

Fei Zou

List of Publications by Year in descending order

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45
papers

2,367
citations

471509

17
h-index

254184

43
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47
all docs

47
docs citations

47
times ranked

3460
citing authors

#	ARTICLE	IF	CITATIONS
1	Joint Gene Network Construction by Single-Cell RNA Sequencing Data. <i>Biometrics</i> , 2023, 79, 915-925.	1.4	1
2	On polygenic risk scores for complex traits prediction. <i>Biometrics</i> , 2022, 78, 499-511.	1.4	2
3	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. <i>PLoS Medicine</i> , 2022, 19, e1003928.	8.4	13
4	eQTL mapping using allele-specific count data is computationally feasible, powerful, and provides individual-specific estimates of genetic effects. <i>PLoS Genetics</i> , 2022, 18, e1010076.	3.5	13
5	Inadvertent Transfer of Murine VL30 Retrotransposons to CAR-T Cells. <i>Advances in Cell and Gene Therapy</i> , 2022, 2022, 1-21.	0.9	1
6	An interaction of inorganic arsenic exposure with body weight and composition on type 2 diabetes indicators in Diversity Outbred mice. <i>Mammalian Genome</i> , 2022, 33, 575-589.	2.2	4
7	Permutation-based identification of important biomarkers for complex diseases via machine learning models. <i>Nature Communications</i> , 2021, 12, 3008.	12.8	48
8	Improved Metabolite Prediction Using Microbiome Data-Based Elastic Net Models. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 734416.	3.9	7
9	An efficient integrative resampling method for gene-trait association analysis. <i>Genetic Epidemiology</i> , 2020, 44, 197-207.	1.3	1
10	Differential DNA methylation following chemotherapy for breast cancer is associated with lack of memory improvement at one year. <i>Epigenetics</i> , 2020, 15, 499-510.	2.7	20
11	Pay-it-forward gonorrhoea and chlamydia testing among men who have sex with men in China: a randomised controlled trial. <i>Lancet Infectious Diseases</i> , The, 2020, 20, 976-982.	9.1	30
12	Antipsychotic Behavioral Phenotypes in the Mouse Collaborative Cross Recombinant Inbred Inter-Crosses (RIX). <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3165-3177.	1.8	4
13	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. <i>Cancer Epidemiology</i> , 2019, 61, 165-171.	1.9	6
14	Interfrontal Bone Among Inbred Strains of Mice and QTL Mapping. <i>Frontiers in Genetics</i> , 2019, 10, 291.	2.3	6
15	Bagging and Deep Learning in Optimal Individualized Treatment Rules. <i>Biometrics</i> , 2019, 75, 674-684.	1.4	22
16	Joint Analysis of Strain and Parent-of-Origin Effects for Recombinant Inbred Intercrosses Generated from Multiparent Populations with the Collaborative Cross as an Example. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 599-605.	1.8	3
17	Airway Mucosal Host Defense Is Key to Genomic Regulation of Cystic Fibrosis Lung Disease Severity. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2018, 197, 79-93.	5.6	46
18	A family-based study of gene variants and maternal folate and choline in neuroblastoma: a report from the Children's Oncology Group. <i>Cancer Causes and Control</i> , 2016, 27, 1209-1218.	1.8	8

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19	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. <i>Reproductive Toxicology</i> , 2016, 61, 28-38.	2.9	26
20	Fast eQTL Analysis for Twin Studies. <i>Genetic Epidemiology</i> , 2015, 39, 357-365.	1.3	9
21	Analyses of allele-specific gene expression in highly divergent mouse crosses identifies pervasive allelic imbalance. <i>Nature Genetics</i> , 2015, 47, 353-360.	21.4	204
22	High-Dimensional Variable Selection in Meta-Analysis for Censored Data. <i>Biometrics</i> , 2011, 67, 504-512.	1.4	8
23	Control of Population Stratification by Correlation-Selected Principal Components. <i>Biometrics</i> , 2011, 67, 967-974.	1.4	29
24	Bayesian Multiple Quantitative Trait Loci Mapping for Recombinant Inbred Intercrosses. <i>Genetics</i> , 2011, 188, 189-195.	2.9	7
25	An approximate Bayesian approach for quantitative trait loci estimation. <i>Computational Statistics and Data Analysis</i> , 2010, 54, 565-574.	1.2	0
26	Gaussian Process Based Bayesian Semiparametric Quantitative Trait Loci Interval Mapping. <i>Biometrics</i> , 2010, 66, 222-232.	1.4	2
27	Nonparametric Bayesian Variable Selection With Applications to Multiple Quantitative Trait Loci Mapping With Epistasis and Gene-Environment Interaction. <i>Genetics</i> , 2010, 186, 385-394.	2.9	20
28	Quantification of Population Structure Using Correlated SNPs by Shrinkage Principal Components. <i>Human Heredity</i> , 2010, 70, 9-22.	0.8	48
29	A Semiparametric Bayesian Approach for Estimating the Gene Expression Distribution. <i>Journal of Biopharmaceutical Statistics</i> , 2010, 20, 267-280.	0.8	2
30	A robust QTL mapping procedure. <i>Journal of Statistical Planning and Inference</i> , 2009, 139, 978-989.	0.6	7
31	QTL Mapping in Intercross and Backcross Populations. <i>Methods in Molecular Biology</i> , 2009, 573, 157-173.	0.9	11
32	Comment on a Simple and Improved Correction for Population Stratification. <i>American Journal of Human Genetics</i> , 2008, 82, 524-526.	6.2	13
33	Bayesian Multiple Quantitative Trait Loci Mapping for Complex Traits Using Markers of the Entire Genome. <i>Genetics</i> , 2007, 176, 2529-2540.	2.9	13
34	Empirical likelihood-based inference for genetic mixture models. <i>Canadian Journal of Statistics</i> , 2007, 35, 563-574.	0.9	3
35	Proximity Model for Expression Quantitative Trait Loci (eQTL) Detection. <i>Biometrics</i> , 2007, 63, 1108-1116.	1.4	14
36	Assessing the Significance of Quantitative Trait Loci in Replicable Mapping Populations. <i>Genetics</i> , 2006, 174, 1063-1068.	2.9	12

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37	Quantitative Trait Locus Analysis Using Recombinant Inbred Intercrosses. <i>Genetics</i> , 2005, 170, 1299-1311.	2.9	75
38	Improving Quantitative Trait Loci Mapping Resolution in Experimental Crosses by the Use of Genotypically Selected Samples. <i>Genetics</i> , 2005, 170, 401-408.	2.9	50
39	Practical FDR-based sample size calculations in microarray experiments. <i>Bioinformatics</i> , 2005, 21, 3264-3272.	4.1	54
40	An Efficient Resampling Method for Assessing Genome-Wide Statistical Significance in Mapping Quantitative Trait Loci. <i>Genetics</i> , 2004, 168, 2307-2316.	2.9	49
41	Nonparametric estimation of the effects of quantitative trait loci. <i>Biostatistics</i> , 2004, 5, 501-513.	1.5	16
42	The Collaborative Cross, a community resource for the genetic analysis of complex traits. <i>Nature Genetics</i> , 2004, 36, 1133-1137.	21.4	1,034
43	The nature and identification of quantitative trait loci: a community's view. <i>Nature Reviews Genetics</i> , 2003, 4, 911-916.	16.3	390
44	Rank-Based Statistical Methodologies for Quantitative Trait Locus Mapping. <i>Genetics</i> , 2003, 165, 1599-1605.	2.9	15
45	Statistical Issues in the Analysis of Quantitative Traits in Combined Crosses. <i>Genetics</i> , 2001, 158, 1339-1346.	2.9	18