

Wei Zhou

List of Publications by Citations

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Version: 2024-04-26

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

40
papers

2,646
citations

19
h-index

51
g-index

54
ext. papers

4,357
ext. citations

22.3
avg, IF

3.94
L-index

#	Paper	IF	Citations
40	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017 , 542, 186-190	50.4	412
39	Efficiently controlling for case-control imbalance and sample relatedness in large-scale genetic association studies. <i>Nature Genetics</i> , 2018 , 50, 1335-1341	36.3	375
38	Exome-wide association study of plasma lipids in >300,000 individuals. <i>Nature Genetics</i> , 2017 , 49, 1758-1766	36.3	310
37	Shared genetic origin of asthma, hay fever and eczema elucidates allergic disease biology. <i>Nature Genetics</i> , 2017 , 49, 1752-1757	36.3	256
36	Biobank-driven genomic discovery yields new insight into atrial fibrillation biology. <i>Nature Genetics</i> , 2018 , 50, 1234-1239	36.3	254
35	Systematic evaluation of coding variation identifies a candidate causal variant in TM6SF2 influencing total cholesterol and myocardial infarction risk. <i>Nature Genetics</i> , 2014 , 46, 345-51	36.3	213
34	GREGOR: evaluating global enrichment of trait-associated variants in epigenomic features using a systematic, data-driven approach. <i>Bioinformatics</i> , 2015 , 31, 2601-6	7.2	96
33	Deep-coverage whole genome sequences and blood lipids among 16,324 individuals. <i>Nature Communications</i> , 2018 , 9, 3391	17.4	90
32	Exome chip meta-analysis identifies novel loci and East Asian-specific coding variants that contribute to lipid levels and coronary artery disease. <i>Nature Genetics</i> , 2017 , 49, 1722-1730	36.3	83
31	Evidence of a causal relationship between body mass index and psoriasis: A mendelian randomization study. <i>PLoS Medicine</i> , 2019 , 16, e1002739	11.6	77
30	Exome-wide association analysis reveals novel coding sequence variants associated with lipid traits in Chinese. <i>Nature Communications</i> , 2015 , 6, 10206	17.4	60
29	Genome-wide analysis yields new loci associating with aortic valve stenosis. <i>Nature Communications</i> , 2018 , 9, 987	17.4	56
28	Genome-wide Study of Atrial Fibrillation Identifies Seven Risk Loci and Highlights Biological Pathways and Regulatory Elements Involved in Cardiac Development. <i>American Journal of Human Genetics</i> , 2018 , 102, 103-115	11	53
27	Scalable generalized linear mixed model for region-based association tests in large biobanks and cohorts. <i>Nature Genetics</i> , 2020 , 52, 634-639	36.3	41
26	Exploring and visualizing large-scale genetic associations by using PheWeb. <i>Nature Genetics</i> , 2020 , 52, 550-552	36.3	41
25	A genome-wide association study with 1,126,563 individuals identifies new risk loci for Alzheimer's disease. <i>Nature Genetics</i> , 2021 , 53, 1276-1282	36.3	40
24	The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021 ,	50.4	24

23	UK Biobank Whole-Exome Sequence Binary Phenome Analysis with Robust Region-Based Rare-Variant Test. <i>American Journal of Human Genetics</i> , 2020 , 106, 3-12	11	21
22	GWAS of thyroid stimulating hormone highlights pleiotropic effects and inverse association with thyroid cancer. <i>Nature Communications</i> , 2020 , 11, 3981	17.4	21
21	Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. <i>Nature Communications</i> , 2020 , 11, 6417	17.4	17
20	Improving power of association tests using multiple sets of imputed genotypes from distributed reference panels. <i>Genetic Epidemiology</i> , 2017 , 41, 744-755	2.6	13
19	Age-of-onset information helps identify 76 genetic variants associated with allergic disease. <i>PLoS Genetics</i> , 2020 , 16, e1008725	6	10
18	Scalable generalized linear mixed model for region-based association tests in large biobanks and cohorts		7
17	Genetic insight into sick sinus syndrome. <i>European Heart Journal</i> , 2021 , 42, 1959-1971	9.5	7
16	Global Biobank Meta-analysis Initiative: powering genetic discovery across human diseases		6
15	Efficiently controlling for case-control imbalance and sample relatedness in large-scale genetic association studies		6
14	Systematic single-variant and gene-based association testing of 3,700 phenotypes in 281,850 UK Biobank exomes		6
13	Robust meta-analysis of biobank-based genome-wide association studies with unbalanced binary phenotypes. <i>Genetic Epidemiology</i> , 2019 , 43, 462-476	2.6	5
12	An efficient and accurate frailty model approach for genome-wide survival association analysis controlling for population structure and relatedness in large-scale biobanks		5
11	Discovery and systematic characterization of risk variants and genes for coronary artery disease in over a million participants		5
10	Genome-wide association study of 1 million people identifies 111 loci for atrial fibrillation		4
9	MEPE loss-of-function variant associates with decreased bone mineral density and increased fracture risk. <i>Nature Communications</i> , 2020 , 11, 4093	17.4	4
8	Mendelian randomization of genetically independent aging phenotypes identifies LPA and VCAM1 as biological targets for human aging. <i>Nature Aging</i> , 2022 , 2, 19-30		3
7	The HUNT Study: a population-based cohort for genetic research		3
6	Global biobank analyses provide lessons for computing polygenic risk scores across diverse cohorts		3

5	Efficient mixed model approach for large-scale genome-wide association studies of ordinal categorical phenotypes. <i>American Journal of Human Genetics</i> , 2021 , 108, 825-839	11	3
4	Evidence of a common causal relationship between body mass index and inflammatory skin disease: a Mendelian Randomization study		2
3	UK-Biobank Whole Exome Sequence Binary Phenome Analysis with Robust Region-based Rare Variant Test		1
2	Set-based rare variant association tests for biobank scale sequencing data sets		1
1	Meta-analysis fine-mapping is often miscalibrated at single-variant resolution		1