

Ting Qi

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/415412/publications.pdf>

Version: 2024-02-01

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