Wei Zhou

List of Publications by Year in Descending Order

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	Mendelian randomization of genetically independent aging phenotypes identifies LPA and VCAM1 as biological targets for human aging. *Nature Aging*, **2022**, 2, 19-30		3
39	The power of genetic diversity in genome-wide association studies of lipids. *Nature*, **2021**,	50.4	24
38	Efficient mixed model approach for large-scale genome-wide association studies of ordinal categorical phenotypes. *American Journal of Human Genetics*, **2021**, 108, 825-839	11	3
37	Genetic insight into sick sinus syndrome. *European Heart Journal*, **2021**, 42, 1959-1971	9.5	7
36	A genome-wide association study with 1,126,563 individuals identifies new risk loci for Alzheimer's disease. *Nature Genetics*, **2021**, 53, 1276-1282	36.3	40
35	Scalable generalized linear mixed model for region-based association tests in large biobanks and cohorts. *Nature Genetics*, **2020**, 52, 634-639	36.3	41
34	Exploring and visualizing large-scale genetic associations by using PheWeb. *Nature Genetics*, **2020**, 52, 550-552	36.3	41
33	Age-of-onset information helps identify 76 genetic variants associated with allergic disease. *PLoS Genetics*, **2020**, 16, e1008725	6	10
32	UK Biobank Whole-Exome Sequence Binary Phenome Analysis with Robust Region-Based Rare-Variant Test. *American Journal of Human Genetics*, **2020**, 106, 3-12	11	21
31	GWAS of thyroid stimulating hormone highlights pleiotropic effects and inverse association with thyroid cancer. *Nature Communications*, **2020**, 11, 3981	17.4	21
30	MEPE loss-of-function variant associates with decreased bone mineral density and increased fracture risk. *Nature Communications*, **2020**, 11, 4093	17.4	4
29	Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. *Nature Communications*, **2020**, 11, 6417	17.4	17
28	Evidence of a causal relationship between body mass index and psoriasis: A mendelian randomization study. *PLoS Medicine*, **2019**, 16, e1002739	11.6	77
27	Robust meta-analysis of biobank-based genome-wide association studies with unbalanced binary phenotypes. *Genetic Epidemiology*, **2019**, 43, 462-476	2.6	5
26	Genome-wide analysis yields new loci associating with aortic valve stenosis. *Nature Communications* , **2018**, 9, 987	17.4	56
25	Genome-wide Study of Atrial Fibrillation Identifies Seven Risk Loci and Highlights Biological Pathways and Regulatory Elements Involved in Cardiac Development. *American Journal of Human Genetics*, **2018**, 102, 103-115	11	53
24	Biobank-driven genomic discovery yields new insight into atrial fibrillation biology. *Nature Genetics*, **2018**, 50, 1234-1239	36.3	254

23	Efficiently controlling for case-control imbalance and sample relatedness in large-scale genetic association studies. *Nature Genetics*, **2018**, 50, 1335-1341	36.3	375
22	Deep-coverage whole genome sequences and blood lipids among 16,324 individuals. *Nature Communications*, **2018**, 9, 3391	17.4	90
21	Rare and low-frequency coding variants alter human adult height. *Nature*, **2017**, 542, 186-190	50.4	412
20	Exome-wide association study of plasma lipids in >300,000 individuals. *Nature Genetics*, **2017**, 49, 1758-1766	36.3	310
19	Exome chip meta-analysis identifies novel loci and East Asian-specific coding variants that contribute to lipid levels and coronary artery disease. *Nature Genetics*, **2017**, 49, 1722-1730	36.3	83
18	Shared genetic origin of asthma, hay fever and eczema elucidates allergic disease biology. *Nature Genetics*, **2017**, 49, 1752-1757	36.3	256
17	Improving power of association tests using multiple sets of imputed genotypes from distributed reference panels. *Genetic Epidemiology*, **2017**, 41, 744-755	2.6	13
16	GREGOR: evaluating global enrichment of trait-associated variants in epigenomic features using a systematic, data-driven approach. *Bioinformatics*, **2015**, 31, 2601-6	7.2	96
15	Exome-wide association analysis reveals novel coding sequence variants associated with lipid traits in Chinese. *Nature Communications*, **2015**, 6, 10206	17.4	60
14	Systematic evaluation of coding variation identifies a candidate causal variant in TM6SF2 influencing total cholesterol and myocardial infarction risk. *Nature Genetics*, **2014**, 46, 345-51	36.3	213
13	The HUNT Study: a population-based cohort for genetic research		3
12	Global Biobank Meta-analysis Initiative: powering genetic discovery across human diseases		6
11	Global biobank analyses provide lessons for computing polygenic risk scores across diverse cohorts		3
10	Evidence of a common causal relationship between body mass index and inflammatory skin disease: a Mendelian Randomization study		2
9	UK-Biobank Whole Exome Sequence Binary Phenome Analysis with Robust Region-based Rare Variant Test		1
8	An efficient and accurate frailty model approach for genome-wide survival association analysis controlling for population structure and relatedness in large-scale biobanks		5
7	Efficiently controlling for case-control imbalance and sample relatedness in large-scale genetic association studies		6
6	Genome-wide association study of 1 million people identifies 111 loci for atrial fibrillation		4

5	Scalable generalized linear mixed model for region-based association tests in large biobanks and cohorts	7
4	Discovery and systematic characterization of risk variants and genes for coronary artery disease in over a million participants	5
3	Systematic single-variant and gene-based association testing of 3,700 phenotypes in 281,850 UK Biobank exomes	6
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