

Biao Zeng

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11135483/publications.pdf>

Version: 2024-02-01

11
papers

2,097
citations

1040056

9
h-index

1199594

12
g-index

14
all docs

14
docs citations

14
times ranked

5600
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. <i>Nature Genetics</i> , 2021, 53, 1300-1310.	21.4	590
2	Genome-wide genetic changes during modern breeding of maize. <i>Nature Genetics</i> , 2012, 44, 812-815.	21.4	352
3	Dynamic Transcriptome Landscape of Maize Embryo and Endosperm Development. <i>Plant Physiology</i> , 2014, 166, 252-264.	4.8	274
4	The Genetic Architecture of Gene Expression in Peripheral Blood. <i>American Journal of Human Genetics</i> , 2017, 100, 228-237.	6.2	178
5	Ribosome profiling reveals dynamic translational landscape in maize seedlings under drought stress. <i>Plant Journal</i> , 2015, 84, 1206-1218.	5.7	162
6	Genome-wide high resolution parental-specific DNA and histone methylation maps uncover patterns of imprinting regulation in maize. <i>Genome Research</i> , 2014, 24, 167-176.	5.5	140
7	Constraints on eQTL Fine Mapping in the Presence of Multisite Local Regulation of Gene Expression. <i>Genes, Genomes, Genetics</i> , 2017, 7, 2533-2544.	1.8	23
8	Comprehensive Multiple eQTL Detection and Its Application to GWAS Interpretation. <i>Genetics</i> , 2019, 212, 905-918.	2.9	23
9	Autosomal genetic control of human gene expression does not differ across the sexes. <i>Genome Biology</i> , 2016, 17, 248.	8.8	15
10	PolyQTL: Bayesian multiple eQTL detection with control for population structure and sample relatedness. <i>Bioinformatics</i> , 2019, 35, 1061-1063.	4.1	6
11	TreeMap: a structured approach to fine mapping of eQTL variants. <i>Bioinformatics</i> , 2021, 37, 1125-1134.	4.1	6