## Lily Wang

## List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Gene set analysis of genome-wide association studies: Methodological issues and perspectives. Genomics, 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. Nucleic Acids Research, 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. Inflammatory Bowel Diseases, 2020, 26, 797-808.	1.9	133
4	Validation of serum neurofilaments as prognostic and potential pharmacodynamic biomarkers for ALS. Neurology, 2020, 95, e59-e69.	1.1	119
5	Multi-omics analysis identifies therapeutic vulnerabilities in triple-negative breast cancer subtypes. Nature Communications, 2021, 12, 6276.	12.8	89
6	ldentification of a fiveâ€IncRNA signature for predicting the risk of tumor recurrence in patients with breast cancer. International Journal of Cancer, 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. Nature Communications, 2020, 11, 6114.	12.8	75
8	Supervised principal component analysis for gene set enrichment of microarray data with continuous or survival outcomes. Bioinformatics, 2008, 24, 2474-2481.	4.1	73
9	An evaluation of supervised methods for identifying differentially methylated regions in Illumina methylation arrays. Briefings in Bioinformatics, 2019, 20, 2224-2235.	6.5	72
10	Convergent Pathways in Idiopathic Autism Revealed by Time Course Transcriptomic Analysis of Patient-Derived Neurons. Scientific Reports, 2018, 8, 8423.	3.3	67
11	Genome-wide brain DNA methylation analysis suggests epigenetic reprogramming in Parkinson disease. Neurology: Genetics, 2019, 5, e342.	1.9	50
12	Pathwayâ€based analysis for genomeâ€wide association studies using supervised principal components. Genetic Epidemiology, 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. Nucleic Acids Research, 2019, 47, e98-e98.	14.5	28
14	Sex-specific DNA methylation differences in Alzheimer's disease pathology. Acta Neuropathologica Communications, 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. Environmental Health, 2019, 18, 100.	4.0	22
16	RNA editing alterations in a multi-ethnic Alzheimer disease cohort converge on immune and endocytic molecular pathways. Human Molecular Genetics, 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. Frontiers in Genetics, 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. Frontiers in Genetics, 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. Molecular Pharmacology, 2016, 89, 226-232.	2.3	8
20	PathwayPCA: an R/Bioconductor Package for Pathway Based Integrative Analysis of Multiâ€Omics Data. Proteomics, 2020, 20, e1900409.	2.2	8
21	MethReg: estimating the regulatory potential of DNA methylation in gene transcription. Nucleic Acids Research, 2022, 50, e51-e51.	14.5	8
22	Network module-based model in the differential expression analysis for RNA-seq. Bioinformatics, 2017, 33, 2699-2705.	4.1	5
23	PathwaySplice: an R package for unbiased pathway analysis of alternative splicing in RNA-Seq data. Bioinformatics, 2018, 34, 3220-3222.	4.1	3
24	Machine learning-based estimation of cognitive performance using regional brain MRI markers: the Northern Manhattan Study. Brain Imaging and Behavior, 2020, 15, 1270-1278.	2.1	2
25	Genetic architecture of RNA editing regulation in Alzheimer's disease across diverse ancestral populations. Human Molecular Genetics, 2022, 31, 2876-2886.	2.9	2
26	O2â€01â€05: MULTIâ€ETHNIC ALZHEIMER'S DISEASE RELATED CHANGES OF RNA EDITING AFFECT IMMUNE REGULATION, ENDOCYTOSIS, AND AMYLOID PRECURSOR PROTEIN CATABOLISM. Alzheimer's and Dementia, 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. Cancer Research, 2022, 82, PD3-04-PD3-04.	0.9	0
28	Sexâ€specific analysis of DNA methylation changes implicates new loci in Alzheimer's disease pathology. Alzheimer's and Dementia, 2021, 17, e049363.	0.8	0
29	Estimating the regulatory potential of DNA methylation in Alzheimer's disease. Alzheimer's and Dementia. 2021. 17. e049365.	0.8	0