

Zhi-xiang Lu

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

20
papers

1,693
citations

12
h-index

22
g-index

22
ext. papers

2,482
ext. citations

13.2
avg, IF

4.34
L-index

#	Paper	IF	Citations
20	A Semi-Quantitative Isothermal Diagnostic Assay Utilizing Competitive Amplification. <i>Analytical Chemistry</i> , 2021 , 93, 9541-9548	7.8	1
19	Barcoded microbial system for high-resolution object provenance. <i>Science</i> , 2020 , 368, 1135-1140	33.3	9
18	An enhanced isothermal amplification assay for viral detection 2020 ,		6
17	An enhanced isothermal amplification assay for viral detection. <i>Nature Communications</i> , 2020 , 11, 5920	17.4	54
16	Concerted effects of heterogeneous nuclear ribonucleoprotein C1/C2 to control vitamin D-directed gene transcription and RNA splicing in human bone cells. <i>Nucleic Acids Research</i> , 2017 , 45, 606-618	20.1	9
15	The contribution of Alu exons to the human proteome. <i>Genome Biology</i> , 2016 , 17, 15	18.3	30
14	m(6)A-LAIC-seq reveals the census and complexity of the m(6)A epitranscriptome. <i>Nature Methods</i> , 2016 , 13, 692-8	21.6	211
13	Species-specific exon loss in human transcriptomes. <i>Molecular Biology and Evolution</i> , 2015 , 32, 481-94	8.3	6
12	Transcriptome-wide landscape of pre-mRNA alternative splicing associated with metastatic colonization. <i>Molecular Cancer Research</i> , 2015 , 13, 305-18	6.6	44
11	Discover hidden splicing variations by mapping personal transcriptomes to personal genomes. <i>Nucleic Acids Research</i> , 2015 , 43, 10612-22	20.1	12
10	Gene self-control: when pre-mRNA splicing variants become competing endogenous RNAs. <i>Frontiers in Genetics</i> , 2014 , 5, 405	4.5	1
9	rMATS: robust and flexible detection of differential alternative splicing from replicate RNA-Seq data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, E5593-601	11.5	857
8	GLiMMPS: robust statistical model for regulatory variation of alternative splicing using RNA-seq data. <i>Genome Biology</i> , 2013 , 14, R74	18.3	60
7	Transcriptome landscape of the human placenta. <i>BMC Genomics</i> , 2012 , 13, 115	4.5	65
6	Genetic variation of pre-mRNA alternative splicing in human populations. <i>Wiley Interdisciplinary Reviews RNA</i> , 2012 , 3, 581-92	9.3	37
5	MATS: a Bayesian framework for flexible detection of differential alternative splicing from RNA-Seq data. <i>Nucleic Acids Research</i> , 2012 , 40, e61	20.1	240
4	Context-dependent robustness to 5bsplice site polymorphisms in human populations. <i>Human Molecular Genetics</i> , 2011 , 20, 1084-96	5.6	18

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| 3 | Functional characterization of the human-specific (type II) form of kallikrein 8, a gene involved in learning and memory. <i>Cell Research</i> , 2009 , 19, 259-67 | 24-7 | 9 |
| 2 | A human-specific mutation leads to the origin of a novel splice form of neuropsin (KLK8), a gene involved in learning and memory. <i>Human Mutation</i> , 2007 , 28, 978-84 | 4-7 | 23 |
| 1 | Forensic microbial system for high-resolution object provenance | | 1 |