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	A data-adaptive Bayesian regression approach for polygenic risk prediction. Bioinformatics, 2022, 38, 1938-1946.	4.1	1
2	Cell type annotation of single-cell chromatin accessibility data via supervised Bayesian embedding. Nature Machine Intelligence, 2022, 4, 116-126.	16.0	42
3	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
4	Multi-Cell-Type Openness-Weighted Association Studies for Trait-Associated Genomic Segments Prioritization. Genes, 2022, 13, 1220.	2.4	0
5	A Set of Efficient Methods to Generate High-Dimensional Binary Data With Specified Correlation Structures. American Statistician, 2021, 75, 310-322.	1.6	15
6	Transcriptome wide association studies: general framework and methods. Quantitative Biology, 2021, 9, 141-150.	0.5	2
7	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
8	Detecting local genetic correlations with scan statistics. Nature Communications, 2021, 12, 2033.	12.8	23
9	Openness weighted association studies: leveraging personal genome information to prioritize non-coding variants. Bioinformatics, 2021, 37, 4737-4743.	4.1	3
10	A novel transcriptional risk score for risk prediction of complex human diseases. Genetic Epidemiology, 2021, 45, 811-820.	1.3	3
11	A Pan-Cancer Analysis of Predictive Methylation Signatures of Response to Cancer Immunotherapy. Frontiers in Immunology, 2021, 12, 796647.	4.8	16
12	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
13	Interplay of tRNA-Derived Fragments and T Cell Activation in Breast Cancer Patient Survival. Cancers, 2020, 12, 2230.	3.7	21
14	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
15	Prediction and differential analysis of RNA secondary structure. Quantitative Biology, 2020, 8, 109-118.	0.5	12
16	Identification of trans-eQTLs using mediation analysis with multiple mediators. BMC Bioinformatics, 2019, 20, 126.	2.6	34
17	Transcriptional Profiling of Ectoderm Specification to Keratinocyte Fate in Human Embryonic Stem Cells. PLoS ONE, 2015, 10, e0122493.	2.5	13
18	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

#	Article	IF	Citations
19	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
20	Phosphorylation of GATA-6 is required for vascular smooth muscle cell differentiation after mTORC1 inhibition. Science Signaling, 2015, 8, ra44.	3.6	39
21	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
22	Guilt by rewiring: gene prioritization through network rewiring in Genome Wide Association Studies. Human Molecular Genetics, 2014, 23, 2780-2790.	2.9	54
23	Admixture mapping analysis in the context of GWAS with GAW18 data. BMC Proceedings, 2014, 8, S3.	1.6	12
24	Adjustment of familial relatedness in association test for rare variants. BMC Proceedings, 2014, 8, S39.	1.6	1
25	A penalized linear mixed model for genomic prediction using pedigree structures. BMC Proceedings, 2014, 8, S67.	1.6	2
26	Identification of rare variants for hypertension with incorporation of linkage information. BMC Proceedings, 2014, 8, S109.	1.6	5
27	A review of post-GWAS prioritization approaches. Frontiers in Genetics, 2013, 4, 280.	2.3	77
28	Quantifying concordant genetic effects of de novo mutations on multiple disorders. ELife, 0, 11, .	6.0	3