Yun Li

List of Publications by Year
in descending order

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Version: 2024-02-01

		57631	21474
121	16,049	44	114
papers	citations	h-index	g-index

123	123	123	25402
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Rare-Variant Association Testing for Sequencing Data with the Sequence Kernel Association Test. American Journal of Human Genetics, 2011, 89, 82-93.	2.6	2,060
2	MaCH: using sequence and genotype data to estimate haplotypes and unobserved genotypes. Genetic Epidemiology, 2010, 34, 816-834.	0.6	1,718
3	An epigenetic biomarker of aging for lifespan and healthspan. Aging, 2018, 10, 573-591.	1.4	1,552
4	DNA methylation GrimAge strongly predicts lifespan and healthspan. Aging, 2019, 11, 303-327.	1.4	1,128
5	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. Nature Genetics, 2018, 50, 524-537.	9.4	1,124
6	A Compendium of Chromatin Contact Maps Reveals Spatially Active Regions in the Human Genome. Cell Reports, 2016, 17, 2042-2059.	2.9	745
7	An Abundance of Rare Functional Variants in 202 Drug Target Genes Sequenced in 14,002 People. Science, 2012, 337, 100-104.	6.0	626
8	Epigenetic clock for skin and blood cells applied to Hutchinson Gilford Progeria Syndrome and ex vivo studies. Aging, 2018, 10, 1758-1775.	1.4	406
9	The 3D Genome Browser: a web-based browser for visualizing 3D genome organization and long-range chromatin interactions. Genome Biology, 2018, 19, 151.	3.8	393
10	The Polygenic and Monogenic Basis of Blood Traits and Diseases. Cell, 2020, 182, 1214-1231.e11.	13.5	388
11	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. Cell, 2020, 182, 1198-1213.e14.	13.5	353
12	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	9.4	341
13	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, 4464-4479.	1.4	289
14	Low-coverage sequencing: Implications for design of complex trait association studies. Genome Research, 2011, 21, 940-951.	2.4	273
15	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. Nature Genetics, 2022, 54, 560-572.	9.4	250
16	DNA methylation-based estimator of telomere length. Aging, 2019, 11, 5895-5923.	1.4	198
17	Genomic analysis of oesophageal squamous-cell carcinoma identifies alcohol drinking-related mutation signature and genomic alterations. Nature Communications, 2017, 8, 15290.	5.8	195
18	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. American Journal of Human Genetics, 2014, 94, 233-245.	2.6	193

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19	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. American Journal of Human Genetics, 2017, 101, 888-902.	2.6	154
20	Blood Leukocyte DNA Methylation Predicts Risk of Future Myocardial Infarction and Coronary Heart Disease. Circulation, 2019, 140, 645-657.	1.6	151
21	Mapping cis-regulatory chromatin contacts in neural cells links neuropsychiatric disorder risk variants to target genes. Nature Genetics, 2019, 51, 1252-1262.	9.4	139
22	Genome-wide association analysis identifies six new loci associated with forced vital capacity. Nature Genetics, 2014, 46, 669-677.	9.4	131
23	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.	2.6	123
24	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.	2.6	123
25	Multiethnic genome-wide meta-analysis of ectopic fat depots identifies loci associated with adipocyte development and differentiation. Nature Genetics, 2017, 49, 125-130.	9.4	116
26	Multi-ancestry genome-wide geneâ€“smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. Nature Genetics, 2019, 51, 636-648.	9.4	112
27	Cell-type-specific 3D epigenomes in the developing human cortex. Nature, 2020, 587, 644-649.	13.7	110
28	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.	4.5	110
29	SAFE-clustering: Single-cell Aggregated (from Ensemble) clustering for single-cell RNA-seq data. Bioinformatics, 2019, 35, 1269-1277.	1.8	104
30	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.	1.5	98
31	Genetic loci associated with heart rate variability and their effects on cardiac disease risk. Nature Communications, 2017, 8, 15805.	5.8	95
32	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. PLoS ONE, 2018, 13, e0198166.	1.1	94
33	MAPS: Model-based analysis of long-range chromatin interactions from PLAC-seq and HiChIP experiments. PLoS Computational Biology, 2019, 15, e1006982.	1.5	94
34	Non-coding variability at the APOE locus contributes to the Alzheimerâ€™s risk. Nature Communications, 2019, 10, 3310.	5.8	91
35	Single-Cell Heterogeneity Analysis and CRISPR Screen Identify Key Î²-Cell-Specific Disease Genes. Cell Reports, 2019, 26, 3132-3144.e7.	2.9	90
36	To Identify Associations with Rare Variants, Just WHaIT: Weighted Haplotype and Imputation-Based Tests. American Journal of Human Genetics, 2010, 87, 728-735.	2.6	86

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37	Multiethnic meta-analysis identifies ancestry-specific and cross-ancestry loci for pulmonary function. Nature Communications, 2018, 9, 2976.	5.8	85
38	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	1.6	85
39	DNA Methylation Signatures of Depressive Symptoms in Middle-aged and Elderly Persons. JAMA Psychiatry, 2018, 75, 949.	6.0	78
40	Identification of genetic risk factors in the Chinese population implicates a role of immune system in Alzheimerâ€™s disease pathogenesis. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 1697-1706.	3.3	71
41	HUGIn: Hi-C Unifying Genomic Interrogator. Bioinformatics, 2017, 33, 3793-3795.	1.8	69
42	Common DNA sequence variation influences 3-dimensional conformation of the human genome. Genome Biology, 2019, 20, 255.	3.8	65
43	Meta-analysis of lipid-traits in Hispanics identifies novel loci, population-specific effects and tissue-specific enrichment of eQTLs. Scientific Reports, 2016, 6, 19429.	1.6	63
44	Gene regulation in the 3D genome. Human Molecular Genetics, 2018, 27, R228-R233.	1.4	61
45	Methylome-wide association study provides evidence of particulate matter air pollution-associated DNA methylation. Environment International, 2019, 132, 104723.	4.8	58
46	Common genetic risk variants identified in the SPARK cohort support DDHD2 as a candidate risk gene for autism. Translational Psychiatry, 2020, 10, 265.	2.4	56
47	Increased burden of ultra-rare structural variants localizing to boundaries of topologically associated domains in schizophrenia. Nature Communications, 2020, 11, 1842.	5.8	56
48	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.	1.5	53
49	Neuronal and glial 3D chromatin architecture informs the cellular etiology of brain disorders. Nature Communications, 2021, 12, 3968.	5.8	48
50	Genome of the Netherlands population-specific imputations identify an ABCA6 variant associated with cholesterol levels. Nature Communications, 2015, 6, 6065.	5.8	45
51	Common Î±-globin variants modify hematologic and other clinical phenotypes in sickle cell trait and disease. PLoS Genetics, 2018, 14, e1007293.	1.5	45
52	Genome- and exome-wide association study of serum lipoprotein (a) in the Jackson Heart Study. Journal of Human Genetics, 2015, 60, 755-761.	1.1	42
53	D-Dimer in African Americans. Arteriosclerosis, Thrombosis, and Vascular Biology, 2017, 37, 2220-2227.	1.1	40
54	Meta-analysis of 49â€…549 individuals imputed with the 1000 Genomes Project reveals an exonic damaging variant inANGPTL4determining fasting TG levels. Journal of Medical Genetics, 2016, 53, 441-449.	1.5	34

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55	The circadian clock shapes the Arabidopsis transcriptome by regulating alternative splicing and alternative polyadenylation. Journal of Biological Chemistry, 2020, 295, 7608-7619.	1.6	34
56	A multi-ancestry genome-wide study incorporating geneâ€“smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. Human Molecular Genetics, 2019, 28, 2615-2633.	1.4	31
57	Genome-Wide Association Scan for Variants Associated with Early-Onset Prostate Cancer. PLoS ONE, 2014, 9, e93436.	1.1	25
58	Gene Level Meta-Analysis of Quantitative Traits by Functional Linear Models. Genetics, 2015, 200, 1089-1104.	1.2	25
59	TOP-LD: A tool to explore linkage disequilibrium with TOPMed whole-genome sequence data. American Journal of Human Genetics, 2022, 109, 1175-1181.	2.6	25
60	TGFBI (ÂIG-H3) is a diabetes-risk gene based on mouse and human genetic studies. Human Molecular Genetics, 2014, 23, 4597-4611.	1.4	24
61	Elevated D-dimer levels in African Americans with sickle cell trait. Blood, 2016, 127, 2261-2263.	0.6	24
62	Leveraging Multi-ethnic Evidence for Mapping Complex Traits in Minority Populations: An Empirical Bayes Approach. American Journal of Human Genetics, 2015, 96, 740-752.	2.6	22
63	FIREcaller: Detecting frequently interacting regions from Hi-C data. Computational and Structural Biotechnology Journal, 2021, 19, 355-362.	1.9	22
64	Trans-ancestry Fine Mapping and Molecular Assays Identify Regulatory Variants at the ANGPTL8 HDL-C GWAS Locus. G3: Genes, Genomes, Genetics, 2017, 7, 3217-3227.	0.8	19
65	Epigenome-wide association study of diet quality in the Womenâ€™s Health Initiative and TwinsUK cohort. International Journal of Epidemiology, 2021, 50, 675-684.	0.9	19
66	Meta-analysis of Complex Diseases at Gene Level with Generalized Functional Linear Models. Genetics, 2016, 202, 457-470.	1.2	18
67	Genome-wide association study of heart rate and its variability in Hispanic/Latino cohorts. Heart Rhythm, 2017, 14, 1675-1684.	0.3	18
68	Genetic architecture of lipid traits in the Hispanic community health study/study of Latinos. Lipids in Health and Disease, 2017, 16, 200.	1.2	18
69	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.	2.6	18
70	Variant Near FGF5 Has Stronger Effects on Blood Pressure in Chinese With a Higher Body Mass Index. American Journal of Hypertension, 2015, 28, 1031-1037.	1.0	17
71	A robust and powerful twoâ€step testing procedure for local ancestry adjusted allelic association analysis in admixed populations. Genetic Epidemiology, 2018, 42, 288-302.	0.6	17
72	Leukocyte Traits and Exposure to Ambient Particulate Matter Air Pollution in the Womenâ€™s Health Initiative and Atherosclerosis Risk in Communities Study. Environmental Health Perspectives, 2020, 128, 17004.	2.8	17

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73	HiC-ACT: improved detection of chromatin interactions from Hi-C data via aggregated Cauchy test. American Journal of Human Genetics, 2021, 108, 257-268.	2.6	17
74	Functional coordination of nonâ€myocytes plays a key role in adult zebrafish heart regeneration. EMBO Reports, 2021, 22, e52901.	2.0	17
75	Single Nucleotide Polymorphism (SNP) Detection and Genotype Calling from Massively Parallel Sequencing (MPS) Data. Statistics in Biosciences, 2013, 5, 3-25.	0.6	15
76	A comprehensive comparison on cell-type composition inference for spatial transcriptomics data. Briefings in Bioinformatics, 2022, 23, .	3.2	15
77	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, 1019-1024.	3.3	14
78	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.	2.7	14
79	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.	0.7	13
80	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.	1.5	11
81	Adiponectin GWAS loci harboring extensive allelic heterogeneity exhibit distinct molecular consequences. PLoS Genetics, 2020, 16, e1009019.	1.5	11
82	Transcriptome-Wide Association Study of Blood Cell Traits in African Ancestry and Hispanic/Latino Populations. Genes, 2021, 12, 1049.	1.0	11
83	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.	0.2	11
84	Accurate Inference of Local Phased Ancestry of Modern Admixed Populations. Scientific Reports, 2015, 4, 5800.	1.6	10
85	Acrossâ€Platform Imputation of DNA Methylation Levels Incorporating Nonlocal Information Using Penalized Functional Regression. Genetic Epidemiology, 2016, 40, 333-340.	0.6	10
86	On the substructure controls in rare variant analysis: Principal components or variance components?. Genetic Epidemiology, 2018, 42, 276-287.	0.6	10
87	SVSI: Fast and Powerful Setâ€Valued System Identification Approach to Identifying Rare Variants in Sequencing Studies for Ordered Categorical Traits. Annals of Human Genetics, 2015, 79, 294-309.	0.3	9
88	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.	1.5	9
89	Allelic Heterogeneity at the CRP Locus Identified by Whole-Genome Sequencing in Multi-ancestry Cohorts. American Journal of Human Genetics, 2020, 106, 112-120.	2.6	9
90	Mapping chromatin loops in single cells. Trends in Genetics, 2022, 38, 637-640.	2.9	9

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91	Testing Genetic Association With Rare Variants in Admixed Populations. Genetic Epidemiology, 2013, 37, 38-47.	0.6	8
92	Fine mapping the CETP region reveals a common intronic insertion associated to HDL-C. Npj Aging and Mechanisms of Disease, 2015, 1, 15011.	4.5	8
93	Age-related DNA hydroxymethylation is enriched for gene expression and immune system processes in human peripheral blood. Epigenetics, 2020, 15, 294-306.	1.3	8
94	A SNP panel and online tool for checking genotype concordance through comparing QR codes. PLoS ONE, 2017, 12, e0182438.	1.1	8
95	Genome-wide Association Study of Susceptibility to Particulate Matterâ€“Associated QT Prolongation. Environmental Health Perspectives, 2017, 125, 067002.	2.8	7
96	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.	1.1	7
97	Soluble Urokinase Plasminogen Activator Receptor: Genetic Variation and Cardiovascular Disease Risk in Black Adults. Circulation Genomic and Precision Medicine, 2021, 14, CIRCGEN121003421.	1.6	7
98	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.	3.7	7
99	Optimism is not associated with two indicators of DNA methylation aging. Aging, 2019, 11, 4970-4989.	1.4	6
100	Genome-Wide Association of Kidney Traits in Hispanics/Latinos Using Dense Imputed Whole-Genome Sequencing Data. Circulation Genomic and Precision Medicine, 2020, 13, e002891.	1.6	6
101	LAIT: a local ancestry inference toolkit. BMC Genetics, 2017, 18, 83.	2.7	5
102	Likelihood-based complex trait association testing for arbitrary depth sequencing data. Bioinformatics, 2015, 31, 2955-2962.	1.8	4
103	Genome-wide association study and meta-analysis identify loci associated with ventricular and supraventricular ectopy. Scientific Reports, 2018, 8, 5675.	1.6	4
104	STEPS: an efficient prospective likelihood approach to genetic association analyses of secondary traits in extreme phenotype sequencing. Biostatistics, 2020, 21, 33-49.	0.9	4
105	SMART-Q:Â An Integrative Pipeline Quantifying Cell Type-Specific RNA Transcription. PLoS ONE, 2020, 15, e0228760.	1.1	4
106	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.	3.7	4
107	Super interactive promoters provide insight into cell type-specific regulatory networks in blood lineage cell types. PLoS Genetics, 2022, 18, e1009984.	1.5	4
108	Assessing the Cumulative Contribution of New and Established Common Genetic Risk Factors to Early-Onset Prostate Cancer. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 766-772.	1.1	3

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109	Analysis of genetic and nongenetic factors influencing triglycerides-lowering drug effects based on paired observations. BMC Proceedings, 2018, 12, 46.	1.8	3
110	A systematic evaluation of Hi-C data enhancement methods for enhancing PLAC-seq and HiChIP data. Briefings in Bioinformatics, 2022, 23, .	3.2	3
111	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, .	0.2	2
112	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.	1.1	1
113	CUE: CpG impUtation ensemble for DNA methylation levels across the human methylation450 (HM450) and EPIC (HM850) BeadChip platforms. Epigenetics, 2021, 16, 851-861.	1.3	1
114	Association Studies with Imputed Variants Using Expectation-Maximization Likelihood-Ratio Tests. PLoS ONE, 2014, 9, e110679.	1.1	1
115	Abstract P261: Genome-wide Association Study of Susceptibility to Particulate Matter-associated Reduced Heart Rate Variability. Circulation, 2016, 133, .	1.6	0
116	Abstract 225: Coordinated Transcriptome and Cell State Dynamics of Non-myocytes in Heart Regeneration. Circulation Research, 2020, 127, .	2.0	0
117	SMART-Q: An Integrative Pipeline Quantifying Cell Type-Specific RNA Transcription. , 2020, 15, e0228760.		0
118	SMART-Q: An Integrative Pipeline Quantifying Cell Type-Specific RNA Transcription. , 2020, 15, e0228760.		0
119	SMART-Q: An Integrative Pipeline Quantifying Cell Type-Specific RNA Transcription. , 2020, 15, e0228760.		0
120	SMART-Q: An Integrative Pipeline Quantifying Cell Type-Specific RNA Transcription. , 2020, 15, e0228760.		0
121	DNA Methylation Imputation Across Platforms. Methods in Molecular Biology, 2022, 2432, 137-151.	0.4	0