Zhili Zheng

List of Publications by Year in descending order

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		471509	610901
25	7,026	17	24
papers	citations	h-index	g-index
36	36	36	12617
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	Assessing the contribution of rare variants to complex trait heritability from whole-genome sequence data. Nature Genetics, 2022, 54, 263-273.	21.4	156
2	Widespread signatures of natural selection across human complex traits and functional genomic categories. Nature Communications, 2021 , 12 , 1164 .	12.8	50
3	Phenotypic covariance across the entire spectrum of relatedness for 86 billion pairs of individuals. Nature Communications, 2021, 12, 1050.	12.8	19
4	A Comparison of Ten Polygenic Score Methods for Psychiatric Disorders Applied Across Multiple Cohorts. Biological Psychiatry, 2021, 90, 611-620.	1.3	103
5	Tumor Mutational Burden Is Polygenic and Genetically Associated with Complex Traits and Diseases. Cancer Research, 2021, 81, 1230-1239.	0.9	14
6	A generalized linear mixed model association tool for biobank-scale data. Nature Genetics, 2021, 53, 1616-1621.	21.4	168
7	Improved analyses of GWAS summary statistics by reducing data heterogeneity and errors. Nature Communications, 2021, 12, 7117.	12.8	31
8	Promoter-anchored chromatin interactions predicted from genetic analysis of epigenomic data. Nature Communications, 2020, 11, 2061.	12.8	8
9	The Effects of Spatial Frequency on the Accommodative Responses of Myopic and Emmetropic Chinese Children. Translational Vision Science and Technology, 2019, 8, 65.	2.2	6
10	F87COMMON GENETIC VARIATION EXPLAINS A HIGH PROPORTION OF THE ELEVATED RISK OF PSYCHIATRIC DISORDERS IN CHILDREN OF YOUNGER MOTHERS. European Neuropsychopharmacology, 2019, 29, S1156-S1157.	0.7	0
11	Genome-wide association study of medication-use and associated disease in the UK Biobank. Nature Communications, 2019, 10, 1891.	12.8	140
12	Improved polygenic prediction by Bayesian multiple regression on summary statistics. Nature Communications, 2019, 10, 5086.	12.8	291
13	A resource-efficient tool for mixed model association analysis of large-scale data. Nature Genetics, 2019, 51, 1749-1755.	21.4	294
14	Integrative analysis of omics summary data reveals putative mechanisms underlying complex traits. Nature Communications, 2018, 9, 918.	12.8	250
15	Causal associations between risk factors and common diseases inferred from GWAS summary data. Nature Communications, 2018, 9, 224.	12.8	629
16	Global genetic differentiation of complex traits shaped by natural selection in humans. Nature Communications, 2018, 9, 1865.	12.8	70
17	Association Between Population Density and Genetic Risk for Schizophrenia. JAMA Psychiatry, 2018, 75, 901.	11.0	67
18	Gene discovery and polygenic prediction from a genome-wide association study of educational attainment in 1.1 million individuals. Nature Genetics, 2018, 50, 1112-1121.	21.4	1,835

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#	Article	IF	CITATION
19	Genome-wide association analyses identify 143 risk variants and putative regulatory mechanisms for type 2 diabetes. Nature Communications, 2018, 9, 2941.	12.8	570
20	Meta-analysis of genome-wide association studies for height and body mass index in â ¹ / ₄ 700000 individuals of European ancestry. Human Molecular Genetics, 2018, 27, 3641-3649.	2.9	1,541
21	Identifying gene targets for brain-related traits using transcriptomic and methylomic data from blood. Nature Communications, 2018, 9, 2282.	12.8	294
22	Comparison of three monocular methods for measuring accommodative stimulus–response curves. Australasian journal of optometry, The, 2017, 100, 155-161.	1.3	14
23	Quantifying the mapping precision of genome-wide association studies using whole-genome sequencing data. Genome Biology, 2017, 18, 86.	8.8	84
24	Genetic signatures of high-altitude adaptation in Tibetans. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 4189-4194.	7.1	181
25	The effects of spatial frequency on the accommodation responses of myopes and emmetropes under various detection demands. Vision Research, 2015, 115, 1-7.	1.4	8