Yun Li

List of Publications by Year in Descending Order

114 papers	9,212 citations	38 h-index	95 g-index
123 ext. papers	13,060 ext. citations	10.5 avg, IF	5.79 L-index

#	Paper	IF	Citations
114	Super interactive promoters provide insight into cell type-specific regulatory networks in blood lineage cell types.. *PLoS Genetics*, **2022**, 18, e1009984	6	0
113	Mapping chromatin loops in single cells.. *Trends in Genetics*, **2022**,	8.5	1
112	DNA Methylation Imputation Across Platforms.. *Methods in Molecular Biology*, **2022**, 2432, 137-151	1.4	
111	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation.. *Nature Genetics*, **2022**,	36.3	7
110	Gaseous air pollutants and DNA methylation in a methylome-wide association study of an ethnically and environmentally diverse population of U.S. adults.. *Environmental Research*, **2022**, 212, 113360	7.9	0
109	Soluble Urokinase Plasminogen Activator Receptor: Genetic Variation and Cardiovascular Disease Risk in Blacks. *Circulation Genomic and Precision Medicine*, **2021**, CIRCGEN121003421	5.2	1
108	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
107	Discovery and fine-mapping of height loci via high-density imputation of GWASs in individuals of African ancestry. *American Journal of Human Genetics*, **2021**, 108, 564-582	11	7
106	The trans-ancestral genomic architecture of glycemic traits. *Nature Genetics*, **2021**, 53, 840-860	36.3	44
105	Neuronal and glial 3D chromatin architecture informs the cellular etiology of brain disorders. *Nature Communications*, **2021**, 12, 3968	17.4	2
104	Epigenome-wide association study of diet quality in the Women's Health Initiative and TwinsUK cohort. *International Journal of Epidemiology*, **2021**, 50, 675-684	7.8	8
103	Whole genome sequence analyses of eGFR in 23,732 people representing multiple ancestries in the NHLBI trans-omics for precision medicine (TOPMed) consortium. *EBioMedicine*, **2021**, 63, 103157	8.8	3
102	FIREcaller: Detecting frequently interacting regions from Hi-C data. *Computational and Structural Biotechnology Journal*, **2021**, 19, 355-362	6.8	13
101	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
100	Epigenetically mediated electrocardiographic manifestations of sub-chronic exposures to ambient particulate matter air pollution in the Women's Health Initiative and Atherosclerosis Risk in Communities Study. *Environmental Research*, **2021**, 198, 111211	7.9	
99	Functional coordination of non-myocytes plays a key role in adult zebrafish heart regeneration. *EMBO Reports*, **2021**, 22, e52901	6.5	1
98	Robust Hi-C Maps of Enhancer-Promoter Interactions Reveal the Function of Non-coding Genome in Neural Development and Diseases. *Molecular Cell*, **2020**, 79, 521-534.e15	17.6	38

97	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
96	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
95	SMART-Q:An Integrative Pipeline Quantifying Cell Type-Specific RNA Transcription. *PLoS ONE*, **2020**, 15, e0228760	3.7	2
94	STEPS: an efficient prospective likelihood approach to genetic association analyses of secondary traits in extreme phenotype sequencing. *Biostatistics*, **2020**, 21, 33-49	3.7	2
93	Leukocyte Traits and Exposure to Ambient Particulate Matter Air Pollution in the Women's Health Initiative and Atherosclerosis Risk in Communities Study. *Environmental Health Perspectives*, **2020**, 128, 17004	8.4	11
92	The Polygenic and Monogenic Basis of Blood Traits and Diseases. *Cell*, **2020**, 182, 1214-1231.e11	56.2	96
91	Cell-type-specific 3D epigenomes in the developing human cortex. *Nature*, **2020**, 587, 644-649	50.4	37
90	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
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	Adiponectin GWAS loci harboring extensive allelic heterogeneity exhibit distinct molecular consequences. *PLoS Genetics*, **2020**, 16, e1009019	6	3
87	Age-related DNA hydroxymethylation is enriched for gene expression and immune system processes in human peripheral blood. *Epigenetics*, **2020**, 15, 294-306	5.7	3
86	Increased burden of ultra-rare structural variants localizing to boundaries of topologically associated domains in schizophrenia. *Nature Communications*, **2020**, 11, 1842	17.4	22
85	The circadian clock shapes the s transcriptome by regulating alternative splicing and alternative polyadenylation. *Journal of Biological Chemistry*, **2020**, 295, 7608-7619	5.4	12
84	SMART-Q: An Integrative Pipeline Quantifying Cell Type-Specific RNA Transcription **2020**, 15, e0228760		
83	SMART-Q: An Integrative Pipeline Quantifying Cell Type-Specific RNA Transcription **2020**, 15, e0228760		
82	SMART-Q: An Integrative Pipeline Quantifying Cell Type-Specific RNA Transcription **2020**, 15, e0228760		
81	SMART-Q: An Integrative Pipeline Quantifying Cell Type-Specific RNA Transcription **2020**, 15, e0228760		
80	Optimism is not associated with two indicators of DNA methylation aging. *Aging*, **2019**, 11, 4970-4989	5.6	5

79	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. *American Journal of Epidemiology*, **2019**, 188, 1033-1054	3.8	39
78	Methylome-wide association study provides evidence of particulate matter air pollution-associated DNA methylation. *Environment International*, **2019**, 132, 104723	12.9	35
77	DNA methylation GrimAge strongly predicts lifespan and healthspan. *Aging*, **2019**, 11, 303-327	5.6	424
76	MAPS: Model-based analysis of long-range chromatin interactions from PLAC-seq and HiChIP experiments. *PLoS Computational Biology*, **2019**, 15, e1006982	5	45
75	Single-Cell Heterogeneity Analysis and CRISPR Screen Identify Key Cell-Specific Disease Genes. *Cell Reports*, **2019**, 26, 3132-3144.e7	10.6	38
74	A multi-ancestry genome-wide study incorporating gene-smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. *Human Molecular Genetics*, **2019**, 28, 2615-2633	5.6	14
73	Multi-ancestry genome-wide gene-smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. *Nature Genetics*, **2019**, 51, 636-648	36.3	59
72	Blood Leukocyte DNA Methylation Predicts Risk of Future Myocardial Infarction and Coronary Heart Disease. *Circulation*, **2019**, 140, 645-657	16.7	65
71	Non-coding variability at the APOE locus contributes to the Alzheimer's risk. *Nature Communications*, **2019**, 10, 3310	17.4	42
70	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
69	DNA methylation-based estimator of telomere length. *Aging*, **2019**, 11, 5895-5923	5.6	69
68	Common DNA sequence variation influences 3-dimensional conformation of the human genome. *Genome Biology*, **2019**, 20, 255	18.3	36
67	SAFE-clustering: Single-cell Aggregated (from Ensemble) clustering for single-cell RNA-seq data. *Bioinformatics*, **2019**, 35, 1269-1277	7.2	54
66	Genome-wide association study and meta-analysis identify loci associated with ventricular and supraventricular ectopy. *Scientific Reports*, **2018**, 8, 5675	4.9	1
65	Identification of genetic risk factors in the Chinese population implicates a role of immune system in Alzheimer's disease pathogenesis. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, 1697-1706	11.5	40
64	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. *American Journal of Human Genetics*, **2018**, 102, 375-400	11	59
63	On the substructure controls in rare variant analysis: Principal components or variance components?. *Genetic Epidemiology*, **2018**, 42, 276-287	2.6	5
62	Genome-wide association study of homocysteine in African Americans from the Jackson Heart Study, the Multi-Ethnic Study of Atherosclerosis, and the Coronary Artery Risk in Young Adults study. *Journal of Human Genetics*, **2018**, 63, 327-337	4.3	5

61	DNA Methylation Signatures of Depressive Symptoms in Middle-aged and Elderly Persons: Meta-analysis of Multiethnic Epigenome-wide Studies. *JAMA Psychiatry*, **2018**, 75, 949-959	14.5	51
60	Multiethnic meta-analysis identifies ancestry-specific and cross-ancestry loci for pulmonary function. *Nature Communications*, **2018**, 9, 2976	17.4	45
59	Common β-globin variants modify hematologic and other clinical phenotypes in sickle cell trait and disease. *PLoS Genetics*, **2018**, 14, e1007293	6	25
58	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. *PLoS ONE*, **2018**, 13, e0198166	3.7	31
57	Epigenetic clock for skin and blood cells applied to Hutchinson Gilford Progeria Syndrome and studies. *Aging*, **2018**, 10, 1758-1775	5.6	187
56	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. *Nature Genetics*, **2018**, 50, 524-537	36.3	536
55	A robust and powerful two-step testing procedure for local ancestry adjusted allelic association analysis in admixed populations. *Genetic Epidemiology*, **2018**, 42, 288-302	2.6	8
54	An epigenetic biomarker of aging for lifespan and healthspan. *Aging*, **2018**, 10, 573-591	5.6	658
53	The 3D Genome Browser: a web-based browser for visualizing 3D genome organization and long-range chromatin interactions. *Genome Biology*, **2018**, 19, 151	18.3	226
52	Analysis of genetic and nongenetic factors influencing triglycerides-lowering drug effects based on paired observations. *BMC Proceedings*, **2018**, 12, 46	2.3	3
51	Gene regulation in the 3D genome. *Human Molecular Genetics*, **2018**, 27, R228-R233	5.6	26
50	A genome-wide interaction analysis of tricyclic/tetracyclic antidepressants and RR and QT intervals: a pharmacogenomics study from the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) consortium. *Journal of Medical Genetics*, **2017**, 54, 313-323	5.8	5
49	Multiethnic genome-wide meta-analysis of ectopic fat depots identifies loci associated with adipocyte development and differentiation. *Nature Genetics*, **2017**, 49, 125-130	36.3	80
48	Genetic loci associated with heart rate variability and their effects on cardiac disease risk. *Nature Communications*, **2017**, 8, 15805	17.4	50
47	Genome-wide association study of heart rate and its variability in Hispanic/Latino cohorts. *Heart Rhythm*, **2017**, 14, 1675-1684	6.7	11
46	HUGIn: Hi-C Unifying Genomic Interrogator. *Bioinformatics*, **2017**, 33, 3793-3795	7.2	41
45	Genomic analysis of oesophageal squamous-cell carcinoma identifies alcohol drinking-related mutation signature and genomic alterations. *Nature Communications*, **2017**, 8, 15290	17.4	109
44	LAIT: a local ancestry inference toolkit. *BMC Genetics*, **2017**, 18, 83	2.6	5

43	Genome-wide Association Study of Susceptibility to Particulate Matter-Associated QT Prolongation. *Environmental Health Perspectives*, **2017**, 125, 067002	8.4	5
42	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
41	-ancestry Fine Mapping and Molecular Assays Identify Regulatory Variants at the HDL-C GWAS Locus. *G3: Genes, Genomes, Genetics*, **2017**, 7, 3217-3227	3.2	14
40	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. *American Journal of Human Genetics*, **2017**, 101, 888-902	11	83
39	Genetic architecture of lipid traits in the Hispanic community health study/study of Latinos. *Lipids in Health and Disease*, **2017**, 16, 200	4.4	11
38	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
37	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
36	A SNP panel and online tool for checking genotype concordance through comparing QR codes. *PLoS ONE*, **2017**, 12, e0182438	3.7	1
35	Meta-analysis of lipid-traits in Hispanics identifies novel loci, population-specific effects, and tissue-specific enrichment of eQTLs. *Scientific Reports*, **2016**, 6, 19429	4.9	51
34	A Compendium of Chromatin Contact Maps Reveals Spatially Active Regions in the Human Genome. *Cell Reports*, **2016**, 17, 2042-2059	10.6	453
33	Assessing the Cumulative Contribution of New and Established Common Genetic Risk Factors to Early-Onset Prostate Cancer. *Cancer Epidemiology Biomarkers and Prevention*, **2016**, 25, 766-72	4	3
32	Meta-analysis of Complex Diseases at Gene Level with Generalized Functional Linear Models. *Genetics*, **2016**, 202, 457-70	4	13
31	Across-Platform Imputation of DNA Methylation Levels Incorporating Nonlocal Information Using Penalized Functional Regression. *Genetic Epidemiology*, **2016**, 40, 333-40	2.6	8
30	Meta-analysis of 49 549 individuals imputed with the 1000 Genomes Project reveals an exonic damaging variant in ANGPTL4 determining fasting TG levels. *Journal of Medical Genetics*, **2016**, 53, 441-9	5.8	27
29	Elevated D-dimer levels in African Americans with sickle cell trait. *Blood*, **2016**, 127, 2261-3	2.2	24
28	Variant Near FGF5 Has Stronger Effects on Blood Pressure in Chinese With a Higher Body Mass Index. *American Journal of Hypertension*, **2015**, 28, 1031-7	2.3	10
27	Epigenome-wide association study (EWAS) of BMI, BMI change and waist circumference in African American adults identifies multiple replicated loci. *Human Molecular Genetics*, **2015**, 24, 4464-79	5.6	219
26	Leveraging Multi-ethnic Evidence for Mapping Complex Traits in Minority Populations: An Empirical Bayes Approach. *American Journal of Human Genetics*, **2015**, 96, 740-52	11	11

25	Removing reference mapping biases using limited or no genotype data identifies allelic differences in protein binding at disease-associated loci. *BMC Medical Genomics*, **2015**, 8, 43	3.7	9
24	Gene Level Meta-Analysis of Quantitative Traits by Functional Linear Models. *Genetics*, **2015**, 200, 1089-104	4	24
23	Genome of The Netherlands population-specific imputations identify an ABCA6 variant associated with cholesterol levels. *Nature Communications*, **2015**, 6, 6065	17.4	32
22	Genome- and exome-wide association study of serum lipoprotein (a) in the Jackson Heart Study. *Journal of Human Genetics*, **2015**, 60, 755-61	4.3	35
21	Fine mapping the region reveals a common intronic insertion associated to HDL-C. *Npj Aging and Mechanisms of Disease*, **2015**, 1, 15011	5.5	5
20	SVSI: fast and powerful set-valued system identification approach to identifying rare variants in sequencing studies for ordered categorical traits. *Annals of Human Genetics*, **2015**, 79, 294-309	2.2	5
19	Relatively Small Contribution of Methylation and Genomic Copy Number Aberration to the Aberrant Expression of Inflammation-Related Genes in HBV-Related Hepatocellular Carcinoma. *PLoS ONE*, **2015**, 10, e0126836	3.7	1
18	One Size Doesn't Fit All - RefEditor: Building Personalized Diploid Reference Genome to Improve Read Mapping and Genotype Calling in Next Generation Sequencing Studies. *PLoS Computational Biology*, **2015**, 11, e1004448	5	6
17	Likelihood-based complex trait association testing for arbitrary depth sequencing data. *Bioinformatics*, **2015**, 31, 2955-62	7.2	2
16	Integrative analysis of sequencing and array genotype data for discovering disease associations with rare mutations. *Proceedings of the National Academy of Sciences of the United States of America*, **2015**, 112, 1019-24	11.5	12
15	Rare variant testing across methods and thresholds using the multi-kernel sequence kernel association test (MK-SKAT). *Statistics and Its Interface*, **2015**, 8, 495-505	0.4	8
14	Whole-exome sequencing identifies rare and low-frequency coding variants associated with LDL cholesterol. *American Journal of Human Genetics*, **2014**, 94, 233-45	11	170
13	Genome-wide association analysis identifies six new loci associated with forced vital capacity. *Nature Genetics*, **2014**, 46, 669-77	36.3	104
12	Accurate inference of local phased ancestry of modern admixed populations. *Scientific Reports*, **2014**, 4, 5800	4.9	9
11	Genome-wide association scan for variants associated with early-onset prostate cancer. *PLoS ONE*, **2014**, 9, e93436	3.7	19
10	TGFBI (IG-H3) is a diabetes-risk gene based on mouse and human genetic studies. *Human Molecular Genetics*, **2014**, 23, 4597-611	5.6	19
9	Association studies with imputed variants using expectation-maximization likelihood-ratio tests. *PLoS ONE*, **2014**, 9, e110679	3.7	1
8	Single Nucleotide Polymorphism (SNP) Detection and Genotype Calling from Massively Parallel Sequencing (MPS) Data. *Statistics in Biosciences*, **2013**, 5, 3-25	1.5	14

7	Testing genetic association with rare variants in admixed populations. *Genetic Epidemiology*, **2013**, 37, 38-47	2.6	8
6	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
5	An abundance of rare functional variants in 202 drug target genes sequenced in 14,002 people. *Science*, **2012**, 337, 100-4	33.3	523
4	Rare-variant association testing for sequencing data with the sequence kernel association test. *American Journal of Human Genetics*, **2011**, 89, 82-93	11	1573
3	Low-coverage sequencing: implications for design of complex trait association studies. *Genome Research*, **2011**, 21, 940-51	9.7	231
2	To identify associations with rare variants, just WHaIT: Weighted haplotype and imputation-based tests. *American Journal of Human Genetics*, **2010**, 87, 728-35	11	78
1	MaCH: using sequence and genotype data to estimate haplotypes and unobserved genotypes. *Genetic Epidemiology*, **2010**, 34, 816-34	2.6	1535