

# ABySS: A parallel assembler for short read sequence data

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Citation Report

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1	Pebble and Rock Band: Heuristic Resolution of Repeats and Scaffolding in the Velvet Short-Read de Novo Assembler. PLoS ONE, 2009, 4, e8407.	1.1	196
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1681	SKESA: strategic k-mer extension for scrupulous assemblies. <i>Genome Biology</i> , 2018, 19, 153.	3.8	375
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1845	Understanding UCEs: A Comprehensive Primer on Using Ultraconserved Elements for Arthropod Phylogenomics. <i>Insect Systematics and Diversity</i> , 2019, 3, .	0.7	35
1846	Assexon: Assembling Exon Using Gene Capture Data. <i>Evolutionary Bioinformatics</i> , 2019, 15, 117693431987479.	0.6	15
1847	Population Genomic Approaches for Weed Science. <i>Plants</i> , 2019, 8, 354.	1.6	14
1848	Using Genomics to Adapt Crops to Climate Change. , 2019, , 91-109.		4
1849	Aligning optical maps to de Bruijn graphs. <i>Bioinformatics</i> , 2019, 35, 3250-3256.	1.8	4
1850	Genomic resources for the Neotropical tree genus <i>Cedrela</i> (Meliaceae) and its relatives. <i>BMC Genomics</i> , 2019, 20, 58.	1.2	15
1851	Genomic Sequence of a Megrivirus Strain Identified in Laying Hens in Brazil. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	1
1852	Genomic Characterization and Virulence Potential of Two <i>Fusarium oxysporum</i> Isolates Cultured from the International Space Station. <i>MSystems</i> , 2019, 4, .	1.7	26
1853	Draft Genome Sequence from a Putative New Genus and Species in the Family <i>Methanoregulaceae</i> Isolated from the Anoxic Basin of Lake Untersee in East Antarctica. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	3
1854	MULKSG: MULTiple K Simultaneous Graph Assembly. <i>Lecture Notes in Computer Science</i> , 2019, , 125-136.	1.0	1



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1856	<i>Araucaria angustifolia</i> chloroplast genome sequence and its relation to other Araucariaceae. <i>Genetics and Molecular Biology</i> , 2019, 42, 671-676.	0.6	6
1857	Effect of de novo transcriptome assembly on transcript quantification. <i>Scientific Reports</i> , 2019, 9, 8304.	1.6	36
1858	The Red Fox Y-Chromosome in Comparative Context. <i>Genes</i> , 2019, 10, 409.	1.0	6
1859	Genomic characterization of a well-differentiated grade 3 pancreatic neuroendocrine tumor. <i>Journal of Physical Education and Sports Management</i> , 2019, 5, a003814.	0.5	17
1860	A SNP in a Steroidogenic Enzyme Is Associated with Phenotypic Sex in <i>Seriola</i> Fishes. <i>Current Biology</i> , 2019, 29, 1901-1909.e8.	1.8	79
1861	The complete mitogenome of clam <i>Corbicula fluminea</i> determined using next-generation and PacBio sequencing. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1660-1661.	0.2	6
1862	A Review on Role of Bloom Filter on DNA Assembly. <i>IEEE Access</i> , 2019, 7, 66939-66954.	2.6	7
1863	Landscape genomics of an obligate mutualism: Concordant and discordant population structures between the leafcutter ant <i>Atta texana</i> and its two main fungal symbiont types. <i>Molecular Ecology</i> , 2019, 28, 2831-2845.	2.0	18
1864	Current challenges and solutions of <i>de novo</i> assembly. <i>Quantitative Biology</i> , 2019, 7, 90-109.	0.3	46
1865	Unravelling the molecular mechanisms of nickel in woodlice. <i>Environmental Research</i> , 2019, 176, 108507.	3.7	3
1866	Biosynthetic SPAdes: reconstructing biosynthetic gene clusters from assembly graphs. <i>Genome Research</i> , 2019, 29, 1352-1362.	2.4	55
1867	Complete Genome Sequence of <i>Qipengyuania sediminis</i> CGMCC 1.12928T, Shed Light on Its Role in Matter-Cycle and Cold Adaption Mechanism of the Genus <i>Qipengyuania</i> . <i>Current Microbiology</i> , 2019, 76, 988-994.	1.0	6
1868	Genome Sequencing Revealed the Biotechnological Potential of an Obligate Thermophile <i>Geobacillus thermoleovorans</i> Strain RL Isolated from Hot Water Spring. <i>Indian Journal of Microbiology</i> , 2019, 59, 351-355.	1.5	10
1869	Genome Resequencing. <i>Compendium of Plant Genomes</i> , 2019, , 205-218.	0.3	0
1870	Extensive loss of cell-cycle and DNA repair genes in an ancient lineage of bipolar budding yeasts. <i>PLoS Biology</i> , 2019, 17, e3000255.	2.6	116
1871	Insect genomes: progress and challenges. <i>Insect Molecular Biology</i> , 2019, 28, 739-758.	1.0	115
1872	Quantitative Genetic Mapping and Genome Assembly in the Lesser Wax Moth <i>Achroia grisella</i> . <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2349-2361.	0.8	3

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1874	OMGS: Optical Map-Based Genome Scaffolding. <i>Lecture Notes in Computer Science</i> , 2019, , 190-207.	1.0	1
1875	Chloroplast Genome of the Soap Bark Tree <i>Quillaja saponaria</i> . <i>Frontiers in Ecology and Evolution</i> , 2019, 7, .	1.1	3
1876	Pervasive hybridizations in the history of wheat relatives. <i>Science Advances</i> , 2019, 5, eaav9188.	4.7	79
1877	De novo transcriptome assembly: A comprehensive cross-species comparison of short-read RNA-Seq assemblers. <i>GigaScience</i> , 2019, 8, .	3.3	150
1878	An Efficient, Scalable and Exact Representation of High-Dimensional Color Information Enabled via de Bruijn Graph Search. <i>Lecture Notes in Computer Science</i> , 2019, , 1-18.	1.0	9
1879	Genome- and MS-based mining of antibacterial chlorinated chromones and xanthenes from the phytopathogenic fungus <i>Bipolaris sorokiniana</i> strain 11134. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 5167-5181.	1.7	18
1880	TransLiG: a de novo transcriptome assembler that uses line graph iteration. <i>Genome Biology</i> , 2019, 20, 81.	3.8	30
1881	The <i>Lactococcus lactis</i> Pan-Plasmidome. <i>Frontiers in Microbiology</i> , 2019, 10, 707.	1.5	22
1882	Mitotic Recombination and Rapid Genome Evolution in the Invasive Forest Pathogen <i>Phytophthora ramorum</i> . <i>MBio</i> , 2019, 10, .	1.8	50
1883	Genome Sequence Resource of the Wide-Host-Range Anthracnose Pathogen <i>Colletotrichum siamense</i> . <i>Molecular Plant-Microbe Interactions</i> , 2019, 32, 931-934.	1.4	14
1884	Keanu: a novel visualization tool to explore biodiversity in metagenomes. <i>BMC Bioinformatics</i> , 2019, 20, 103.	1.2	4
1885	A draft genome of <i>Prunus avium</i> "Karina"™ as a tool for genomic studies. <i>Acta Horticulturae</i> , 2019, , 85-92.	0.1	2
1886	Composition and Origin of the Fermentation Microbiota of Mahewu, a Zimbabwean Fermented Cereal Beverage. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	46
1887	Carriage meningococcal isolates with capsule null locus dominate among high school students in a non-endemic period, Italy, 2012-2013. <i>International Journal of Medical Microbiology</i> , 2019, 309, 182-188.	1.5	7
1888	Sequencing-based methods and resources to study antimicrobial resistance. <i>Nature Reviews Genetics</i> , 2019, 20, 356-370.	7.7	263
1889	GMASS: a novel measure for genome assembly structural similarity. <i>BMC Bioinformatics</i> , 2019, 20, 147.	1.2	4
1890	Cloudy with a chance of speciation: integrative taxonomy reveals extraordinary divergence within a Mesoamerican cloud forest bird. <i>Biological Journal of the Linnean Society</i> , 2019, 126, 1-15.	0.7	28

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1892	Uncovering carbohydrate metabolism through a genotype-phenotype association study of 56 lactic acid bacteria genomes. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 3135-3152.	1.7	61
1893	Museum genomics reveals the speciation history of <i>Dendrortyx</i> wood-partridges in the Mesoamerican highlands. <i>Molecular Phylogenetics and Evolution</i> , 2019, 136, 29-34.	1.2	21
1894	Parallel pattern of differentiation at a genomic island shared between clinal and mosaic hybrid zones in a complex of cryptic seahorse lineages. <i>Evolution; International Journal of Organic Evolution</i> , 2019, 73, 817-835.	1.1	28
1895	A precedented nuclear genetic code with all three termination codons reassigned as sense codons in the syndinean <i>Amoebophrya</i> sp. ex <i>Karlodinium veneficum</i> . <i>PLoS ONE</i> , 2019, 14, e0212912.	1.1	12
1896	Complete Genome Sequence of Highly Virulent <i>Aeromonas hydrophila</i> Strain D4, Isolated from a Diseased Blunt-Snout Bream in China. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	18
1897	Draft Genome Sequence of <i>Trypanosoma equiperdum</i> Strain IVM-t1. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	12
1898	Stepwise large genome assembly approach: a case of Siberian larch ( <i>Larix sibirica</i> Ledeb). <i>BMC Bioinformatics</i> , 2019, 20, 37.	1.2	40
1899	Development of 15 microsatellite loci in the endangered <i>Streptanthus glandulosus</i> subsp. <i>niger</i> (Brassicaceae). <i>Applications in Plant Sciences</i> , 2019, 7, e01215.	0.8	2
1900	Improving Illumina assemblies with Hi-C and long reads: An example with the North African dromedary. <i>Molecular Ecology Resources</i> , 2019, 19, 1015-1026.	2.2	67
1901	Analyses of 202 plastid genomes elucidate the phylogeny of <i>Solanum</i> section <i>Petota</i> . <i>Scientific Reports</i> , 2019, 9, 4454.	1.6	34
1902	The survey and reference assisted assembly of the <i>Octopus vulgaris</i> genome. <i>Scientific Data</i> , 2019, 6, 13.	2.4	60
1903	In vivo recombination of <i>Saccharomyces eubayanus</i> maltose-transporter genes yields a chimeric transporter that enables maltotriose fermentation. <i>PLoS Genetics</i> , 2019, 15, e1007853.	1.5	29
1904	Genome Sequencing and Transcriptome Analysis of the Hop Downy Mildew Pathogen <i>Pseudoperonospora humuli</i> Reveal Species-Specific Genes for Molecular Detection. <i>Phytopathology</i> , 2019, 109, 1354-1366.	1.1	43
1905	An Insect Counteradaptation against Host Plant Defenses Evolved through Concerted Neofunctionalization. <i>Molecular Biology and Evolution</i> , 2019, 36, 930-941.	3.5	41
1906	Transcriptomics Identifies Modules of Differentially Expressed Genes and Novel Cyclotides in <i>Viola pubescens</i> . <i>Frontiers in Plant Science</i> , 2019, 10, 156.	1.7	12
1907	Integrating a newly developed BAC-based physical mapping resource for <i>Lolium perenne</i> with a genome-wide association study across a <i>L. perenne</i> European ecotype collection identifies genomic contexts associated with agriculturally important traits. <i>Annals of Botany</i> , 2019, 123, 977-992.	1.4	6
1908	The Two Prevalent Genotypes of an Emerging Infectious Disease, Deformed Wing Virus, Cause Equally Low Pupal Mortality and Equally High Wing Deformities in Host Honey Bees. <i>Viruses</i> , 2019, 11, 114.	1.5	65

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1910	<i>Taraxacum kok-saghyz</i> (rubber dandelion) genomic microsatellite loci reveal modest genetic diversity and cross-amplify broadly to related species. <i>Scientific Reports</i> , 2019, 9, 1915.	1.6	17
1911	The Genome Sequence of the Eastern Woodchuck ( <i>Marmota monax</i> ) â€œ A Preclinical Animal Model for Chronic Hepatitis B. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3943-3952.	0.8	13
1912	Greenlip Abalone ( <i>Haliotis laevigata</i> ) Genome and Protein Analysis Provides Insights into Maturation and Spawning. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3067-3078.	0.8	14
1913	Data Provenance Management of Bioinformatics Workflows in Federated Clouds. , 2019, , .		1
1914	Characterization of the Complete Chloroplast Genome of <i>Acer truncatum</i> Bunge (Sapindales:) Tj ETQq1 1 0.784314 rgBT /Over 2019, 2019, 1-13.	0.9	12
1915	A New Approach for De Bruijn Graph Construction in De Novo Genome Assembling. , 2019, , .		2
1916	Paragraph: a graph-based structural variant genotyper for short-read sequence data. <i>Genome Biology</i> , 2019, 20, 291.	3.8	104
1917	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
1918	<i>De Novo</i> Assembly and Annotation from Parental and F1 Puma Genomes of the Florida Panther Genetic Restoration Program. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3531-3536.	0.8	12
1919	Assembly and phylogenetic analysis of the complete chloroplast genome sequence of <i>Actinidia setosa</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3679-3680.	0.2	1
1920	Overlap graphs and <i>de Bruijn</i> graphs: data structures for <i>de novo</i> genome assembly in the big data era. <i>Quantitative Biology</i> , 2019, 7, 278-292.	0.3	30
1921	Phylogenomics and mitochondrial genome evolution of the gall-associated doryctine wasp genera (Hymenoptera: Braconidae). <i>Systematics and Biodiversity</i> , 2019, 17, 731-744.	0.5	8
1922	The complete chloroplast genome of <i>Actinidia fulvicoma</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 4089-4090.	0.2	2
1923	Review, Evaluation, and Directions for Gene-Targeted Assembly for Ecological Analyses of Metagenomes. <i>Frontiers in Genetics</i> , 2019, 10, 957.	1.1	8
1924	Comparison of different annotation tools for characterization of the complete chloroplast genome of <i>Corylus avellana</i> cv Tombul. <i>BMC Genomics</i> , 2019, 20, 874.	1.2	13
1925	Regional epigenetic variation in asexual snail populations among urban and rural lakes. <i>Environmental Epigenetics</i> , 2019, 5, dvz020.	0.9	16
1926	Taxogenomics and Systematics of the Genus <i>Pantoea</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 2463.	1.5	31

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1927	High Prevalence of Integrative and Conjugative Elements Encoding Transcription Activator-Like Effector Repeats in <i>Mycoplasma hominis</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 2385.	1.5	13
1928	PaKman: Scalable Assembly of Large Genomes on Distributed Memory Machines. , 2019, , .		4
1929	Bioinformatics Workflows With NoSQL Database in Cloud Computing. <i>Evolutionary Bioinformatics</i> , 2019, 15, 117693431988997.	0.6	4
1930	Programmed Cell Death in <i>Neurospora crassa</i> Is Controlled by the Allorecognition Determinant <i>rcd-1</i> . <i>Genetics</i> , 2019, 213, 1387-1400.	1.2	32
1931	Extracellular DNA: A Nutritional Trigger of <i>Mycoplasma bovis</i> Cytotoxicity. <i>Frontiers in Microbiology</i> , 2019, 10, 2753.	1.5	16
1932	SCOP: a novel scaffolding algorithm based on contig classification and optimization. <i>Bioinformatics</i> , 2019, 35, 1142-1150.	1.8	13
1933	Genomic analyses of a novel bacteriophage (VB_PmIS-Isfahan) within Siphoviridae family infecting <i>Proteus mirabilis</i> . <i>Genomics</i> , 2019, 111, 1283-1291.	1.3	13
1934	Host Specificity and Spatial Distribution Preference of Three <i>Pseudomonas</i> Isolates. <i>Frontiers in Microbiology</i> , 2018, 9, 3263.	1.5	17
1935	Plant genome sequences: past, present, future. <i>Current Opinion in Plant Biology</i> , 2019, 48, 1-8.	3.5	107
1936	Influence of Recombination and GC-biased Gene Conversion on the Adaptive and Nonadaptive Substitution Rate in Mammals versus Birds. <i>Molecular Biology and Evolution</i> , 2019, 36, 458-471.	3.5	41
1937	Description of <i>Wenzhouxiangella salilacus</i> sp. nov., a moderate halophilic bacterium isolated from a salt lake in Xinjiang Province, China. <i>Antonie Van Leeuwenhoek</i> , 2019, 112, 847-855.	0.7	5
1938	Comparative genomics of the major parasitic worms. <i>Nature Genetics</i> , 2019, 51, 163-174.	9.4	377
1939	SGTK: a toolkit for visualization and assessment of scaffold graphs. <i>Bioinformatics</i> , 2019, 35, 2303-2305.	1.8	8
1940	An LTR retrotransposon insertion was the cause of world's first low erucic acid <i>Brassica rapa</i> oilseed cultivar. <i>Molecular Breeding</i> , 2019, 39, 1.	1.0	4
1941	Datasets for genome assembly of six underutilized Indonesian fruits. <i>Data in Brief</i> , 2019, 22, 960-963.	0.5	6
1942	A critical comparison of technologies for a plant genome sequencing project. <i>GigaScience</i> , 2019, 8, .	3.3	41
1943	Exploring the unmapped DNA and RNA reads in a songbird genome. <i>BMC Genomics</i> , 2019, 20, 19.	1.2	21
1944	Prophage induction, but not production of phage particles, is required for lethal disease in a microbiome-replete murine model of enterohemorrhagic <i>E. coli</i> infection. <i>PLoS Pathogens</i> , 2019, 15, e1007494.	2.1	43

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1945	Whole-genome sequence of the oriental lung fluke <i>Paragonimus westermani</i> . GigaScience, 2019, 8, .	3.3	29
1946	First assembly of the genome of <i>Lolium multiflorum</i> and comparison to other Poaceae genomes. Grassland Science, 2019, 65, 125-134.	0.6	20
1947	Pooled DNA sequencing to identify SNPs associated with a major QTL for bacterial wilt resistance in Italian ryegrass ( <i>Lolium multiflorum</i> Lam.). Theoretical and Applied Genetics, 2019, 132, 947-958.	1.8	26
1948	Genomic characterisation of Cuiaba and Charleville viruses: arboviruses (family Rhabdoviridae, genus Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 587 Td (Subgenus	0.7	10
1949	Insights into the Evolution of the New World Diploid Cottons ( <i>Gossypium</i> sp.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 587 Td (Subgenus	1.1	45
1950	Computational aspects underlying genome to phenome analysis in plants. Plant Journal, 2019, 97, 182-198.	2.8	50
1951	Identification of Rickettsial Infections ( <i>Rickettsia</i> sp. TH2014) in <i>Ctenocephalides orientis</i> Fleas (Siphonaptera: Pulicidae). Journal of Medical Entomology, 2019, 56, 526-532.	0.9	4
1952	Draft genomes and genomic divergence of two <i>Lepidurus</i> tadpole shrimp species (Crustacea,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 587 Td (Subgenus	2.2	14
1953	Exploring Microbial Diversity and Function in Petroleum Hydrocarbon Associated Environments Through Omics Approaches. , 2019, , 171-194.		10
1954	Population genomics reveals evolution and variation of <i>Saccharomyces cerevisiae</i> in the human and insects gut. Environmental Microbiology, 2019, 21, 50-71.	1.8	30
1955	Kmerind: A Flexible Parallel Library for K-mer Indexing of Biological Sequences on Distributed Memory Systems. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1117-1131.	1.9	10
1956	FastEch: A Fast Sketch-Based Assembler for Genomes. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1091-1106.	1.9	4
1957	Whole genome sequence analysis of Geitlerinema sp. FC II unveils competitive edge of the strain in marine cultivation system for biofuel production. Genomics, 2019, 111, 465-472.	1.3	5
1958	Safely Filling Gaps with Partial Solutions Common to All Solutions. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 617-626.	1.9	2
1959	IsoTree: A New Framework for de novo Transcriptome Assembly from RNA-seq Reads. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 938-948.	1.9	4
1960	MEC: Misassembly Error Correction in Contigs based on Distribution of Paired-End Reads and Statistics of GC-contents. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 847-857.	1.9	17
1961	An Efficient Trimming Algorithm based on Multi-Feature Fusion Scoring Model for NGS Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 728-738.	1.9	14
1962	New approaches for metagenome assembly with short reads. Briefings in Bioinformatics, 2020, 21, 584-594.	3.2	140

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1963	Improving de novo Assembly Based on Read Classification. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 177-188.	1.9	19
1964	Transcriptome characterization and expression profiling in chestnut cultivars resistant or susceptible to the gall wasp <i>Dryocosmus kuriphilus</i> . Molecular Genetics and Genomics, 2020, 295, 107-120.	1.0	11
1965	Discovery of Novel Sequences in 1,000 Swedish Genomes. Molecular Biology and Evolution, 2020, 37, 18-30.	3.5	25
1966	An efficient discrete PSO coupled with a fast local search heuristic for the DNA fragment assembly problem. Information Sciences, 2020, 512, 880-908.	4.0	17
1967	<i>Anaerophilus nitritogenes</i> gen. nov., sp. nov., isolated from salt lake sediment in Xinjiang Province, China. Antonie Van Leeuwenhoek, 2020, 113, 417-425.	0.7	1
1968	Accuracy of <i>de novo</i> assembly of DNA sequences from double-digest libraries varies substantially among software. Molecular Ecology Resources, 2020, 20, 360-370.	2.2	13
1969	Phylogenomics Identifies an Ancestral Burst of Gene Duplications Predating the Diversification of Aphidomorpha. Molecular Biology and Evolution, 2020, 37, 730-756.	3.5	29
1970	Transposons played a major role in the diversification between the closely related almond and peach genomes: results from the almond genome sequence. Plant Journal, 2020, 101, 455-472.	2.8	94
1971	Gene duplication and transposition of mobile elements drive evolution of the Rpv3 resistance locus in grapevine. Plant Journal, 2020, 101, 529-542.	2.8	36
1972	On Bubble Generators in Directed Graphs. Algorithmica, 2020, 82, 898-914.	1.0	0
1973	Contribution of introns to the species diversity associated with the apicomplexan parasite, <i>Neospora caninum</i> . Parasitology Research, 2020, 119, 431-445.	0.6	2
1974	Extensive chromosomal rearrangements and rapid evolution of novel effector superfamilies contribute to host adaptation and speciation in the basal ascomycetous fungi. Molecular Plant Pathology, 2020, 21, 330-348.	2.0	22
1975	Parallel Seed Color Adaptation during Multiple Domestication Attempts of an Ancient New World Grain. Molecular Biology and Evolution, 2020, 37, 1407-1419.	3.5	47
1976	Counting Kmers for Biological Sequences at Large Scale. Interdisciplinary Sciences, Computational Life Sciences, 2020, 12, 99-108.	2.2	5
1977	Phylogeography of moose in western North America. Journal of Mammalogy, 2020, 101, 10-23.	0.6	11
1978	Evolutionary History, Genomic Adaptation to Toxic Diet, and Extinction of the Carolina Parakeet. Current Biology, 2020, 30, 108-114.e5.	1.8	24
1979	The underdog invader: Breeding system and colony genetic structure of the dark rover ant ( <i>Brachymyrmex patagonicus</i> Mayr). Ecology and Evolution, 2020, 10, 493-505.	0.8	6
1980	OMGS: Optical Map-Based Genome Scaffolding. Journal of Computational Biology, 2020, 27, 519-533.	0.8	14



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1982	GPU acceleration of Darwin read overlapper for de novo assembly of long DNA reads. BMC Bioinformatics, 2020, 21, 388.	1.2	4
1983	Bifrost: highly parallel construction and indexing of colored and compacted de Bruijn graphs. Genome Biology, 2020, 21, 249.	3.8	92
1985	The methylome is altered for plants in a high CO <sub>2</sub> world: Insights into the response of a wild plant population to multigenerational exposure to elevated atmospheric [CO <sub>2</sub> ]. Global Change Biology, 2020, 26, 6474-6492.	4.2	13
1986	Sequence analysis of the <i>Petunia inflata</i> S-locus region containing 17 <i>S-locus Box</i> genes and the <i>S-RNase</i> gene involved in self-incompatibility. Plant Journal, 2020, 104, 1348-1368.	2.8	14
1987	Phylogenomics of Parasitic and Nonparasitic Lice (Insecta: Psocodea): Combining Sequence Data and Exploring Compositional Bias Solutions in Next Generation Data Sets. Systematic Biology, 2021, 70, 719-738.	2.7	43
1988	Transcriptomic profiling of the digestive tract of the rat flea, Xenopsylla cheopis, following blood feeding and infection with Yersinia pestis. PLoS Neglected Tropical Diseases, 2020, 14, e0008688.	1.3	11
1989	Phylogenomics of the Neotropical fish family Serrasalminae with a novel intrafamilial classification (Teleostei: Characiformes). Molecular Phylogenetics and Evolution, 2020, 153, 106945.	1.2	15
1990	Estimates of the reproductive numbers and demographic reconstruction of outbreak associated with C:P1.5â€”1,10â€”8:F3â€”6:STâ€”11(cc11) Neisseria meningitidis strains. Infection, Genetics and Evolution, 2020, 1.0 84, 104360.	1.0	0
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1992	Genetic Traces of the Francisella tularensis Colonization of Spain, 1998â€”2020. Microorganisms, 2020, 8, 1784.	1.6	1
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2107	Biological computation and computational biology: survey, challenges, and discussion. <i>Artificial Intelligence Review</i> , 2021, 54, 4169-4235.	9.7	7
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2122	Integrative analysis of DNA, macroscopic remains and stable isotopes of dog coprolites to reconstruct community diet. <i>Scientific Reports</i> , 2021, 11, 3113.	1.6	12
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2137	Development and Characterization of 15 Novel Genomic SSRs for <i>Viburnum farreri</i> . <i>Plants</i> , 2021, 10, 487.	1.6	4
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