

Jue Ruan

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8958813/publications.pdf>

Version: 2024-02-01

40
papers

62,468
citations

236612

25
h-index

329751

37
g-index

48
all docs

48
docs citations

48
times ranked

100807
citing authors

#	ARTICLE	IF	CITATIONS
1	The Sequence Alignment/Map format and SAMtools. <i>Bioinformatics</i> , 2009, 25, 2078-2079.	1.8	49,124
2	De novo assembly of human genomes with massively parallel short read sequencing. <i>Genome Research</i> , 2010, 20, 265-272.	2.4	2,516
3	Mapping short DNA sequencing reads and calling variants using mapping quality scores. <i>Genome Research</i> , 2008, 18, 1851-1858.	2.4	2,275
4	The genome of the cucumber, <i>Cucumis sativus</i> L.. <i>Nature Genetics</i> , 2009, 41, 1275-1281.	9.4	1,317
5	Genomic variation in 3,010 diverse accessions of Asian cultivated rice. <i>Nature</i> , 2018, 557, 43-49.	13.7	1,091
6	The sequence and de novo assembly of the giant panda genome. <i>Nature</i> , 2010, 463, 311-317.	13.7	1,058
7	Accurate circular consensus long-read sequencing improves variant detection and assembly of a human genome. <i>Nature Biotechnology</i> , 2019, 37, 1155-1162.	9.4	1,010
8	Fast and accurate long-read assembly with wtdbg2. <i>Nature Methods</i> , 2020, 17, 155-158.	9.0	917
9	The diploid genome sequence of an Asian individual. <i>Nature</i> , 2008, 456, 60-65.	13.7	834
10	A genetic variation map for chicken with 2.8 million single-nucleotide polymorphisms. <i>Nature</i> , 2004, 432, 717-722.	13.7	391
11	DBG2OLC: Efficient Assembly of Large Genomes Using Long Erroneous Reads of the Third Generation Sequencing Technologies. <i>Scientific Reports</i> , 2016, 6, 31900.	1.6	268
12	A chromosome-scale genome assembly of cucumber (<i>Cucumis sativus</i> L.). <i>GigaScience</i> , 2019, 8, .	3.3	138
13	Population sequencing enhances understanding of tea plant evolution. <i>Nature Communications</i> , 2020, 11, 4447.	5.8	123
14	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, 12042-12047.	3.3	117
15	Genomic analysis of snub-nosed monkeys (<i>Rhinopithecus</i>) identifies genes and processes related to high-altitude adaptation. <i>Nature Genetics</i> , 2016, 48, 947-952.	9.4	109
16	SMARTdenovo: a de novo assembler using long noisy reads. <i>GigaByte</i> , 0, 2021, 1-9.	0.0	109
17	African lungfish genome sheds light on the vertebrate water-to-land transition. <i>Cell</i> , 2021, 184, 1362-1376.e18.	13.5	99
18	A super pan-genomic landscape of rice. <i>Cell Research</i> , 2022, 32, 878-896.	5.7	99

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19	The nearly complete genome of <i>Ginkgo biloba</i> illuminates gymnosperm evolution. <i>Nature Plants</i> , 2021, 7, 748-756.	4.7	98
20	novoBreak: local assembly for breakpoint detection in cancer genomes. <i>Nature Methods</i> , 2017, 14, 65-67.	9.0	93
21	Genome analysis of <i>Taraxacum kok-saghyz</i> Rodin provides new insights into rubber biosynthesis. <i>National Science Review</i> , 2018, 5, 78-87.	4.6	90
22	The <i>Cycas</i> genome and the early evolution of seed plants. <i>Nature Plants</i> , 2022, 8, 389-401.	4.7	80
23	From asymmetrical to balanced genomic diversification during rediploidization: Subgenomic evolution in allotetraploid fish. <i>Science Advances</i> , 2020, 6, eaaz7677.	4.7	59
24	LRScarf: improving draft genomes using long noisy reads. <i>BMC Genomics</i> , 2019, 20, 955.	1.2	53
25	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.	5.8	43
26	Understanding divergent domestication traits from the whole-genome sequencing of swamp- and river-buffalo populations. <i>National Science Review</i> , 2020, 7, 686-701.	4.6	43
27	Structural variation during dog domestication: insights from gray wolf and dhole genomes. <i>National Science Review</i> , 2019, 6, 110-122.	4.6	30
28	Sequencing of Chinese castor lines reveals genetic signatures of selection and yield-associated loci. <i>Nature Communications</i> , 2019, 10, 3418.	5.8	26
29	Comparison of Long Non-Coding RNA Expression Profiles of Cattle and Buffalo Differing in Muscle Characteristics. <i>Frontiers in Genetics</i> , 2020, 11, 98.	1.1	19
30	A Chromosome-level Genome Assembly of Wild Castor Provides New Insights into its Adaptive Evolution in Tropical Desert. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 42-59.	3.0	18
31	Novel sequences, structural variations and gene presence variations of Asian cultivated rice. <i>Scientific Data</i> , 2018, 5, 180079.	2.4	14
32	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.	1.3	12
33	pBACode: a random-barcode-based high-throughput approach for BAC paired-end sequencing and physical clone mapping. <i>Nucleic Acids Research</i> , 2017, 45, gkw1261.	6.5	9
34	The First High-quality Reference Genome of Sika Deer Provides Insights into High-tannin Adaptation. <i>Genomics, Proteomics and Bioinformatics</i> , 2023, 21, 203-215.	3.0	9
35	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
36	The Evolution of Small Insertions and Deletions in the Coding Genes of <i>Drosophila melanogaster</i> . <i>Molecular Biology and Evolution</i> , 2013, 30, 2699-2708.	3.5	6

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37	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.	1.3	6
38	Reference-Free Comparative Genomics of 174 Chloroplasts. <i>PLoS ONE</i> , 2012, 7, e48995.	1.1	4
39	Transcriptome Analysis of <i>Ginkgo biloba</i> L. Leaves across Late Developmental Stages Based on RNA-Seq and Co-Expression Network. <i>Forests</i> , 2021, 12, 315.	0.9	1
40	En Route to Completion: What Is An Ideal Reference Genome?. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 1-3.	3.0	0