

Jianjun Zhang

List of Publications by Year in descending order

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Version: 2024-02-01

14
papers

40
citations

2258059

3
h-index

1872680

6
g-index

17
all docs

17
docs citations

17
times ranked

58
citing authors

#	ARTICLE	IF	CITATIONS
1	A fast and powerful eQTL weighted method to detect genes associated with complex trait using GWAS summary data. Genetic Epidemiology, 2020, 44, 550-563.	1.3	10
2	Powerful statistical method to detect disease-associated genes using publicly available genome-wide association studies summary data. Genetic Epidemiology, 2019, 43, 941-951.	1.3	9
3	Test Gene-Environment Interactions for Multiple Traits in Sequencing Association Studies. Human Heredity, 2019, 84, 170-196.	0.8	4
4	Testing gene-environment interactions for rare and/or common variants in sequencing association studies. PLoS ONE, 2020, 15, e0229217.	2.5	4
5	A general statistic to test an optimally weighted combination of common and/or rare variants. Genetic Epidemiology, 2019, 43, 966-979.	1.3	3
6	Polya tree priors and their estimation with multi-group data. Statistical Papers, 2019, 60, 849-875.	1.2	2
7	Methods to evaluate rare variants gene-age interaction for triglycerides. BMC Proceedings, 2018, 12, 49.	1.6	1
8	A gene based approach to test genetic association based on an optimally weighted combination of multiple traits. PLoS ONE, 2019, 14, e0220914.	2.5	1
9	EM-test for homogeneity in a two-sample problem with a mixture structure. Journal of Applied Statistics, 2020, 47, 724-738.	1.3	1
10	TS: a powerful truncated test to detect novel disease associated genes using publicly available gWAS summary data. BMC Bioinformatics, 2020, 21, 172.	2.6	1
11	Title is missing!. , 2020, 15, e0229217.		0
12	Title is missing!. , 2020, 15, e0229217.		0
13	Title is missing!. , 2020, 15, e0229217.		0
14	Title is missing!. , 2020, 15, e0229217.		0