Lin Hou

List of Publications by Year
in descending order

28 papers	727 citations	759233 12 h-index	610901 24 g-index
35 all docs	35 docs citations	35 times ranked	1726 citing authors

#	Article	IF	Citations
1	Temperature-dependent innate defense against the common cold virus limits viral replication at warm temperature in mouse airway cells. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 827-832.	7.1	199
2	A review of post-GWAS prioritization approaches. Frontiers in Genetics, 2013, 4, 280.	2.3	77
3	A Multipurpose, High-Throughput Single-Nucleotide Polymorphism Chip for the Dengue and Yellow Fever Mosquito, *Aedes aegypti*. G3: Genes, Genomes, Genetics, 2015, 5, 711-718.	1.8	56
4	Guilt by rewiring: gene prioritization through network rewiring in Genome Wide Association Studies. Human Molecular Genetics, 2014, 23, 2780-2790.	2.9	54
5	Cell type annotation of single-cell chromatin accessibility data via supervised Bayesian embedding. Nature Machine Intelligence, 2022, 4, 116-126.	16.0	42
6	Phosphorylation of GATA-6 is required for vascular smooth muscle cell differentiation after mTORC1 inhibition. Science Signaling, 2015, 8, ra44.	3.6	39
7	Identification of trans-eQTLs using mediation analysis with multiple mediators. BMC Bioinformatics, 2019, 20, 126.	2.6	34
8	Global COVID-19 pandemic demands joint interventions for the suppression of future waves. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 26151-26157.	7.1	33
9	Leveraging effect size distributions to improve polygenic risk scores derived from summary statistics of genome-wide association studies. PLoS Computational Biology, 2020, 16, e1007565.	3.2	32
10	Detecting local genetic correlations with scan statistics. Nature Communications, 2021, 12, 2033.	12.8	23
11	Interplay of tRNA-Derived Fragments and T Cell Activation in Breast Cancer Patient Survival. Cancers, 2020, 12, 2230.	3.7	21
12	A Pan-Cancer Analysis of Predictive Methylation Signatures of Response to Cancer Immunotherapy. Frontiers in Immunology, 2021, 12, 796647.	4.8	16
13	A Set of Efficient Methods to Generate High-Dimensional Binary Data With Specified Correlation Structures. American Statistician, 2021, 75, 310-322.	1.6	15
14	Transcriptional Profiling of Ectoderm Specification to Keratinocyte Fate in Human Embryonic Stem Cells. PLoS ONE, 2015, 10, e0122493.	2.5	13
15	Admixture mapping analysis in the context of GWAS with GAW18 data. BMC Proceedings, 2014, 8, S3.	1.6	12
16	Prediction and differential analysis of RNA secondary structure. Quantitative Biology, 2020, 8, 109-118.	0.5	12
17	Leveraging LD eigenvalue regression to improve the estimation of SNP heritability and confounding inflation. American Journal of Human Genetics, 2022, 109, 802-811.	6.2	12
18	Identification of rare variants for hypertension with incorporation of linkage information. BMC Proceedings, 2014, 8, S109.	1.6	5

#	ARTICLE	IF	CITATIONS
19	Openness weighted association studies: leveraging personal genome information to prioritize non-coding variants. Bioinformatics, 2021, 37, 4737-4743.	4.1	3
20	A novel transcriptional risk score for risk prediction of complex human diseases. Genetic Epidemiology, 2021, 45, 811-820.	1.3	3
21	Quantifying concordant genetic effects of de novo mutations on multiple disorders. ELife, 0, 11, .	6.0	3
22	Incorporating functional annotation information in prioritizing disease associated SNPs from genome wide association studies. Science China Life Sciences, 2014, 57, 1072-1079.	4.9	2
23	A penalized linear mixed model for genomic prediction using pedigree structures. BMC Proceedings, 2014, 8, S67.	1.6	2
24	Transcriptome wide association studies: general framework and methods. Quantitative Biology, 2021, 9, 141-150.	0.5	2
25	Reduction of Human Mobility Matters during Early COVID-19 Outbreaks: Evidence from India, Japan and China. International Journal of Environmental Research and Public Health, 2021, 18, 2826.	2.6	2
26	Adjustment of familial relatedness in association test for rare variants. BMC Proceedings, 2014, 8, S39.	1.6	1
27	A data-adaptive Bayesian regression approach for polygenic risk prediction. Bioinformatics, 2022, 38, 1938-1946.	4.1	1
28	Multi-Cell-Type Openness-Weighted Association Studies for Trait-Associated Genomic Segments Prioritization. Genes, 2022, 13, 1220.	2.4	0