Fen in Northwestern Russia. <i>Microbiology</i> , 2021, 90, 598-606.	0.5	8
4652	Whole-Genome Sequencing of <i>Sinocyclocheilus maitianheensis</i> Reveals Phylogenetic Evolution and Immunological Variances in Various <i>Sinocyclocheilus</i> Fishes. <i>Frontiers in Genetics</i> , 2021, 12, 736500.	1.1	2
4653	Neurogenomic divergence during speciation by reinforcement of mating behaviors in chorus frogs (<i>Pseudacris</i>). <i>BMC Genomics</i> , 2021, 22, 711.	1.2	3
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5479	Chromosome-Level Genome Assembly of the Rare and Endangered Tropical Plant <i>Speranskia yunnanensis</i> (Euphorbiaceae). <i>Frontiers in Genetics</i> , 2021, 12, 755564.	1.1	1
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5483	Chromosome-level <i>Thlaspi arvense</i> genome provides new tools for translational research and for a newly domesticated cash cover crop of the cooler climates. <i>Plant Biotechnology Journal</i> , 2022, 20, 944-963.	4.1	18

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5524	TransPi—a comprehensive TRanscriptome ANalysis Pipeline for <i>de novo</i> transcriptome assembly. <i>Molecular Ecology Resources</i> , 2022, 22, 2070-2086.	2.2	14
5526	Cytology, transcriptomics, and mass spectrometry imaging reveal changes in late-maturation elm (<i>Ulmus pumila</i>) seeds. <i>Journal of Plant Physiology</i> , 2022, 271, 153639.	1.6	1

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5534	Long-read sequencing of the zebrafish genome reorganizes genomic architecture. <i>BMC Genomics</i> , 2022, 23, 116.	1.2	9
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5649	Whole-Genome Sequence Resource of <i>Fusarium oxysporum</i> Strain TH15, a Plant Growth Promoting Endophytic Fungus Isolated from <i>Tetrastigma hemsleyanum</i> . <i>PhytoFrontiers</i> , 2022, 2, 314-319.	0.8	4

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5690	Draft genomes assembly and annotation of <i>Carex parvula</i> and <i>Carex kokanica</i> reveals stress-specific genes. <i>Scientific Reports</i> , 2022, 12, 4970.	1.6	7
5691	Accurate prediction of metagenome-assembled genome completeness by MAGISTA, a random forest model built on alignment-free intra-bin statistics. <i>Environmental Microbiomes</i> , 2022, 17, 9.	2.2	3
5692	The genome of an apodid holothuroid (<i>Chiridota heheva</i>) provides insights into its adaptation to a deep-sea reducing environment. <i>Communications Biology</i> , 2022, 5, 224.	2.0	15
5694	Haplotype-resolved Chinese male genome assembly based on high-fidelity sequencing. <i>Fundamental Research</i> , 2022, 2, 946-953.	1.6	11
5695	Detection of a novel Cry2Ab toxin against <i>Etiella zinckenella</i> Treitschke from the <i>Bacillus thuringiensis</i> serovar <i>canadensis</i> SP142 strain. <i>Plant Protection Science</i> , 2022, 58, 158-169.	0.7	0

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5697	Comparative genomics of plant pathogenic <i>Diaporthe</i> species and transcriptomics of <i>Diaporthe caulivora</i> during host infection reveal insights into pathogenic strategies of the genus. <i>BMC Genomics</i> , 2022, 23, 175.	1.2	12
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5700	Transcriptional Regulation of Reproductive Diapause in the Convergent Lady Beetle, <i>Hippodamia convergens</i> . <i>Insects</i> , 2022, 13, 343.	1.0	4
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5713	An Enigmatic Stramenopile Sheds Light on Early Evolution in Ochrophyta Plastid Organogenesis. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	8
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5716	Extensive sequence divergence between the reference genomes of two zebrafish strains, Tuebingen and AB. <i>Molecular Ecology Resources</i> , 2022, , .	2.2	1
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5720	Metagenomic clustering reveals microbial contamination as an essential consideration in ultraconserved element design for phylogenomics with insect museum specimens. <i>Ecology and Evolution</i> , 2022, 12, e8625.	0.8	6
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5729	Complete Genome Sequence of <i>Brevibacterium frigoritolerans</i> Ant232, Isolated from Antarctic Snow. <i>Microbiology Resource Announcements</i> , 2022, , e0015222.	0.3	2
5730	Chromosome-level genome assembly of grass carp (<i>Ctenopharyngodon idella</i>) provides insights into its genome evolution. <i>BMC Genomics</i> , 2022, 23, 271.	1.2	21
5731	The first genome for the Cape Primrose <i>Streptocarpus rexii</i> (Gesneriaceae), a model plant for studying meristem-driven shoot diversity. <i>Plant Direct</i> , 2022, 6, e388.	0.8	4
5732	Chromosome-Level Genome Assembly Reveals Dynamic Sex Chromosomes in Neotropical Leaf-Litter Geckos (<i>Sphaerodactylidae</i> : <i>Sphaerodactylus</i>). <i>Journal of Heredity</i> , 2022, 113, 272-287.	1.0	19
5733	A chromosome-scale genome assembly of the Mongolian oak (<i>Quercus mongolica</i>). <i>Molecular Ecology Resources</i> , 2022, 22, 2396-2410.	2.2	25
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5736	The <i>Gastrodia menghaiensis</i> (Orchidaceae) genome provides new insights of orchid mycorrhizal interactions. <i>BMC Plant Biology</i> , 2022, 22, 179.	1.6	13
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5758	Transcriptome analysis of <i>Macrobrachium rosenbergii</i> : Identification of precocious puberty and slow-growing information. <i>Journal of Invertebrate Pathology</i> , 2022, 190, 107752.	1.5	7
5759	Insight into the genome data of commercially important giant kelp <i>Macrocystis pyrifera</i> . <i>Data in Brief</i> , 2022, 42, 108068.	0.5	2
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5768	Genome assembly, annotation, and comparative analysis of the cattail <i>Typha latifolia</i> . <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	6
5770	The genome sequence of the European nightjar, <i>Caprimulgus europaeus</i> (Linnaeus, 1758). <i>Wellcome Open Research</i> , 2021, 6, 332.	0.9	0
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5774	Comparative de novo transcriptome analysis identifies salinity stress responsive genes and metabolic pathways in sugarcane and its wild relative <i>Erianthus arundinaceus</i> [Retzius] Jeswiet. <i>Scientific Reports</i> , 2021, 11, 24514.	1.6	5
5777	Comparative Transcriptome Analysis of Female and Male Fine-Patterned Puffer: Identification of Candidate Genes Associated with Growth and Sex Differentiation. <i>Fishes</i> , 2021, 6, 79.	0.7	4
5778	Whole-Genome Sequencing of <i>Acer catalpifolium</i> Reveals Evolutionary History of Endangered Species. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	7
5779	Evolutionary assembly of cooperating cell types in an animal chemical defense system. <i>Cell</i> , 2021, 184, 6138-6156.e28.	13.5	13

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5782	The genome sequence of the tapered dronefly, <i>Eristalis pertinax</i> (Scopoli, 1763). <i>Wellcome Open Research</i> , 0, 6, 292.	0.9	1
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5793	Chromosomal-Level Assembly of Antarctic Scaly Rockcod, <i>Trematomus loennbergii</i> Genome Using Long-Read Sequencing and Chromosome Conformation Capture (Hi-C) Technologies. <i>Diversity</i> , 2021, 13, 668.	0.7	3
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5803	Draft Genome Sequence of <i>Aestuarius halophilus</i> Type Strain JC2043. <i>Microbiology Resource Announcements</i> , 2021, 10, e0109321.	0.3	1
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5852	Genomic Analysis Based on Chromosome-Level Genome Assembly Reveals an Expansion of Terpene Biosynthesis of <i>Azadirachta indica</i> . <i>Frontiers in Plant Science</i> , 2022, 13, 853861.	1.7	5
5853	Oogenesis and lipid metabolism in the deep-sea sponge <i>Phakellia ventilabrum</i> (Linnaeus, 1767). <i>Scientific Reports</i> , 2022, 12, 6317.	1.6	8
5854	Inferring Species Compositions of Complex Fungal Communities from Long- and Short-Read Sequence Data. <i>MBio</i> , 2022, 13, e0244421.	1.8	2
5855	Whole genome sequencing of spotted stem borer, <i>Chilo partellus</i> , reveals multiple genes encoding enzymes for detoxification of insecticides. <i>Functional and Integrative Genomics</i> , 2022, , 1.	1.4	0
5856	The relationship between sexual dimorphism and androgen response element proliferation in primate genomes. <i>Evolution; International Journal of Organic Evolution</i> , 2022, , .	1.1	3
5857	An ancient truncated duplication of the anti- μ 1/2 allergen receptor type 2 gene is a potential conserved master sex determinant in the Pangasiidae catfish family. <i>Molecular Ecology Resources</i> , 2022, 22, 2411-2428.	2.2	13
5859	Genome Sequence Analysis of <i>Exiguobacterium</i> sp. Strain TBG-PICH-001, Isolated from Pichavaram Mangrove Forest in South India. <i>Microbiology Resource Announcements</i> , 2022, 11, e0009622.	0.3	2
5860	Lifestyle, mating type and mitochondrial genome features of the plant pathogen <i>Calonectria hawksworthii</i> (Hypocreales, Nectriaceae) as revealed by genome analyses. <i>Canadian Journal of Plant Pathology</i> , 2022, 44, 723-736.	0.8	1
5861	Dynamics of maternal gene expression in <i>Rhodnius prolixus</i> . <i>Scientific Reports</i> , 2022, 12, 6538.	1.6	4
5862	A chromosome-level genome assembly of chia provides insights into high omega-3 content and coat color variation of its seeds. <i>Plant Communications</i> , 2022, 3, 100326.	3.6	14
5863	Draft Genomes of Six Philippine <i>Erwinia mallotivora</i> Isolates: Comparative Genomics and Genome-Wide Analysis of Candidate Secreted Proteins. <i>Current Microbiology</i> , 2022, 79, 164.	1.0	1
5864	The <i>Cycas</i> genome and the early evolution of seed plants. <i>Nature Plants</i> , 2022, 8, 389-401.	4.7	80
5865	Cross-species transcriptomes reveal species-specific and shared molecular adaptations for plants development on iron-rich rocky outcrops soils. <i>BMC Genomics</i> , 2022, 23, 313.	1.2	2
5866	Genome sequencing of <i>Inonotus obliquus</i> reveals insights into candidate genes involved in secondary metabolite biosynthesis. <i>BMC Genomics</i> , 2022, 23, 314.	1.2	20
5868	High-quality chromosome-scale de novo assembly of the <i>Paspalum notatum</i> "Flugge" genome. <i>BMC Genomics</i> , 2022, 23, 293.	1.2	1
5870	Genome-Wide Study of Conidiation-Related Genes in the Aphid-Obligate Fungal Pathogen <i>Conidiobolus obscurus</i> (Entomophthoromycotina). <i>Journal of Fungi</i> (Basel, Switzerland), 2022, 8, 389.	1.5	4
5871	Metatranscriptomic Assessment of the Microbial Community Associated With the Flavescence dorée Phytoplasma Insect Vector <i>Scaphoideus titanus</i> . <i>Frontiers in Microbiology</i> , 2022, 13, 866523.	1.5	4

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5874	Genetic Basis of Dorper Sheep (<i>Ovis aries</i>) Revealed by Long-Read De Novo Genome Assembly. <i>Frontiers in Genetics</i> , 2022, 13, 846449.	1.1	8
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5877	Natural variation and improved genome annotation of the emerging biofuel crop field pennycress (<i>Thlaspi arvense</i>). <i>G3: Genes, Genomes, Genetics</i> , 2022, , .	0.8	5
5878	De novo transcriptome assembly and development of EST-SSR markers for <i>Pterocarpus santalinus</i> L. f. (Red sanders), a threatened and endemic tree of India. <i>Genetic Resources and Crop Evolution</i> , 2022, 69, 2469-2484.	0.8	3
5879	Chromosomal-level genome assembly of the orchid tree <i>Bauhinia variegata</i> (Leguminosae); Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 29, .	1.5	4
5880	A chromosome-level genome of the kuruma shrimp (<i>Marsupenaeus japonicus</i>) provides insights into its evolution and cold-resistance mechanism. <i>Genomics</i> , 2022, 114, 110373.	1.3	8
5881	Genome analysis of five recently described species of the CUG-Ser clade uncovers <i>Candida theae</i> as a new hybrid lineage with pathogenic potential in the <i>Candida parapsilosis</i> species complex. <i>DNA Research</i> , 2022, , .	1.5	4
5883	The SITE-100 Project: Site-Based Biodiversity Genomics for Species Discovery, Community Ecology, and a Global Tree-of-Life. <i>Frontiers in Ecology and Evolution</i> , 2022, 10, .	1.1	6
6469	Deletion and tandem duplications of biosynthetic genes drive the diversity of triterpenoids in <i>Aralia elata</i> . <i>Nature Communications</i> , 2022, 13, 2224.	5.8	34
6470	Genomes of leafy and leafless <i>Platanthera</i> orchids illuminate the evolution of mycoheterotrophy. <i>Nature Plants</i> , 2022, 8, 373-388.	4.7	36
6471	Genome sequences of <i>Rhizopogon roseolus</i> , <i>Mariannaea elegans</i> , <i>Myrothecium verrucaria</i> and <i>Sphaerostilbella broomeana</i> and the identification of biosynthetic gene clusters for fungal peptide natural products. <i>G3: Genes, Genomes, Genetics</i> , 2022, , .	0.8	0
6473	De novo screening of disease-resistant genes from the chromosome-level genome of rare minnow using CRISPR-cas9 random mutation. <i>GigaScience</i> , 2021, 10, .	3.3	2
6474	Genome of the ramshorn snail <i>Biomphalaria straminea</i> -an obligate intermediate host of schistosomiasis.. <i>GigaScience</i> , 2022, 11, .	3.3	11
6475	Characterisation of the symbionts in the Mediterranean fruit fly gut. <i>Microbial Genomics</i> , 2022, 8, .	1.0	3
6476	<i>Wolbachia</i> endosymbionts in two <i>Anopheles</i> species indicates independent acquisitions and lack of prophage elements. <i>Microbial Genomics</i> , 2022, 8, .	1.0	3
6477	Early branching arbuscular mycorrhizal fungus <i>Paraglomus occultum</i> carries a small and repeat-poor genome compared to relatives in the Glomeromycotina. <i>Microbial Genomics</i> , 2022, 8, .	1.0	14

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6481	The Australian dingo is an early offshoot of modern breed dogs. <i>Science Advances</i> , 2022, 8, eabm5944.	4.7	14
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6483	Genome Mining Shows Ubiquitous Presence and Extensive Diversity of Toxin-Antitoxin Systems in <i>Pseudomonas syringae</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 815911.	1.5	5
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6487	The Unusual Metalloprotease-Rich Venom Proteome of the Australian Elapid Snake <i>Hoplocephalus stephensii</i> . <i>Toxins</i> , 2022, 14, 314.	1.5	2
6488	Speciation with gene flow between two Neotropical sympatric species (<i>Pitcairnia</i> spp.): Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 342	0.8	4
6489	A High-Quality Haplotype-Resolved Genome of Common Bermudagrass (<i>Cynodon dactylon</i> L.) Provides Insights Into Polyploid Genome Stability and Prostrate Growth. <i>Frontiers in Plant Science</i> , 2022, 13, 890980.	1.7	4
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6492	Social insect colony size is correlated with rates of molecular evolution. <i>Insectes Sociaux</i> , 2022, 69, 147-157.	0.7	4
6493	An Improved Genome Sequence Resource of <i>Bipolaris maydis</i>, Causal Agent of Southern Corn Leaf Blight. <i>Phytopathology</i> , 2022, , PHYTO11210490A.	1.1	3
6495	Transcriptome annotation reveals minimal immunogenetic diversity among Wyoming toads, <i>Anaxyrus baxteri</i> . <i>Conservation Genetics</i> , 2022, 23, 669-681.	0.8	2
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6500	Pitaya Genome and Multiomics Database (PGMD): A Comprehensive and Integrative Resource of <i>Selenicereus undatus</i> . <i>Genes</i> , 2022, 13, 745.	1.0	16
6501	Chromosome-Level Genome Assembly of the Hemiparasitic <i>Taxillus chinensis</i> (DC.) Danser. <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	2
6502	Gene expression and allergenic potential of <i>Pseudoterranova bulbosa</i> L3 from different infection sites in North Atlantic cod (<i>Gadus morhua</i>). <i>Journal of Fish Diseases</i> , 2022, 45, 1073-1086.	0.9	2
6503	Complete Genome Sequences of Four Strains of <i>Erwinia tracheiphila</i> : A Resource for Studying a Bacterial Plant Pathogen with a Highly Complex Genome. <i>Molecular Plant-Microbe Interactions</i> , 2022, 35, 500-504.	1.4	4
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6505	Using ultraconserved elements to reconstruct the termite tree of life. <i>Molecular Phylogenetics and Evolution</i> , 2022, 173, 107520.	1.2	11
6506	Genomic insights into the origin, adaptive evolution, and herbicide resistance of <i>Leptochloa chinensis</i> , a devastating tetraploid weedy grass in rice fields. <i>Molecular Plant</i> , 2022, 15, 1045-1058.	3.9	15
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6508	Draft Genome Sequence of <i>Ralstonia syzygii</i> subsp. <i>celebesensis</i> from Indonesia, the Causal Agent of Blood Disease of Banana. <i>Phytopathology</i> , 2022, , PHYTO10210443A.	1.1	4
6509	Draft Genome Assembly of an Iconic Arctic Species: Muskox (<i>Ovibos moschatus</i>). <i>Genes</i> , 2022, 13, 809.	1.0	1
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6512	The genome sequencing and comparative analysis of a wild kiwifruit <i>Actinidia eriantha</i> . <i>Molecular Horticulture</i> , 2022, 2, .	2.3	13
6514	Elucidation of host and symbiont contributions to peptidoglycan metabolism based on comparative genomics of eight aphid subfamilies and their <i>Buchnera</i> . <i>PLoS Genetics</i> , 2022, 18, e1010195.	1.5	11
6515	Functional repertoire convergence of distantly related eukaryotic plankton lineages abundant in the sunlit ocean. <i>Cell Genomics</i> , 2022, 2, 100123.	3.0	70
6516	Pathways to polar adaptation in fishes revealed by long-read sequencing. <i>Molecular Ecology</i> , 2023, 32, 1381-1397.	2.0	8

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6518	Identification of genes differentially expressed between prostrate shoots and erect shoots in the lycophyte <i>Selaginella nipponica</i> using an RNA-seq approach. <i>AoB PLANTS</i> , 2022, 14, .	1.2	1
6519	Comparative Genomics Reveals Insights into the Divergent Evolution of Astigmatic Mites and Household Pest Adaptations. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	13
6520	Chromosome-level genome assembly of <i>Mentha longifolia</i> L. reveals gene organization underlying disease resistance and essential oil traits. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	8
6521	Highly transmissible cytoplasmic incompatibility by the extracellular insect symbiont <i>Spiroplasma</i> . <i>IScience</i> , 2022, 25, 104335.	1.9	20
6522	Gaur genome reveals expansion of sperm odorant receptors in domesticated cattle. <i>BMC Genomics</i> , 2022, 23, 344.	1.2	3
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6526	The Mantle Transcriptome of <i>Chamelea gallina</i> (Mollusca: Bivalvia) and Shell Biomineralization. <i>Animals</i> , 2022, 12, 1196.	1.0	1
6527	Three-Dimensional Genome Map of the Filamentous Fungus <i>Penicillium oxalicum</i> . <i>Microbiology Spectrum</i> , 2022, 10, e0212121.	1.2	11
6528	Chromosomal rearrangements with stable repertoires of genes and transposable elements in an invasive forest-pathogenic fungus. , 0, 2, .		1
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6530	The flying spider-monkey tree fern genome provides insights into fern evolution and arborescence. <i>Nature Plants</i> , 2022, 8, 500-512.	4.7	42
6531	Assembly of a hybrid mangrove, <i>Bruguiera hainesii</i> , and its two ancestral contributors, <i>Bruguiera cylindrica</i> and <i>Bruguiera gymnorhiza</i> . <i>Genomics</i> , 2022, 114, 110382.	1.3	5
6532	Chromosome-level genome assembly of Asian yellow pond turtle (<i>Mauremys mutica</i>) with temperature-dependent sex determination system. <i>Scientific Reports</i> , 2022, 12, 7905.	1.6	7
6533	Evidence of multiple genome duplication events in <i>Mytilus</i> evolution. <i>BMC Genomics</i> , 2022, 23, 340.	1.2	12
6534	Draft Genome Sequence of a <i>Lactobacillus gasseri</i> Strain Isolated from the Catheterized Urine of a Healthy Postmenopausal Woman. <i>Microbiology Resource Announcements</i> , 2022, , e0002122.	0.3	1
6535	Palaeogenomic analysis of black rat (<i>Rattus rattus</i>) reveals multiple European introductions associated with human economic history. <i>Nature Communications</i> , 2022, 13, 2399.	5.8	12

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6537	Daily patterns in parasite processes: diel variation in fish louse transcriptomes. <i>International Journal for Parasitology</i> , 2022, 52, 509-518.	1.3	1
6538	SunUp and Sunset genomes revealed impact of particle bombardment mediated transformation and domestication history in papaya. <i>Nature Genetics</i> , 2022, 54, 715-724.	9.4	26
6539	The combined effect of folic acid and 365-405 nm light emitting diode for inactivation of foodborne pathogens and its bactericidal mechanisms. <i>International Journal of Food Microbiology</i> , 2022, 373, 109704.	2.1	6
6540	Generation of a chromosome-level genome assembly for Pacific halibut (<i>Hippoglossus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 587 T Resources, 2022, 22, 2685-2700.	2.2	15
6541	A Draft Reference Genome Assembly of the Critically Endangered Black Abalone, <i>Haliotis cracherodii</i> . <i>Journal of Heredity</i> , 2022, 113, 665-672.	1.0	4
6542	A catalogue of resistance gene homologs and a chromosome-scale reference sequence support resistance gene mapping in winter wheat. <i>Plant Biotechnology Journal</i> , 2022, 20, 1730-1742.	4.1	21
6543	Landscape Connectivity and Genetic Structure in a Mainstem and a Tributary Stonefly (Plecoptera) Species Using a Novel Reference Genome. <i>Journal of Heredity</i> , 2022, 113, 453-471.	1.0	1
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6546	The state of Medusozoa genomics: current evidence and future challenges. <i>GigaScience</i> , 2022, 11, .	3.3	8
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6549	Transcriptomic Responses of Adult Versus Juvenile Atlantids to Ocean Acidification. <i>Frontiers in Marine Science</i> , 2022, 9, .	1.2	2
6550	A deep dive into genome assemblies of non-vertebrate animals. , 0, 2, .		4
6551	First Chromosome-Scale Assembly and Deep Floral-Bud Transcriptome of a Male Kiwifruit. <i>Frontiers in Genetics</i> , 2022, 13, .	1.1	9
6552	High-Quality Genome Assembly of <i>Olea europaea</i> subsp. <i>cuspidata</i> Provides Insights Into Its Resistance to Fungal Diseases in the Summer Rain Belt in East Asia. <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	5
6553	Evaluation of cold tolerance and gene expression patterns associated with low-temperature stress in giant freshwater prawn <i>Macrobrachium rosenbergii</i> . <i>Aquaculture Reports</i> , 2022, 24, 101172.	0.7	4
6554	Multiple long-range host shifts of major <i>Wolbachia</i> supergroups infecting arthropods. <i>Scientific Reports</i> , 2022, 12, 8131.	1.6	10

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6561	Improved genome assembly of Chinese sucker (<i>Myxocyprinus asiaticus</i>) provides insights into the identification and characterization of pharyngeal teeth related maker genes in Cyprinoidei. , 2022, 1, 100049.		1
6563	Isolation and characterization of acid-tolerant Stichococcus-like Microalga (<i>Tetrastichococcus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 6	1.5	4
6564	Genome Assembly and Population Resequencing Reveal the Geographical Divergence of Shanmei (<i>Rubus</i>) Tj ETQq1_1_0.784314 rgBT (D	3.0	3
6565	From head to rootlet: comparative transcriptomic analysis of a rhizocephalan barnacle <i>Peltogaster reticulata</i> (Crustacea: Rhizocephala). <i>F1000Research</i> , 0, 11, 583.	0.8	4
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6569	Expression Level Dominance and Homeolog Expression Bias Upon Cold Stress in the F1 Hybrid Between the Invasive <i>Sphagneticola trilobata</i> and the Native <i>S. calendulacea</i> in South China, and Implications for Its Invasiveness. <i>Frontiers in Genetics</i> , 2022, 13, .	1.1	1
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6572	Construction and characterization of a de novo draft genome of garden cress (<i>Lepidium sativum</i> L.). <i>Functional and Integrative Genomics</i> , 2022, 22, 879-889.	1.4	2
6573	Draft Genome Sequences of 18 <i>Streptococcus</i> Strains Isolated from Live Dietary Supplements and Cultured Food Products. <i>Microbiology Resource Announcements</i> , 0, , .	0.3	2
6577	Evolutionary Conservation Genomics Reveals Recent Speciation and Local Adaptation in Threatened Takins. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	7
6578	De Novo Transcriptome of the Flagellate <i>Isochrysis galbana</i> Identifies Genes Involved in the Metabolism of Antiproliferative Metabolites. <i>Biology</i> , 2022, 11, 771.	1.3	5
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6582	Development and validation of sex-specific markers in <i>Piaractus mesopotamicus</i> . <i>Aquaculture</i> , 2022, 558, 738374.	1.7	1
6583	A High-Quality Genome of the Dobsonfly <i>Neoneuromus Ignobilis</i> Reveals Molecular Convergences in Aquatic Insects. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
6584	Genome Announcement: The Draft Genome of the Carrot Cyst Nematode <i>Heterodera carotae</i> . <i>Journal of Nematology</i> , 2022, 54, .	0.4	0
6585	A time-course transcriptome analysis of gonads from yellow catfish (<i>Pelteobagrus fulvidraco</i>) reveals genes associated with gonad development. <i>BMC Genomics</i> , 2022, 23, .	1.2	3

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6590	Whole-Genome Sequencing and Analysis of the White-Rot Fungus <i>Ceriporia lacerata</i> Reveals Its Phylogenetic Status and the Genetic Basis of Lignocellulose Degradation and Terpenoid Synthesis. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	4
6591	Pan-Genomes Provide Insights into the Genetic Basis of <i>Auricularia heimuer</i> Domestication. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 581.	1.5	1
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6816	The chromosome-scale genome provides insights into pigmentation in <i>Acer rubrum</i> . <i>Plant Physiology and Biochemistry</i> , 2022, 186, 322-333.	2.8	1
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6930	The final piece of the Triangle of U: Evolution of the tetraploid <i>Brassica carinata</i> genome. <i>Plant Cell</i> , 2022, 34, 4143-4172.	3.1	18
6931	First De novo whole genome sequencing and assembly of mutant <i>Dendrobium</i> hybrid cultivar "Emma White". <i>GigaByte</i> , 0, 2022, 1-8.	0.0	0
6932	Genomic evidence of contemporary hybridization between <i>Schistosoma</i> species. <i>PLoS Pathogens</i> , 2022, 18, e1010706.	2.1	4
6933	Complete Genome Sequence of <i>Methylococcus capsulatus</i> MIR, a Methanotroph Capable of Growth on Methanol. <i>Microbiology Resource Announcements</i> , 2022, 11, .	0.3	3
6934	Jackfruit genome and population genomics provide insights into fruit evolution and domestication history in China. <i>Horticulture Research</i> , 2022, 9, .	2.9	5
6935	The chromosome-scale genome sequence of <i>Triadica sebifera</i> provides insight into fatty acids and anthocyanin biosynthesis. <i>Communications Biology</i> , 2022, 5, .	2.0	6
6936	Phylotranscriptomic and Evolutionary Analyses of the Green Algal Order Chaetophorales (Chlorophyceae, Chlorophyta). <i>Genes</i> , 2022, 13, 1389.	1.0	1
6937	A Beary Good Genome: Haplotype-Resolved, Chromosome-Level Assembly of the Brown Bear (<i>Ursus</i>)	1.1	1
6941	Investigating calcification-related candidates in a non-symbiotic scleractinian coral, <i>Tubastraea</i> spp.. <i>Scientific Reports</i> , 2022, 12, .	1.6	4
6942	<i>Lightella neohaematopini</i> : A new lineage of highly reduced endosymbionts coevolving with chipmunk lice of the genus <i>Neohaematopinus</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
6943	Transcriptomic Differences between Free-Living and Parasitic <i>Chilodonella uncinata</i> (Alveolata)	1.6	10
6944	Complete Genome Sequences of Three <i>Lactobacillus gasseri</i> Urine Isolates Obtained from Postmenopausal Women. <i>Microbiology Resource Announcements</i> , 0, , .	0.3	0
6945	Draft Genome Sequence of <i>Fusarium oxysporum</i> f. sp. <i>cubense</i> Tropical Race 4 from Peru, Obtained by Nanopore and Illumina Hybrid Assembly. <i>Microbiology Resource Announcements</i> , 2022, 11, .	0.3	4
6946	Energetics, but not development, is impacted in coral embryos exposed to ocean acidification. <i>Journal of Experimental Biology</i> , 2022, 225, .	0.8	1
6947	Analysis of flavonol regulator evolution in the Brassicaceae reveals MYB12, MYB111 and MYB21 duplications and MYB11 and MYB24 gene loss. <i>BMC Genomics</i> , 2022, 23, .	1.2	5
6948	De Novo Long-Read Whole-Genome Assemblies and the Comparative Pan-Genome Analysis of Ascochyta Blight Pathogens Affecting Field Pea. <i>Journal of Fungi</i> (Basel, Switzerland), 2022, 8, 884.	1.5	0
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6952	Transcriptome Analysis of <i>Podoscypha petalodes</i> Strain GGF6 Reveals the Diversity of Proteins Involved in Lignocellulose Degradation and Lignolytic Function. Indian Journal of Microbiology, 2022, 62, 569-582.	1.5	3
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6958	Developmental RNA-Seq transcriptomics of haploid germ cells and spermatozoa uncovers novel pathways associated with teleost spermiogenesis. Scientific Reports, 2022, 12, .	1.6	3
6959	Structural and genetic insights into a poly- γ -glutamic acid with in vitro antioxidant activity of <i>Bacillus velezensis</i> VCN56. World Journal of Microbiology and Biotechnology, 2022, 38, .	1.7	7
6960	Cascading effects of prey identity on gene expression in a kleptoplastidic ciliate. Journal of Eukaryotic Microbiology, 0, , .	0.8	2
6961	Pulmonate slug evolution is reflected in the de novo genome of <i>Arion vulgaris</i> Moquin-Tandon, 1855. Scientific Reports, 2022, 12, .	1.6	2
6963	Improved genome assembly provides new insights into the environmental adaptation of the American cockroach, <i>Periplaneta americana</i> . Archives of Insect Biochemistry and Physiology, 2022, 111, .	0.6	3
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6967	Genome sequencing of adapted diploid potato clones. Frontiers in Plant Science, 0, 13, .	1.7	4
6968	Twinkle twinkle brittle star: the draft genome of <i>Ophioderma brevispinum</i> (Echinodermata:). Tj ETQq1 1 0.784314 rgBT /Overlock 10 TFS	1.2	5
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6978	The nearly complete assembly of the <i>Cercis chinensis</i> genome and Fabaceae phylogenomic studies provide insights into new gene evolution. <i>Plant Communications</i> , 2023, 4, 100422.	3.6	4
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6980	Gene expression underlying parenting and being parented shows limited plasticity in response to different ambient temperatures. <i>Molecular Ecology</i> , 0, , .	2.0	3
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6983	Draft Genome Sequence of a Multiple Antibiotic Resistant <i>Staphylococcus aureus</i> NCTC 6571-UB Laboratory Strain. <i>Microbiology Resource Announcements</i> , 0, , .	0.3	0
6984	Chromosome-level and graphic genomes provide insights into metabolism of bioactive metabolites and cold-adaption of <i>Pueraria lobata</i> var. <i>montana</i> . <i>DNA Research</i> , 2022, 29, .	1.5	7
6986	Assembly of high-quality genomes of the locoweed <i>Oxytropis ochrocephala</i> and its endophyte <i>Alternaria oxytropis</i> provides new evidence for their symbiotic relationship and swainsonine biosynthesis. <i>Molecular Ecology Resources</i> , 2023, 23, 253-272.	2.2	4
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6991	Genomic Insights into Genetic Diploidization in the Homosporous Fern <i>Adiantum nelumboides</i> . <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	7
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6996	A high-quality genome of the dobsonfly <i>Neoneuromus ignobilis</i> reveals molecular convergences in aquatic insects. <i>Genomics</i> , 2022, 114, 110437.	1.3	0
6997	Transcriptional response of short-term nanoplastic exposure in <i>Monodonta labio</i> . <i>Marine Pollution Bulletin</i> , 2022, 182, 114005.	2.3	3
6998	The toxic effects of chronic atrazine exposure on the intestinal microbiota, metabolism and transcriptome of <i>Pelophylax nigromaculatus</i> larvae. <i>Journal of Hazardous Materials</i> , 2022, 440, 129817.	6.5	7
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7004	Functional genomics analysis reveals the evolutionary adaptation and demographic history of pygmy lorises. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	5
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7013	Oxidative stress, apoptosis, and transcriptional responses in <i>Acropora microphthalma</i> under simulated diving activities. <i>Marine Pollution Bulletin</i> , 2022, 183, 114084.	2.3	5
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7015	Genome sequencing and comparative analysis of <i>Ficus benghalensis</i> and <i>Ficus religiosa</i> species reveal evolutionary mechanisms of longevity. <i>IScience</i> , 2022, 25, 105100.	1.9	12

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7020	Rooting Species Trees Using Gene Tree-Species Tree Reconciliation. <i>Methods in Molecular Biology</i> , 2022, , 189-211.	0.4	3
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7027	Metagenomic approaches for understanding microbial communities in contaminated environments: Bioinformatic tools, case studies and future outlook. , 2023, , 103-156.		1
7028	Genome analysis of <i>Phrixothrix hirtus</i> (Phengodidae) railroad worm shows the expansion of odorant-binding gene families and positive selection on morphogenesis and sex determination genes. <i>Gene</i> , 2023, 850, 146917.	1.0	1
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7031	Chromosome-Level Genome Assembly of a Fragrant Japonica Rice Cultivar ‘Changxianggeng 1813’™ Provides Insights into Genomic Variations between Fragrant and Non-Fragrant Japonica Rice. <i>International Journal of Molecular Sciences</i> , 2022, 23, 9705.	1.8	5
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7033	WGS-Based Lineage and Antimicrobial Resistance Pattern of <i>Salmonella Typhimurium</i> Isolated during 2000–2017 in Peru. <i>Antibiotics</i> , 2022, 11, 1170.	1.5	7
7034	Near-Complete Whole-Genome Sequencing of Two <i>Burkholderia pseudomallei</i> Strains Harboring Novel Molecular Class D Beta-Lactamase Genes, Isolated from Malaysia. <i>Microbiology Resource Announcements</i> , 0, , .	0.3	1

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7049	A chromosome-scale genome assembly of <i>Quercus gilva</i> : Insights into the evolution of <i>Quercus</i> section <i>Cyclobalanopsis</i> (Fagaceae). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	8
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7062	Whole-genome assembly and analysis of a medicinal fungus: <i>Inonotus hispidus</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
7063	Multi-omics provides new insights into the domestication and improvement of dark jute (<i>T. ETQq1 1 0.784314 rBT /Overlock 10</i>)	2.8	1
7064	Transcriptome analysis of five different tissues of bitter melon (<i>Momordica charantia</i> L.) fruit identifies full-length genes involved in seed oil biosynthesis. <i>Scientific Reports</i> , 2022, 12, .	1.6	0
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7076	Chromosome-level genome assembly of <i>Amomum tsao-ko</i> provides insights into the biosynthesis of flavor compounds. <i>Horticulture Research</i> , 2022, 9, .	2.9	5
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7081	A High-quality genome assembly of <i>Lactarius hatsudake</i> strain JH5. <i>G3: Genes, Genomes, Genetics</i> , 0, , .	0.8	0
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7084	Whole genome analyses based on single, field collected spores of the arbuscular mycorrhizal fungus <i>Funneliformis geosporum</i> . Mycorrhiza, 2022, 32, 361-371.	1.3	6
7085	Genetic Diversity of <i>Actinobacillus pleuropneumoniae</i> Serovars in Hungary. Veterinary Sciences, 2022, 9, 511.	0.6	6
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7088	The genetic architecture of phenotypic diversity in the Betta fish (<i>Betta splendens</i>). Science Advances, 2022, 8, .	4.7	10
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7099	The Gain and Loss of Cryptochrome/Photolyase Family Members during Evolution. Genes, 2022, 13, 1613.	1.0	11
7100	The coral <i>Acropora loripes</i> genome reveals an alternative pathway for cysteine biosynthesis in animals. Science Advances, 2022, 8, .	4.7	10
7101	Whole-genome sequence analysis for evaluating the safety and probiotic potential of <i>Lactiplantibacillus pentosus</i> 9D3, a gamma-aminobutyric acid (GABA)-producing strain isolated from Thai pickled weed. Frontiers in Microbiology, 0, 13, .	1.5	8

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7104	High-Quality Genome Sequence Resource of <i>Lasiodiplodia theobromae</i> JMB122, a Fungal Pathogen Causing Peach Gummosis. <i>Molecular Plant-Microbe Interactions</i> , 2022, 35, 938-940.	1.4	3
7105	Genome-wide characterization of two <i>Aubrieta</i> taxa: <i>Aubrieta canescens</i> subsp. <i>canescens</i> and <i>Au. macrostyla</i> (Brassicaceae). <i>AoB PLANTS</i> , 2022, 14, .	1.2	0
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7109	Calcium homeostasis disruption initiates rapid growth after micro-fragmentation in the scleractinian coral <i>Porites lobata</i> . <i>Ecology and Evolution</i> , 2022, 12, .	0.8	4
7110	A chromosome-level assembly of the widely used Rockefeller strain of <i>Aedes aegypti</i> , the yellow fever mosquito. <i>G3: Genes, Genomes, Genetics</i> , 0, , .	0.8	1
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7113	Evidence for evolutionary adaptation of mixotrophic nanoflagellates to warmer temperatures. <i>Global Change Biology</i> , 2022, 28, 7094-7107.	4.2	9
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7116	A genome for <i>Cissus</i> illustrates features underlying its evolutionary success in dry savannas. <i>Horticulture Research</i> , 2022, 9, .	2.9	3
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7120	Targeted Mutagenesis of the Multicopy Myrosinase Gene Family in Allotetraploid Brassica juncea Reduces Pungency in Fresh Leaves across Environments. <i>Plants</i> , 2022, 11, 2494.	1.6	11
7121	Chromosome-level genome assembly and resequencing of camphor tree (<i>Cinnamomum</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tj ETQq1 biosynthesis of <i>Cinnamomum</i> . <i>Horticulture Research</i> , 2022, 9, .	2.9	5
7122	A chromosome-scale genome assembly of turmeric provides insights into curcumin biosynthesis and tuber formation mechanism. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
7123	Characterization of defense responses against bacterial pathogens in duckweeds lacking <i>EDS1</i> . <i>New Phytologist</i> , 2022, 236, 1838-1855.	3.5	9

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7134	PacBio Full-Length and Illumina Transcriptomes of the Gill Reveal the Molecular Response of <i>Corbicula fluminea</i> under Aerial Exposure. <i>International Journal of Molecular Sciences</i> , 2022, 23, 11474.	1.8	1
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7141	Genome assembly of the Brassicaceae diploid <i>Orychophragmus violaceus</i> reveals complex whole-genome duplication and evolution of dihydroxy fatty acid metabolism. <i>Plant Communications</i> , 2023, 4, 100432.	3.6	7
7142	Dynamic Transcriptional Landscape of Grass Carp (<i>Ctenopharyngodon idella</i>) Reveals Key Transcriptional Features Involved in Fish Development. <i>International Journal of Molecular Sciences</i> , 2022, 23, 11547.	1.8	2
7143	Draft Genome Sequence of an <i>Aspergillus</i> Strain Isolated from a Honey Bee Pupa. <i>Microbiology Resource Announcements</i> , 2022, 11, .	0.3	1
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7146	Combined “omics framework reveals how ant symbionts benefit the Neotropical ant-plant <i>Tococa quadralata</i> at different levels. <i>IScience</i> , 2022, 25, 105261.	1.9	3
7147	Genomic insight into the nocturnal adaptation of the black-crowned night heron (<i>Nycticorax</i>) Tj ETQq0 0 0 rgBT /Oyerlock 10 Tf 50 662	1.2	2
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7149	Novel genome sequence of Chinese cavefish (<i>Triplophysa rosa</i>) reveals pervasive relaxation of natural selection in cavefish genomes. <i>Molecular Ecology</i> , 2022, 31, 5831-5845.	2.0	12
7150	De novo genome assembly of the medicinal plant <i>Gentiana macrophylla</i> provides insights into the genomic evolution and biosynthesis of iridoids. <i>DNA Research</i> , 2022, 29, .	1.5	10
7152	Mating strategy predicts gene presence/absence patterns in a genus of simultaneously hermaphroditic flatworms. <i>Evolution; International Journal of Organic Evolution</i> , 0, , .	1.1	1
7153	Draft genome and multi-tissue transcriptome assemblies of the Neotropical leaf-frog <i>Phyllomedusa bahiana</i> . <i>G3: Genes, Genomes, Genetics</i> , 0, , .	0.8	0
7155	Comparative genomics of <i>Sarcoptes scabiei</i> provide new insights into adaptation to permanent parasitism and within-host species divergence. <i>Transboundary and Emerging Diseases</i> , 2022, 69, 3468-3484.	1.3	4
7156	A chromosome-level genome assembly for <i>Dracaena cochinchinensis</i> reveals the molecular basis of its longevity and formation of dragon’s blood. <i>Plant Communications</i> , 2022, 3, 100456.	3.6	6
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7164	Genomes of Two Flying Squid Species Provide Novel Insights into Adaptations of Cephalopods to Pelagic Life. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 1053-1065.	3.0	0
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7172	Genome Resources for <i>Ensete ventricosum</i> (Enset) and Related Species. <i>Compendium of Plant Genomes</i> , 2022, , 355-371.	0.3	1
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7179	Phylogenomics provides insights into the evolution of cactophily and host plant shifts in <i>Drosophila</i> . <i>Molecular Phylogenetics and Evolution</i> , 2023, 178, 107653.	1.2	4
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7183	Brain de novo transcriptome assembly of a toad species showing polymorphic anti-predatory behavior. <i>Scientific Data</i> , 2022, 9, .	2.4	3
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7185	Genome Assembly of the Medicinal Plant <i>Voacanga thouarsii</i> . <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	4
7186	Genome report: chromosome-level draft assemblies of the snow leopard, African leopard, and tiger (<i>Panthera uncia</i> , <i>Panthera pardus pardus</i> , and <i>Panthera tigris</i>). <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	5
7187	A reference-grade genome assembly for <i>Astragalus mongholicus</i> and insights into the biosynthesis and high accumulation of triterpenoids and flavonoids in its roots. <i>Plant Communications</i> , 2023, 4, 100469.	3.6	8
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7189	The pangenome of the wheat pathogen <i>Pyrenophora tritici-repentis</i> reveals novel transposons associated with necrotrophic effectors ToxA and ToxB. <i>BMC Biology</i> , 2022, 20, .	1.7	15
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7199	Transcriptome-based Phylogeny of the Semi-aquatic Bugs (Hemiptera: Heteroptera: Gerromorpha) Reveals Patterns of Lineage Expansion in a Series of New Adaptive Zones. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	4
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7201	Genome Sequence Resource of <i>Serratia ureilytica</i> HNU47: a strain with Biocontrol Potential Against Bacterial Wilt Pathogen <i>Ralstonia solanacearum</i> . <i>Plant Disease</i> , 0, , .	0.7	0
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7210	The genome and lifestage-specific transcriptomes of a plant-parasitic nematode and its host reveal susceptibility genes involved in trans-kingdom synthesis of vitamin B5. <i>Nature Communications</i> , 2022, 13, .	5.8	28
7211	Genome Resources for Four <i>Clariireedia</i> Species Causing Dollar Spot on Diverse Turfgrasses. <i>Plant Disease</i> , 2023, 107, 929-934.	0.7	2
7212	The genome of single-petal jasmine (<i>Jasminum sambac</i>) provides insights into heat stress tolerance and aroma compound biosynthesis. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
7215	Comparative Transcriptome Analysis to Reveal Differentially Expressed Cytochrome P450 in Response to Imidacloprid in the Aphid <i>Lion</i> , <i>Chrysoperla zastrowi sillemi</i> (Esben-Petersen). <i>Insects</i> , 2022, 13, 900.	1.0	0

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7227	Gene Recruitments and Dismissals in the Argonaut Genome Provide Insights into Pelagic Lifestyle Adaptation and Shell-like Eggcase Reacquisition. <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	6
7228	<i>Streptomyces solincola</i> sp. nov., isolated from soil in Malaysia. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	1
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7231	The rate and role of pseudogenes of the <i>Mycobacterium tuberculosis</i> complex. <i>Microbial Genomics</i> , 2022, 8, .	1.0	3
7232	Telomere-to-telomere genome assembly of bitter melon (<i>Momordica charantia</i> L. var.) Tj ETQq1 1 0.784314 rgBT /Overlock 10. <i>Horticulture Research</i> , 2023, 10, .	2.9	16
7233	High-quality genome resource of a novel Venturiaceae sp. KMAF11, isolated from diseased <i>Colobanthus quitensis</i> , an Antarctic flowering plant. <i>Plant Disease</i> , 0, , .	0.7	0
7234	De novo genome assembly and annotation of <i>Holothuria scabra</i> (Jaeger, 1833) from nanopore sequencing reads. <i>Genes and Genomics</i> , 2022, 44, 1487-1498.	0.5	3
7235	BuscoPhylo: a webserver for Busco-based phylogenomic analysis for non-specialists. <i>Scientific Reports</i> , 2022, 12, .	1.6	6
7236	The reference genome and organelle genomes of wasabi (<i>Eutrema japonicum</i>). <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1

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7238	Genome of the endangered Guatemalan Beaded Lizard, <i>Heloderma charlesbogerti</i> , reveals evolutionary relationships of squamates and declines in effective population sizes. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	2
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7240	A contiguous <i>de novo</i> genome assembly of sugar beet EL10 (<i>Beta vulgaris</i> L.). <i>DNA Research</i> , 2023, 30, .	1.5	15
7241	Assessment of the Genetic Diversity and Population Structure of <i>Rhizophora apiculata</i> Blume (Rhizophoraceae) in Thailand. <i>Biology</i> , 2022, 11, 1449.	1.3	4
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7249	Multi-Organ Transcriptome Response of Lumpfish (<i>Cyclopterus lumpus</i>) to <i>Aeromonas salmonicida</i> Subspecies <i>salmonicida</i> Systemic Infection. <i>Microorganisms</i> , 2022, 10, 2113.	1.6	6
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7252	Compensatory Genetic and Transcriptional Cytonuclear Coordination in Allopolyploid Lager Yeast (<i>Saccharomyces pastorianus</i>). <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	1
7253	A chromosome-level genome of <i>Semiothisa cinerearia</i> provides insights into its genome evolution and control. <i>BMC Genomics</i> , 2022, 23, .	1.2	1
7254	Assembly-free discovery of human novel sequences using long reads. <i>DNA Research</i> , 2022, 29, .	1.5	2
7255	De novo assembly and characterization of the draft genome of the cashew (<i>Anacardium occidentale</i>) Tj ETQq0 0 0 ggBT /Over lock 10 Tf	1.6	4
7256	Phylogenomics and gene selection in <i>Aspergillus welwitschiae</i> : Possible implications in the pathogenicity in <i>Agave sisalana</i> . <i>Genomics</i> , 2022, 114, 110517.	1.3	3
7257	Gene family expansions in Antarctic winged midge as a strategy for adaptation to cold environments. <i>Scientific Reports</i> , 2022, 12, .	1.6	7
7260	De Novo Assembly of a Sarcocarp Transcriptome Set Identifies AaMYB1 as a Regulator of Anthocyanin Biosynthesis in <i>Actinidia arguta</i> var. <i>purpurea</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 12120.	1.8	0

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7743	PANAS: Pipeline and a Case Study to Obtain Synonymous and Nonsynonymous Substitution Rates in Genes of Platyhelminthes. <i>Comparative Parasitology</i> , 2023, 90, .	0.0	1
7745	Gene expression responses of <i>Bactrocera tryoni</i> larvae feeding on different ripening stages of tomato fruit. <i>Journal of Applied Entomology</i> , 2023, 147, 205-230.	0.8	0
7746	A high-quality reference genome for the fission yeast <i>Schizosaccharomyces osmophilus</i> . <i>G3: Genes, Genomes, Genetics</i> , 2023, 13, .	0.8	13
7747	Macroevolutionary diversity of traits and genomes in the model yeast genus <i>Saccharomyces</i> . <i>Nature Communications</i> , 2023, 14, .	5.8	8
7748	Insights into the convergent evolution of fructan biosynthesis in angiosperms from the highly characteristic chicory genome. <i>New Phytologist</i> , 2023, 238, 1245-1262.	3.5	4
7749	Genome Report: Genome sequence of 1S1, a transformable and highly regenerable diploid potato for use as a model for gene editing and genetic engineering. <i>G3: Genes, Genomes, Genetics</i> , 2023, 13, .	0.8	1
7750	A chromosome-level reference genome of the wax gourd (<i>Benincasa hispida</i>). <i>Scientific Data</i> , 2023, 10, .	2.4	4
7751	Nectary development in <i>Cleome violacea</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
7752	Genome Sequence and Analysis of <i>Nicotiana benthamiana</i> , the Model Plant for Interactions between Organisms. <i>Plant and Cell Physiology</i> , 2023, 64, 248-257.	1.5	14
7753	Dissecting the genetic basis of heterosis in elite super-hybrid rice. <i>Plant Physiology</i> , 2023, 192, 307-325.	2.3	4
7754	Genome and haplotype provide insights into the population differentiation and breeding improvement of <i>Gossypium barbadense</i> . <i>Journal of Advanced Research</i> , 2023, 54, 15-27.	4.4	2
7755	Insights into the differentiation and adaptation within <i>Circaeasteraceae</i> from <i>Circaeaster agrestis</i> genome sequencing and resequencing. <i>IScience</i> , 2023, 26, 106159.	1.9	0
7756	The genome of <i>Magnolia hypoleuca</i> provides a new insight into cold tolerance and the evolutionary position of magnoliids. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	3
7757	Persistence of <i>Metarhizium brunneum</i> (Ascomycota: Hypocreales) in the Soil Is Affected by Formulation Type as Shown by Strain-Specific DNA Markers. <i>Journal of Fungi (Basel, Switzerland)</i> , 2023, 9, 229.	1.5	2
7758	The subgenome <i>Saccharum spontaneum</i> contributes to sugar accumulation in sugarcane as revealed by full-length transcriptomic analysis. <i>Journal of Advanced Research</i> , 2023, 54, 1-13.	4.4	3
7759	The genome of a vestimentiferan tubeworm (<i>Ridgeia piscesae</i>) provides insights into its adaptation to a deep-sea environment. <i>BMC Genomics</i> , 2023, 24, .	1.2	4
7760	Response of the obligate halophile fungus <i>Aspergillus loretoensis</i> to stress salinity. <i>Journal of Microbiology & Experimentation</i> , 2023, 11, 26-33.	0.1	0

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7761	A Mitosome With Distinct Metabolism in the Uncultured Protist Parasite <i>Paramikrocytos cancri</i> (Rhizaria, Ascetosporea). <i>Genome Biology and Evolution</i> , 2023, 15, .	1.1	3
7762	Draft Genome Sequence of <i>Exophiala</i> Strain HKRS030, a Fungus Capable of Reducing Iron but Not Nitrate. <i>Microbiology Resource Announcements</i> , 2023, 12, .	0.3	0
7763	A chromosomal reference genome sequence for the malaria mosquito, <i>Anopheles gambiae</i> , Giles, 1902, Ifakara strain. <i>Wellcome Open Research</i> , 0, 8, 74.	0.9	1
7764	Genome assembly, resequencing and genome-wide association analyses provide novel insights into the origin, evolution and flower colour variations of flowering cherry. <i>Plant Journal</i> , 2023, 114, 519-533.	2.8	4
7766	Biotechnologically potential genes in a polysaccharide-degrading epibiont of the Indonesian brown algae <i>Hydroclathrus</i> sp.. <i>Journal of Genetic Engineering and Biotechnology</i> , 2023, 21, 18.	1.5	1
7767	<i>Wolbachia</i> and <i>Spiroplasma</i> endosymbionts in the <i>Anurida maritima</i> (Collembola) species group. , 0, .		0
7768	A gap-free and haplotype-resolved lemon genome provides insights into flavor synthesis and huanglongbing (HLB) tolerance. <i>Horticulture Research</i> , 2023, 10, .	2.9	6
7769	Chromosomal-level genome assembly of the high-quality Xian/Indica rice (<i>Oryza sativa</i> L.) Xiangyaxiangzhan. <i>BMC Plant Biology</i> , 2023, 23, .	1.6	0
7770	A chromosome-level genome assembly of <i>Ostrea denselamellosa</i> provides initial insights into its evolution. <i>Genomics</i> , 2023, 115, 110582.	1.3	3
7771	<i>Mucilaginibacter straminoryzae</i> sp. nov., isolated from rice straw used for growing periphyton. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2023, 73, .	0.8	0
7773	An improved reference genome for <i>Trifolium subterraneum</i> L. provides insight into molecular diversity and intra-specific phylogeny. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	5
7774	Chromosome-Level Genome Assembly of the Rough-Toothed Dolphin (<i>Steno bredanensis</i>). <i>Journal of Marine Science and Engineering</i> , 2023, 11, 418.	1.2	2
7776	Dataset of 143 metagenome-assembled genomes from the Arctic and Atlantic Oceans, including 21 for eukaryotic organisms. <i>Data in Brief</i> , 2023, 47, 108990.	0.5	1
7777	polishCLR: A Nextflow Workflow for Polishing PacBio CLR Genome Assemblies. <i>Genome Biology and Evolution</i> , 2023, 15, .	1.1	2
7778	Complete Genome Sequence of <i>Bacillus velezensis</i> TH-1, a Candidate Biocontrol Bacterium from China. <i>Molecular Plant-Microbe Interactions</i> , 2023, 36, 305-308.	1.4	5
7779	Sizing Up the Onychophoran Genome: Repeats, Introns, and Gene Family Expansion Contribute to Genome Gigantism in <i>Epiperipatus broadwayi</i> . <i>Genome Biology and Evolution</i> , 2023, 15, .	1.1	2
7780	Genome survey and genetic characterization of <i>Acacia pachyceras</i> O. Schwartz. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	2
7781	Resequencing of durian genomes reveals large genetic variations among different cultivars. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	0

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7782	Genomics and biochemical analyses reveal a metabolon key to Î²-L-ODAP biosynthesis in <i>Lathyrus sativus</i> . <i>Nature Communications</i> , 2023, 14, .	5.8	10
7783	Identification and expression profile analysis of chemosensory genes in pine needle gall midge, <i>Thecodiplosis japonensis</i> (Diptera: Cecidomyiidae). <i>Frontiers in Physiology</i> , 0, 14, .	1.3	0
7784	First draft genome of <i>Thecaphora frezii</i> , causal agent of peanut smut disease. <i>BMC Genomic Data</i> , 2023, 24, .	0.7	5
7785	The genome of the egg parasitoid <i>Trissolcus basalis</i> (Wollaston) (Hymenoptera, Scelionidae), a model organism and biocontrol agent of stink bugs. <i>Journal of Hymenoptera Research</i> , 0, 95, 31-44.	0.8	1
7786	Whole Genome Sequence of an Edible Mushroom <i>Oudemansiella raphanipes</i> (Changgengu). <i>Journal of Fungi</i> (Basel, Switzerland), 2023, 9, 266.	1.5	3
7787	Phylotranscriptomics and evolution of key genes for terpene biosynthesis in Pinaceae. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	0
7788	Host immune responses to enzootic and invasive pathogen lineages vary in magnitude, timing, and efficacy. <i>Molecular Ecology</i> , 2023, 32, 2252-2270.	2.0	1
7790	Transcriptome-based variations effectively untangling the intraspecific relationships and selection signals in Xinyang Maojian tea population. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	1
7791	Draft genome of the oriental garden lizard (<i>Calotes versicolor</i>). <i>Frontiers in Genetics</i> , 0, 14, .	1.1	0
7792	Chromosome-level genome assembly and population genomics of Mongolian racerunner (<i>Eremias</i>) Tj ETQq1 1 0.784314 rgBT ₂ /Overlook	1.7	0
7793	Genomics of Secondarily Temperate Adaptation in the Only Non-Antarctic Icefish. <i>Molecular Biology and Evolution</i> , 2023, 40, .	3.5	4
7794	High-Quality Nuclear Genome and Mitogenome of <i>Bipolaris sorokiniana</i> LK93, a Devastating Pathogen Causing Wheat Root Rot. <i>Molecular Plant-Microbe Interactions</i> , 2023, 36, 452-456.	1.4	1
7795	Benchmark study for evaluating the quality of reference genomes and gene annotations in 114 species. <i>Frontiers in Veterinary Science</i> , 0, 10, .	0.9	0
7797	Genomic, transcriptomic, and metabolomic analysis of <i>Oldenlandia corymbosa</i> reveals the biosynthesis and mode of action of anti-cancer metabolites. <i>Journal of Integrative Plant Biology</i> , 2023, 65, 1442-1466.	4.1	7
7798	Chromosome-length genome assembly of <i>Teladorsagia circumcincta</i> – a globally important helminth parasite in livestock. <i>BMC Genomics</i> , 2023, 24, .	1.2	4
7799	Two Complete Genomes of Male-Killing <i>Wolbachia</i> Infecting <i>Ostrinia</i> Moth Species Illuminate Their Evolutionary Dynamics and Association with Hosts. <i>Microbial Ecology</i> , 2023, 86, 1740-1754.	1.4	3
7801	Phagocytosis underpins the biotrophic lifestyle of intracellular parasites in the class <i>Phytophyta</i> (Rhizaria). <i>New Phytologist</i> , 2023, 238, 2130-2143.	3.5	2
7802	Diversity of the Antimicrobial Peptide Genes in <i>Collembola</i> . <i>Insects</i> , 2023, 14, 215.	1.0	1

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7803	A chromosome-level genome assembly for <i>Erianthus fulvus</i> provides insights into its biofuel potential and facilitates breeding for improvement of sugarcane. <i>Plant Communications</i> , 2023, 4, 100562.	3.6	4
7804	The Chromosome-Level Assembly of Ramie (<i>Boehmeria nivea</i> L.) Genome Provides Insights into Molecular Regulation of Fiber Fineness. <i>Journal of Natural Fibers</i> , 2023, 20, .	1.7	3
7805	Chromosome Fissions and Fusions Act as Barriers to Gene Flow between <i>Brenthis</i> Fritillary Butterflies. <i>Molecular Biology and Evolution</i> , 2023, 40, .	3.5	17
7806	Giant proteins in a giant cell: Molecular basis of ultrafast Ca ²⁺ -dependent cell contraction. <i>Science Advances</i> , 2023, 9, .	4.7	4
7807	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. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	0
7808	Functional annotation and comparative analysis of four <i>Botrytis cinerea</i> mitogenomes reported from Punjab, Pakistan. <i>Saudi Journal of Biological Sciences</i> , 2023, 30, 103605.	1.8	1
7809	Ancient Rapid Radiation Explains Most Conflicts Among Gene Trees and Well-Supported Phylogenomic Trees of Nostoclean Cyanobacteria. <i>Systematic Biology</i> , 2023, 72, 694-712.	2.7	2
7810	Latitudinal variation and plasticity in response to temperature in <i>Geukensia demissa</i> . <i>Ecology and Evolution</i> , 2023, 13, .	0.8	3
7811	Transcriptomic thermal plasticity underlying gonadal development in a turtle with ZZ/ZW sex chromosomes despite canalized genotypic sex determination. <i>Ecology and Evolution</i> , 2023, 13, .	0.8	5
7813	Transposable element and host silencing activity in gigantic genomes. <i>Frontiers in Cell and Developmental Biology</i> , 0, 11, .	1.8	3
7814	A genome and single-nucleus cerebral cortex transcriptome atlas of the short-finned pilot whale <i>Globicephala macrorhynchus</i> . <i>Molecular Ecology Resources</i> , 2023, 23, 1108-1123.	2.2	1
7816	Transcriptome analysis of gall oak (<i>Quercus infectoria</i>): De novo assembly, functional annotation and metabolic pathways analysis. <i>Genomics</i> , 2023, 115, 110588.	1.3	3
7817	Weak range-wide population structure in the blackfin tuna (<i>Thunnus atlanticus</i>) revealed by analysis of genome-wide SNPs. <i>ICES Journal of Marine Science</i> , 0, , .	1.2	0
7818	Adaptations of <i>Pseudoxylaria</i> towards a comb-associated lifestyle in fungus-farming termite colonies. <i>ISME Journal</i> , 2023, 17, 733-747.	4.4	4
7819	Core cellular and tissue-specific mechanisms enable desiccation tolerance in <i>Craterostigma</i> . <i>Plant Journal</i> , 2023, 114, 231-245.	2.8	9
7820	A global phylogenomic analysis of the shiitake genus <i>Lentinula</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	3.3	5
7821	Assembling Quality Genomes of Flax Fungal Pathogens from Oxford Nanopore Technologies Data. <i>Journal of Fungi</i> (Basel, Switzerland), 2023, 9, 301.	1.5	3
7822	The origin of human pathogenicity and biological interactions in Chaetothyriales. <i>Fungal Diversity</i> , 0, , .	4.7	3

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7823	A population of stem cells with strong regenerative potential discovered in deer antlers. <i>Science</i> , 2023, 379, 840-847.	6.0	28
7824	Enhanced mercury phytoremediation by <i>Pseudomonodictys pantanalensis</i> sp. nov. A73 and <i>Westerdykella aquatica</i> P71. <i>Brazilian Journal of Microbiology</i> , 0, , .	0.8	2
7825	Introgressive hybridization in the west Pacific pen shells (genus <i>Atrina</i>): Restricted interspecies gene flow within the genome. <i>Molecular Ecology</i> , 2023, 32, 2945-2963.	2.0	0
7828	Genome sequence of the cacao pathogen <i>Monilophthora roreri</i> belonging to the invasive <i>A1B1</i> mating type: a resource for genomic efforts in cacao pathology. <i>PhytoFrontiers</i> , 0, , .	0.8	0
7829	Full-Length Transcriptomes and Sex-Based Differentially Expressed Genes in the Brain and Ganglia of Giant River Prawn <i>Macrobrachium rosenbergii</i> . <i>Biomolecules</i> , 2023, 13, 460.	1.8	2
7830	Dual domestications and origin of traits in grapevine evolution. <i>Science</i> , 2023, 379, 892-901.	6.0	60
7831	Pangenomic analysis identifies structural variation associated with heat tolerance in pearl millet. <i>Nature Genetics</i> , 2023, 55, 507-518.	9.4	31
7832	Heritability and gene functions associated with sclerotia formation of <i>Rhizoctonia solani</i> AG-7 using whole genome sequencing and genome-wide association study. <i>Microbial Genomics</i> , 2023, 9, .	1.0	0
7833	Chromosome-level reference genome of <i>Tetrastigma hemsleyanum</i> (Vitaceae) provides insights into genomic evolution and the biosynthesis of phenylpropanoids and flavonoids. <i>Plant Journal</i> , 2023, 114, 805-823.	2.8	5
7834	Tapping Culture Collections for Fungal Endophytes: First Genome Assemblies for Three Genera and Five Species in the <i>Ascomycota</i> . <i>Genome Biology and Evolution</i> , 2023, 15, .	1.1	3
7835	The revised reference genome of the leopard gecko (<i>Eublepharis macularius</i>) provides insight into the considerations of genome phasing and assembly. <i>Journal of Heredity</i> , 2023, 114, 513-520.	1.0	9
7836	Omics in the Red Palm Weevil <i>Rhynchophorus ferrugineus</i> (Olivier) (Coleoptera: Curculionidae): A Bridge to the Pest. <i>Insects</i> , 2023, 14, 255.	1.0	9
7837	Investigating the genetic basis of vertebrate dispersal combining <i>scRNA-seq</i> , <i>scRAD-seq</i> and quantitative genetics. <i>Molecular Ecology</i> , 2023, 32, 3060-3075.	2.0	3
7838	Genomes of two Extinct Wild reptiles from Christmas Island reveal distinct evolutionary histories and conservation insights. <i>Molecular Ecology Resources</i> , 0, , .	2.2	1
7840	Chromosome-Scale Assembly of the Complete Genome Sequence of <i>Leishmania</i> (Mundinia) <i>procaviensis</i> Isolate 253, Strain LV425. <i>Microbiology Resource Announcements</i> , 2023, 12, .	0.3	0
7841	Near-Complete Whole-Genome Sequence of <i>Paenibacillus</i> sp. nov. Strain J5C2022, a Sucrotolerant and Endospore-Forming Bacterium Isolated from Highly Concentrated Sugar Brine. <i>Microbiology Resource Announcements</i> , 2023, 12, .	0.3	0
7842	Identifying Genes Associated with Female Flower Development of <i>Phellodendron amurense</i> Rupr. Using a Transcriptomics Approach. <i>Genes</i> , 2023, 14, 661.	1.0	2
7844	Genomic Resources of Four <i>Colletotrichum</i> Species (<i>C. fiorinae</i> , <i>C. chrysophilum</i> , <i>C. Tj ETQq1</i> 1 0.784314 rgBT /Overlock 10 Eastern U.S.. <i>Molecular Plant-Microbe Interactions</i> , 0, , .	1.4	0

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7846	The terrestrial isopod symbiont <i>Candidatus</i> Hepatincola porcellionum TM is a potential nutrient scavenger related to <i>Holosporales</i> symbionts of protists. <i>ISME Communications</i> , 2023, 3, .	1.7	2
7847	Transcriptome analysis and exploration of genes involved in the biosynthesis of secoiridoids in <i>Gentiana rhodantha</i> . <i>PeerJ</i> , 0, 11, e14968.	0.9	0
7848	Unique gene duplications and conserved microsynteny potentially associated with resistance to wood decay in the Lauraceae. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	0
7849	The giant diploid faba genome unlocks variation in a global protein crop. <i>Nature</i> , 2023, 615, 652-659.	13.7	40
7850	Chromosome-level genome assembly of <i>Phrynocephalus forsythii</i> using third-generation DNA sequencing and Hi-C analysis. <i>DNA Research</i> , 2023, 30, .	1.5	0
7851	Chromosome-scale Genome Assembly of the Yellow Nutsedge (<i>Cyperus esculentus</i>). <i>Genome Biology and Evolution</i> , 2023, 15, .	1.1	2
7852	Genomics, Population Divergence, and Historical Demography of the World's Largest and Endangered Butterfly, The Queen Alexandra's Birdwing. <i>Genome Biology and Evolution</i> , 2023, 15, .	1.1	4
7853	Transcriptomic analysis of mosaic brain differentiation underlying complex division of labor in a social insect. <i>Journal of Comparative Neurology</i> , 2023, 531, 853-865.	0.9	2
7855	Chromosome-level genome of the three-spot damselfish, <i>Dascyllus trimaculatus</i> . <i>G3: Genes, Genomes, Genetics</i> , 2023, 13, .	0.8	2
7856	The chromosome-scale genome assembly of <i>Jasminum sambac</i> var. <i>unifoliatum</i> provides insights into the formation of floral fragrance. <i>Horticultural Plant Journal</i> , 2023, 9, 1131-1148.	2.3	2
7859	Comparative genomics and transcriptomic response to root exudates of six rice root-associated <i>Burkholderia sensu lato</i> species. , 0, 3, .		1
7860	Testosterone Coordinates Gene Expression Across Different Tissues to Produce Carotenoid-Based Red Ornamentation. <i>Molecular Biology and Evolution</i> , 2023, 40, .	3.5	4
7861	<i>iGDP</i> : An integrated genome decontamination pipeline for wild ciliated microeukaryotes. <i>Molecular Ecology Resources</i> , 2023, 23, 1182-1193.	2.2	2
7862	Draft Genome Sequence of <i>Granulicatella</i> sp. Strain S8, Isolated from a Marine Fish, <i>Seriola quinqueradiata</i> . <i>Microbiology Resource Announcements</i> , 2023, 12, .	0.3	1
7863	The first chromosome-level <i>Fallopia multiflora</i> genome assembly provides insights into stilbene biosynthesis. <i>Horticulture Research</i> , 2023, 10, .	2.9	1
7864	Draft Genome Sequence of a <i>Delftia</i> sp., a Member of an Electroactive Community Enriched from Wastewater from the Indian Institute of Technology Delhi, India. <i>Microbiology Resource Announcements</i> , 2023, 12, .	0.3	2
7865	Pleomorphic Variants of <i>Borrelia</i> (syn. <i>Borrelia</i>) <i>burgdorferi</i> Express Evolutionary Distinct Transcriptomes. <i>International Journal of Molecular Sciences</i> , 2023, 24, 5594.	1.8	0
7866	An improved germline genome assembly for the sea lamprey <i>Petromyzon marinus</i> illuminates the evolution of germline-specific chromosomes. <i>Cell Reports</i> , 2023, 42, 112263.	2.9	17

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7893	Stop or Not: Genome-Wide Profiling of Reassigned Stop Codons in Ciliates. <i>Molecular Biology and Evolution</i> , 2023, 40, .	3.5	2
7894	The genome sequence of the Golden-tailed Leafwalker, <i>Xylota sylvarum</i> (Linnaeus, 1758). <i>Wellcome Open Research</i> , 0, 8, 134.	0.9	0
7895	Multiple gene co-options underlie the rapid evolution of sexually deceptive flowers in <i>Gorteria diffusa</i> . <i>Current Biology</i> , 2023, 33, 1502-1512.e8.	1.8	6
7896	Genomes of four <i>Streptomyces</i> strains reveal insights into putative new species and pathogenicity of scab-causing organisms. <i>BMC Genomics</i> , 2023, 24, .	1.2	1
7897	The genome sequence of the Oak-tree Pug, <i>Eupithecia dodoneata</i> (Guenée, 1858). <i>Wellcome Open Research</i> , 0, 8, 133.	0.9	1
7898	Paralog editing tunes rice stomatal density to maintain photosynthesis and improve drought tolerance. <i>Plant Physiology</i> , 2023, 192, 1168-1182.	2.3	6
7901	Metabiotics Signature through Genome Sequencing and In Vitro Inhibitory Assessment of a Novel <i>Lactococcus lactis</i> Strain UTNCys6-1 Isolated from Amazonian Camu-Camu Fruits. <i>International Journal of Molecular Sciences</i> , 2023, 24, 6127.	1.8	2
7905	Comprehensive genomic analyses of <i>Vigna unguiculata</i> provide insights into population differentiation and the genetic basis of key agricultural traits. <i>Plant Biotechnology Journal</i> , 2023, 21, 1426-1439.	4.1	2
7908	An improved reference of the grapevine genome reasserts the origin of the PN40024 highly homozygous genotype. <i>G3: Genes, Genomes, Genetics</i> , 2023, 13, .	0.8	13
7909	Pan-genome inversion index reveals evolutionary insights into the subpopulation structure of Asian rice. <i>Nature Communications</i> , 2023, 14, .	5.8	13
7910	De novo transcriptome assemblies of five major European oilseed rape insect pests. <i>BMC Genomic Data</i> , 2023, 24, .	0.7	2
7912	Convergent and complementary selection shaped gains and losses of eusociality in sweat bees. <i>Nature Ecology and Evolution</i> , 2023, 7, 557-569.	3.4	9
7913	Draft genome sequence of <i>Enterobacter chengduensis</i> ECC445, isolated from fresh water in the West Indies. <i>BMC Genomic Data</i> , 2023, 24, .	0.7	1
7914	Genome and Genetic Engineering of the House Cricket (<i>Acheta domesticus</i>): A Resource for Sustainable Agriculture. <i>Biomolecules</i> , 2023, 13, 589.	1.8	4
7915	Assembling highly repetitive <i>Xanthomonas</i> TALomes using Oxford Nanopore sequencing. <i>BMC Genomics</i> , 2023, 24, .	1.2	3
7916	Benchmarking datasets for assembly-based variant calling using high-fidelity long reads. <i>BMC Genomics</i> , 2023, 24, .	1.2	4
7918	Resequencing of a Pekin duck breeding population provides insights into the genomic response to short-term artificial selection. <i>GigaScience</i> , 2023, 12, .	3.3	1

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7919	The genome sequence of the malaria mosquito, <i>Anopheles funestus</i> , Giles, 1900. Wellcome Open Research, 0, 7, 287.	0.9	2
7921	Preadapted to adapt: underpinnings of adaptive plasticity revealed by the downy brome genome. Communications Biology, 2023, 6, .	2.0	7
7922	Genome sequences of four isolates of <i>Xanthomonas campestris</i> pv. <i>campestris</i> , the causal agent of black rot. PhytoFrontiers, 0, , .	0.8	0
7923	The genome sequence of the Brindled Pug, <i>Eupithecia abbreviata</i> (Stephens, 1831). Wellcome Open Research, 0, 8, 140.	0.9	0
7924	The Australasian dingo archetype: <i>de novo</i> chromosome-length genome assembly, DNA methylome, and cranial morphology. GigaScience, 2023, 12, .	3.3	0
7925	The genome sequence of the Common Carder Bee, <i>Bombus pascuorum</i> (Scopoli, 1763). Wellcome Open Research, 0, 8, 142.	0.9	3
7926	The genome of <i>Lactuca saligna</i> , a wild relative of lettuce, provides insight into non-host resistance to the downy mildew <i>Bremia lactucae</i> . Plant Journal, 2023, 115, 108-126.	2.8	2
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