

Zhe Ji

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3262140/publications.pdf>

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 | Unannotated proteins expand the MHC-I-restricted immunopeptidome in cancer. <i>Nature Biotechnology</i> , 2022, 40, 209-217. | 17.5 | 127 |
| 2 | Low-input RNase footprinting for simultaneous quantification of cytosolic and mitochondrial translation. <i>Genome Research</i> , 2022, 32, 545-557. | 5.5 | 15 |
| 3 | Noncanonical open reading frames encode functional proteins essential for cancer cell survival. <i>Nature Biotechnology</i> , 2021, 39, 697-704. | 17.5 | 85 |
| 4 | 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 |
| 5 | A PRC2-independent function for EZH2 in regulating rRNA 2â€²-O methylation and IRES-dependent translation. <i>Nature Cell Biology</i> , 2021, 23, 341-354. | 10.3 | 54 |
| 6 | 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 |
| 7 | CD95/Fas protects triple negative breast cancer from anti-tumor activity of NK cells. <i>IScience</i> , 2021, 24, 103348. | 4.1 | 10 |
| 8 | 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 |
| 9 | 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 |
| 10 | 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 |
| 11 | 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 |
| 12 | RibORF: Identifying Genome-wide Translated Open Reading Frames Using Ribosome Profiling. <i>Current Protocols in Molecular Biology</i> , 2018, 124, e67. | 2.9 | 33 |
| 13 | 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 |
| 14 | Comprehensive comparative analysis of 5â€²-end RNA-sequencing methods. <i>Nature Methods</i> , 2018, 15, 505-511. | 19.0 | 90 |
| 15 | 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 |
| 16 | Genome-wide identification and differential analysis of translational initiation. <i>Nature Communications</i> , 2017, 8, 1749. | 12.8 | 100 |
| 17 | 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 |
| 18 | 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 |

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 19 | Transcriptome-scale RNase-footprinting of RNA-protein complexes. <i>Nature Biotechnology</i> , 2016, 34, 410-413. | 17.5 | 49 |
| 20 | 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 |
| 21 | 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 |
| 22 | 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 |
| 23 | 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 |
| 24 | Analysis of alternative cleavage and polyadenylation by 3' region extraction and deep sequencing. <i>Nature Methods</i> , 2013, 10, 133-139. | 19.0 | 386 |
| 25 | 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 |
| 26 | 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 |
| 27 | Star-PAP Control of BIK Expression and Apoptosis Is Regulated by Nuclear PIPK β and PKC ζ Signaling. <i>Molecular Cell</i> , 2012, 45, 25-37. | 9.7 | 57 |
| 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 | The β ,CstF-64 Polyadenylation Protein Controls Genome Expression in Testis. <i>PLoS ONE</i> , 2012, 7, e48373. | 2.5 | 26 |
| 30 | Transcriptional activity regulates alternative cleavage and polyadenylation. <i>Molecular Systems Biology</i> , 2011, 7, 534. | 7.2 | 111 |
| 31 | 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 |
| 32 | 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 |
| 33 | 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 |