

Qi Zhang

List of Publications by Year in descending order

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Version: 2024-02-01

14
papers

217
citations

1651377

6
h-index

1336881

12
g-index

16
all docs

16
docs citations

16
times ranked

360
citing authors

#	ARTICLE	IF	CITATIONS
1	High-Dimensional Mediation Analysis with Applications to Causal Gene Identification. <i>Statistics in Biosciences</i> , 2022, 14, 432-451.	0.6	8
2	Gene by environment interaction mouse model reveals a functional role for 5-hydroxymethylcytosine in neurodevelopmental disorders. <i>Genome Research</i> , 2022, 32, 266-279.	2.4	6
3	Genome-wide mediation analysis: an empirical study to connect phenotype with genotype via intermediate transcriptomic data in maize. <i>Genetics</i> , 2022, 221, .	1.2	8
4	An Empirical Bayes approach for the identification of long-range chromosomal interaction from Hi-C data. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2021, 20, 1-15.	0.2	0
5	TGCnA: temporal gene coexpression network analysis using a low-rank plus sparse framework. <i>Journal of Applied Statistics</i> , 2020, 47, 1064-1083.	0.6	2
6	Data Analysis of ChIP-Seq Experiments. , 2019, , 67-77.		0
7	Metabolic Dynamics of Developing Rice Seeds Under High Night-Time Temperature Stress. <i>Frontiers in Plant Science</i> , 2019, 10, 1443.	1.7	50
8	An empirical Bayes test for allelic-imbalance detection in ChIP-seq. <i>Biostatistics</i> , 2018, 19, 546-561.	0.9	6
9	Using single-index ODEs to study dynamic gene regulatory network. <i>PLoS ONE</i> , 2018, 13, e0192833.	1.1	8
10	Sex-specific hippocampal 5-hydroxymethylcytosine is disrupted in response to acute stress. <i>Neurobiology of Disease</i> , 2016, 96, 54-66.	2.1	24
11	Systematic evaluation of the impact of ChIP-seq read designs on genome coverage, peak identification, and allele-specific binding detection. <i>BMC Bioinformatics</i> , 2016, 17, 96.	1.2	6
12	Genome-wide alterations in hippocampal 5-hydroxymethylcytosine links plasticity genes to acute stress. <i>Neurobiology of Disease</i> , 2016, 86, 99-108.	2.1	48
13	Genome-wide disruption of 5-hydroxymethylcytosine in a mouse model of autism. <i>Human Molecular Genetics</i> , 2015, 24, ddv411.	1.4	38
14	CNV-guided multi-read allocation for ChIP-seq. <i>Bioinformatics</i> , 2014, 30, 2860-2867.	1.8	10