

Ji Wan

List of Publications by Year in descending order

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Version: 2024-02-01

26
papers

3,154
citations

430874

18
h-index

552781

26
g-index

26
all docs

26
docs citations

26
times ranked

5243
citing authors

#	ARTICLE	IF	CITATIONS
1	MATHLA: a robust framework for HLA-peptide binding prediction integrating bidirectional LSTM and multiple head attention mechanism. BMC Bioinformatics, 2021, 22, 7.	2.6	11
2	Relaxed initiation pausing of ribosomes drives oncogenic translation. Science Advances, 2021, 7, .	10.3	7
3	Chromogranin A pathway: from pathogenic molecule to renal disease. Journal of Hypertension, 2020, 38, 456-466.	0.5	3
4	Clustering single-cell RNA-seq data with a model-based deep learning approach. Nature Machine Intelligence, 2019, 1, 191-198.	16.0	189
5	SEN3-mediated host defense response contains HBV replication and restores protein synthesis. PLoS ONE, 2019, 14, e0209179.	2.5	7
6	N6-Methyladenosine Guides mRNA Alternative Translation during Integrated Stress Response. Molecular Cell, 2018, 69, 636-647.e7.	9.7	215
7	A Comprehensive Survey of Immune Cytolytic Activity-Associated Gene Co-Expression Networks across 17 Tumor and Normal Tissue Types. Cancers, 2018, 10, 307.	3.7	4
8	A Coding Sequence-Embedded Principle Governs Translational Reading Frame Fidelity. Research, 2018, 2018, 7089174.	5.7	4
9	m6A Facilitates eIF4F-Independent mRNA Translation. Molecular Cell, 2017, 68, 504-514.e7.	9.7	197
10	Competition between translation initiation factor eIF5 and its mimic protein 5MP determines non-AUG initiation rate genome-wide. Nucleic Acids Research, 2017, 45, 11941-11953.	14.5	63
11	Codon optimality controls differential mRNA translation during amino acid starvation. Rna, 2016, 22, 1719-1727.	3.5	47
12	Genome-Wide Profiling of Alternative Translation Initiation Sites. Methods in Molecular Biology, 2016, 1358, 303-316.	0.9	6
13	Dynamic m6A mRNA methylation directs translational control of heat shock response. Nature, 2015, 526, 591-594.	27.8	990
14	Quantitative profiling of initiating ribosomes in vivo. Nature Methods, 2015, 12, 147-153.	19.0	222
15	TISdb: a database for alternative translation initiation in mammalian cells. Nucleic Acids Research, 2014, 42, D845-D850.	14.5	84
16	Fip1 regulates mRNA alternative polyadenylation to promote stem cell self-renewal. EMBO Journal, 2014, 33, 878-889.	7.8	136
17	Human-specific microRNA regulation of FOXO1: implications for microRNA recognition element evolution. Human Molecular Genetics, 2014, 23, 2593-2603.	2.9	19
18	Ribosome profiling reveals sequence-independent post-initiation pausing as a signature of translation. Cell Research, 2014, 24, 842-851.	12.0	48

#	ARTICLE	IF	CITATIONS
19	CP Poly(C) Binding Proteins Act as Global Regulators of Alternative Polyadenylation. <i>Molecular and Cellular Biology</i> , 2013, 33, 2560-2573.	2.3	40
20	Overlapping and distinct functions of CstF64 and CstF64 β , in mammalian mRNA 3' processing. <i>Rna</i> , 2013, 19, 1781-1790.	3.5	59
21	Genome-Wide Determination of a Broad ESRP-Regulated Posttranscriptional Network by High-Throughput Sequencing. <i>Molecular and Cellular Biology</i> , 2012, 32, 1468-1482.	2.3	127
22	Transcriptome-wide analyses of CstF64-RNA interactions in global regulation of mRNA alternative polyadenylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 18773-18778.	7.1	194
23	Structure and activity of putative intronic miRNA promoters. <i>Rna</i> , 2010, 16, 495-505.	3.5	313
24	Meta-prediction of phosphorylation sites with weighted voting and restricted grid search parameter selection. <i>Nucleic Acids Research</i> , 2008, 36, e22-e22.	14.5	64
25	In Silico Prediction of Peptide-MHC Binding Affinity Using SVRMHC. <i>Methods in Molecular Biology</i> , 2007, 409, 283-291.	0.9	12
26	SVRMHC prediction server for MHC-binding peptides. <i>BMC Bioinformatics</i> , 2006, 7, 463.	2.6	93