Yun Li

List of Publications by Year in Descending Order

107 papers	18,073 citations	33 h-index	134 g-index
138 ext. papers	22,631 ext. citations	12.6 avg, IF	6.28 L-index

#	Paper	IF	Citations
107	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**, e12885	4.6	1
106	Super interactive promoters provide insight into cell type-specific regulatory networks in blood lineage cell types.. *PLoS Genetics*, **2022**, 18, e1009984	6	0
105	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	0.8	
104	Placental genomics mediates genetic associations with complex health traits and disease.. *Nature Communications*, **2022**, 13, 706	17.4	0
103	From GWAS variant to function: A study of ~148,000 variants for blood cell traits.. *Human Genetics and Genomics Advances*, **2022**, 3, 100063	0.8	1
102	Innovative computational approaches shed light on genetic mechanisms underlying cognitive impairment among children born extremely preterm.. *Journal of Neurodevelopmental Disorders*, **2022**, 14, 16	4.6	0
101	THUNDER: A reference-free deconvolution method to infer cell type proportions from bulk Hi-C data.. *PLoS Genetics*, **2022**, 18, e1010102	6	0
100	Common variants contribute to intrinsic human brain functional networks.. *Nature Genetics*, **2022**, 54, 508-517	36.3	1
99	DNA Methylation Imputation Across Platforms.. *Methods in Molecular Biology*, **2022**, 2432, 137-151	1.4	
98	SnapHiC2: A computationally efficient loop caller for single cell Hi-C data. *Computational and Structural Biotechnology Journal*, **2022**, 20, 2778-2783	6.8	0
97	Large-scale GWAS reveals genetic architecture of brain white matter microstructure and genetic overlap with cognitive and mental health traits (n = 17,706). *Molecular Psychiatry*, **2021**, 26, 3943-3955	15.1	35
96	Soluble Urokinase Plasminogen Activator Receptor: Genetic Variation and Cardiovascular Disease Risk in Blacks. *Circulation Genomic and Precision Medicine*, **2021**, CIRCGEN121003421	5.2	1
95	CUE: CpG impUtation ensemble for DNA methylation levels across the human methylation450 (HM450) and EPIC (HM850) BeadChip platforms. *Epigenetics*, **2021**, 16, 851-861	5.7	0
94	MOSTWAS: Multi-Omic Strategies for Transcriptome-Wide Association Studies. *PLoS Genetics*, **2021**, 17, e1009398	6	9
93	MRLocus: Identifying causal genes mediating a trait through Bayesian estimation of allelic heterogeneity. *PLoS Genetics*, **2021**, 17, e1009455	6	4
92	Single cell dual-omics reveals the transcriptomic and epigenomic diversity of cardiac non-myocytes. *Cardiovascular Research*, **2021**,	9.9	5
91	iSMNN: batch effect correction for single-cell RNA-seq data via iterative supervised mutual nearest neighbor refinement. *Briefings in Bioinformatics*, **2021**, 22,	13.4	3

90	Whole-genome sequencing association analysis of quantitative red blood cell phenotypes: The NHLBI TOPMed program. *American Journal of Human Genetics*, **2021**, 108, 874-893	11	5
89	Transcriptome-wide association analysis of brain structures yields insights into pleiotropy with complex neuropsychiatric traits. *Nature Communications*, **2021**, 12, 2878	17.4	2
88	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	4.5	0
87	Common genetic variation influencing human white matter microstructure. *Science*, **2021**, 372,	33.3	18
86	Neuronal and glial 3D chromatin architecture informs the cellular etiology of brain disorders. *Nature Communications*, **2021**, 12, 3968	17.4	2
85	SMNN: batch effect correction for single-cell RNA-seq data via supervised mutual nearest neighbor detection. *Briefings in Bioinformatics*, **2021**, 22,	13.4	8
84	TWO-SIGMA: A novel two-component single cell model-based association method for single-cell RNA-seq data. *Genetic Epidemiology*, **2021**, 45, 142-153	2.6	2
83	SCDC: bulk gene expression deconvolution by multiple single-cell RNA sequencing references. *Briefings in Bioinformatics*, **2021**, 22, 416-427	13.4	34
82	Super hotspots and super coldspots in the repair of UV-induced DNA damage in the human genome. *Journal of Biological Chemistry*, **2021**, 296, 100581	5.4	4
81	Machine Learning and Deep Learning in Genetics and Genomics **2021**, 163-181		
80	FIREcaller: Detecting frequently interacting regions from Hi-C data. *Computational and Structural Biotechnology Journal*, **2021**, 19, 355-362	6.8	13
79	HiC-ACT: improved detection of chromatin interactions from Hi-C data via aggregated Cauchy test. *American Journal of Human Genetics*, **2021**, 108, 257-268	11	3
78	SnapHiC: a computational pipeline to identify chromatin loops from single-cell Hi-C data. *Nature Methods*, **2021**, 18, 1056-1059	21.6	4
77	Analyses of biomarker traits in diverse UK biobank participants identify associations missed by European-centric analysis strategies. *Journal of Human Genetics*, **2021**,	4.3	6
76	Host Genetic Risk Factors for Chlamydia trachomatis-Related Infertility in Women. *Journal of Infectious Diseases*, **2021**, 224, S64-S71	7	0
75	HPRep: Quantifying Reproducibility in HiChIP and PLAC-Seq Datasets. *Current Issues in Molecular Biology*, **2021**, 43, 1156-1170	2.9	0
74	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	11	1
73	Parallel characterization of cis-regulatory elements for multiple genes using CRISPRpath. *Science Advances*, **2021**, 7, eabi4360	14.3	2

72	Whole genome sequence analysis of platelet traits in the NHLBI trans-omics for precision medicine initiative. *Human Molecular Genetics*, **2021**,	5.6	2
71	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	4.5	8
70	Genome-Wide Association of Kidney Traits in Hispanics/Latinos Using Dense Imputed Whole-Genome Sequencing Data: The Hispanic Community Health Study/Study of Latinos. *Circulation Genomic and Precision Medicine*, **2020**, 13, e002891	5.2	1
69	Allelic Heterogeneity at the CRP Locus Identified by Whole-Genome Sequencing in Multi-ancestry Cohorts. *American Journal of Human Genetics*, **2020**, 106, 112-120	11	2
68	SMART-Q:An Integrative Pipeline Quantifying Cell Type-Specific RNA Transcription. *PLoS ONE*, **2020**, 15, e0228760	3.7	2
67	SAME-clustering: Single-cell Aggregated Clustering via Mixture Model Ensemble. *Nucleic Acids Research*, **2020**, 48, 86-95	20.1	27
66	The Polygenic and Monogenic Basis of Blood Traits and Diseases. *Cell*, **2020**, 182, 1214-1231.e11	56.2	96
65	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. *Nature*, **2020**, 586, 763-768	50.4	127
64	Cell-type-specific 3D epigenomes in the developing human cortex. *Nature*, **2020**, 587, 644-649	50.4	37
63	Common genetic risk variants identified in the SPARK cohort support DDHD2 as a candidate risk gene for autism. *Translational Psychiatry*, **2020**, 10, 265	8.6	19
62	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. *Cell*, **2020**, 182, 1198-1213.e14	56.2	88
61	Adiponectin GWAS loci harboring extensive allelic heterogeneity exhibit distinct molecular consequences. *PLoS Genetics*, **2020**, 16, e1009019	6	3
60	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	36.3	33
59	Increased burden of ultra-rare structural variants localizing to boundaries of topologically associated domains in schizophrenia. *Nature Communications*, **2020**, 11, 1842	17.4	22
58	Generalized multi-SNP mediation intersection-union test. *Biometrics*, **2020**,	1.8	2
57	Multi-SNP mediation intersection-union test. *Bioinformatics*, **2019**, 35, 4724-4729	7.2	9
56	MAPS: Model-based analysis of long-range chromatin interactions from PLAC-seq and HiChIP experiments. *PLoS Computational Biology*, **2019**, 15, e1006982	5	45
55	Single-Cell Heterogeneity Analysis and CRISPR Screen Identify Key Cell-Specific Disease Genes. *Cell Reports*, **2019**, 26, 3132-3144.e7	10.6	38

54	Heritability of Regional Brain Volumes in Large-Scale Neuroimaging and Genetic Studies. *Cerebral Cortex*, **2019**, 29, 2904-2914	5.1	10
53	Mapping cis-regulatory chromatin contacts in neural cells links neuropsychiatric disorder risk variants to target genes. *Nature Genetics*, **2019**, 51, 1252-1262	36.3	68
52	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	36.3	69
51	Common DNA sequence variation influences 3-dimensional conformation of the human genome. *Genome Biology*, **2019**, 20, 255	18.3	36
50	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	6	90
49	SAFE-clustering: Single-cell Aggregated (from Ensemble) clustering for single-cell RNA-seq data. *Bioinformatics*, **2019**, 35, 1269-1277	7.2	54
48	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. *Nature Genetics*, **2018**, 50, 668-681	36.3	1301
47	Common globin variants modify hematologic and other clinical phenotypes in sickle cell trait and disease. *PLoS Genetics*, **2018**, 14, e1007293	6	25
46	Integrative functional genomic analysis of human brain development and neuropsychiatric risks. *Science*, **2018**, 362,	33.3	277
45	Gene regulation in the 3D genome. *Human Molecular Genetics*, **2018**, 27, R228-R233	5.6	26
44	HUGIn: Hi-C Unifying Genomic Interrogator. *Bioinformatics*, **2017**, 33, 3793-3795	7.2	41
43	D-Dimer in African Americans: Whole Genome Sequence Analysis and Relationship to Cardiovascular Disease Risk in the Jackson Heart Study. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2017**, 37, 2220-2227	9.4	22
42	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	6	60
41	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	6	38
40	A Compendium of Chromatin Contact Maps Reveals Spatially Active Regions in the Human Genome. *Cell Reports*, **2016**, 17, 2042-2059	10.6	453
39	Meta-analysis of Complex Diseases at Gene Level with Generalized Functional Linear Models. *Genetics*, **2016**, 202, 457-70	4	13
38	A hidden Markov random field-based Bayesian method for the detection of long-range chromosomal interactions in Hi-C data. *Bioinformatics*, **2016**, 32, 650-6	7.2	32
37	Across-Platform Imputation of DNA Methylation Levels Incorporating Nonlocal Information Using Penalized Functional Regression. *Genetic Epidemiology*, **2016**, 40, 333-40	2.6	8

36	FastHiC: a fast and accurate algorithm to detect long-range chromosomal interactions from Hi-C data. *Bioinformatics*, **2016**, 32, 2692-5	7.2	20
35	Gene Level Meta-Analysis of Quantitative Traits by Functional Linear Models. *Genetics*, **2015**, 200, 1089-104	4	24
34	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. *Nature Genetics*, **2014**, 46, 234-44	36.3	784
33	A comprehensive SNP and indel imputability database. *Bioinformatics*, **2013**, 29, 528-31	7.2	14
32	MaCH-admix: genotype imputation for admixed populations. *Genetic Epidemiology*, **2013**, 37, 25-37	2.6	100
31	Imputation of coding variants in African Americans: better performance using data from the exome sequencing project. *Bioinformatics*, **2013**, 29, 2744-9	7.2	30
30	Genotype imputation of Metabochip SNPs using a study-specific reference panel of ~4,000 haplotypes in African Americans from the Women's Health Initiative. *Genetic Epidemiology*, **2012**, 36, 107-17	2.6	49
29	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	11	103
28	Population-specific coding variant underlies genome-wide association with adiponectin level. *Human Molecular Genetics*, **2012**, 21, 463-71	5.6	35
27	Rare-variant association testing for sequencing data with the sequence kernel association test. *American Journal of Human Genetics*, **2011**, 89, 82-93	11	1573
26	METAL: fast and efficient meta-analysis of genomewide association scans. *Bioinformatics*, **2010**, 26, 2190-1	7.2	2697
25	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. *Nature Genetics*, **2010**, 42, 105-16	36.3	1673
24	MaCH: using sequence and genotype data to estimate haplotypes and unobserved genotypes. *Genetic Epidemiology*, **2010**, 34, 816-34	2.6	1535
23	Genome-wide association study identifies variants in TMPRSS6 associated with hemoglobin levels. *Nature Genetics*, **2009**, 41, 1170-2	36.3	179
22	Genotype imputation. *Annual Review of Genomics and Human Genetics*, **2009**, 10, 387-406	9.7	812
21	Newly identified loci that influence lipid concentrations and risk of coronary artery disease. *Nature Genetics*, **2008**, 40, 161-9	36.3	1304
20	On the asymptotics of penalized splines. *Biometrika*, **2008**, 95, 415-436	2	96
19	A second generation human haplotype map of over 3.1 million SNPs. *Nature*, **2007**, 449, 851-61	50.4	3647

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18	MAPS: model-based analysis of long-range chromatin interactions from PLAC-seq and HiChIP experiments	1
17	SAME-clustering: Single-cell Aggregated Clustering via Mixture Model Ensemble	2
16	Generalized Multi-SNP Mediation Intersection-Union Test	1
15	SnapHiC: a computational pipeline to map chromatin contacts from single cell Hi-C data	1
14	3D Epigenomic Characterization Reveals Insights Into Gene Regulation and Lineage Specification During Corticogenesis	3
13	Nucleotide excision repair hotspots and coldspots of UV-induced DNA damage in the human genome	3
12	MOSTWAS: Multi-Omic Strategies for Transcriptome-Wide Association Studies	1
11	Neuronal and glial 3D chromatin architecture illustrates cellular etiology of brain disorders	3
10	Common genetic variation influencing human white matter microstructure	5
9	Whole genome sequencing association analysis of quantitative red blood cell phenotypes: the NHLBI TOPMed program	1
8	SAFE-clustering: Single-cell Aggregated (From Ensemble) Clustering for Single-cell RNA-seq Data	8
7	FIREcaller: Detecting Frequently Interacting Regions from Hi-C Data	5
6	SMNN: Batch Effect Correction for Single-cell RNA-seq data via Supervised Mutual Nearest Neighbor Detection	2
5	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	2
4	SCDC: Bulk Gene Expression Deconvolution by Multiple Single-Cell RNA Sequencing References	5
3	HUGIn: Hi-C Unifying Genomic Interrogator	1
2	From GWAS Variant to Function: a Study of ~148,000 Variants for Blood Cell Traits	1
1	Whole genome sequencing identifies common and rare structural variants contributing to hematologic traits in the NHLBI TOPMed program	1