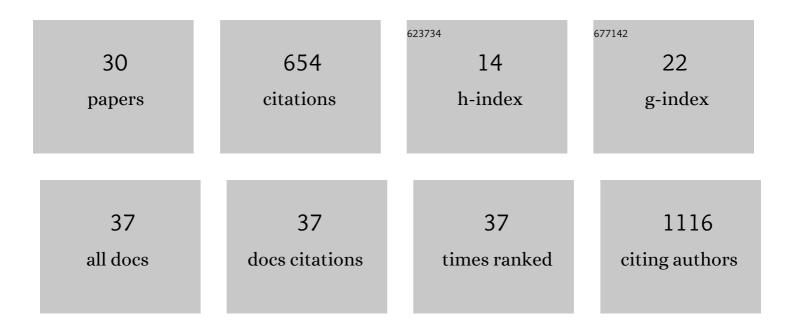
Chong Wu

List of Publications by Year in descending order

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Сномс Ми

#	Article	IF	CITATIONS
1	A Powerful Framework for Integrating eQTL and GWAS Summary Data. Genetics, 2017, 207, 893-902.	2.9	72
2	An adaptive association test for microbiome data. Genome Medicine, 2016, 8, 56.	8.2	69
3	Imaging-wide association study: Integrating imaging endophenotypes in GWAS. NeuroImage, 2017, 159, 159-169.	4.2	57
4	A Review of Integrative Imputation for Multi-Omics Datasets. Frontiers in Genetics, 2020, 11, 570255.	2.3	57
5	Accurate recognition of colorectal cancer with semi-supervised deep learning on pathological images. Nature Communications, 2021, 12, 6311.	12.8	51
6	Integration of Enhancer-Promoter Interactions with GWAS Summary Results Identifies Novel Schizophrenia-Associated Genes and Pathways. Genetics, 2018, 209, 699-709.	2.9	34
7	A powerful fine-mapping method for transcriptome-wide association studies. Human Genetics, 2020, 139, 199-213.	3.8	32
8	An integrative multi-omics analysis to identify candidate DNA methylation biomarkers related to prostate cancer risk. Nature Communications, 2020, 11, 3905.	12.8	28
9	A Transcriptome-Wide Association Study Identifies Candidate Susceptibility Genes for Pancreatic Cancer Risk. Cancer Research, 2020, 80, 4346-4354.	0.9	28
10	An integrative multiomics analysis identifies putative causal genes for COVID-19 severity. Genetics in Medicine, 2021, 23, 2076-2086.	2.4	25
11	A transcriptome-wide association study of Alzheimer's disease using prediction models of relevant tissues identifies novel candidate susceptibility genes. Genome Medicine, 2021, 13, 141.	8.2	25
12	Integrating eQTL data with GWAS summary statistics in pathwayâ€based analysis with application to schizophrenia. Genetic Epidemiology, 2018, 42, 303-316.	1.3	20
13	Integration of methylation QTL and enhancer–target gene maps with schizophrenia GWAS summary results identifies novel genes. Bioinformatics, 2019, 35, 3576-3583.	4.1	19
14	Asymptotically independent U-statistics in high-dimensional testing. Annals of Statistics, 2021, 49, 154-181.	2.6	19
15	Associations between Genetically Predicted Blood Protein Biomarkers and Pancreatic Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 1501-1508.	2.5	18
16	Adaptive SNP-Set Association Testing in Generalized Linear Mixed Models with Application to Family Studies. Behavior Genetics, 2018, 48, 55-66.	2.1	13
17	Imputation of missing covariate values in epigenome-wide analysis of DNA methylation data. Epigenetics, 2016, 11, 132-139.	2.7	10
18	Multi-trait Genome-Wide Analyses of the Brain Imaging Phenotypes in UK Biobank. Genetics, 2020, 215, 947-958.	2.9	10

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19	Associations Between Genetically Predicted Protein Levels and COVID-19 Severity. Journal of Infectious Diseases, 2021, 223, 19-22.	4.0	10
20	A transcriptomeâ€wide association study identifies novel candidate susceptibility genes for prostate cancer risk. International Journal of Cancer, 2022, 150, 80-90.	5.1	9
21	Comparison between two post-dentin bond strength measurement methods. Scientific Reports, 2018, 8, 2350.	3.3	8
22	Integrating DNA sequencing and transcriptomic data for association analyses of low-frequency variants and lipid traits. Human Molecular Genetics, 2020, 29, 515-526.	2.9	7
23	A gene-level methylome-wide association analysis identifies novel Alzheimer's disease genes. Bioinformatics, 2021, 37, 1933-1940.	4.1	7
24	A transcriptome-wide association study identifies novel blood-based gene biomarker candidates for Alzheimer's disease risk. Human Molecular Genetics, 2021, 31, 289-299.	2.9	7
25	Novel strategy for disease risk prediction incorporating predicted gene expression and DNA methylation data: a multiâ€phased study of prostate cancer. Cancer Communications, 2021, 41, 1387-1397.	9.2	6
26	InTACT: An adaptive and powerful framework for jointâ€ŧissue transcriptomeâ€wide association studies. Genetic Epidemiology, 2021, 45, 848-859.	1.3	4
27	An adaptive test for metaâ€analysis of rare variant association studies. Genetic Epidemiology, 2020, 44, 104-116.	1.3	2
28	Leveraging existing GWAS summary data of genetically correlated and uncorrelated traits to improve power for a new GWAS. Genetic Epidemiology, 2020, 44, 717-732.	1.3	2
29	A Regularization-Based Adaptive Test for High-Dimensional Generalized Linear Models. Journal of Machine Learning Research, 2020, 21, .	62.4	1
30	Using R for Cell-Type Composition Imputation in Epigenome-Wide Association Studies. Methods in Molecular Biology, 2022, 2432, 49-56.	0.9	0