

Jue Ruan

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

41
papers

40,149
citations

22
h-index

48
g-index

48
ext. papers

54,832
ext. citations

17.3
avg, IF

7
L-index

#	Paper	IF	Citations
41	The Sequence Alignment/Map format and SAMtools. <i>Bioinformatics</i> , 2009 , 25, 2078-9	7.2	30805
40	De novo assembly of human genomes with massively parallel short read sequencing. <i>Genome Research</i> , 2010 , 20, 265-72	9.7	2084
39	Mapping short DNA sequencing reads and calling variants using mapping quality scores. <i>Genome Research</i> , 2008 , 18, 1851-8	9.7	2002
38	The genome of the cucumber, <i>Cucumis sativus</i> L. <i>Nature Genetics</i> , 2009 , 41, 1275-81	36.3	1031
37	The sequence and de novo assembly of the giant panda genome. <i>Nature</i> , 2010 , 463, 311-7	50.4	864
36	The diploid genome sequence of an Asian individual. <i>Nature</i> , 2008 , 456, 60-5	50.4	744
35	Genomic variation in 3,010 diverse accessions of Asian cultivated rice. <i>Nature</i> , 2018 , 557, 43-49	50.4	582
34	Accurate circular consensus long-read sequencing improves variant detection and assembly of a human genome. <i>Nature Biotechnology</i> , 2019 , 37, 1155-1162	44.5	427
33	Fast and accurate long-read assembly with wtdbg2. <i>Nature Methods</i> , 2020 , 17, 155-158	21.6	374
32	A genetic variation map for chicken with 2.8 million single-nucleotide polymorphisms. <i>Nature</i> , 2004 , 432, 717-22	50.4	341
31	DBG2OLC: Efficient Assembly of Large Genomes Using Long Erroneous Reads of the Third Generation Sequencing Technologies. <i>Scientific Reports</i> , 2016 , 6, 31900	4.9	186
30	Rapid growth of a hepatocellular carcinoma and the driving mutations revealed by cell-population genetic analysis of whole-genome data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 12042-7	11.5	110
29	A chromosome-scale genome assembly of cucumber (<i>Cucumis sativus</i> L.). <i>GigaScience</i> , 2019 , 8,	7.6	68
28	novoBreak: local assembly for breakpoint detection in cancer genomes. <i>Nature Methods</i> , 2017 , 14, 65-67	21.6	67
27	Fast and accurate long-read assembly with wtdbg2		64
26	Genomic analysis of snub-nosed monkeys (<i>Rhinopithecus</i>) identifies genes and processes related to high-altitude adaptation. <i>Nature Genetics</i> , 2016 , 48, 947-52	36.3	58
25	Genome analysis of <i>Taraxacum kok-saghyz</i> Rodin provides new insights into rubber biosynthesis. <i>National Science Review</i> , 2018 , 5, 78-87	10.8	47

24	Population sequencing enhances understanding of tea plant evolution. <i>Nature Communications</i> , 2020 , 11, 4447	17.4	40
23	Highly-accurate long-read sequencing improves variant detection and assembly of a human genome		29
22	African lungfish genome sheds light on the vertebrate water-to-land transition. <i>Cell</i> , 2021 , 184, 1362-1376.e1827	36.2	1827
21	Understanding divergent domestication traits from the whole-genome sequencing of swamp- and river-buffalo populations. <i>National Science Review</i> , 2020 , 7, 686-701	10.8	23
20	SMARTdenovo: a de novo assembler using long noisy reads. <i>GigaByte</i> , 2021, 1-9		22
19	From asymmetrical to balanced genomic diversification during rediploidization: Subgenomic evolution in allotetraploid fish. <i>Science Advances</i> , 2020 , 6, eaaz7677	14.3	21
18	Structural variation during dog domestication: insights from gray wolf and dhole genomes. <i>National Science Review</i> , 2019 , 6, 110-122	10.8	19
17	LRScarf: improving draft genomes using long noisy reads. <i>BMC Genomics</i> , 2019 , 20, 955	4.5	17
16	Genome and single-cell RNA-sequencing of the earthworm <i>Eisenia andrei</i> identifies cellular mechanisms underlying regeneration. <i>Nature Communications</i> , 2020 , 11, 2656	17.4	16
15	Sequencing of Chinese castor lines reveals genetic signatures of selection and yield-associated loci. <i>Nature Communications</i> , 2019 , 10, 3418	17.4	14
14	The nearly complete genome of <i>Ginkgo biloba</i> illuminates gymnosperm evolution. <i>Nature Plants</i> , 2021 , 7, 748-756	11.5	11
13	Novel sequences, structural variations and gene presence variations of Asian cultivated rice. <i>Scientific Data</i> , 2018 , 5, 180079	8.2	10
12	Comparison of Long Non-Coding RNA Expression Profiles of Cattle and Buffalo Differing in Muscle Characteristics. <i>Frontiers in Genetics</i> , 2020 , 11, 98	4.5	7
11	The evolution of small insertions and deletions in the coding genes of <i>Drosophila melanogaster</i> . <i>Molecular Biology and Evolution</i> , 2013 , 30, 2699-708	8.3	6
10	pBACode: a random-barcode-based high-throughput approach for BAC paired-end sequencing and physical clone mapping. <i>Nucleic Acids Research</i> , 2017 , 45, e52	20.1	6
9	The <i>Cycas</i> genome and the early evolution of seed plants.. <i>Nature Plants</i> , 2022 ,	11.5	5
8	Reference-free comparative genomics of 174 chloroplasts. <i>PLoS ONE</i> , 2012 , 7, e48995	3.7	4
7	High-quality reference genome of <i>Fasciola gigantica</i> : Insights into the genomic signatures of transposon-mediated evolution and specific parasitic adaption in tropical regions. <i>PLoS Neglected Tropical Diseases</i> , 2021 , 15, e0009750	4.8	4

6	Screening and identification of female-specific DNA sequences in octaploid sturgeon using comparative genomics with high-throughput sequencing. <i>Genomics</i> , 2021 , 113, 4237-4244	4.3	3
5	A Chromosome-level Assembly of A Wild Castor Genome Provides New Insights into the Adaptive Evolution in A Tropical Desert. <i>Genomics, Proteomics and Bioinformatics</i> , 2021 ,	6.5	3
4	Automated assembly of high-quality diploid human reference genomes		3
3	A genome-wide survey of copy number variations reveals an asymmetric evolution of duplicated genes in rice. <i>BMC Biology</i> , 2020 , 18, 73	7.3	2
2	Population sequencing enhances understanding of tea plant evolution		1
1	Transcriptome Analysis of Ginkgo biloba L. Leaves across Late Developmental Stages Based on RNA-Seq and Co-Expression Network. <i>Forests</i> , 2021 , 12, 315	2.8	0