Wei Zhou

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/1301919/publications.pdf

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28 papers	5,566 citations	331538 21 h-index	434063 31 g-index
54 all docs	54 docs citations	54 times ranked	11395 citing authors

#	Article	IF	Citations
1	Efficiently controlling for case-control imbalance and sample relatedness in large-scale genetic association studies. Nature Genetics, 2018, 50, 1335-1341.	9.4	896
2	Biobank-driven genomic discovery yields new insight into atrial fibrillation biology. Nature Genetics, 2018, 50, 1234-1239.	9.4	547
3	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	13.7	544
4	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	9.4	470
5	Shared genetic origin of asthma, hay fever and eczema elucidates allergic disease biology. Nature Genetics, 2017, 49, 1752-1757.	9.4	432
6	A genome-wide association study with 1,126,563 individuals identifies new risk loci for Alzheimerâ€™s disease. Nature Genetics, 2021, 53, 1276-1282.	9.4	430
7	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	13.7	353
8	Systematic evaluation of coding variation identifies a candidate causal variant in TM6SF2 influencing total cholesterol and myocardial infarction risk. Nature Genetics, 2014, 46, 345-351.	9.4	268
9	GREGOR: evaluating global enrichment of trait-associated variants in epigenomic features using a systematic, data-driven approach. Bioinformatics, 2015, 31, 2601-2606.	1.8	146
10	Evidence of a causal relationship between body mass index and psoriasis: A mendelian randomization study. PLoS Medicine, 2019, 16, e1002739.	3.9	144
11	Deep-coverage whole genome sequences and blood lipids among 16,324 individuals. Nature Communications, 2018, 9, 3391.	5.8	140
12	Exome chip meta-analysis identifies novel loci and East Asianâ€“specific coding variants that contribute to lipid levels and coronary artery disease. Nature Genetics, 2017, 49, 1722-1730.	9.4	129
13	Exploring and visualizing large-scale genetic associations by using PheWeb. Nature Genetics, 2020, 52, 550-552.	9.4	129
14	Scalable generalized linear mixed model for region-based association tests in large biobanks and cohorts. Nature Genetics, 2020, 52, 634-639.	9.4	124
15	Genome-wide analysis yields new loci associating with aortic valve stenosis. Nature Communications, 2018, 9, 987.	5.8	91
16	Exome-wide association analysis reveals novel coding sequence variants associated with lipid traits in Chinese. Nature Communications, 2015, 6, 10206.	5.8	86
17	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.	2.6	86
18	GWAS of thyroid stimulating hormone highlights pleiotropic effects and inverse association with thyroid cancer. Nature Communications, 2020, 11, 3981.	5.8	86

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19	UK Biobank Whole-Exome Sequence Binary Phenome Analysis with Robust Region-Based Rare-Variant Test. American Journal of Human Genetics, 2020, 106, 3-12.	2.6	56
20	Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. Nature Communications, 2020, 11, 6417.	5.8	39
21	Improving power of association tests using multiple sets of imputed genotypes from distributed reference panels. Genetic Epidemiology, 2017, 41, 744-755.	0.6	27
22	Age-of-onset information helps identify 76 genetic variants associated with allergic disease. PLoS Genetics, 2020, 16, e1008725.	1.5	27
23	Genetic insight into sick sinus syndrome. European Heart Journal, 2021, 42, 1959-1971.	1.0	27
24	Efficient mixed model approach for large-scale genome-wide association studies of ordinal categorical phenotypes. American Journal of Human Genetics, 2021, 108, 825-839.	2.6	25
25	MEPE loss-of-function variant associates with decreased bone mineral density and increased fracture risk. Nature Communications, 2020, 11, 4093.	5.8	24
26	Mendelian randomization of genetically independent aging phenotypes identifies LPA and VCAM1 as biological targets for human aging. Nature Aging, 2022, 2, 19-30.	5.3	17
27	Genome-wide meta-analysis of iron status biomarkers and the effect of iron on all-cause mortality in HUNT. Communications Biology, 2022, 5, .	2.0	11
28	Robust metaâ€analysis of biobankâ€based genomeâ€wide association studies with unbalanced binary phenotypes. Genetic Epidemiology, 2019, 43, 462-476.	0.6	7