

# Ruibang Luo

## List of Publications by Year in descending order

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Version: 2024-02-01

64  
papers

35,268  
citations

236925

25  
h-index

149698

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. <i>Nature Machine Intelligence</i> , 2022, 4, 32-40.	16.0	29
2	HKG: an open genetic variant database of 205 Hong Kong cantonese exomes. <i>NAR Genomics and Bioinformatics</i> , 2022, 4, lqac005.	3.2	2
3	Temporal Control of the WNT Signaling Pathway During Cardiac Differentiation Impacts Upon the Maturation State of Human Pluripotent Stem Cell Derived Cardiomyocytes. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 714008.	3.5	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. <i>BMC Medical Genomics</i> , 2022, 15, 43.	1.5	7
5	Same-Cell Co-Occurrence of RAS Hotspot and BRAF V600E Mutations in Treatment-Naive Colorectal Cancer. <i>JCO Precision Oncology</i> , 2022, 6, e2100365.	3.0	1
6	Detecting structural variations with precise breakpoints using low-depth WGS data from a single oxford nanopore MinION flowcell. <i>Scientific Reports</i> , 2022, 12, 4519.	3.3	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. <i>Theranostics</i> , 2021, 11, 2170-2181.	10.0	14
8	High Prevalence and Mechanism Associated With Extended Spectrum Beta-Lactamase-Positive Phenotype in <i>Laribacter hongkongensis</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 618894.	3.5	3
9	<sc>SARS-CoV-2 biology and variants: anticipation of viral evolution and what needs to be done. <i>Environmental Microbiology</i> , 2021, 23, 2339-2363.	3.8	30
10	RENET2: high-performance full-text gene-disease relation extraction with iterative training data expansion. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab062.	3.2	4
11	Building a Chinese pan-genome of 486 individuals. <i>Communications Biology</i> , 2021, 4, 1016.	4.4	13
12	Applications and potentials of nanopore sequencing in the (epi)genome and (epi)transcriptome era. <i>Innovation(China)</i> , 2021, 2, 100153.	9.1	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. <i>Clinical Infectious Diseases</i> , 2021, 73, e4154-e4165.	5.8	42
14	Identification of Cooperative Gene Regulation Among Transcription Factors, LncRNAs, and MicroRNAs in Diabetic Nephropathy Progression. <i>Frontiers in Genetics</i> , 2020, 11, 1008.	2.3	8
15	CONNET: Accurate Genome Consensus in Assembling Nanopore Sequencing Data via Deep Learning. <i>IScience</i> , 2020, 23, 101128.	4.1	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. <i>BMC Genomics</i> , 2020, 21, 500.	2.8	6
18	High-quality bacterial genomes of a partial-nitritation/anammox system by an iterative hybrid assembly method. <i>Microbiome</i> , 2020, 8, 155.	11.1	29

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19	Exploring the limit of using a deep neural network on pileup data for germline variant calling. <i>Nature Machine Intelligence</i> , 2020, 2, 220-227.	16.0	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. <i>International Journal of Computational Biology and Drug Design</i> , 2020, 13, 431.	0.3	2
23	Translocator. , 2020, , .		0
24	RENET: A Deep Learning Approach for Extracting Gene-Disease Associations from Literature. <i>Lecture Notes in Computer Science</i> , 2019, , 272-284.	1.3	45
25	A multi-task convolutional deep neural network for variant calling in single molecule sequencing. <i>Nature Communications</i> , 2019, 10, 998.	12.8	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. <i>Biomedicines</i> , 2018, 6, 41.	3.2	5
28	AC-DIAMOND v1: accelerating large-scale DNAâ€“protein alignment. <i>Bioinformatics</i> , 2018, 34, 3744-3746.	4.1	8
29	16GT: a fast and sensitive variant caller using a 16-genotype probabilistic model. <i>GigaScience</i> , 2017, 6, 1-4.	6.4	11
30	Serine peptidase inhibitor Kazal type 1 (SPINK1) as novel downstream effector of the cadherin-17/ $\beta$ -catenin axis in hepatocellular carcinoma. <i>Cellular Oncology (Dordrecht)</i> , 2017, 40, 443-456.	4.4	13
31	First Draft Genome Sequence of the Pathogenic Fungus <i>Lomentospora prolificans</i> (Formerly) Tj ETQq1 1 0.784314 rgBT /Overl 1.8 11		
32	LRSim: A Linked-Reads Simulator Generating Insights for Better Genome Partitioning. <i>Computational and Structural Biotechnology Journal</i> , 2017, 15, 478-484.	4.1	42
33	MegaGTA: a sensitive and accurate metagenomic gene-targeted assembler using iterative de Bruijn graphs. <i>BMC Bioinformatics</i> , 2017, 18, 408.	2.6	11
34	AC-DIAMOND: Accelerating Protein Alignment via Better SIMD Parallelization and Space-Efficient Indexing. <i>Lecture Notes in Computer Science</i> , 2016, , 426-433.	1.3	1
35	BASE: a practical de novo assembler for large genomes using long NGS reads. <i>BMC Genomics</i> , 2016, 17, 499.	2.8	6
36	MEGAHIT v1.0: A fast and scalable metagenome assembler driven by advanced methodologies and community practices. <i>Methods</i> , 2016, 102, 3-11.	3.8	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.	2.6	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.	6.6	125
39	De novo assembly of a haplotype-resolved human genome. Nature Biotechnology, 2015, 33, 617-622.	17.5	73
40	MEGAHIT: an ultra-fast single-node solution for large and complex metagenomics assembly via succinct <i>de Bruijn</i> graph. Bioinformatics, 2015, 31, 1674-1676.	4.1	4,864
41	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	27.8	13,998
42	database.bio: a web application for interpreting human variations. Bioinformatics, 2015, 31, 4035-4037.	4.1	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.	2.5	27
44	FaSD-somatic: a fast and accurate somatic SNV detection algorithm for cancer genome sequencing data. Bioinformatics, 2014, 30, 2498-2500.	4.1	18
45	SOAPdenovo-Trans: <i>de novo</i> transcriptome assembly with short RNA-Seq reads. Bioinformatics, 2014, 30, 1660-1666.	4.1	826
46	BALSA: integrated secondary analysis for whole-genome and whole-exome sequencing, accelerated by GPU. PeerJ, 2014, 2, e421.	2.0	16
47	Abstract 4269: Exome sequencing of tumor cell lines: Optimizing for cancer variants. , 2014, , .		0
48	Assemblathon 2: evaluating <i>de novo</i> methods of genome assembly in three vertebrate species. GigaScience, 2013, 2, 10.	6.4	582
49	SOAP3-dp: Fast, Accurate and Sensitive GPU-Based Short Read Aligner. PLoS ONE, 2013, 8, e65632.	2.5	104
50	Efficient SNP-sensitive alignment and database-assisted SNP calling for low coverage samples. , 2012, , .		0
51	COPE: an accurate <i>k</i> -mer-based pair-end reads connection tool to facilitate genome assembly. Bioinformatics, 2012, 28, 2870-2874.	4.1	145
52	SOAP3: ultra-fast GPU-based parallel alignment tool for short reads. Bioinformatics, 2012, 28, 878-879.	4.1	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.	2.8	266
54	SOAPdenovo2: an empirically improved memory-efficient short-read <i>de novo</i> assembler. GigaScience, 2012, 1, 18.	6.4	4,510

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55	The oyster genome reveals stress adaptation and complexity of shell formation. <i>Nature</i> , 2012, 490, 49-54.	27.8	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.. <i>Blood</i> , 2012, 120, 2414-2414.	1.4	3
57	Structural variation in two human genomes mapped at single-nucleotide resolution by whole genome de novo assembly. <i>Nature Biotechnology</i> , 2011, 29, 723-730.	17.5	113
58	Mapping copy number variation by population-scale genome sequencing. <i>Nature</i> , 2011, 470, 59-65.	27.8	991
59	Assemblathon 1: A competitive assessment of de novo short read assembly methods. <i>Genome Research</i> , 2011, 21, 2224-2241.	5.5	443
60	Sequencing of 50 Human Exomes Reveals Adaptation to High Altitude. <i>Science</i> , 2010, 329, 75-78.	12.6	1,339
61	International network of cancer genome projects. <i>Nature</i> , 2010, 464, 993-998.	27.8	2,114
62	Building the sequence map of the human pan-genome. <i>Nature Biotechnology</i> , 2010, 28, 57-63.	17.5	237
63	Archaeology Augments Tibet's Genetic Historyâ€™Response. <i>Science</i> , 2010, 329, 1467-1468.	12.6	3
64	The DNA Methylome of Human Peripheral Blood Mononuclear Cells. <i>PLoS Biology</i> , 2010, 8, e1000533.	5.6	290