Ting Qi

List of Publications by Year
in descending order

14 papers	1,582 citations	840776 11 h-index	1058476 14 g-index
16 all docs	16 docs citations	16 times ranked	3914 citing authors

#	Article	IF	Citations
1	Large-scale cis- and trans-eQTL analyses identify thousands of genetic loci and polygenic scores that regulate blood gene expression. Nature Genetics, 2021, 53, 1300-1310.	21.4	590
2	Identifying gene targets for brain-related traits using transcriptomic and methylomic data from blood. Nature Communications, 2018, 9, 2282.	12.8	294
3	Integrative analysis of omics summary data reveals putative mechanisms underlying complex traits. Nature Communications, 2018, 9, 918.	12.8	250
4	Genomic variation associated with local adaptation of weedy rice during de-domestication. Nature Communications, 2017, 8, 15323.	12.8	132
5	Analysis of DNA methylation associates the cystine–glutamate antiporter SLC7A11 with risk of Parkinson's disease. Nature Communications, 2020, 11, 1238.	12.8	85
6	Conditional GWAS analysis to identify disorder-specific SNPs for psychiatric disorders. Molecular Psychiatry, 2021, 26, 2070-2081.	7.9	48
7	Mixed Linear Model Approaches of Association Mapping for Complex Traits Based on Omics Variants. Scientific Reports, 2015, 5, 10298.	3.3	47
8	Tissue specific regulation of transcription in endometrium and association with disease. Human Reproduction, 2020, 35, 377-393.	0.9	43
9	Genetic regulation of methylation in human endometrium and blood and gene targets for reproductive diseases. Clinical Epigenetics, 2019, 11, 49.	4.1	26
10	Multivariate Dimensionality Reduction Approaches to Identify Gene-Gene and Gene-Environment Interactions Underlying Multiple Complex Traits. PLoS ONE, 2014, 9, e108103.	2.5	18
11	Mixed linear model approach for mapping quantitative trait loci underlying crop seed traits. Heredity, 2014, 113, 224-232.	2.6	18
12	Functional characterisation of the amyotrophic lateral sclerosis risk locus GPX3/TNIP1. Genome Medicine, 2022, 14, 7.	8.2	12
13	Promoter-anchored chromatin interactions predicted from genetic analysis of epigenomic data. Nature Communications, 2020, 11, 2061.	12.8	8
14	Dissecting Genetic Architecture Underlying Seed Traits in Multiple Environments. Genetics, 2015, 199, 61-71.	2.9	4