

Lin Hou

List of Publications by Year in descending order

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Version: 2024-02-01

28
papers

727
citations

759055

12
h-index

610775

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. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 827-832. | 3.3 | 199 |
| 2 | A review of post-GWAS prioritization approaches. <i>Frontiers in Genetics</i> , 2013, 4, 280. | 1.1 | 77 |
| 3 | A Multipurpose, High-Throughput Single-Nucleotide Polymorphism Chip for the Dengue and Yellow Fever Mosquito, <i>Aedes aegypti</i> . <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 711-718. | 0.8 | 56 |
| 4 | Guilt by rewiring: gene prioritization through network rewiring in Genome Wide Association Studies. <i>Human Molecular Genetics</i> , 2014, 23, 2780-2790. | 1.4 | 54 |
| 5 | Cell type annotation of single-cell chromatin accessibility data via supervised Bayesian embedding. <i>Nature Machine Intelligence</i> , 2022, 4, 116-126. | 8.3 | 42 |
| 6 | Phosphorylation of GATA-6 is required for vascular smooth muscle cell differentiation after mTORC1 inhibition. <i>Science Signaling</i> , 2015, 8, ra44. | 1.6 | 39 |
| 7 | Identification of trans-eQTLs using mediation analysis with multiple mediators. <i>BMC Bioinformatics</i> , 2019, 20, 126. | 1.2 | 34 |
| 8 | Global COVID-19 pandemic demands joint interventions for the suppression of future waves. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 26151-26157. | 3.3 | 33 |
| 9 | Leveraging effect size distributions to improve polygenic risk scores derived from summary statistics of genome-wide association studies. <i>PLoS Computational Biology</i> , 2020, 16, e1007565. | 1.5 | 32 |
| 10 | Detecting local genetic correlations with scan statistics. <i>Nature Communications</i> , 2021, 12, 2033. | 5.8 | 23 |
| 11 | Interplay of tRNA-Derived Fragments and T Cell Activation in Breast Cancer Patient Survival. <i>Cancers</i> , 2020, 12, 2230. | 1.7 | 21 |
| 12 | A Pan-Cancer Analysis of Predictive Methylation Signatures of Response to Cancer Immunotherapy. <i>Frontiers in Immunology</i> , 2021, 12, 796647. | 2.2 | 16 |
| 13 | A Set of Efficient Methods to Generate High-Dimensional Binary Data With Specified Correlation Structures. <i>American Statistician</i> , 2021, 75, 310-322. | 0.9 | 15 |
| 14 | Transcriptional Profiling of Ectoderm Specification to Keratinocyte Fate in Human Embryonic Stem Cells. <i>PLoS ONE</i> , 2015, 10, e0122493. | 1.1 | 13 |
| 15 | Admixture mapping analysis in the context of GWAS with GAW18 data. <i>BMC Proceedings</i> , 2014, 8, S3. | 1.8 | 12 |
| 16 | Prediction and differential analysis of RNA secondary structure. <i>Quantitative Biology</i> , 2020, 8, 109-118. | 0.3 | 12 |
| 17 | Leveraging LD eigenvalue regression to improve the estimation of SNP heritability and confounding inflation. <i>American Journal of Human Genetics</i> , 2022, 109, 802-811. | 2.6 | 12 |
| 18 | Identification of rare variants for hypertension with incorporation of linkage information. <i>BMC Proceedings</i> , 2014, 8, S109. | 1.8 | 5 |

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|----|---|-----|-----------|
| 19 | Openness weighted association studies: leveraging personal genome information to prioritize non-coding variants. <i>Bioinformatics</i> , 2021, 37, 4737-4743. | 1.8 | 3 |
| 20 | A novel transcriptional risk score for risk prediction of complex human diseases. <i>Genetic Epidemiology</i> , 2021, 45, 811-820. | 0.6 | 3 |
| 21 | Quantifying concordant genetic effects of de novo mutations on multiple disorders. <i>ELife</i> , 0, 11, . | 2.8 | 3 |
| 22 | Incorporating functional annotation information in prioritizing disease associated SNPs from genome wide association studies. <i>Science China Life Sciences</i> , 2014, 57, 1072-1079. | 2.3 | 2 |
| 23 | A penalized linear mixed model for genomic prediction using pedigree structures. <i>BMC Proceedings</i> , 2014, 8, S67. | 1.8 | 2 |
| 24 | Transcriptome wide association studies: general framework and methods. <i>Quantitative Biology</i> , 2021, 9, 141-150. | 0.3 | 2 |
| 25 | Reduction of Human Mobility Matters during Early COVID-19 Outbreaks: Evidence from India, Japan and China. <i>International Journal of Environmental Research and Public Health</i> , 2021, 18, 2826. | 1.2 | 2 |
| 26 | Adjustment of familial relatedness in association test for rare variants. <i>BMC Proceedings</i> , 2014, 8, S39. | 1.8 | 1 |
| 27 | A data-adaptive Bayesian regression approach for polygenic risk prediction. <i>Bioinformatics</i> , 2022, 38, 1938-1946. | 1.8 | 1 |
| 28 | Multi-Cell-Type Openness-Weighted Association Studies for Trait-Associated Genomic Segments Prioritization. <i>Genes</i> , 2022, 13, 1220. | 1.0 | 0 |