Xiang Zhou

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/4469727/publications.pdf

Version: 2024-02-01

79 papers	7,202 citations	159585 30 h-index	79698 73 g-index
97 all docs	97 docs citations	97 times ranked	10222 citing authors

#	Article	IF	Citations
1	Genome-wide efficient mixed-model analysis for association studies. Nature Genetics, 2012, 44, 821-824.	21.4	2,577
2	Efficient multivariate linear mixed model algorithms for genome-wide association studies. Nature Methods, 2014, 11, 407-409.	19.0	698
3	Polygenic Modeling with Bayesian Sparse Linear Mixed Models. PLoS Genetics, 2013, 9, e1003264.	3.5	686
4	Statistical analysis of spatial expression patterns for spatially resolved transcriptomic studies. Nature Methods, 2020, 17, 193-200.	19.0	264
5	Accuracy, robustness and scalability of dimensionality reduction methods for single-cell RNA-seq analysis. Genome Biology, 2019, 20, 269.	8.8	140
6	Spatially informed cell-type deconvolution for spatial transcriptomics. Nature Biotechnology, 2022, 40, 1349-1359.	17.5	121
7	Non-parametric genetic prediction of complex traits with latent Dirichlet process regression models. Nature Communications, 2017, 8, 456.	12.8	102
8	Detecting epistasis with the marginal epistasis test in genetic mapping studies of quantitative traits. PLoS Genetics, 2017, 13, e1006869.	3.5	100
9	Causal effects of blood lipids on amyotrophic lateral sclerosis: a Mendelian randomization study. Human Molecular Genetics, 2019, 28, 688-697.	2.9	99
10	The genetic architecture of gene expression levels in wild baboons. ELife, 2015, 4, .	6.0	99
11	A unified framework for variance component estimation with summary statistics in genome-wide association studies. Annals of Applied Statistics, 2017, 11, 2027-2051.	1.1	98
12	VIPER: variability-preserving imputation for accurate gene expression recovery in single-cell RNA sequencing studies. Genome Biology, 2018, 19, 196.	8.8	97
13	A Flexible, Efficient Binomial Mixed Model for Identifying Differential DNA Methylation in Bisulfite Sequencing Data. PLoS Genetics, 2015, 11, e1005650.	3.5	93
14	Adaptive, convergent origins of the pygmy phenotype in African rainforest hunter-gatherers. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E3596-603.	7.1	91
15	SPARK-X: non-parametric modeling enables scalable and robust detection of spatial expression patterns for large spatial transcriptomic studies. Genome Biology, 2021, 22, 184.	8.8	90
16	Accurate and Scalable Construction of Polygenic Scores in Large Biobank Data Sets. American Journal of Human Genetics, 2020, 106, 679-693.	6.2	80
17	Testing and controlling for horizontal pleiotropy with probabilistic Mendelian randomization in transcriptome-wide association studies. Nature Communications, 2020, 11, 3861.	12.8	79
18	Efficient Genome-Wide Sequencing and Low-Coverage Pedigree Analysis from Noninvasively Collected Samples. Genetics, 2016, 203, 699-714.	2.9	76

#	Article	IF	Citations
19	Epigenetic modifications are associated with inter-species gene expression variation in primates. Genome Biology, 2014, 15, 547.	8.8	72
20	Demystifying â€œdrop-outsâ€•in single-cell UMI data. Genome Biology, 2020, 21, 196.	8.8	72
21	Cancer PRSweb: An Online Repository with Polygenic Risk Scores for Major Cancer Traits and Their Evaluation in Two Independent Biobanks. American Journal of Human Genetics, 2020, 107, 815-836.	6.2	65
22	A Scalable Bayesian Method for Integrating Functional Information in Genome-wide Association Studies. American Journal of Human Genetics, 2017, 101, 404-416.	6.2	63
23	Causal association of type 2 diabetes with amyotrophic lateral sclerosis: new evidence from Mendelian randomization using GWAS summary statistics. BMC Medicine, 2019, 17, 225.	5.5	63
24	Differential expression analysis for RNAseq using Poisson mixed models. Nucleic Acids Research, 2017, 45, e106-e106.	14.5	60
25	Heritability estimation and differential analysis of count data with generalized linear mixed models in genomic sequencing studies. Bioinformatics, 2019, 35, 487-496.	4.1	60
26	Chromosome 1q21.2 and additional loci influence risk of spontaneous coronary artery dissection and myocardial infarction. Nature Communications, 2020, 11, 4432.	12.8	60
27	Genetic Architecture of Gene Expression in European and African Americans: An eQTL Mapping Study in GENOA. American Journal of Human Genetics, 2020, 106, 496-512.	6.2	56
28	Statistical methods for Mendelian randomization in genome-wide association studies: A review. Computational and Structural Biotechnology Journal, 2022, 20, 2338-2351.	4.1	56
29	Genetic prediction of complex traits with polygenic scores: a statistical review. Trends in Genetics, 2021, 37, 995-1011.	6.7	55
30	GeneNetwork: framework for web-based genetics. Journal of Open Source Software, 2016, 1, 25.	4.6	51
31	Integrative differential expression and gene set enrichment analysis using summary statistics for scRNA-seq studies. Nature Communications, 2020, 11, 1585.	12.8	43
32	Statistical methods for SNP heritability estimation and partition: A review. Computational and Structural Biotechnology Journal, 2020, 18, 1557-1568.	4.1	41
33	Statistical methods for mediation analysis in the era of high-throughput genomics: Current successes and future challenges. Computational and Structural Biotechnology Journal, 2021, 19, 3209-3224.	4.1	40
34	Epigenetic age acceleration is associated with cardiometabolic risk factors and clinical cardiovascular disease risk scores in African Americans. Clinical Epigenetics, 2021, 13, 55.	4.1	37
35	CoMM: a collaborative mixed model to dissecting genetic contributions to complex traits by leveraging regulatory information. Bioinformatics, 2019, 35, 1644-1652.	4.1	36
36	Multi-trait transcriptome-wide association studies with probabilistic Mendelian randomization. American Journal of Human Genetics, 2021, 108, 240-256.	6.2	35

#	Article	IF	Citations
37	Pleiotropic mapping and annotation selection in genome-wide association studies with penalized Gaussian mixture models. Bioinformatics, 2018, 34, 2797-2807.	4.1	34
38	Genetic investigation of fibromuscular dysplasia identifies risk loci and shared genetics with common cardiovascular diseases. Nature Communications, 2021, 12, 6031.	12.8	34
39	Bayesian Approximate Kernel Regression With Variable Selection. Journal of the American Statistical Association, 2018, 113, 1710-1721.	3.1	33
40	Controlling for Confounding Effects in Single Cell RNA Sequencing Studies Using both Control and Target Genes. Scientific Reports, 2017, 7, 13587.	3.3	32
41	On cross-ancestry cancer polygenic risk scores. PLoS Genetics, 2021, 17, e1009670.	3.5	32
42	CoMM-S2: a collaborative mixed model using summary statistics in transcriptome-wide association studies. Bioinformatics, 2020, 36, 2009-2016.	4.1	30
43	Identifying and exploiting trait-relevant tissues with multiple functional annotations in genome-wide association studies. PLoS Genetics, 2018, 14, e1007186.	3.5	30
44	Prediction of gene expression with cis-SNPs using mixed models and regularization methods. BMC Genomics, 2017, 18, 368.	2.8	29
45	Joint dimension reduction and clustering analysis of single-cell RNA-seq and spatial transcriptomics data. Nucleic Acids Research, 2022, 50, e72-e72.	14.5	26
46	Leveraging gene co-expression patterns to infer trait-relevant tissues in genome-wide association studies. PLoS Genetics, 2020, 16, e1008734.	3.5	25
47	Aggregating multiple expression prediction models improves the power of transcriptome-wide association studies. Human Molecular Genetics, 2021, 30, 939-951.	2.9	24
48	Modeling zero inflation is not necessary for spatial transcriptomics. Genome Biology, 2022, 23, 118.	8.8	23
49	SNV identification from single-cell RNA sequencing data. Human Molecular Genetics, 2019, 28, 3569-3583.	2.9	22
50	Transcriptomeâ€wide association studies: a view from Mendelian randomization. Quantitative Biology, 2021, 9, 107-121.	0.5	22
51	Assessing the Relationship Between Leukocyte Telomere Length and Cancer Risk/Mortality in UK Biobank and TCGA Datasets With the Genetic Risk Score and Mendelian Randomization Approaches. Frontiers in Genetics, 2020, 11, 583106.	2.3	17
52	Multi-scale inference of genetic trait architecture using biologically annotated neural networks. PLoS Genetics, 2021, 17, e1009754.	3.5	13
53	Likelihood-based Mendelian randomization analysis with automated instrument selection and horizontal pleiotropic modeling. Science Advances, 2022, 8, eabl5744.	10.3	13
54	Effective and scalable single-cell data alignment with non-linear canonical correlation analysis. Nucleic Acids Research, 2022, 50, e21-e21.	14.5	13

#	Article	IF	Citations
55	IMAGE: high-powered detection of genetic effects on DNA methylation using integrated methylation QTL mapping and allele-specific analysis. Genome Biology, 2019, 20, 220.	8.8	12
56	Epigenetic loci for blood pressure are associated with hypertensive target organ damage in older African Americans from the genetic epidemiology network of Arteriopathy (GENOA) study. BMC Medical Genomics, 2020, 13, 131.	1.5	12
57	Accurate genetic and environmental covariance estimation with composite likelihood in genome-wide association studies. PLoS Genetics, 2021, 17, e1009293.	3.5	12
58	PGS-server: accuracy, robustness and transferability of polygenic score methods for biobank scale studies. Briefings in Bioinformatics, 2022, 23, .	6.5	12
59	METRO: Multi-ancestry transcriptome-wide association studies for powerful gene-trait association detection. American Journal of Human Genetics, 2022, 109, 783-801.	6.2	12
60	Transcriptome-Wide Association Study of Blood Cell Traits in African Ancestry and Hispanic/Latino Populations. Genes, 2021, 12, 1049.	2.4	11
61	An improved variable selection procedure for adaptive Lasso in high-dimensional survival analysis. Lifetime Data Analysis, 2019, 25, 569-585.	0.9	10
62	Epigenome-wide association study identifies DNA methylation sites associated with target organ damage in older African Americans. Epigenetics, 2021, 16, 862-875.	2.7	10
63	Mendelian randomization under the omnigenic architecture. Briefings in Bioinformatics, 2021, 22, .	6.5	9
64	Screening for geneâ€“environment (GÃ—E) interaction using omics data from exposed individuals: an application to gene-arsenic interaction. Mammalian Genome, 2018, 29, 101-111.	2.2	7
65	Longitudinal analysis of epigenome-wide DNA methylation reveals novel smoking-related loci in African Americans. Epigenetics, 2019, 14, 171-184.	2.7	7
66	A Review of Statistical Methods for Identifying Trait-Relevant Tissues and Cell Types. Frontiers in Genetics, 2020, 11, 587887.	2.3	7
67	Pinpointing miRNA and genes enrichment over trait-relevant tissue network in Genome-Wide Association Studies. BMC Medical Genomics, 2020, 13, 191.	1.5	6
68	Epigenetics of single-site and multi-site atherosclerosis in African Americans from the Genetic Epidemiology Network of Arteriopathy (GENOA). Clinical Epigenetics, 2022, 14, 10.	4.1	6
69	Subset-Based Analysis Using Gene-Environment Interactions for Discovery of Genetic Associations across Multiple Studies or Phenotypes. Human Heredity, 2018, 83, 283-314.	0.8	5
70	Genome-Wide Association Meta-Analysis of Individuals of European Ancestry Identifies Suggestive Loci for Sodium Intake, Potassium Intake, and Their Ratio Measured from 24-Hour or Half-Day Urine Samples. Journal of Nutrition, 2020, 150, 2635-2645.	2.9	4
71	MCC-SP: a powerful integration method for identification of causal pathways from genetic variants to complex disease. BMC Genetics, 2020, 21, 90.	2.7	3
72	Efficient and effective control of confounding in eQTL mapping studies through joint differential expression and Mendelian randomization analyses. Bioinformatics, 2021, 37, 296-302.	4.1	3

#	Article	IF	Citations
73	False discovery control for penalized variable selections with high-dimensional covariates. Statistical Applications in Genetics and Molecular Biology, 2018, 17, .	0.6	1
74	Epidemiologic and Genetic Associations of Erythropoietin With Blood Pressure, Hypertension, and Coronary Artery Disease. Hypertension, 2021, 78, 1555-1566.	2.7	1
75	Title is missing!. , 2021, 17, e1009293.		0
76	Title is missing!. , 2021, 17, e1009293.		0
77	Title is missing!. , 2021, 17, e1009293.		0
78	Title is missing!. , 2021, 17, e1009293.		0
79	Statistical analysis of spatially resolved transcriptomic data by incorporating multiomics auxiliary information. Genetics, 2022, 221, .	2.9	0