# Chong Wu

List of Publications by Year
in descending order



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|---|---|---|---|
| 30 papers | 654 citations | 623734 14 h-index | 677142 22 g-index |
| 37 all docs | 37 docs citations | 37 times ranked | 1116 citing authors |

| # | 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 Alzheimerâ€™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 enhancerâ€“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 |

| # | Article | IF | Citations |
|---|---|---|---|
| 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 Alzheimerâ€™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 Alzheimerâ€™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€tissue 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 |