

# Jun-Hao Li

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/853800/publications.pdf>

Version: 2024-02-01

23  
papers

6,744  
citations

516710

16  
h-index

752698

20  
g-index

27  
all docs

27  
docs citations

27  
times ranked

9388  
citing authors

#	ARTICLE	IF	CITATIONS
1	Cellular and genetic drivers of RNA editing variation in the human brain. <i>Nature Communications</i> , 2022, 13, .	12.8	18
2	Single-Cell Sequencing of Brain Cell Transcriptomes and Epigenomes. <i>Neuron</i> , 2021, 109, 11-26.	8.1	135
3	Genome-wide identification of microRNA targets reveals positive regulation of the Hippo pathway by miR-122 during liver development. <i>Cell Death and Disease</i> , 2021, 12, 1161.	6.3	7
4	Using the Power of Single-Nucleus Epigenomics to Map the Molecular Complexity of the Adult Brain. <i>Biological Psychiatry</i> , 2020, 87, S61-S62.	1.3	0
5	Evolution of regulatory signatures in primate cortical neurons at cell-type resolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 28422-28432.	7.1	18
6	Inhibition of the JNK/MAPK signaling pathway by myogenesis-associated miRNAs is required for skeletal muscle development. <i>Cell Death and Differentiation</i> , 2018, 25, 1581-1597.	11.2	79
7	Environmental enrichment increases transcriptional and epigenetic differentiation between mouse dorsal and ventral dentate gyrus. <i>Nature Communications</i> , 2018, 9, 298.	12.8	106
8	A unique role for DNA (hydroxy)methylation in epigenetic regulation of human inhibitory neurons. <i>Science Advances</i> , 2018, 4, eaau6190.	10.3	92
9	Single-cell methylomes identify neuronal subtypes and regulatory elements in mammalian cortex. <i>Science</i> , 2017, 357, 600-604.	12.6	445
10	tRF2Cancer: A web server to detect tRNA-derived small RNA fragments (tRFs) and their expression in multiple cancers. <i>Nucleic Acids Research</i> , 2016, 44, W185-W193.	14.5	113
11	deepBase v2.0: identification, expression, evolution and function of small RNAs, LncRNAs and circular RNAs from deep-sequencing data. <i>Nucleic Acids Research</i> , 2016, 44, D196-D202.	14.5	203
12	RMBase: a resource for decoding the landscape of RNA modifications from high-throughput sequencing data. <i>Nucleic Acids Research</i> , 2016, 44, D259-D265.	14.5	166
13	Integrative analysis reveals clinical phenotypes and oncogenic potentials of long non-coding RNAs across 15 cancer types. <i>Oncotarget</i> , 2016, 7, 35044-35055.	1.8	17
14	MtiBase: a database for decoding microRNA target sites located within CDS and 5'UTR regions from CLIP-Seq and expression profile datasets. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav102.	3.0	23
15	StarScan: a web server for scanning small RNA targets from degradome sequencing data. <i>Nucleic Acids Research</i> , 2015, 43, W480-W486.	14.5	36
16	Conservation and divergence of transcriptional coregulations between box C/D snoRNA and ribosomal protein genes in Ascomycota. <i>Rna</i> , 2014, 20, 1376-1385.	3.5	6
17	A distinct set of long non-coding RNAs in childhood MLL-rearranged acute lymphoblastic leukemia: biology and epigenetic target. <i>Human Molecular Genetics</i> , 2014, 23, 3278-3288.	2.9	49
18	starBase v2.0: decoding miRNA-ceRNA, miRNA-ncRNA and protein-RNA interaction networks from large-scale CLIP-Seq data. <i>Nucleic Acids Research</i> , 2014, 42, D92-D97.	14.5	4,113

#	ARTICLE	IF	CITATIONS
19	Discovery of Protein-ncRNA Interactions by Integrating Large-Scale CLIP-Seq and RNA-Seq Datasets. <i>Frontiers in Bioengineering and Biotechnology</i> , 2014, 2, 88.	4.1	73
20	ChIPBase: a database for decoding the transcriptional regulation of long non-coding RNA and microRNA genes from ChIP-Seq data. <i>Nucleic Acids Research</i> , 2013, 41, D177-D187.	14.5	293
21	starBase: a database for exploring microRNA-mRNA interaction maps from Argonaute CLIP-Seq and Degradome-Seq data. <i>Nucleic Acids Research</i> , 2011, 39, D202-D209.	14.5	738
22	Genome-Wide Identification of MicroRNA Targets Reveals Positive Regulation of the Hippo Pathway by miR-122 During Liver Development. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
23	Dnmt3a knockout in excitatory neurons impairs postnatal synapse maturation and increases the repressive histone modification H3K27me3. <i>ELife</i> , 0, 11, .	6.0	10