

Zhe Ji

List of Publications by Year in descending order

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Version: 2024-02-01

33
papers

3,428
citations

279798

23
h-index

395702

33
g-index

40
all docs

40
docs citations

40
times ranked

4857
citing authors

#	ARTICLE	IF	CITATIONS
1	Progressive lengthening of 3' untranslated regions of mRNAs by alternative polyadenylation during mouse embryonic development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 7028-7033.	7.1	545
2	Many lncRNAs, 5' UTRs, and pseudogenes are translated and some are likely to express functional proteins. <i>ELife</i> , 2015, 4, e08890.	6.0	439
3	Analysis of alternative cleavage and polyadenylation by 3' region extraction and deep sequencing. <i>Nature Methods</i> , 2013, 10, 133-139.	19.0	386
4	Reprogramming of 3' Untranslated Regions of mRNAs by Alternative Polyadenylation in Generation of Pluripotent Stem Cells from Different Cell Types. <i>PLoS ONE</i> , 2009, 4, e8419.	2.5	245
5	Systematic Profiling of Poly(A) ⁺ Transcripts Modulated by Core 3' End Processing and Splicing Factors Reveals Regulatory Rules of Alternative Cleavage and Polyadenylation. <i>PLoS Genetics</i> , 2015, 11, e1005166.	3.5	217
6	Selectivity of ORC binding sites and the relation to replication timing, fragile sites, and deletions in cancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E4810-9.	7.1	164
7	Inflammatory regulatory network mediated by the joint action of NF- κ B, STAT3, and AP-1 factors is involved in many human cancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 9453-9462.	7.1	147
8	Unannotated proteins expand the MHC-I-restricted immunopeptidome in cancer. <i>Nature Biotechnology</i> , 2022, 40, 209-217.	17.5	127
9	Transcriptional activity regulates alternative cleavage and polyadenylation. <i>Molecular Systems Biology</i> , 2011, 7, 534.	7.2	111
10	Alternative to the soft-agar assay that permits high-throughput drug and genetic screens for cellular transformation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 5708-5713.	7.1	105
11	Phylogenetic analysis of mRNA polyadenylation sites reveals a role of transposable elements in evolution of the 3'-end of genes. <i>Nucleic Acids Research</i> , 2008, 36, 5581-5590.	14.5	100
12	Genome-wide identification and differential analysis of translational initiation. <i>Nature Communications</i> , 2017, 8, 1749.	12.8	100
13	Comprehensive comparative analysis of 5'-end RNA-sequencing methods. <i>Nature Methods</i> , 2018, 15, 505-511.	19.0	90
14	Noncanonical open reading frames encode functional proteins essential for cancer cell survival. <i>Nature Biotechnology</i> , 2021, 39, 697-704.	17.5	85
15	Analysis of <i>C. elegans</i> intestinal gene expression and polyadenylation by fluorescence-activated nuclei sorting and 3'-end-seq. <i>Nucleic Acids Research</i> , 2012, 40, 6304-6318.	14.5	69
16	Star-PAP Control of BIK Expression and Apoptosis Is Regulated by Nuclear PIPKII α and PKC δ Signaling. <i>Molecular Cell</i> , 2012, 45, 25-37.	9.7	57
17	A PRC2-independent function for EZH2 in regulating rRNA 2'-O methylation and IRES-dependent translation. <i>Nature Cell Biology</i> , 2021, 23, 341-354.	10.3	54
18	Transcriptome-scale RNase-footprinting of RNA-protein complexes. <i>Nature Biotechnology</i> , 2016, 34, 410-413.	17.5	49

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19	LINC00520 is induced by Src, STAT3, and PI3K and plays a functional role in breast cancer. <i>Oncotarget</i> , 2016, 7, 81981-81994.	1.8	48
20	The Conserved Intronic Cleavage and Polyadenylation Site of CstF-77 Gene Imparts Control of 3' End Processing Activity through Feedback Autoregulation and by U1 snRNP. <i>PLoS Genetics</i> , 2013, 9, e1003613.	3.5	44
21	RibORF: Identifying Genome-Wide Translated Open Reading Frames Using Ribosome Profiling. <i>Current Protocols in Molecular Biology</i> , 2018, 124, e67.	2.9	33
22	Distinct regulation of alternative polyadenylation and gene expression by nuclear poly(A) polymerases. <i>Nucleic Acids Research</i> , 2017, 45, 8930-8942.	14.5	31
23	The β ,CstF-64 Polyadenylation Protein Controls Genome Expression in Testis. <i>PLoS ONE</i> , 2012, 7, e48373.	2.5	26
24	Genome-scale identification of transcription factors that mediate an inflammatory network during breast cellular transformation. <i>Nature Communications</i> , 2018, 9, 2068.	12.8	24
25	Antibody targeting tumor-derived soluble NKG2D ligand sMIC reprograms NK cell homeostatic survival and function and enhances melanoma response to PDL1 blockade therapy. <i>Journal of Hematology and Oncology</i> , 2020, 13, 74.	17.0	17
26	Low-input RNase footprinting for simultaneous quantification of cytosolic and mitochondrial translation. <i>Genome Research</i> , 2022, 32, 545-557.	5.5	15
27	Mapping 3' mRNA Isoforms on a Genomic Scale. <i>Current Protocols in Molecular Biology</i> , 2015, 110, 4.23.1-4.23.17.	2.9	14
28	Transcription termination between polo and snap, two closely spaced tandem genes of <i>D. melanogaster</i> . <i>Transcription</i> , 2012, 3, 198-212.	3.1	13
29	Tumor-derived NKG2D ligand sMIC reprograms NK cells to an inflammatory phenotype through CBM signalosome activation. <i>Communications Biology</i> , 2021, 4, 905.	4.4	10
30	CD95/Fas protects triple negative breast cancer from anti-tumor activity of NK cells. <i>iScience</i> , 2021, 24, 103348.	4.1	10
31	Rfoot: Transcriptome-scale Identification of RNA-Protein Complexes from Ribosome Profiling Data. <i>Current Protocols in Molecular Biology</i> , 2018, 124, e66.	2.9	8
32	Spike-in normalization for single-cell RNA-seq reveals dynamic global transcriptional activity mediating anticancer drug response. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab054.	3.2	5
33	TBIO-26. NON-CANONICAL OPEN READING FRAMES ENCODE FUNCTIONAL PROTEINS ESSENTIAL FOR CANCER CELL SURVIVAL. <i>Neuro-Oncology</i> , 2020, 22, iii471-iii471.	1.2	0