

Chong Wu

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6415155/publications.pdf>

Version: 2024-02-01

30
papers

654
citations

623574

14
h-index

677027

22
g-index

37
all docs

37
docs citations

37
times ranked

1116
citing authors

#	ARTICLE	IF	CITATIONS
1	A transcriptome-wide association study identifies novel candidate susceptibility genes for prostate cancer risk. <i>International Journal of Cancer</i> , 2022, 150, 80-90.	2.3	9
2	Using R for Cell-Type Composition Imputation in Epigenome-Wide Association Studies. <i>Methods in Molecular Biology</i> , 2022, 2432, 49-56.	0.4	0
3	Associations Between Genetically Predicted Protein Levels and COVID-19 Severity. <i>Journal of Infectious Diseases</i> , 2021, 223, 19-22.	1.9	10
4	A gene-level methylome-wide association analysis identifies novel Alzheimer's disease genes. <i>Bioinformatics</i> , 2021, 37, 1933-1940.	1.8	7
5	Asymptotically independent U-statistics in high-dimensional testing. <i>Annals of Statistics</i> , 2021, 49, 154-181.	1.4	19
6	An integrative multiomics analysis identifies putative causal genes for COVID-19 severity. <i>Genetics in Medicine</i> , 2021, 23, 2076-2086.	1.1	25
7	InTACT: An adaptive and powerful framework for joint-tissue transcriptome-wide association studies. <i>Genetic Epidemiology</i> , 2021, 45, 848-859.	0.6	4
8	A transcriptome-wide association study identifies novel blood-based gene biomarker candidates for Alzheimer's disease risk. <i>Human Molecular Genetics</i> , 2021, 31, 289-299.	1.4	7
9	A transcriptome-wide association study of Alzheimer's disease using prediction models of relevant tissues identifies novel candidate susceptibility genes. <i>Genome Medicine</i> , 2021, 13, 141.	3.6	25
10	Novel strategy for disease risk prediction incorporating predicted gene expression and DNA methylation data: a multi-phased study of prostate cancer. <i>Cancer Communications</i> , 2021, 41, 1387-1397.	3.7	6
11	Accurate recognition of colorectal cancer with semi-supervised deep learning on pathological images. <i>Nature Communications</i> , 2021, 12, 6311.	5.8	51
12	An adaptive test for meta-analysis of rare variant association studies. <i>Genetic Epidemiology</i> , 2020, 44, 104-116.	0.6	2
13	A powerful fine-mapping method for transcriptome-wide association studies. <i>Human Genetics</i> , 2020, 139, 199-213.	1.8	32
14	Leveraging existing GWAS summary data of genetically correlated and uncorrelated traits to improve power for a new GWAS. <i>Genetic Epidemiology</i> , 2020, 44, 717-732.	0.6	2
15	An integrative multi-omics analysis to identify candidate DNA methylation biomarkers related to prostate cancer risk. <i>Nature Communications</i> , 2020, 11, 3905.	5.8	28
16	A Transcriptome-Wide Association Study Identifies Candidate Susceptibility Genes for Pancreatic Cancer Risk. <i>Cancer Research</i> , 2020, 80, 4346-4354.	0.4	28
17	A Review of Integrative Imputation for Multi-Omics Datasets. <i>Frontiers in Genetics</i> , 2020, 11, 570255.	1.1	57
18	Multi-trait Genome-Wide Analyses of the Brain Imaging Phenotypes in UK Biobank. <i>Genetics</i> , 2020, 215, 947-958.	1.2	10

#	ARTICLE	IF	CITATIONS
19	Integrating DNA sequencing and transcriptomic data for association analyses of low-frequency variants and lipid traits. <i>Human Molecular Genetics</i> , 2020, 29, 515-526.	1.4	7
20	Associations between Genetically Predicted Blood Protein Biomarkers and Pancreatic Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020, 29, 1501-1508.	1.1	18
21	A Regularization-Based Adaptive Test for High-Dimensional Generalized Linear Models. <i>Journal of Machine Learning Research</i> , 2020, 21, .	62.4	1
22	Integration of methylation QTL and enhancerâ€target gene maps with schizophrenia GWAS summary results identifies novel genes. <i>Bioinformatics</i> , 2019, 35, 3576-3583.	1.8	19
23	Comparison between two post-dentin bond strength measurement methods. <i>Scientific Reports</i> , 2018, 8, 2350.	1.6	8
24	Integrating eQTL data with GWAS summary statistics in pathwayâ€based analysis with application to schizophrenia. <i>Genetic Epidemiology</i> , 2018, 42, 303-316.	0.6	20
25	Integration of Enhancer-Promoter Interactions with GWAS Summary Results Identifies Novel Schizophrenia-Associated Genes and Pathways. <i>Genetics</i> , 2018, 209, 699-709.	1.2	34
26	Adaptive SNP-Set Association Testing in Generalized Linear Mixed Models with Application to Family Studies. <i>Behavior Genetics</i> , 2018, 48, 55-66.	1.4	13
27	A Powerful Framework for Integrating eQTL and GWAS Summary Data. <i>Genetics</i> , 2017, 207, 893-902.	1.2	72
28	Imaging-wide association study: Integrating imaging endophenotypes in GWAS. <i>NeuroImage</i> , 2017, 159, 159-169.	2.1	57
29	An adaptive association test for microbiome data. <i>Genome Medicine</i> , 2016, 8, 56.	3.6	69
30	Imputation of missing covariate values in epigenome-wide analysis of DNA methylation data. <i>Epigenetics</i> , 2016, 11, 132-139.	1.3	10