Yun Li

List of Publications by Year
in descending order

99 papers	25,585 citations	94433 37 h-index	37204 96 g-index
138 all docs	138 docs citations	138 times ranked	38109 citing authors

#	Article	IF	Citations
1	A second generation human haplotype map of over 3.1 million SNPs. Nature, 2007, 449, 851-861.	27.8	4,137
2	METAL: fast and efficient meta-analysis of genomewide association scans. Bioinformatics, 2010, 26, 2190-2191.	4.1	4,046
3	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. Nature Genetics, 2018, 50, 668-681.	21.4	2,224
4	Rare-Variant Association Testing for Sequencing Data with the Sequence Kernel Association Test. American Journal of Human Genetics, 2011, 89, 82-93.	6.2	2,060
5	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. Nature Genetics, 2010, 42, 105-116.	21.4	1,982
6	MaCH: using sequence and genotype data to estimate haplotypes and unobserved genotypes. Genetic Epidemiology, 2010, 34, 816-834.	1.3	1,718
7	Newly identified loci that influence lipid concentrations and risk of coronary artery disease. Nature Genetics, 2008, 40, 161-169.	21.4	1,488
8	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. Nature Genetics, 2014, 46, 234-244.	21.4	959
9	Genotype Imputation. Annual Review of Genomics and Human Genetics, 2009, 10, 387-406.	6.2	920
10	A Compendium of Chromatin Contact Maps Reveals Spatially Active Regions in the Human Genome. Cell Reports, 2016, 17, 2042-2059.	6.4	745
11	Integrative functional genomic analysis of human brain development and neuropsychiatric risks. Science, 2018, 362, .	12.6	516
12	The Polygenic and Monogenic Basis of Blood Traits and Diseases. Cell, 2020, 182, 1214-1231.e11.	28.9	388
13	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. Nature, 2020, 586, 763-768.	27.8	376
14	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. Cell, 2020, 182, 1198-1213.e14.	28.9	353
15	Genome-wide association study identifies variants in TMPRSS6 associated with hemoglobin levels. Nature Genetics, 2009, 41, 1170-1172.	21.4	217
16	Use of >100,000 NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium whole genome sequences improves imputation quality and detection of rare variant associations in admixed African and Hispanic/Latino populations. PLoS Genetics, 2019, 15, e1008500.	3.5	203
17	Genome-wide association analysis of 19,629 individuals identifies variants influencing regional brain volumes and refines their genetic co-architecture with cognitive and mental health traits. Nature Genetics, 2019, 51, 1637-1644.	21.4	186
18	SCDC: bulk gene expression deconvolution by multiple single-cell RNA sequencing references. Briefings in Bioinformatics, 2021, 22, 416-427.	6.5	156

#	Article	IF	Citations
19	Dynamic incorporation of multiple in silico functional annotations empowers rare variant association analysis of large whole-genome sequencing studies at scale. Nature Genetics, 2020, 52, 969-983.	21.4	146
20	Mapping cis-regulatory chromatin contacts in neural cells links neuropsychiatric disorder risk variants to target genes. Nature Genetics, 2019, 51, 1252-1262.	21.4	139
21	On the asymptotics of penalized splines. Biometrika, 2008, 95, 415-436.	2.4	126
22	Imputation of Exome Sequence Variants into Population- Based Samples and Blood-Cell-Trait-Associated Loci in African Americans: NHLBI GO Exome Sequencing Project. American Journal of Human Genetics, 2012, 91, 794-808.	6.2	123
23	MaCHâ€Admix: Genotype Imputation for Admixed Populations. Genetic Epidemiology, 2013, 37, 25-37.	1.3	113
24	Cell-type-specific 3D epigenomes in the developing human cortex. Nature, 2020, 587, 644-649.	27.8	110
25	Common genetic variation influencing human white matter microstructure. Science, 2021, 372, .	12.6	106
26	SAFE-clustering: Single-cell Aggregated (from Ensemble) clustering for single-cell RNA-seq data. Bioinformatics, 2019, 35, 1269-1277.	4.1	104
27	Large-scale GWAS reveals genetic architecture of brain white matter microstructure and genetic overlap with cognitive and mental health traits (nâ€‰=â€‰17,706). Molecular Psychiatry, 2021, 26, 3943-3955.	7.9	100
28	Discovery and fine-mapping of adiposity loci using high density imputation of genome-wide association studies in individuals of African ancestry: African Ancestry Anthropometry Genetics Consortium. PLoS Genetics, 2017, 13, e1006719.	3.5	98
29	MAPS: Model-based analysis of long-range chromatin interactions from PLAC-seq and HiChIP experiments. PLoS Computational Biology, 2019, 15, e1006982.	3.2	94
30	Single-Cell Heterogeneity Analysis and CRISPR Screen Identify Key Î²-Cell-Specific Disease Genes. Cell Reports, 2019, 26, 3132-3144.e7.	6.4	90
31	HUGIn: Hi-C Unifying Genomic Interrogator. Bioinformatics, 2017, 33, 3793-3795.	4.1	69
32	Common DNA sequence variation influences 3-dimensional conformation of the human genome. Genome Biology, 2019, 20, 255.	8.8	65
33	Gene regulation in the 3D genome. Human Molecular Genetics, 2018, 27, R228-R233.	2.9	61
34	Genotype Imputation of <scp>M</scp>etabochip<scp>SNPs</scp> Using a Studyâ€Specific Reference Panel of â¼4,000 Haplotypes in <scp>A</scp>frican <scp>A</scp>mericans From the Women's Health Initiative. Genetic Epidemiology, 2012, 36, 107-117.	1.3	57
35	Common genetic risk variants identified in the SPARK cohort support DDHD2 as a candidate risk gene for autism. Translational Psychiatry, 2020, 10, 265.	4.8	56
36	Increased burden of ultra-rare structural variants localizing to boundaries of topologically associated domains in schizophrenia. Nature Communications, 2020, 11, 1842.	12.8	56

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37	SAME-clustering: Single-cell Aggregated Clustering via Mixture Model Ensemble. Nucleic Acids Research, 2020, 48, 86-95.	14.5	55
38	Genome-wide association study of red blood cell traits in Hispanics/Latinos: The Hispanic Community Health Study/Study of Latinos. PLoS Genetics, 2017, 13, e1006760.	3.5	53
39	Neuronal and glial 3D chromatin architecture informs the cellular etiology of brain disorders. Nature Communications, 2021, 12, 3968.	12.8	48
40	A hidden Markov random field-based Bayesian method for the detection of long-range chromosomal interactions in Hi-C data. Bioinformatics, 2016, 32, 650-656.	4.1	47
41	MOSTWAS: Multi-Omic Strategies for Transcriptome-Wide Association Studies. PLoS Genetics, 2021, 17, e1009398.	3.5	46
42	SnapHiC: a computational pipeline to identify chromatin loops from single-cell Hi-C data. Nature Methods, 2021, 18, 1056-1059.	19.0	46
43	Common Î±-globin variants modify hematologic and other clinical phenotypes in sickle cell trait and disease. PLoS Genetics, 2018, 14, e1007293.	3.5	45
44	FastHiC: a fast and accurate algorithm to detect long-range chromosomal interactions from Hi-C data. Bioinformatics, 2016, 32, 2692-2695.	4.1	40
45	D-Dimer in African Americans. Arteriosclerosis, Thrombosis, and Vascular Biology, 2017, 37, 2220-2227.	2.4	40
46	Population-specific coding variant underlies genome-wide association with adiponectin level. Human Molecular Genetics, 2012, 21, 463-471.	2.9	37
47	Common variants contribute to intrinsic human brain functional networks. Nature Genetics, 2022, 54, 508-517.	21.4	37
48	Imputation of coding variants in African Americans: better performance using data from the exome sequencing project. Bioinformatics, 2013, 29, 2744-2749.	4.1	36
49	Heritability of Regional Brain Volumes in Large-Scale Neuroimaging and Genetic Studies. Cerebral Cortex, 2019, 29, 2904-2914.	2.9	36
50	Single-cell dual-omics reveals the transcriptomic and epigenomic diversity of cardiac non-myocytes. Cardiovascular Research, 2022, 118, 1548-1563.	3.8	31
51	Whole-genome sequencing association analysis of quantitative red blood cell phenotypes: The NHLBI TOPMed program. American Journal of Human Genetics, 2021, 108, 874-893.	6.2	28
52	Analyses of biomarker traits in diverse UK biobank participants identify associations missed by European-centric analysis strategies. Journal of Human Genetics, 2022, 67, 87-93.	2.3	27
53	Gene Level Meta-Analysis of Quantitative Traits by Functional Linear Models. Genetics, 2015, 200, 1089-1104.	2.9	25
54	Transcriptome-wide association analysis of brain structures yields insights into pleiotropy with complex neuropsychiatric traits. Nature Communications, 2021, 12, 2878.	12.8	25

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55	MRLocus: Identifying causal genes mediating a trait through Bayesian estimation of allelic heterogeneity. PLoS Genetics, 2021, 17, e1009455.	3.5	24
56	Multi-SNP mediation intersection-union test. Bioinformatics, 2019, 35, 4724-4729.	4.1	23
57	FIREcaller: Detecting frequently interacting regions from Hi-C data. Computational and Structural Biotechnology Journal, 2021, 19, 355-362.	4.1	22
58	Placental genomics mediates genetic associations with complex health traits and disease. Nature Communications, 2022, 13, 706.	12.8	20
59	Ancestry-specific associations identified in genome-wide combined-phenotype study of red blood cell traits emphasize benefits of diversity in genomics. BMC Genomics, 2020, 21, 228.	2.8	19
60	A comprehensive SNP and indel imputability database. Bioinformatics, 2013, 29, 528-531.	4.1	18
61	Meta-analysis of Complex Diseases at Gene Level with Generalized Functional Linear Models. Genetics, 2016, 202, 457-470.	2.9	18
62	SMNN: batch effect correction for single-cell RNA-seq data via supervised mutual nearest neighbor detection. Briefings in Bioinformatics, 2021, 22, .	6.5	17
63	HiC-ACT: improved detection of chromatin interactions from Hi-C data via aggregated Cauchy test. American Journal of Human Genetics, 2021, 108, 257-268.	6.2	17
64	Parallel characterization of cis-regulatory elements for multiple genes using CRISPRpath. Science Advances, 2021, 7, eabi4360.	10.3	16
65	Whole-genome sequencing in diverse subjects identifies genetic correlates of leukocyte traits: The NHLBI TOPMed program. American Journal of Human Genetics, 2021, 108, 1836-1851.	6.2	14
66	Super hotspots and super coldspots in the repair of UV-induced DNA damage in the human genome. Journal of Biological Chemistry, 2021, 296, 100581.	3.4	13
67	Adiponectin GWAS loci harboring extensive allelic heterogeneity exhibit distinct molecular consequences. PLoS Genetics, 2020, 16, e1009019.	3.5	11
68	TWOâ€SIGMA: A novel twoâ€component single cell modelâ€based association method for singleâ€cell RNAâ€seq data. Genetic Epidemiology, 2021, 45, 142-153.	1.3	11
69	Transcriptome-Wide Association Study of Blood Cell Traits in African Ancestry and Hispanic/Latino Populations. Genes, 2021, 12, 1049.	2.4	11
70	Acrossâ€Platform Imputation of DNA Methylation Levels Incorporating Nonlocal Information Using Penalized Functional Regression. Genetic Epidemiology, 2016, 40, 333-340.	1.3	10
71	Allelic Heterogeneity at the CRP Locus Identified by Whole-Genome Sequencing in Multi-ancestry Cohorts. American Journal of Human Genetics, 2020, 106, 112-120.	6.2	9
72	Whole genome sequence analysis of platelet traits in the NHLBI Trans-Omics for Precision Medicine (TOPMed) initiative. Human Molecular Genetics, 2022, 31, 347-361.	2.9	9

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73	From GWAS variant to function: A study of âˆ¼148,000 variants for blood cell traits. Human Genetics and Genomics Advances, 2022, 3, 100063.	1.7	9
74	THUNDER: A reference-free deconvolution method to infer cell type proportions from bulk Hi-C data. PLoS Genetics, 2022, 18, e1010102.	3.5	9
75	iSMNN: batch effect correction for single-cell RNA-seq data via iterative supervised mutual nearest neighbor refinement. Briefings in Bioinformatics, 2021, 22, .	6.5	8
76	Generalized multiâ€SNP mediation intersectionâ€“union test. Biometrics, 2022, 78, 364-375.	1.4	7
77	Soluble Urokinase Plasminogen Activator Receptor: Genetic Variation and Cardiovascular Disease Risk in Black Adults. Circulation Genomic and Precision Medicine, 2021, 14, CIRCGEN121003421.	3.6	7
78	Understanding Regulatory Mechanisms of Brain Function and Disease through 3D Genome Organization. Genes, 2022, 13, 586.	2.4	7
79	SnapHiC2: A computationally efficient loop caller for single cell Hi-C data. Computational and Structural Biotechnology Journal, 2022, 20, 2778-2783.	4.1	7
80	Genome-Wide Association of Kidney Traits in Hispanics/Latinos Using Dense Imputed Whole-Genome Sequencing Data. Circulation Genomic and Precision Medicine, 2020, 13, e002891.	3.6	6
81	Multi-ethnic genome-wide association analyses of white blood cell and platelet traits in the Population Architecture using Genomics and Epidemiology (PAGE) study. BMC Genomics, 2021, 22, 432.	2.8	6
82	Leveraging TOPMed imputation server and constructing a cohort-specific imputation reference panel to enhance genotype imputation among cystic fibrosis patients. Human Genetics and Genomics Advances, 2022, 3, 100090.	1.7	6
83	Transcriptome-wide association study in UK Biobank Europeans identifies associations with blood cell traits. Human Molecular Genetics, 2022, 31, 2333-2347.	2.9	6
84	eSCAN: scan regulatory regions for aggregate association testing using whole-genome sequencing data. Briefings in Bioinformatics, 2022, 23, .	6.5	5
85	TWO-SIGMA-G: a new competitive gene set testing framework for scRNA-seq data accounting for inter-gene and cellâ€“cell correlation. Briefings in Bioinformatics, 2022, 23, .	6.5	5
86	SMART-Q:Â An Integrative Pipeline Quantifying Cell Type-Specific RNA Transcription. PLoS ONE, 2020, 15, e0228760.	2.5	4
87	Host Genetic Risk Factors for Chlamydia trachomatis-Related Infertility in Women. Journal of Infectious Diseases, 2021, 224, S64-S71.	4.0	4
88	HPRep: Quantifying Reproducibility in HiChIP and PLAC-Seq Datasets. Current Issues in Molecular Biology, 2021, 43, 1156-1170.	2.4	4
89	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. Pediatric Obesity, 2022, 17, e12885.	2.8	4
90	Super interactive promoters provide insight into cell type-specific regulatory networks in blood lineage cell types. PLoS Genetics, 2022, 18, e1009984.	3.5	4

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91	Machine Learning and Deep Learning in Genetics and Genomics. , 2021, , 163-181.		3
92	ExpressHeart: Web Portal to Visualize Transcriptome Profiles of Non-Cardiomyocyte Cells. International Journal of Molecular Sciences, 2021, 22, 8943.	4.1	3
93	A systematic evaluation of Hi-C data enhancement methods for enhancing PLAC-seq and HiChIP data. Briefings in Bioinformatics, 2022, 23, .	6.5	3
94	Full title: A largeâ€scale transcriptomeâ€wide association study (TWAS) of 10 blood cell phenotypes reveals complexities of TWAS fineâ€mapping. Genetic Epidemiology, 2021, , .	1.3	2
95	GMEPS: a fast and efficient likelihood approach for genome-wide mediation analysis under extreme phenotype sequencing. Statistical Applications in Genetics and Molecular Biology, 2022, 21, .	0.6	2
96	Innovative computational approaches shed light on genetic mechanisms underlying cognitive impairment among children born extremely preterm. Journal of Neurodevelopmental Disorders, 2022, 14, 16.	3.1	2
97	CUE: CpG impUtation ensemble for DNA methylation levels across the human methylation450 (HM450) and EPIC (HM850) BeadChip platforms. Epigenetics, 2021, 16, 851-861.	2.7	1
98	MUNIn: A statistical framework for identifying long-range chromatin interactions from multiple samples. Human Genetics and Genomics Advances, 2021, 2, 100036.	1.7	0
99	DNA Methylation Imputation Across Platforms. Methods in Molecular Biology, 2022, 2432, 137-151.	0.9	0