

Lily Wang

List of Publications by Year in descending order

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Version: 2024-02-01

29
papers

1,285
citations

567247

15
h-index

610883

24
g-index

36
all docs

36
docs citations

36
times ranked

3077
citing authors

#	ARTICLE	IF	CITATIONS
1	Gene set analysis of genome-wide association studies: Methodological issues and perspectives. <i>Genomics</i> , 2011, 98, 1-8.	2.9	180
2	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.	14.5	143
3	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.	1.9	133
4	Validation of serum neurofilaments as prognostic and potential pharmacodynamic biomarkers for ALS. <i>Neurology</i> , 2020, 95, e59-e69.	1.1	119
5	Multi-omics analysis identifies therapeutic vulnerabilities in triple-negative breast cancer subtypes. <i>Nature Communications</i> , 2021, 12, 6276.	12.8	89
6	Identification of a five-lncRNA signature for predicting the risk of tumor recurrence in patients with breast cancer. <i>International Journal of Cancer</i> , 2018, 143, 2150-2160.	5.1	84
7	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.	12.8	75
8	Supervised principal component analysis for gene set enrichment of microarray data with continuous or survival outcomes. <i>Bioinformatics</i> , 2008, 24, 2474-2481.	4.1	73
9	An evaluation of supervised methods for identifying differentially methylated regions in Illumina methylation arrays. <i>Briefings in Bioinformatics</i> , 2019, 20, 2224-2235.	6.5	72
10	Convergent Pathways in Idiopathic Autism Revealed by Time Course Transcriptomic Analysis of Patient-Derived Neurons. <i>Scientific Reports</i> , 2018, 8, 8423.	3.3	67
11	Genome-wide brain DNA methylation analysis suggests epigenetic reprogramming in Parkinson disease. <i>Neurology: Genetics</i> , 2019, 5, e342.	1.9	50
12	Pathway-based analysis for genome-wide association studies using supervised principal components. <i>Genetic Epidemiology</i> , 2010, 34, 716-724.	1.3	48
13	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.	14.5	28
14	Sex-specific DNA methylation differences in Alzheimer's disease pathology. <i>Acta Neuropathologica Communications</i> , 2021, 9, 77.	5.2	26
15	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.	4.0	22
16	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.	2.9	19
17	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.	2.3	9
18	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.	2.3	9

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19	Arsenic Attenuates GLI Signaling, Increasing or Decreasing its Transcriptional Program in a Context-Dependent Manner. <i>Molecular Pharmacology</i> , 2016, 89, 226-232.	2.3	8
20	PathwayPCA: an R/Bioconductor Package for Pathway Based Integrative Analysis of Multi-Omics Data. <i>Proteomics</i> , 2020, 20, e1900409.	2.2	8
21	MethReg: estimating the regulatory potential of DNA methylation in gene transcription. <i>Nucleic Acids Research</i> , 2022, 50, e51-e51.	14.5	8
22	Network module-based model in the differential expression analysis for RNA-seq. <i>Bioinformatics</i> , 2017, 33, 2699-2705.	4.1	5
23	PathwaySplice: an R package for unbiased pathway analysis of alternative splicing in RNA-Seq data. <i>Bioinformatics</i> , 2018, 34, 3220-3222.	4.1	3
24	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.	2.1	2
25	Genetic architecture of RNA editing regulation in Alzheimer's disease across diverse ancestral populations. <i>Human Molecular Genetics</i> , 2022, 31, 2876-2886.	2.9	2
26	O20105: MULTI-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.	0.8	0
27	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.	0.9	0
28	Sex-specific analysis of DNA methylation changes implicates new loci in Alzheimer's disease pathology. <i>Alzheimer's and Dementia</i> , 2021, 17, e049363.	0.8	0
29	Estimating the regulatory potential of DNA methylation in Alzheimer's disease. <i>Alzheimer's and Dementia</i> , 2021, 17, e049365.	0.8	0