

Lily Wang

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6372803/publications.pdf>

Version: 2024-02-01

29
papers

1,285
citations

643344

15
h-index

685536

24
g-index

36
all docs

36
docs citations

36
times ranked

3394
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 1 | MethReg: estimating the regulatory potential of DNA methylation in gene transcription. <i>Nucleic Acids Research</i> , 2022, 50, e51-e51. | 6.5 | 8 |
| 2 | Abstract PD3-04: Multi-omics characterization of triple-negative breast cancer identifies therapeutic vulnerabilities and epigenetic immune suppression in the mesenchymal subtype. <i>Cancer Research</i> , 2022, 82, PD3-04-PD3-04. | 0.4 | 0 |
| 3 | Genetic architecture of RNA editing regulation in Alzheimer's disease across diverse ancestral populations. <i>Human Molecular Genetics</i> , 2022, 31, 2876-2886. | 1.4 | 2 |
| 4 | Sex-specific DNA methylation differences in Alzheimer's disease pathology. <i>Acta Neuropathologica Communications</i> , 2021, 9, 77. | 2.4 | 26 |
| 5 | LR Hunting: A Random Forest Based Cell-Cell Interaction Discovery Method for Single-Cell Gene Expression Data. <i>Frontiers in Genetics</i> , 2021, 12, 708835. | 1.1 | 9 |
| 6 | Multi-omics analysis identifies therapeutic vulnerabilities in triple-negative breast cancer subtypes. <i>Nature Communications</i> , 2021, 12, 6276. | 5.8 | 89 |
| 7 | Sex-specific analysis of DNA methylation changes implicates new loci in Alzheimer's disease pathology. <i>Alzheimer's and Dementia</i> , 2021, 17, e049363. | 0.4 | 0 |
| 8 | Estimating the regulatory potential of DNA methylation in Alzheimer's disease. <i>Alzheimer's and Dementia</i> , 2021, 17, e049365. | 0.4 | 0 |
| 9 | PathwayMultiomics: An R Package for Efficient Integrative Analysis of Multi-Omics Datasets With Matched or Un-matched Samples. <i>Frontiers in Genetics</i> , 2021, 12, 783713. | 1.1 | 9 |
| 10 | Epigenome-wide meta-analysis of DNA methylation differences in prefrontal cortex implicates the immune processes in Alzheimer's disease. <i>Nature Communications</i> , 2020, 11, 6114. | 5.8 | 75 |
| 11 | Machine learning-based estimation of cognitive performance using regional brain MRI markers: the Northern Manhattan Study. <i>Brain Imaging and Behavior</i> , 2020, 15, 1270-1278. | 1.1 | 2 |
| 12 | PathwayPCA: an R/Bioconductor Package for Pathway Based Integrative Analysis of Multi-Omics Data. <i>Proteomics</i> , 2020, 20, e1900409. | 1.3 | 8 |
| 13 | Expression of SARS-CoV-2 Entry Molecules ACE2 and TMPRSS2 in the Gut of Patients With IBD. <i>Inflammatory Bowel Diseases</i> , 2020, 26, 797-808. | 0.9 | 133 |
| 14 | Validation of serum neurofilaments as prognostic and potential pharmacodynamic biomarkers for ALS. <i>Neurology</i> , 2020, 95, e59-e69. | 1.5 | 119 |
| 15 | coMethDMR: accurate identification of co-methylated and differentially methylated regions in epigenome-wide association studies with continuous phenotypes. <i>Nucleic Acids Research</i> , 2019, 47, e98-e98. | 6.5 | 28 |
| 16 | Genome-wide brain DNA methylation analysis suggests epigenetic reprogramming in Parkinson disease. <i>Neurology: Genetics</i> , 2019, 5, e342. | 0.9 | 50 |
| 17 | RNA editing alterations in a multi-ethnic Alzheimer disease cohort converge on immune and endocytic molecular pathways. <i>Human Molecular Genetics</i> , 2019, 28, 3053-3061. | 1.4 | 19 |
| 18 | Transcriptome-wide analysis of changes in the fetal placenta associated with prenatal arsenic exposure in the New Hampshire Birth Cohort Study. <i>Environmental Health</i> , 2019, 18, 100. | 1.7 | 22 |

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|----|---|-----|-----------|
| 19 | An evaluation of supervised methods for identifying differentially methylated regions in Illumina methylation arrays. <i>Briefings in Bioinformatics</i> , 2019, 20, 2224-2235. | 3.2 | 72 |
| 20 | PathwaySplice: an R package for unbiased pathway analysis of alternative splicing in RNA-Seq data. <i>Bioinformatics</i> , 2018, 34, 3220-3222. | 1.8 | 3 |
| 21 | Identification of a five-miRNA signature for predicting the risk of tumor recurrence in patients with breast cancer. <i>International Journal of Cancer</i> , 2018, 143, 2150-2160. | 2.3 | 84 |
| 22 | miR-105: MULTIPLE ETHNIC ALZHEIMER'S DISEASE RELATED CHANGES OF RNA EDITING AFFECT IMMUNE REGULATION, ENDOCYTOSIS, AND AMYLOID PRECURSOR PROTEIN CATABOLISM. <i>Alzheimer's and Dementia</i> , 2018, 14, P609. | 0.4 | 0 |
| 23 | Data Portal for the Library of Integrated Network-based Cellular Signatures (LINCS) program: integrated access to diverse large-scale cellular perturbation response data. <i>Nucleic Acids Research</i> , 2018, 46, D558-D566. | 6.5 | 143 |
| 24 | Convergent Pathways in Idiopathic Autism Revealed by Time Course Transcriptomic Analysis of Patient-Derived Neurons. <i>Scientific Reports</i> , 2018, 8, 8423. | 1.6 | 67 |
| 25 | Network module-based model in the differential expression analysis for RNA-seq. <i>Bioinformatics</i> , 2017, 33, 2699-2705. | 1.8 | 5 |
| 26 | Arsenic Attenuates GLI Signaling, Increasing or Decreasing its Transcriptional Program in a Context-Dependent Manner. <i>Molecular Pharmacology</i> , 2016, 89, 226-232. | 1.0 | 8 |
| 27 | Gene set analysis of genome-wide association studies: Methodological issues and perspectives. <i>Genomics</i> , 2011, 98, 1-8. | 1.3 | 180 |
| 28 | Pathway-based analysis for genome-wide association studies using supervised principal components. <i>Genetic Epidemiology</i> , 2010, 34, 716-724. | 0.6 | 48 |
| 29 | Supervised principal component analysis for gene set enrichment of microarray data with continuous or survival outcomes. <i>Bioinformatics</i> , 2008, 24, 2474-2481. | 1.8 | 73 |