Zhili Zheng

List of Publications by Year
in descending order

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

#	Article	IF	Citations
1	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
2	Meta-analysis of genome-wide association studies for height and body mass index in â^¼700000 individuals of European ancestry. Human Molecular Genetics, 2018, 27, 3641-3649.	2.9	1,541
3	Causal associations between risk factors and common diseases inferred from GWAS summary data. Nature Communications, 2018, 9, 224.	12.8	629
4	Genome-wide association analyses identify 143 risk variants and putative regulatory mechanisms for type 2 diabetes. Nature Communications, 2018, 9, 2941.	12.8	570
5	Identifying gene targets for brain-related traits using transcriptomic and methylomic data from blood. Nature Communications, 2018, 9, 2282.	12.8	294
6	A resource-efficient tool for mixed model association analysis of large-scale data. Nature Genetics, 2019, 51, 1749-1755.	21.4	294
7	Improved polygenic prediction by Bayesian multiple regression on summary statistics. Nature Communications, 2019, 10, 5086.	12.8	291
8	Integrative analysis of omics summary data reveals putative mechanisms underlying complex traits. Nature Communications, 2018, 9, 918.	12.8	250
9	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
10	A generalized linear mixed model association tool for biobank-scale data. Nature Genetics, 2021, 53, 1616-1621.	21.4	168
11	Assessing the contribution of rare variants to complex trait heritability from whole-genome sequence data. Nature Genetics, 2022, 54, 263-273.	21.4	156
12	Genome-wide association study of medication-use and associated disease in the UK Biobank. Nature Communications, 2019, 10, 1891.	12.8	140
13	A Comparison of Ten Polygenic Score Methods for Psychiatric Disorders Applied Across Multiple Cohorts. Biological Psychiatry, 2021, 90, 611-620.	1.3	103
14	Quantifying the mapping precision of genome-wide association studies using whole-genome sequencing data. Genome Biology, 2017, 18, 86.	8.8	84
15	Global genetic differentiation of complex traits shaped by natural selection in humans. Nature Communications, 2018, 9, 1865.	12.8	70
16	Association Between Population Density and Genetic Risk for Schizophrenia. JAMA Psychiatry, 2018, 75, 901.	11.0	67
17	Widespread signatures of natural selection across human complex traits and functional genomic categories. Nature Communications, 2021, 12, 1164.	12.8	50
18	Improved analyses of GWAS summary statistics by reducing data heterogeneity and errors. Nature Communications, 2021, 12, 7117.	12.8	31

#	Article	IF	Citations
19	Phenotypic covariance across the entire spectrum of relatedness for 86 billion pairs of individuals. Nature Communications, 2021, 12, 1050.	12.8	19
20	Comparison of three monocular methods for measuring accommodative stimulusâ€“response curves. Australasian journal of optometry, The, 2017, 100, 155-161.	1.3	14
21	Tumor Mutational Burden Is Polygenic and Genetically Associated with Complex Traits and Diseases. Cancer Research, 2021, 81, 1230-1239.	0.9	14
22	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
23	Promoter-anchored chromatin interactions predicted from genetic analysis of epigenomic data. Nature Communications, 2020, 11, 2061.	12.8	8
24	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
25	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