

# Qi Zhang

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/572953/publications.pdf>

Version: 2024-02-01

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	High-Dimensional Mediation Analysis with Applications to Causal Gene Identification. Statistics in Biosciences, 2022, 14, 432-451.	1.2	8
2	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
3	Genome-wide mediation analysis: an empirical study to connect phenotype with genotype via intermediate transcriptomic data in maize. Genetics, 2022, 221, .	2.9	8
4	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
5	TGCnA: temporal gene coexpression network analysis using a low-rank plus sparse framework. Journal of Applied Statistics, 2020, 47, 1064-1083.	1.3	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. Frontiers in Plant Science, 2019, 10, 1443.	3.6	50
8	An empirical Bayes test for allelic-imbalance detection in ChIP-seq. Biostatistics, 2018, 19, 546-561.	1.5	6
9	Using single-index ODEs to study dynamic gene regulatory network. PLoS ONE, 2018, 13, e0192833.	2.5	8
10	Sex-specific hippocampal 5-hydroxymethylcytosine is disrupted in response to acute stress. Neurobiology of Disease, 2016, 96, 54-66.	4.4	24
11	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
12	Genome-wide alterations in hippocampal 5-hydroxymethylcytosine links plasticity genes to acute stress. Neurobiology of Disease, 2016, 86, 99-108.	4.4	48
13	Genome-wide disruption of 5-hydroxymethylcytosine in a mouse model of autism. Human Molecular Genetics, 2015, 24, ddv411.	2.9	38
14	CNV-guided multi-read allocation for ChIP-seq. Bioinformatics, 2014, 30, 2860-2867.	4.1	10