Qi Zhang

List of Publications by Year
in descending order

14 papers	217 citations	1478505 6 h-index	1199594 12 g-index
16 all docs	16 docs citations	16 times ranked	326 citing authors

#	Article	IF	Citations
1	Metabolic Dynamics of Developing Rice Seeds Under High Night-Time Temperature Stress. Frontiers in Plant Science, 2019, 10, 1443.	3.6	50
2	Genome-wide alterations in hippocampal 5-hydroxymethylcytosine links plasticity genes to acute stress. Neurobiology of Disease, 2016, 86, 99-108.	4.4	48
3	Genome-wide disruption of 5-hydroxymethylcytosine in a mouse model of autism. Human Molecular Genetics, 2015, 24, ddv411.	2.9	38
4	Sex-specific hippocampal 5-hydroxymethylcytosine is disrupted in response to acute stress. Neurobiology of Disease, 2016, 96, 54-66.	4.4	24
5	CNV-guided multi-read allocation for ChIP-seq. Bioinformatics, 2014, 30, 2860-2867.	4.1	10
6	Using single-index ODEs to study dynamic gene regulatory network. PLoS ONE, 2018, 13, e0192833.	2.5	8
7	High-Dimensional Mediation Analysis with Applications to Causal Gene Identification. Statistics in Biosciences, 2022, 14, 432-451.	1.2	8
8	Genome-wide mediation analysis: an empirical study to connect phenotype with genotype via intermediate transcriptomic data in maize. Genetics, 2022, 221, .	2.9	8
9	Systematic evaluation of the impact of ChIP-seq read designs on genome coverage, peak identification, and allele-specific binding detection. BMC Bioinformatics, 2016, 17, 96.	2.6	6
10	An empirical Bayes test for allelic-imbalance detection in ChIP-seq. Biostatistics, 2018, 19, 546-561.	1.5	6
11	Gene by environment interaction mouse model reveals a functional role for 5-hydroxymethylcytosine in neurodevelopmental disorders. Genome Research, 2022, 32, 266-279.	5.5	6
12	TGCnA: temporal gene coexpression network analysis using a low-rank plus sparse framework. Journal of Applied Statistics, 2020, 47, 1064-1083.	1.3	2
13	Data Analysis of ChIP-Seq Experiments. , 2019, , 67-77.		0
14	An Empirical Bayes approach for the identification of long-range chromosomal interaction from Hi-C data. Statistical Applications in Genetics and Molecular Biology, 2021, 20, 1-15.	0.6	0