

Yi Zhang

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7677006/publications.pdf>

Version: 2024-02-01

45
papers

2,332
citations

331670

21
h-index

289244

40
g-index

48
all docs

48
docs citations

48
times ranked

3969
citing authors

#	ARTICLE	IF	CITATIONS
1	Direct Conversion of Fibroblasts to Neurons by Reprogramming PTB-Regulated MicroRNA Circuits. <i>Cell</i> , 2013, 152, 82-96.	28.9	508
2	Genome-wide Analysis of PTB-RNA Interactions Reveals a Strategy Used by the General Splicing Repressor to Modulate Exon Inclusion or Skipping. <i>Molecular Cell</i> , 2009, 36, 996-1006.	9.7	429
3	Nuclear Matrix Factor hnRNP U/SAF-A Exerts a Global Control of Alternative Splicing by Regulating U2 snRNP Maturation. <i>Molecular Cell</i> , 2012, 45, 656-668.	9.7	146
4	The FOXN3-NEAT1-SIN3A repressor complex promotes progression of hormonally responsive breast cancer. <i>Journal of Clinical Investigation</i> , 2017, 127, 3421-3440.	8.2	146
5	Cyclin-dependent Kinase 1 (CDK1)-mediated Phosphorylation of Enhancer of Zeste 2 (Ezh2) Regulates Its Stability. <i>Journal of Biological Chemistry</i> , 2011, 286, 28511-28519.	3.4	117
6	Annotation and cluster analysis of spatiotemporal- and sex-related lncRNA expression in rhesus macaque brain. <i>Genome Research</i> , 2017, 27, 1608-1620.	5.5	113
7	CELF1 preferentially binds to exon-intron boundary and regulates alternative splicing in HeLa cells. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2017, 1860, 911-921.	1.9	111
8	A comparison of the low temperature transcriptomes of two tomato genotypes that differ in freezing tolerance: <i>Solanum lycopersicum</i> and <i>Solanum habrochaites</i> . <i>BMC Plant Biology</i> , 2015, 15, 132.	3.6	77
9	Transcriptome analysis reveals the complexity of alternative splicing regulation in the fungus <i>Verticillium dahliae</i> . <i>BMC Genomics</i> , 2017, 18, 130.	2.8	71
10	hnRNPD L extensively regulates transcription and alternative splicing. <i>Gene</i> , 2019, 687, 125-134.	2.2	45
11	Comparative study on seasonal hair follicle cycling by analysis of the transcriptomes from cashmere and milk goats. <i>Genomics</i> , 2020, 112, 332-345.	2.9	44
12	A novel antiviral lncRNA, EDAL, shields a T309 O-GlcNAcylation site to promote EZH2 lysosomal degradation. <i>Genome Biology</i> , 2020, 21, 228.	8.8	38
13	The dynamics of FTO binding and demethylation from the m ⁶ A motifs. <i>RNA Biology</i> , 2019, 16, 1179-1189.	3.1	36
14	Tristetraprolin specifically regulates the expression and alternative splicing of immune response genes in HeLa cells. <i>BMC Immunology</i> , 2019, 20, 13.	2.2	34
15	MicroRNA-transcription factor network analysis reveals miRNAs cooperatively suppress RORA in oral squamous cell carcinoma. <i>Oncogenesis</i> , 2018, 7, 79.	4.9	29
16	Transcriptome profiling reveals transcriptional and alternative splicing regulation in the early embryonic development of hair follicles in the cashmere goat. <i>Scientific Reports</i> , 2019, 9, 17735.	3.3	29
17	Concerted folding of a <i>Candida</i> ribozyme into the catalytically active structure posterior to a rapid RNA compaction. <i>Nucleic Acids Research</i> , 2003, 31, 3901-3908.	14.5	26
18	CRKL regulates alternative splicing of cancer-related genes in cervical cancer samples and HeLa cell. <i>BMC Cancer</i> , 2019, 19, 499.	2.6	26

#	ARTICLE	IF	CITATIONS
19	Poly(A)-seq: A method for direct sequencing and analysis of the transcriptomic poly(A)-tails. <i>PLoS ONE</i> , 2020, 15, e0234696.	2.5	24
20	A draft genome assembly of halophyte <i>Suaeda aralocaspica</i> , a plant that performs C4 photosynthesis within individual cells. <i>GigaScience</i> , 2019, 8, .	6.4	23
21	Transcriptome analysis reveals downregulation of virulence-associated genes expression in a low virulence <i>Verticillium dahliae</i> strain. <i>Archives of Microbiology</i> , 2019, 201, 927-941.	2.2	23
22	Regulation of splicing enhancer activities by RNA secondary structures. <i>FEBS Letters</i> , 2010, 584, 4401-4407.	2.8	21
23	Chromatin modifier MTA1 regulates mitotic transition and tumorigenesis by orchestrating mitotic mRNA processing. <i>Nature Communications</i> , 2020, 11, 4455.	12.8	20
24	The susceptibility of sea-island cotton recombinant inbred lines to <i>Fusarium oxysporum</i> f. sp. <i>vasinfectum</i> infection is characterized by altered expression of long noncoding RNAs. <i>Scientific Reports</i> , 2019, 9, 2894.	3.3	19
25	Genome-wide identification of AGO18b-bound miRNAs and phasiRNAs in maize by cRIP-seq. <i>BMC Genomics</i> , 2019, 20, 656.	2.8	18
26	A structured RNA in hepatitis B virus post-transcriptional regulatory element represses alternative splicing in a sequence-independent and position-dependent manner. <i>FEBS Journal</i> , 2011, 278, 1533-1546.	4.7	16
27	DDX41 regulates the expression and alternative splicing of genes involved in tumorigenesis and immune response. <i>Oncology Reports</i> , 2021, 45, 1213-1225.	2.6	16
28	EIF2AK2 selectively regulates the gene transcription in immune response and histones associated with systemic lupus erythematosus. <i>Molecular Immunology</i> , 2021, 132, 132-141.	2.2	15
29	Galectin-RNA interaction map reveals potential regulatory roles in angiogenesis. <i>FEBS Letters</i> , 2021, 595, 623-636.	2.8	13
30	Tristetraprolin-RNA interaction map reveals a novel TTP-RelB regulatory network for innate immunity gene expression. <i>Molecular Immunology</i> , 2020, 121, 59-71.	2.2	12
31	Genome-wide identification of Hami melon miRNAs with putative roles during fruit development. <i>PLoS ONE</i> , 2017, 12, e0180600.	2.5	11
32	Cytokeratin 18 regulates the transcription and alternative splicing of apoptotic-related genes and pathways in HeLa cells. <i>Oncology Reports</i> , 2019, 42, 301-312.	2.6	11
33	SUVA: splicing site usage variation analysis from RNA-seq data reveals highly conserved complex splicing biomarkers in liver cancer. <i>RNA Biology</i> , 2021, 18, 157-171.	3.1	11
34	RBM4 modulates the proliferation and expression of inflammatory factors via the alternative splicing of regulatory factors in HeLa cells. <i>Molecular Genetics and Genomics</i> , 2020, 295, 95-106.	2.1	10
35	MACF1 promotes osteoblast differentiation by sequestering repressors in cytoplasm. <i>Cell Death and Differentiation</i> , 2021, 28, 2160-2178.	11.2	9
36	Comparison of lncRNA and mRNA expression in mouse brains infected by a wild-type and a lab-attenuated Rabies lyssavirus. <i>Journal of General Virology</i> , 2021, 102, .	2.9	8

#	ARTICLE	IF	CITATIONS
37	Hfq Globally Binds and Destabilizes sRNAs and mRNAs in <i>Yersinia pestis</i> . <i>MSystems</i> , 2019, 4, .	3.8	7
38	Protective Role of microRNA-31 in Acetaminophen-Induced Liver Injury: A Negative Regulator of c-Jun N-Terminal Kinase (JNK) Signaling Pathway. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2021, 12, 1789-1807.	4.5	6
39	Repression of the expression of proinflammatory genes by mitochondrial transcription factor A is linked to its alternative splicing regulation in human lung epithelial cells. <i>BMC Immunology</i> , 2021, 22, 74.	2.2	4
40	Attenuated Duck Hepatitis A Virus Infection Is Associated With High mRNA Maintenance in Duckling Liver via m6A Modification. <i>Frontiers in Immunology</i> , 0, 13, .	4.8	4
41	TCTP participates in hepatic metabolism by regulating gene expression involved in insulin resistance. <i>Gene</i> , 2021, 768, 145263.	2.2	3
42	Activation of the intronic cryptic 5' splice site depends on its distance to the upstream cassette exon. <i>Gene</i> , 2017, 619, 30-36.	2.2	1
43	Sex-Specific Development in Haplodiploid Honeybee is Controlled by the Female-Embryo-Specific Activation of Thousands of Intronic lncRNAs. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
44	Sex-Specific Development in Haplodiploid Honeybee Is Controlled by the Female-Embryo-Specific Activation of Thousands of Intronic lncRNAs. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 690167.	3.7	0
45	Two novel RNA-binding proteins identification through computational prediction and experimental validation. <i>Genomics</i> , 2022, 114, 149-160.	2.9	0