Fei Zou

List of Publications by Year
in descending order

45 papers	2,367 citations	471509 17 h-index	254184 43 g-index
47 all docs	47 docs citations	47 times ranked	3460 citing authors

#	Article	IF	Citations
1	The Collaborative Cross, a community resource for the genetic analysis of complex traits. Nature Genetics, 2004, 36, 1133-1137.	21.4	1,034
2	The nature and identification of quantitative trait loci: a community's view. Nature Reviews Genetics, 2003, 4, 911-916.	16.3	390
3	Analyses of allele-specific gene expression in highly divergent mouse crosses identifies pervasive allelic imbalance. Nature Genetics, 2015, 47, 353-360.	21.4	204
4	Quantitative Trait Locus Analysis Using Recombinant Inbred Intercrosses. Genetics, 2005, 170, 1299-1311.	2.9	75
5	Practical FDR-based sample size calculations in microarray experiments. Bioinformatics, 2005, 21, 3264-3272.	4.1	54
6	Improving Quantitative Trait Loci Mapping Resolution in Experimental Crosses by the Use of Genotypically Selected Samples. Genetics, 2005, 170, 401-408.	2.9	50
7	An Efficient Resampling Method for Assessing Genome-Wide Statistical Significance in Mapping Quantitative Trait Loci. Genetics, 2004, 168, 2307-2316.	2.9	49
8	Quantification of Population Structure Using Correlated SNPs by Shrinkage Principal Components. Human Heredity, 2010, 70, 9-22.	0.8	48
9	Permutation-based identification of important biomarkers for complex diseases via machine learning models. Nature Communications, 2021, 12, 3008.	12.8	48
10	Airway Mucosal Host Defense Is Key to Genomic Regulation of Cystic Fibrosis Lung Disease Severity. American Journal of Respiratory and Critical Care Medicine, 2018, 197, 79-93.	5.6	46
11	Pay-it-forward gonorrhoea and chlamydia testing among men who have sex with men in China: a randomised controlled trial. Lancet Infectious Diseases, The, 2020, 20, 976-982.	9.1	30
12	Control of Population Stratification by Correlation-Selected Principal Components. Biometrics, 2011, 67, 967-974.	1.4	29
13	Analysis of maternal polymorphisms in arsenic (+3 oxidation state)-methyltransferase AS3MT and fetal sex in relation to arsenic metabolism and infant birth outcomes: Implications for risk analysis. Reproductive Toxicology, 2016, 61, 28-38.	2.9	26
14	Bagging and Deep Learning in Optimal Individualized Treatment Rules. Biometrics, 2019, 75, 674-684.	1.4	22
15	Nonparametric Bayesian Variable Selection With Applications to Multiple Quantitative Trait Loci Mapping With Epistasis and Gene–Environment Interaction. Genetics, 2010, 186, 385-394.	2.9	20
16	Differential DNA methylation following chemotherapy for breast cancer is associated with lack of memory improvement at one year. Epigenetics, 2020, 15, 499-510.	2.7	20
17	Statistical Issues in the Analysis of Quantitative Traits in Combined Crosses. Genetics, 2001, 158, 1339-1346.	2.9	18
18	Nonparametric estimation of the effects of quantitative trait loci. Biostatistics, 2004, 5, 501-513.	1.5	16

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19	Rank-Based Statistical Methodologies for Quantitative Trait Locus Mapping. Genetics, 2003, 165, 1599-1605.	2.9	15
20	Proximity Model for Expression Quantitative Trait Loci (eQTL) Detection. Biometrics, 2007, 63, 1108-1116.	1.4	14
21	Bayesian Multiple Quantitative Trait Loci Mapping for Complex Traits Using Markers of the Entire Genome. Genetics, 2007, 176, 2529-2540.	2.9	13
22	Comment on a Simple and Improved Correction for Population Stratification. American Journal of Human Genetics, 2008, 82, 524-526.	6.2	13
23	Monetary incentives and peer referral in promoting secondary distribution of HIV self-testing among men who have sex with men in China: A randomized controlled trial. PLoS Medicine, 2022, 19, e1003928.	8.4	13
24	eQTL mapping using allele-specific count data is computationally feasible, powerful, and provides individual-specific estimates of genetic effects. PLoS Genetics, 2022, 18, e1010076.	3.5	13
25	Assessing the Significance of Quantitative Trait Loci in Replicable Mapping Populations. Genetics, 2006, 174, 1063-1068.	2.9	12
26	QTL Mapping in Intercross and Backcross Populations. Methods in Molecular Biology, 2009, 573, 157-173.	0.9	11
27	Fast eQTL Analysis for Twin Studies. Genetic Epidemiology, 2015, 39, 357-365.	1.3	9
28	High-Dimensional Variable Selection in Meta-Analysis for Censored Data. Biometrics, 2011, 67, 504-512.	1.4	8
29	A family-based study of gene variants and maternal folate and choline in neuroblastoma: a report from the Children's Oncology Group. Cancer Causes and Control, 2016, 27, 1209-1218.	1.8	8
30	A robust QTL mapping procedure. Journal of Statistical Planning and Inference, 2009, 139, 978-989.	0.6	7
31	Bayesian Multiple Quantitative Trait Loci Mapping for Recombinant Inbred Intercrosses. Genetics, 2011, 188, 189-195.	2.9	7
32	Improved Metabolite Prediction Using Microbiome Data-Based Elastic Net Models. Frontiers in Cellular and Infection Microbiology, 2021, 11, 734416.	3.9	7
33	Neuroblastoma in relation to joint effects of vitamin A and maternal and offspring variants in vitamin A-related genes: A report of the Children's Oncology Group. Cancer Epidemiology, 2019, 61, 165-171.	1.9	6
34	Interfrontal Bone Among Inbred Strains of Mice and QTL Mapping. Frontiers in Genetics, 2019, 10, 291.	2.3	6
35	Antipsychotic Behavioral Phenotypes in the Mouse Collaborative Cross Recombinant Inbred Inter-Crosses (RIX). G3: Genes, Genomes, Genetics, 2020, 10, 3165-3177.	1.8	4
36	An interaction of inorganic arsenic exposure with body weight and composition on type 2 diabetes indicators in Diversity Outbred mice. Mammalian Genome, 2022, 33, 575-589.	2.2	4

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37	Empirical likelihoodâ€based inference for genetic mixture models. Canadian Journal of Statistics, 2007, 35, 563-574.	0.9	3
38	Joint Analysis of Strain and Parent-of-Origin Effects for Recombinant Inbred Intercrosses Generated from Multiparent Populations with the Collaborative Cross as an Example. G3: Genes, Genomes, Genetics, 2018, 8, 599-605.	1.8	3
39	Gaussian Process Based Bayesian Semiparametric Quantitative Trait Loci Interval Mapping. Biometrics, 2010, 66, 222-232.	1.4	2
40	A Semiparametric Bayesian Approach for Estimating the Gene Expression Distribution. Journal of Biopharmaceutical Statistics, 2010, 20, 267-280.	0.8	2
41	On polygenic risk scores for complex traits prediction. Biometrics, 2022, 78, 499-511.	1.4	2
42	An efficient integrative resampling method for geneâ€"trait association analysis. Genetic Epidemiology, 2020, 44, 197-207.	1.3	1
43	Joint Gene Network Construction by Single-Cell RNA Sequencing Data. Biometrics, 2023, 79, 915-925.	1.4	1
44	Inadvertent Transfer of Murine VL30 Retrotransposons to CAR-T Cells. Advances in Cell and Gene Therapy, 2022, 2022, 1-21.	0.9	1
45	An approximate Bayesian approach for quantitative trait loci estimation. Computational Statistics and Data Analysis, 2010, 54, 565-574.	1.2	0