Yun Li

List of Publications by Citations

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

#	Paper	IF	Citations
107	A second generation human haplotype map of over 3.1 million SNPs. *Nature*, **2007**, 449, 851-61	50.4	3647
106	METAL: fast and efficient meta-analysis of genomewide association scans. *Bioinformatics*, **2010**, 26, 2190-1	7.2	2697
105	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
104	Rare-variant association testing for sequencing data with the sequence kernel association test. *American Journal of Human Genetics*, **2011**, 89, 82-93	11	1573
103	MaCH: using sequence and genotype data to estimate haplotypes and unobserved genotypes. *Genetic Epidemiology*, **2010**, 34, 816-34	2.6	1535
102	Newly identified loci that influence lipid concentrations and risk of coronary artery disease. *Nature Genetics*, **2008**, 40, 161-9	36.3	1304
101	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
100	Genotype imputation. *Annual Review of Genomics and Human Genetics*, **2009**, 10, 387-406	9.7	812
99	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
98	A Compendium of Chromatin Contact Maps Reveals Spatially Active Regions in the Human Genome. *Cell Reports*, **2016**, 17, 2042-2059	10.6	453
97	Integrative functional genomic analysis of human brain development and neuropsychiatric risks. *Science*, **2018**, 362,	33.3	277
96	Genome-wide association study identifies variants in TMPRSS6 associated with hemoglobin levels. *Nature Genetics*, **2009**, 41, 1170-2	36.3	179
95	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. *Nature*, **2020**, 586, 763-768	50.4	127
94	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
93	MaCH-admix: genotype imputation for admixed populations. *Genetic Epidemiology*, **2013**, 37, 25-37	2.6	100
92	On the asymptotics of penalized splines. *Biometrika*, **2008**, 95, 415-436	2	96
91	The Polygenic and Monogenic Basis of Blood Traits and Diseases. *Cell*, **2020**, 182, 1214-1231.e11	56.2	96

90	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
89	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
88	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
87	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
86	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
85	SAFE-clustering: Single-cell Aggregated (from Ensemble) clustering for single-cell RNA-seq data. *Bioinformatics*, **2019**, 35, 1269-1277	7.2	54
84	Genotype imputation of Metabochip SNPs using a study-specific reference panel of ~4,000 haplotypes in African Americans from the Women Health Initiative. *Genetic Epidemiology*, **2012**, 36, 107-17	2.6	49
83	MAPS: Model-based analysis of long-range chromatin interactions from PLAC-seq and HiChIP experiments. *PLoS Computational Biology*, **2019**, 15, e1006982	5	45
82	HUGIn: Hi-C Unifying Genomic Interrogator. *Bioinformatics*, **2017**, 33, 3793-3795	7.2	41
81	Single-Cell Heterogeneity Analysis and CRISPR Screen Identify Key Cell-Specific Disease Genes. *Cell Reports*, **2019**, 26, 3132-3144.e7	10.6	38
80	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
79	Cell-type-specific 3D epigenomes in the developing human cortex. *Nature*, **2020**, 587, 644-649	50.4	37
78	Common DNA sequence variation influences 3-dimensional conformation of the human genome. *Genome Biology*, **2019**, 20, 255	18.3	36
77	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
76	Population-specific coding variant underlies genome-wide association with adiponectin level. *Human Molecular Genetics*, **2012**, 21, 463-71	5.6	35
75	SCDC: bulk gene expression deconvolution by multiple single-cell RNA sequencing references. *Briefings in Bioinformatics*, **2021**, 22, 416-427	13.4	34
74	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
73	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

72	Imputation of coding variants in African Americans: better performance using data from the exome sequencing project. *Bioinformatics*, **2013**, 29, 2744-9	7.2	30
71	SAME-clustering: Single-cell Aggregated Clustering via Mixture Model Ensemble. *Nucleic Acids Research*, **2020**, 48, 86-95	20.1	27
70	Gene regulation in the 3D genome. *Human Molecular Genetics*, **2018**, 27, R228-R233	5.6	26
69	Common globin variants modify hematologic and other clinical phenotypes in sickle cell trait and disease. *PLoS Genetics*, **2018**, 14, e1007293	6	25
68	Gene Level Meta-Analysis of Quantitative Traits by Functional Linear Models. *Genetics*, **2015**, 200, 1089-104	4	24
67	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
66	Increased burden of ultra-rare structural variants localizing to boundaries of topologically associated domains in schizophrenia. *Nature Communications*, **2020**, 11, 1842	17.4	22
65	FastHiC: a fast and accurate algorithm to detect long-range chromosomal interactions from Hi-C data. *Bioinformatics*, **2016**, 32, 2692-5	7.2	20
64	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
63	Common genetic variation influencing human white matter microstructure. *Science*, **2021**, 372,	33.3	18
62	A comprehensive SNP and indel imputability database. *Bioinformatics*, **2013**, 29, 528-31	7.2	14
61	Meta-analysis of Complex Diseases at Gene Level with Generalized Functional Linear Models. *Genetics*, **2016**, 202, 457-70	4	13
60	FIREcaller: Detecting frequently interacting regions from Hi-C data. *Computational and Structural Biotechnology Journal*, **2021**, 19, 355-362	6.8	13
59	Heritability of Regional Brain Volumes in Large-Scale Neuroimaging and Genetic Studies. *Cerebral Cortex*, **2019**, 29, 2904-2914	5.1	10
58	Multi-SNP mediation intersection-union test. *Bioinformatics*, **2019**, 35, 4724-4729	7.2	9
57	MOSTWAS: Multi-Omic Strategies for Transcriptome-Wide Association Studies. *PLoS Genetics*, **2021**, 17, e1009398	6	9
56	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
55	SAFE-clustering: Single-cell Aggregated (From Ensemble) Clustering for Single-cell RNA-seq Data		8

54	Across-Platform Imputation of DNA Methylation Levels Incorporating Nonlocal Information Using Penalized Functional Regression. *Genetic Epidemiology*, **2016**, 40, 333-40	2.6	8
53	SMNN: batch effect correction for single-cell RNA-seq data via supervised mutual nearest neighbor detection. *Briefings in Bioinformatics*, **2021**, 22,	13.4	8
52	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
51	Common genetic variation influencing human white matter microstructure		5
50	FIREcaller: Detecting Frequently Interacting Regions from Hi-C Data		5
49	SCDC: Bulk Gene Expression Deconvolution by Multiple Single-Cell RNA Sequencing References		5
48	Single cell dual-omics reveals the transcriptomic and epigenomic diversity of cardiac non-myocytes. *Cardiovascular Research*, **2021**,	9.9	5
47	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
46	MRLocus: Identifying causal genes mediating a trait through Bayesian estimation of allelic heterogeneity. *PLoS Genetics*, **2021**, 17, e1009455	6	4
45	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
44	SnapHiC: a computational pipeline to identify chromatin loops from single-cell Hi-C data. *Nature Methods*, **2021**, 18, 1056-1059	21.6	4
43	3D Epigenomic Characterization Reveals Insights Into Gene Regulation and Lineage Specification During Corticogenesis		3
42	Nucleotide excision repair hotspots and coldspots of UV-induced DNA damage in the human genome		3
41	Neuronal and glial 3D chromatin architecture illustrates cellular etiology of brain disorders		3
40	Adiponectin GWAS loci harboring extensive allelic heterogeneity exhibit distinct molecular consequences. *PLoS Genetics*, **2020**, 16, e1009019	6	3
39	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
38	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
37	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

36	SMART-Q:An Integrative Pipeline Quantifying Cell Type-Specific RNA Transcription. *PLoS ONE*, **2020**, 15, e0228760	3.7	2
35	SAME-clustering: Single-cell Aggregated Clustering via Mixture Model Ensemble		2
34	SMNN: Batch Effect Correction for Single-cell RNA-seq data via Supervised Mutual Nearest Neighbor Detection		2
33	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
32	Transcriptome-wide association analysis of brain structures yields insights into pleiotropy with complex neuropsychiatric traits. *Nature Communications*, **2021**, 12, 2878	17.4	2
31	Neuronal and glial 3D chromatin architecture informs the cellular etiology of brain disorders. *Nature Communications*, **2021**, 12, 3968	17.4	2
30	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
29	Generalized multi-SNP mediation intersection-union test. *Biometrics*, **2020**,	1.8	2
28	Parallel characterization of cis-regulatory elements for multiple genes using CRISPRpath. *Science Advances*, **2021**, 7, eabi4360	14.3	2
27	Whole genome sequence analysis of platelet traits in the NHLBI trans-omics for precision medicine initiative. *Human Molecular Genetics*, **2021**,	5.6	2
26	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
25	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
24	MAPS: model-based analysis of long-range chromatin interactions from PLAC-seq and HiChIP experiments		1
23	Generalized Multi-SNP Mediation Intersection-Union Test		1
22	Soluble Urokinase Plasminogen Activator Receptor: Genetic Variation and Cardiovascular Disease Risk in Blacks. *Circulation Genomic and Precision Medicine*, **2021**, CIRCGEN121003421	5.2	1
21	SnapHiC: a computational pipeline to map chromatin contacts from single cell Hi-C data		1
20	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
19	MOSTWAS: Multi-Omic Strategies for Transcriptome-Wide Association Studies		1

18	Whole genome sequencing association analysis of quantitative red blood cell phenotypes: the NHLBI TOPMed program		1
17	HUGIn: Hi-C Unifying Genomic Interrogator		1
16	From GWAS Variant to Function: a Study of ~148,000 Variants for Blood Cell Traits		1
15	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
14	Common variants contribute to intrinsic human brain functional networks.. *Nature Genetics*, **2022**, 54, 508-517	36.3	1
13	Whole genome sequencing identifies common and rare structural variants contributing to hematologic traits in the NHLBI TOPMed program		1
12	Super interactive promoters provide insight into cell type-specific regulatory networks in blood lineage cell types.. *PLoS Genetics*, **2022**, 18, e1009984	6	0
11	Placental genomics mediates genetic associations with complex health traits and disease.. *Nature Communications*, **2022**, 13, 706	17.4	0
10	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
9	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
8	Host Genetic Risk Factors for Chlamydia trachomatis-Related Infertility in Women. *Journal of Infectious Diseases*, **2021**, 224, S64-S71	7	0
7	HPRep: Quantifying Reproducibility in HiChIP and PLAC-Seq Datasets. *Current Issues in Molecular Biology*, **2021**, 43, 1156-1170	2.9	0
6	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
5	THUNDER: A reference-free deconvolution method to infer cell type proportions from bulk Hi-C data.. *PLoS Genetics*, **2022**, 18, e1010102	6	0
4	SnapHiC2: A computationally efficient loop caller for single cell Hi-C data. *Computational and Structural Biotechnology Journal*, **2022**, 20, 2778-2783	6.8	0
3	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	
2	Machine Learning and Deep Learning in Genetics and Genomics **2021**, 163-181		
1	DNA Methylation Imputation Across Platforms.. *Methods in Molecular Biology*, **2022**, 2432, 137-151	1.4	