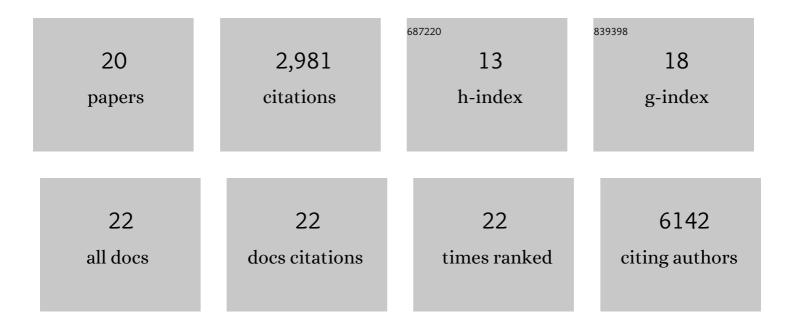
Zhi-xiang Lu

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2026538/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	rMATS: Robust and flexible detection of differential alternative splicing from replicate RNA-Seq data. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E5593-601.	3.3	1,774
2	MATS: a Bayesian framework for flexible detection of differential alternative splicing from RNA-Seq data. Nucleic Acids Research, 2012, 40, e61-e61.	6.5	330
3	m6A-LAIC-seq reveals the census and complexity of the m6A epitranscriptome. Nature Methods, 2016, 13, 692-698.	9.0	310
4	An enhanced isothermal amplification assay for viral detection. Nature Communications, 2020, 11, 5920.	5.8	117
5	Transcriptome landscape of the human placenta. BMC Genomics, 2012, 13, 115.	1.2	83
6	GLiMMPS: Robust statistical model for regulatory variation of alternative splicing using RNA-seq data. Genome Biology, 2013, 14, R74.	13.9	76
7	Transcriptome-wide Landscape of Pre-mRNA Alternative Splicing Associated with Metastatic Colonization. Molecular Cancer Research, 2015, 13, 305-318.	1.5	63
8	Genetic variation of preâ€mRNA alternative splicing in human populations. Wiley Interdisciplinary Reviews RNA, 2012, 3, 581-592.	3.2	42
9	The contribution of Alu exons to the human proteome. Genome Biology, 2016, 17, 15.	3.8	39
10	A human-specific mutation leads to the origin of a novel splice form of neuropsin (KLK8), a gene involved in learning and memory. Human Mutation, 2007, 28, 978-984.	1.1	29
11	Barcoded microbial system for high-resolution object provenance. Science, 2020, 368, 1135-1140.	6.0	27
12	Concerted effects of heterogeneous nuclear ribonucleoprotein C1/C2 to control vitamin D-directed gene transcription and RNA splicing in human bone cells. Nucleic Acids Research, 2017, 45, 606-618.	6.5	20
13	Context-dependent robustness to 5′ splice site polymorphisms in human populations. Human Molecular Genetics, 2011, 20, 1084-1096.	1.4	18
14	Discover hidden splicing variations by mapping personal transcriptomes to personal genomes. Nucleic Acids Research, 2015, 43, 10612-10622.	6.5	13
15	A Semi-Quantitative Isothermal Diagnostic Assay Utilizing Competitive Amplification. Analytical Chemistry, 2021, 93, 9541-9548.	3.2	13
16	Functional characterization of the human-specific (type II) form of kallikrein 8, a gene involved in learning and memory. Cell Research, 2009, 19, 259-267.	5.7	11
17	Species-Specific Exon Loss in Human Transcriptomes. Molecular Biology and Evolution, 2015, 32, 481-494.	3.5	7
18	Gene self-control: when pre-mRNA splicing variants become competing endogenous RNAs. Frontiers in Genetics, 2014, 5, 405.	1.1	1

#	Article	IF	CITATIONS
19	Advances in Computational Genomics. BioMed Research International, 2015, 2015, 1-2.	0.9	0
20	Genetic Control of pre-mRNA Splicing and Diseases. Enliven Journal of Genetics Molecular and Cellular Biology, 2014, 01, .	0.0	0