Ruibang Luo

List of Publications by Year
in descending order

64 papers	35,268 citations	236612 25 h-index	149479 56 g-index
85 all docs	85 docs citations	85 times ranked	61371 citing authors

#	Article	IF	Citations
1	Generalized radiograph representation learning via cross-supervision between images and free-text radiology reports. Nature Machine Intelligence, 2022, 4, 32-40.	8.3	29
2	HKG: an open genetic variant database of 205 Hong Kong cantonese exomes. NAR Genomics and Bioinformatics, 2022, 4, lqac005.	1.5	2
3	Temporal Control of the WNT Signaling Pathway During Cardiac Differentiation Impacts Upon the Maturation State of Human Pluripotent Stem Cell Derived Cardiomyocytes. Frontiers in Molecular Biosciences, 2022, 9, 714008.	1.6	1
4	ECNano: A cost-effective workflow for target enrichment sequencing and accurate variant calling on 4800 clinically significant genes using a single MinION flowcell. BMC Medical Genomics, 2022, 15, 43.	0.7	7
5	Same-Cell Co-Occurrence of RAS Hotspot and BRAF V600E Mutations in Treatment-Naive Colorectal Cancer. JCO Precision Oncology, 2022, 6, e2100365.	1.5	1
6	Detecting structural variations with precise breakpoints using low-depth WGS data from a single oxford nanopore MinION flowcell. Scientific Reports, 2022, 12, 4519.	1.6	5
7	Clinical analysis and pluripotent stem cells-based model reveal possible impacts of ACE2 and lung progenitor cells on infants vulnerable to COVID-19. Theranostics, 2021, 11, 2170-2181.	4.6	14
8	High Prevalence and Mechanism Associated With Extended Spectrum Beta-Lactamase-Positive Phenotype in Laribacter hongkongensis. Frontiers in Microbiology, 2021, 12, 618894.	1.5	3
9	<scp>SARSâ€CoV</scp>â€2 biology and variants: anticipation of viral evolution and what needs to be done. Environmental Microbiology, 2021, 23, 2339-2363.	1.8	30
10	RENET2: high-performance full-text geneâ€“disease relation extraction with iterative training data expansion. NAR Genomics and Bioinformatics, 2021, 3, lqab062.	1.5	4
11	Building a Chinese pan-genome of 486 individuals. Communications Biology, 2021, 4, 1016.	2.0	13
12	Applications and potentials of nanopore sequencing in the (epi)genome and (epi)transcriptome era. Innovation(China), 2021, 2, 100153.	5.2	15
13	Distinct Disease Severity Between Children and Older Adults With Coronavirus Disease 2019 (COVID-19): Impacts of ACE2 Expression, Distribution, and Lung Progenitor Cells. Clinical Infectious Diseases, 2021, 73, e4154-e4165.	2.9	42
14	Identification of Cooperative Gene Regulation Among Transcription Factors, LncRNAs, and MicroRNAs in Diabetic Nephropathy Progression. Frontiers in Genetics, 2020, 11, 1008.	1.1	8
15	CONNET: Accurate Genome Consensus in Assembling Nanopore Sequencing Data via Deep Learning. IScience, 2020, 23, 101128.	1.9	5
16	MC-Explorer: Analyzing and Visualizing Motif-Cliques on Large Networks. , 2020, , .		4
17	MegaPath: sensitive and rapid pathogen detection using metagenomic NGS data. BMC Genomics, 2020, 21, 500.	1.2	6
18	High-quality bacterial genomes of a partial-nitritation/anammox system by an iterative hybrid assembly method. Microbiome, 2020, 8, 155.	4.9	29

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19	Exploring the limit of using a deep neural network on pileup data for germline variant calling. Nature Machine Intelligence, 2020, 2, 220-227.	8.3	87
20	MegaPath-Nano: Accurate Compositional Analysis and Drug-level Antimicrobial Resistance Detection Software for Oxford Nanopore Long-read Metagenomics. , 2020, , .		0
21	ChromSeg: Two-Stage Framework for Overlapping Chromosome Segmentation and Reconstruction. , 2020, , .		4
22	Skyhawk: an artificial neural network-based discriminator for reviewing clinically significant genomic variants. International Journal of Computational Biology and Drug Design, 2020, 13, 431.	0.3	2
23	Translocator. , 2020, , .		0
24	RENET: A Deep Learning Approach for Extracting Gene-Disease Associations from Literature. Lecture Notes in Computer Science, 2019, , 272-284.	1.0	45
25	A multi-task convolutional deep neural network for variant calling in single molecule sequencing. Nature Communications, 2019, 10, 998.	5.8	102
26	MegaPath: Low-Similarity Pathogen Detection from Metagenomic NGS Data (Extended Abstract). , 2018, , .		0
27	Transcriptome Analysis of Acute Phase Liver Graft Injury in Liver Transplantation. Biomedicines, 2018, 6, 41.	1.4	5
28	AC-DIAMOND v1: accelerating large-scale DNAâ€“protein alignment. Bioinformatics, 2018, 34, 3744-3746.	1.8	8
29	16GT: a fast and sensitive variant caller using a 16-genotype probabilistic model. GigaScience, 2017, 6, 1-4.	3.3	11
30	Serine peptidase inhibitor Kazal type 1 (SPINK1) as novel downstream effector of the cadherin-17/Î²-catenin axis in hepatocellular carcinoma. Cellular Oncology (Dordrecht), 2017, 40, 443-456.	2.1	13
31	First Draft Genome Sequence of the Pathogenic Fungus Lomentospora prolificans (Formerly) Tj ETQq1 1 0.784314 rgBT /Overl	0.8	11
32	LRSim: A Linked-Reads Simulator Generating Insights for Better Genome Partitioning. Computational and Structural Biotechnology Journal, 2017, 15, 478-484.	1.9	42
33	MegaGTA: a sensitive and accurate metagenomic gene-targeted assembler using iterative de Bruijn graphs. BMC Bioinformatics, 2017, 18, 408.	1.2	11
34	AC-DIAMOND: Accelerating Protein Alignment via Better SIMD Parallelization and Space-Efficient Indexing. Lecture Notes in Computer Science, 2016, , 426-433.	1.0	1
35	BASE: a practical de novo assembler for large genomes using long NGS reads. BMC Genomics, 2016, 17, 499.	1.2	6
36	MEGAHIT v1.0: A fast and scalable metagenome assembler driven by advanced methodologies and community practices. Methods, 2016, 102, 3-11.	1.9	1,174

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37	MICA: A fast short-read aligner that takes full advantage of Many Integrated Core Architecture (MIC). BMC Bioinformatics, 2015, 16, S10.	1.2	14
38	Genome-Wide Mapping of Structural Variations Reveals a Copy Number Variant That Determines Reproductive Morphology in Cucumber. Plant Cell, 2015, 27, 1595-1604.	3.1	125
39	De novo assembly of a haplotype-resolved human genome. Nature Biotechnology, 2015, 33, 617-622.	9.4	73
40	MEGAHIT: an ultra-fast single-node solution for large and complex metagenomics assembly via succinct de Bruijn graph. Bioinformatics, 2015, 31, 1674-1676.	1.8	4,864
41	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	13.7	13,998
42	database.bio: a web application for interpreting human variations. Bioinformatics, 2015, 31, 4035-4037.	1.8	9
43	From Peer-Reviewed to Peer-Reproduced in Scholarly Publishing: The Complementary Roles of Data Models and Workflows in Bioinformatics. PLoS ONE, 2015, 10, e0127612.	1.1	27
44	FaSD-somatic: a fast and accurate somatic SNV detection algorithm for cancer genome sequencing data. Bioinformatics, 2014, 30, 2498-2500.	1.8	18
45	SOAPdenovo-Trans: de novo transcriptome assembly with short RNA-Seq reads. Bioinformatics, 2014, 30, 1660-1666.	1.8	826
46	BALSA: integrated secondary analysis for whole-genome and whole-exome sequencing, accelerated by GPU. PeerJ, 2014, 2, e421.	0.9	16
47	Abstract 4269: Exome sequencing of tumor cell lines: Optimizing for cancer variants. , 2014, , .		0
48	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. GigaScience, 2013, 2, 10.	3.3	582
49	SOAP3-dp: Fast, Accurate and Sensitive GPU-Based Short Read Aligner. PLoS ONE, 2013, 8, e65632.	1.1	104
50	Efficient SNP-sensitive alignment and database-assisted SNP calling for low coverage samples. , 2012, , .		0
51	COPE: an accurate k-mer-based pair-end reads connection tool to facilitate genome assembly. Bioinformatics, 2012, 28, 2870-2874.	1.8	145
52	SOAP3: ultra-fast GPU-based parallel alignment tool for short reads. Bioinformatics, 2012, 28, 878-879.	1.8	200
53	Single-base resolution maps of cultivated and wild rice methylomes and regulatory roles of DNA methylation in plant gene expression. BMC Genomics, 2012, 13, 300.	1.2	266
54	SOAPdenovo2: an empirically improved memory-efficient short-read de novo assembler. GigaScience, 2012, 1, 18.	3.3	4,510

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55	The oyster genome reveals stress adaptation and complexity of shell formation. Nature, 2012, 490, 49-54.	13.7	1,966
56	Whole Genome Sequencing On Donor Cell Leukemia in a Patient with Multiple Myeloma Identified Gene Mutations That May Provide Insights to Leukemogenesis.. Blood, 2012, 120, 2414-2414.	0.6	3
57	Structural variation in two human genomes mapped at single-nucleotide resolution by whole genome de novo assembly. Nature Biotechnology, 2011, 29, 723-730.	9.4	113
58	Mapping copy number variation by population-scale genome sequencing. Nature, 2011, 470, 59-65.	13.7	991
59	Assemblathon 1: A competitive assessment of de novo short read assembly methods. Genome Research, 2011, 21, 2224-2241.	2.4	443
60	Sequencing of 50 Human Exomes Reveals Adaptation to High Altitude. Science, 2010, 329, 75-78.	6.0	1,339
61	International network of cancer genome projects. Nature, 2010, 464, 993-998.	13.7	2,114
62	Building the sequence map of the human pan-genome. Nature Biotechnology, 2010, 28, 57-63.	9.4	237
63	Archaeology Augments Tibet's Genetic Historyâ€"Response. Science, 2010, 329, 1467-1468.	6.0	3
64	The DNA Methylome of Human Peripheral Blood Mononuclear Cells. PLoS Biology, 2010, 8, e1000533.	2.6	290