

Yun Li

List of Publications by Year in descending order

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Version: 2024-02-01

37
papers

2,900
citations

623734

14
h-index

345221

36
g-index

55
all docs

55
docs citations

55
times ranked

7475
citing authors

#	ARTICLE	IF	CITATIONS
1	Generalized multi-omic SNP mediation intersection union test. <i>Biometrics</i> , 2022, 78, 364-375.	1.4	7
2	Single-cell dual-omics reveals the transcriptomic and epigenomic diversity of cardiac non-myocytes. <i>Cardiovascular Research</i> , 2022, 118, 1548-1563.	3.8	31
3	eSCAN: scan regulatory regions for aggregate association testing using whole-genome sequencing data. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	5
4	Do adverse childhood experiences and genetic obesity risk interact in relation to body mass index in young adulthood? Findings from the National Longitudinal Study of Adolescent to Adult Health. <i>Pediatric Obesity</i> , 2022, 17, e12885.	2.8	4
5	THUNDER: A reference-free deconvolution method to infer cell type proportions from bulk Hi-C data. <i>PLoS Genetics</i> , 2022, 18, e1010102.	3.5	9
6	A systematic evaluation of Hi-C data enhancement methods for enhancing PLAC-seq and HiChIP data. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	3
7	SnapHiC2: A computationally efficient loop caller for single cell Hi-C data. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 2778-2783.	4.1	7
8	CUE: CpG imputation ensemble for DNA methylation levels across the human methylation450 (HM450) and EPIC (HM850) BeadChip platforms. <i>Epigenetics</i> , 2021, 16, 851-861.	2.7	1
9	SMNN: batch effect correction for single-cell RNA-seq data via supervised mutual nearest neighbor detection. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	17
10	TWO-SIGMA: A novel two-component single cell model-based association method for single-cell RNA-seq data. <i>Genetic Epidemiology</i> , 2021, 45, 142-153.	1.3	11
11	Maternal gut microbiota reflecting poor diet quality is associated with spontaneous preterm birth in a prospective cohort study. <i>American Journal of Clinical Nutrition</i> , 2021, 113, 602-611.	4.7	19
12	MOSTWAS: Multi-Omic Strategies for Transcriptome-Wide Association Studies. <i>PLoS Genetics</i> , 2021, 17, e1009398.	3.5	46
13	MRLocus: Identifying causal genes mediating a trait through Bayesian estimation of allelic heterogeneity. <i>PLoS Genetics</i> , 2021, 17, e1009455.	3.5	24
14	Genetic correlations between COVID-19 and a variety of traits and diseases. <i>Innovation(China)</i> , 2021, 2, 100112.	9.1	7
15	ExpressHeart: Web Portal to Visualize Transcriptome Profiles of Non-Cardiomyocyte Cells. <i>International Journal of Molecular Sciences</i> , 2021, 22, 8943.	4.1	3
16	HPRep: Quantifying Reproducibility in HiChIP and PLAC-Seq Datasets. <i>Current Issues in Molecular Biology</i> , 2021, 43, 1156-1170.	2.4	4
17	Soluble Urokinase Plasminogen Activator Receptor: Genetic Variation and Cardiovascular Disease Risk in Black Adults. <i>Circulation Genomic and Precision Medicine</i> , 2021, 14, CIRCGEN121003421.	3.6	7
18	Age-related DNA hydroxymethylation is enriched for gene expression and immune system processes in human peripheral blood. <i>Epigenetics</i> , 2020, 15, 294-306.	2.7	8

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19	SAME-clustering: Single-cell Aggregated Clustering via Mixture Model Ensemble. <i>Nucleic Acids Research</i> , 2020, 48, 86-95.	14.5	55
20	Genome-Wide Association of Kidney Traits in Hispanics/Latinos Using Dense Imputed Whole-Genome Sequencing Data. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, e002891.	3.6	6
21	Bacterial colonization reprograms the neonatal gut metabolome. <i>Nature Microbiology</i> , 2020, 5, 838-847.	13.3	70
22	MAPS: Model-based analysis of long-range chromatin interactions from PLAC-seq and HiChIP experiments. <i>PLoS Computational Biology</i> , 2019, 15, e1006982.	3.2	94
23	Coexpression network analysis identifies transcriptional modules associated with genomic alterations in neuroblastoma. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2018, 1864, 2341-2348.	3.8	35
24	FXR-Dependent Modulation of the Human Small Intestinal Microbiome by the Bile Acid Derivative Obeticholic Acid. <i>Gastroenterology</i> , 2018, 155, 1741-1752.e5.	1.3	82
25	299 - FXR-Dependent Modification of the Human Small Intestinal Microbiome. <i>Gastroenterology</i> , 2018, 154, S-1084.	1.3	0
26	Weighted Gene Co-Expression Network Analysis Reveals Dysregulation of Mitochondrial Oxidative Phosphorylation in Eating Disorders. <i>Genes</i> , 2018, 9, 325.	2.4	14
27	A Multiancestral Genome-Wide Exome Array Study of Alzheimer Disease, Frontotemporal Dementia, and Progressive Supranuclear Palsy. <i>JAMA Neurology</i> , 2015, 72, 414.	9.0	37
28	An Epigenetic Signature in Peripheral Blood Associated with the Haplotype on 17q21.31, a Risk Factor for Neurodegenerative Tauopathy. <i>PLoS Genetics</i> , 2014, 10, e1004211.	3.5	65
29	Dynamic modular architecture of protein-protein interaction networks beyond the dichotomy of "date" and "party" hubs. <i>Scientific Reports</i> , 2013, 3, 1691.	3.3	71
30	A cross-species analysis method to analyze animal models' similarity to human's disease state. <i>BMC Systems Biology</i> , 2012, 6, S18.	3.0	7
31	Rare-Variant Association Testing for Sequencing Data with the Sequence Kernel Association Test. <i>American Journal of Human Genetics</i> , 2011, 89, 82-93.	6.2	2,060
32	EcoBrowser: a web-based tool for visualizing transcriptome data of <i>Escherichia coli</i> . <i>BMC Research Notes</i> , 2011, 4, 405.	1.4	3
33	ASSOCIATION OF FEATURE GENE EXPRESSION WITH STRUCTURAL FINGERPRINTS OF CHEMICAL COMPOUNDS. <i>Journal of Bioinformatics and Computational Biology</i> , 2011, 09, 503-519.	0.8	4
34	GEOGLE: context mining tool for the correlation between gene expression and the phenotypic distinction. <i>BMC Bioinformatics</i> , 2009, 10, 264.	2.6	4
35	MPSQ: a web tool for protein-state searching. <i>Bioinformatics</i> , 2008, 24, 2412-2413.	4.1	4
36	Gene expression module-based chemical function similarity search. <i>Nucleic Acids Research</i> , 2008, 36, e137-e137.	14.5	23

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37	Tree of Life Based on Genome Context Networks. PLoS ONE, 2008, 3, e3357.	2.5	26