

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.	2.5	196
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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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.	1.8	3

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1876	Pervasive hybridizations in the history of wheat relatives. Science Advances, 2019, 5, eaav9188.	10.3	79
1877	De novo transcriptome assembly: A comprehensive cross-species comparison of short-read RNA-Seq assemblers. GigaScience, 2019, 8, .	6.4	150
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1879	Genome- and MS-based mining of antibacterial chlorinated chromones and xanthenes from the phytopathogenic fungus Bipolaris sorokiniana strain 11134. Applied Microbiology and Biotechnology, 2019, 103, 5167-5181.	3.6	18
1880	TransLiG: a de novo transcriptome assembler that uses line graph iteration. Genome Biology, 2019, 20, 81.	8.8	30
1881	The Lactococcus lactis Pan-Plasmidome. Frontiers in Microbiology, 2019, 10, 707.	3.5	22
1882	Mitotic Recombination and Rapid Genome Evolution in the Invasive Forest Pathogen <i>Phytophthora ramorum</i> . MBio, 2019, 10, .	4.1	50
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1896	Complete Genome Sequence of Highly Virulent Aeromonas hydrophila Strain D4, Isolated from a Diseased Blunt-Snout Bream in China. Microbiology Resource Announcements, 2019, 8, .	0.6	18
1897	Draft Genome Sequence of Trypanosoma equiperdum Strain IVM-t1. Microbiology Resource Announcements, 2019, 8, .	0.6	12
1898	Stepwise large genome assembly approach: a case of Siberian larch (Larix sibirica Ledeb). BMC Bioinformatics, 2019, 20, 37.	2.6	40
1899	Development of 15 microsatellite loci in the endangered <i>Streptanthus glandulosus</i> subsp. <i>niger</i> (Brassicaceae). Applications in Plant Sciences, 2019, 7, e01215.	2.1	2
1900	Improving Illumina assemblies with Hi-C and long reads: An example with the North African dromedary. Molecular Ecology Resources, 2019, 19, 1015-1026.	4.8	67
1901	Analyses of 202 plastid genomes elucidate the phylogeny of Solanum section Petota. Scientific Reports, 2019, 9, 4454.	3.3	34
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1903	In vivo recombination of Saccharomyces eubayanus maltose-transporter genes yields a chimeric transporter that enables maltotriose fermentation. PLoS Genetics, 2019, 15, e1007853.	3.5	29
1904	Genome Sequencing and Transcriptome Analysis of the Hop Downy Mildew Pathogen <i>Pseudoperonospora humuli</i> Reveal Species-Specific Genes for Molecular Detection. Phytopathology, 2019, 109, 1354-1366.	2.2	43
1905	An Insect Counteradaptation against Host Plant Defenses Evolved through Concerted Neofunctionalization. Molecular Biology and Evolution, 2019, 36, 930-941.	8.9	41
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1910	Taraxacum kok-saghyz (rubber dandelion) genomic microsatellite loci reveal modest genetic diversity and cross-amplify broadly to related species. Scientific Reports, 2019, 9, 1915.	3.3	17
1911	The Genome Sequence of the Eastern Woodchuck (<i>Marmota monax</i>) â€œ A Preclinical Animal Model for Chronic Hepatitis B. G3: Genes, Genomes, Genetics, 2019, 9, 3943-3952.	1.8	13
1912	Greenlip Abalone (<i>Haliotis laevigata</i>) Genome and Protein Analysis Provides Insights into Maturation and Spawning. G3: Genes, Genomes, Genetics, 2019, 9, 3067-3078.	1.8	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 /Overlo 2019, 2019, 1-13.	1.9	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. Genome Biology, 2019, 20, 291.	8.8	104
1917	Genome Sequencing of <i>Pleurozium schreberi</i>: The Assembled and Annotated Draft Genome of a Pleurocarpous Feather Moss. G3: Genes, Genomes, Genetics, 2019, 9, 2791-2797.	1.8	35
1918	<i>De Novo</i> Assembly and Annotation from Parental and F1 Puma Genomes of the Florida Panther Genetic Restoration Program. G3: Genes, Genomes, Genetics, 2019, 9, 3531-3536.	1.8	12
1919	Assembly and phylogenetic analysis of the complete chloroplast genome sequence of <i>Actinidia setosa</i>. Mitochondrial DNA Part B: Resources, 2019, 4, 3679-3680.	0.4	1
1920	Overlap graphs and <i>b</i> de Bruijn <i>/i> graphs: data structures for <i>b</i> de novo <i>/i> genome assembly in the big data era. Quantitative Biology, 2019, 7, 278-292.	0.5	30
1921	Phylogenomics and mitochondrial genome evolution of the gall-associated doryctine wasp genera (Hymenoptera: Braconidae). Systematics and Biodiversity, 2019, 17, 731-744.	1.2	8
1922	The complete chloroplast genome of Actinidia fulvicoma. Mitochondrial DNA Part B: Resources, 2019, 4, 4089-4090.	0.4	2
1923	Review, Evaluation, and Directions for Gene-Targeted Assembly for Ecological Analyses of Metagenomes. Frontiers in Genetics, 2019, 10, 957.	2.3	8
1924	Comparison of different annotation tools for characterization of the complete chloroplast genome of Corylus avellana cv Tombul. BMC Genomics, 2019, 20, 874.	2.8	13
1925	Regional epigenetic variation in asexual snail populations among urban and rural lakes. Environmental Epigenetics, 2019, 5, dvz020.	1.8	16
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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.	1.2	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.	2.9	32
1931	Extracellular DNA: A Nutritional Trigger of <i>Mycoplasma bovis</i> Cytotoxicity. <i>Frontiers in Microbiology</i> , 2019, 10, 2753.	3.5	16
1932	SCOP: a novel scaffolding algorithm based on contig classification and optimization. <i>Bioinformatics</i> , 2019, 35, 1142-1150.	4.1	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.	2.9	13
1934	Host Specificity and Spatial Distribution Preference of Three <i>Pseudomonas</i> Isolates. <i>Frontiers in Microbiology</i> , 2018, 9, 3263.	3.5	17
1935	Plant genome sequences: past, present, future. <i>Current Opinion in Plant Biology</i> , 2019, 48, 1-8.	7.1	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.	8.9	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.	1.7	5
1938	Comparative genomics of the major parasitic worms. <i>Nature Genetics</i> , 2019, 51, 163-174.	21.4	377
1939	SCTK: a toolkit for visualization and assessment of scaffold graphs. <i>Bioinformatics</i> , 2019, 35, 2303-2305.	4.1	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.	2.1	4
1941	Datasets for genome assembly of six underutilized Indonesian fruits. <i>Data in Brief</i> , 2019, 22, 960-963.	1.0	6
1942	A critical comparison of technologies for a plant genome sequencing project. <i>GigaScience</i> , 2019, 8, .	6.4	41
1943	Exploring the unmapped DNA and RNA reads in a songbird genome. <i>BMC Genomics</i> , 2019, 20, 19.	2.8	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.	4.7	43

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1946	First assembly of the geneâ€space of <i>Lolium multiflorum</i> and comparison to other Poaceae genomes. Grassland Science, 2019, 65, 125-134.	1.1	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.	3.6	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) 2.5 45	1.6	10
1949	Insights into the Evolution of the New World Diploid Cottons (<i>Gossypium</i>), Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 587 Td (Subgenus) 2.5 45	2.5	45
1950	Computational aspects underlying genome to phenome analysis in plants. Plant Journal, 2019, 97, 182-198.	5.7	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.	1.8	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) 4.8 14	4.8	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.	3.8	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.	3.0	10
1956	FastEtc: A Fast Sketch-Based Assembler for Genomes. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1091-1106.	3.0	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.	2.9	5
1958	Safely Filling Gaps with Partial Solutions Common to All Solutions. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 617-626.	3.0	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.	3.0	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.	3.0	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.	3.0	14
1962	New approaches for metagenome assembly with short reads. Briefings in Bioinformatics, 2020, 21, 584-594.	6.5	140

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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.	2.1	11
1965	Discovery of Novel Sequences in 1,000 Swedish Genomes. Molecular Biology and Evolution, 2020, 37, 18-30.	8.9	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.	6.9	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.	1.7	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.	4.8	13
1969	Phylogenomics Identifies an Ancestral Burst of Gene Duplications Predating the Diversification of Aphidomorpha. Molecular Biology and Evolution, 2020, 37, 730-756.	8.9	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.	5.7	94
1971	Gene duplication and transposition of mobile elements drive evolution of the Rpv3 resistance locus in grapevine. Plant Journal, 2020, 101, 529-542.	5.7	36
1972	On Bubble Generators in Directed Graphs. Algorithmica, 2020, 82, 898-914.	1.3	0
1973	Contribution of introns to the species diversity associated with the apicomplexan parasite, <i>Neospora caninum</i> . Parasitology Research, 2020, 119, 431-445.	1.6	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.	4.2	22
1975	Parallel Seed Color Adaptation during Multiple Domestication Attempts of an Ancient New World Grain. Molecular Biology and Evolution, 2020, 37, 1407-1419.	8.9	47
1976	Counting Kmers for Biological Sequences at Large Scale. Interdisciplinary Sciences, Computational Life Sciences, 2020, 12, 99-108.	3.6	5
1977	Phylogeography of moose in western North America. Journal of Mammalogy, 2020, 101, 10-23.	1.3	11
1978	Evolutionary History, Genomic Adaptation to Toxic Diet, and Extinction of the Carolina Parakeet. Current Biology, 2020, 30, 108-114.e5.	3.9	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.	1.9	6
1980	OMGS: Optical Map-Based Genome Scaffolding. Journal of Computational Biology, 2020, 27, 519-533.	1.6	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.	2.6	4
1983	Bifrost: highly parallel construction and indexing of colored and compacted de Bruijn graphs. Genome Biology, 2020, 21, 249.	8.8	92
1985	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]. Global Change Biology, 2020, 26, 6474-6492.	9.5	13
1986	Sequence analysis of the <i>Petunia inflata</i> S-locus region containing 17 S-locus F-box genes and the S-RNase gene involved in self-incompatibility. Plant Journal, 2020, 104, 1348-1368.	5.7	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.	5.6	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.	3.0	11
1989	Phylogenomics of the Neotropical fish family Serrasalminae with a novel intrafamilial classification (Teleostei: Characiformes). Molecular Phylogenetics and Evolution, 2020, 153, 106945.	2.7	15
1990	Estimates of the reproductive numbers and demographic reconstruction of outbreak associated with C:P1.5a1,10a8:F3a6:STa11(cc11) Neisseria meningitidis strains. Infection, Genetics and Evolution, 2020, 23, 84, 104360.	2.3	0
1991	Arthrobacter sedimenti sp. nov., isolated from river sediment in Yuantouzhu park, China. Archives of Microbiology, 2020, 202, 2551-2556.	2.2	4
1992	Genetic Traces of the Francisella tularensis Colonization of Spain, 1998–2020. Microorganisms, 2020, 8, 1784.	3.6	1
1993	Clover: a clustering-oriented de novo assembler for Illumina sequences. BMC Bioinformatics, 2020, 21, 528.	2.6	1
1994	A yeast living ancestor reveals the origin of genomic introgressions. Nature, 2020, 587, 420-425.	27.8	45
1995	Massive gene presence-absence variation shapes an open pan-genome in the Mediterranean mussel. Genome Biology, 2020, 21, 275.	8.8	105
1996	The complete chloroplast genome of Isochrysis galbana and comparison with related haptophyte species. Algal Research, 2020, 50, 101989.	4.6	14
1997	Transcriptional variation of sensory-related genes in natural populations of Aedes albopictus. BMC Genomics, 2020, 21, 547.	2.8	6
1998	PGcloser: Fast Parallel Gap-Closing Tool Using Long-Reads or Contigs to Fill Gaps in Genomes. Evolutionary Bioinformatics, 2020, 16, 117693432091385.	1.2	5
1999	Genome Analysis of Two Novel Synechococcus Phages That Lack Common Auxiliary Metabolic Genes: Possible Reasons and Ecological Insights by Comparative Analysis of Cyanomyoviruses. Viruses, 2020, 12, 800.	3.3	9

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2002	Lousy grouse: Comparing evolutionary patterns in Alaska galliform lice to understand host evolution and host-parasite interactions. Ecology and Evolution, 2020, 10, 8379-8393.	1.9	11
2003	Mating strategy and mating type distribution in six global populations of the Eucalyptus foliar pathogen Teratosphaeria destructans. Fungal Genetics and Biology, 2020, 137, 103350.	2.1	19
2004	Description of Erythrobacter mangrovi sp. nov., an aerobic bacterium from rhizosphere soil of mangrove plant (Kandelia candel). Antonie Van Leeuwenhoek, 2020, 113, 1425-1435.	1.7	10
2005	The Most Frequently Used Sequencing Technologies and Assembly Methods in Different Time Segments of the Bacterial Surveillance and RefSeq Genome Databases. Frontiers in Cellular and Infection Microbiology, 2020, 10, 527102.	3.9	32
2006	Cathepsins L and B in Dysdercus peruvianus, Rhodnius prolixus, and Mahanarva fimbriolata. Looking for enzyme adaptations to digestion. Insect Biochemistry and Molecular Biology, 2020, 127, 103488.	2.7	11
2007	All Pairs Suffix-Prefix Matches using Enhanced Suffix Array. , 2020, , .		0
2008	The Untapped Australasian Diversity of Astaxanthin-Producing Yeasts with Biotechnological Potential Phaffia australis sp. nov. and Phaffia tasmanica sp. nov.. Microorganisms, 2020, 8, 1651.	3.6	9
2009	Mitochondrial evolution in the entomopathogenic fungal genus Beauveria. Archives of Insect Biochemistry and Physiology, 2020, 105, e21754.	1.5	5
2010	RNA-sequencing of the Nyssomyia neivai sialome: a sand fly-vector from a Brazilian endemic area for tegumentary leishmaniasis and pemphigus foliaceus. Scientific Reports, 2020, 10, 17664.	3.3	2
2011	A physiologic overview of the organ-specific transcriptome of the cattle tick Rhipicephalus microplus. Scientific Reports, 2020, 10, 18296.	3.3	23
2012	Succinct dynamic de Bruijn graphs. Bioinformatics, 2021, 37, 1946-1952.	4.1	8
2013	Genome- wide structural and functional variant discovery of rice landraces using genotyping by sequencing. Molecular Biology Reports, 2020, 47, 7391-7402.	2.3	11
2014	Nucleotide diversity of functionally different groups of immune response genes in Old World camels based on newly annotated and reference-guided assemblies. BMC Genomics, 2020, 21, 606.	2.8	15
2015	TransBorrow: genome-guided transcriptome assembly by borrowing assemblies from different assemblers. Genome Research, 2020, 30, 1181-1190.	5.5	15
2016	Complex Virome in a Mesenteric Lymph Node from a Californian Sea Lion (Zalophus californianus) with Polyserositis and Steatitis. Viruses, 2020, 12, 793.	3.3	13
2017	Analysis of Draft Genome Sequences of Two New Pantoea Strains Associated with Wheat Leaf Necrotic Tissues Caused by Xanthomonas translucens Reveals Distinct Species. Microbiology Resource Announcements, 2020, 9, .	0.6	1

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2019	First de novo genome specific development, characterization and validation of simple sequence repeat (SSR) markers in Genus <i>Salvadora</i> . Molecular Biology Reports, 2020, 47, 6997-7008.	2.3	14
2020	Multi-model seascape genomics identifies distinct environmental drivers of selection among sympatric marine species. BMC Evolutionary Biology, 2020, 20, 121.	3.2	11
2021	Fast gap-affine pairwise alignment using the wavefront algorithm. Bioinformatics, 2021, 37, 456-463.	4.1	75
2022	Divergence, gene flow, and the origin of leapfrog geographic distributions: The history of colour pattern variation in <i>Phylllobates</i> poison dart frogs. Molecular Ecology, 2020, 29, 3702-3719.	3.9	14
2023	A Second Genome Sequence of an Enterovirus C99 Detected in a Healthy Chimpanzee. Microbiology Resource Announcements, 2020, 9, .	0.6	2
2024	Isolation and characterization of microsatellite markers for the threatened African endemic tree species <i>Pterocarpus erinaceus</i> Poir.. Ecology and Evolution, 2020, 10, 13403-13411.	1.9	4
2025	Monitoring results of wild boar (<i>Sus scrofa</i>) in The Netherlands: analyses of serological results and the first identification of <i>Brucella suis</i> biovar 2. Infection Ecology and Epidemiology, 2020, 10, 1794668.	0.8	4
2026	Moose genomes reveal past glacial demography and the origin of modern lineages. BMC Genomics, 2020, 21, 854.	2.8	23
2027	<i>Streptococcus xiaochunlingii</i> sp. nov. E24 Isolated From the Oropharynx of Healthy Chinese Children. Frontiers in Microbiology, 2020, 11, 563213.	3.5	2
2028	Variation in the expression of a transmembrane protein influences cell growth in <i>Arabidopsis thaliana</i> petals by altering auxin responses. BMC Plant Biology, 2020, 20, 482.	3.6	0
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2030	Complete Genome Sequence of <i>Mycoplasma bovis</i> Strain XBY01, Isolated from Henan Province, China. Microbiology Resource Announcements, 2020, 9, .	0.6	0
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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