Jian-Hua Yang

List of Publications by Year
in descending order

56 papers	11,512 citations	159585 30 h-index	144013 57 g-index
61 all docs	61 docs citations	61 times ranked	13790 citing authors

#	Article	IF	Citations
1	starBase v2.0: decoding miRNA-ceRNA, miRNA-ncRNA and protein–RNA interaction networks from large-scale CLIP-Seq data. Nucleic Acids Research, 2014, 42, D92-D97.	14.5	4,113
2	Recognition of RNA N6-methyladenosine by IGF2BP proteins enhances mRNA stability and translation. Nature Cell Biology, 2018, 20, 285-295.	10.3	1,650
3	METTL14 Inhibits Hematopoietic Stem/Progenitor Differentiation and Promotes Leukemogenesis via mRNA m6A Modification. Cell Stem Cell, 2018, 22, 191-205.e9.	11.1	749
4	starBase: a database for exploring microRNA–mRNA interaction maps from Argonaute CLIP-Seq and Degradome-Seq data. Nucleic Acids Research, 2011, 39, D202-D209.	14.5	738
5	Histone H3 trimethylation at lysine 36 guides m6A RNA modification co-transcriptionally. Nature, 2019, 567, 414-419.	27.8	452
6	Pachytene piRNAs instruct massive mRNA elimination during late spermiogenesis. Cell Research, 2014, 24, 680-700.	12.0	344
7	RMBase v2.0: deciphering the map of RNA modifications from epitranscriptome sequencing data. Nucleic Acids Research, 2018, 46, D327-D334.	14.5	327
8	ChIPBase: a database for decoding the transcriptional regulation of long non-coding RNA and microRNA genes from ChIP-Seq data. Nucleic Acids Research, 2013, 41, D177-D187.	14.5	293
9	ChIPBase v2.0: decoding transcriptional regulatory networks of non-coding RNAs and protein-coding genes from ChIP-seq data. Nucleic Acids Research, 2017, 45, D43-D50.	14.5	228
10	deepBase v2.0: identification, expression, evolution and function of small RNAs, LncRNAs and circular RNAs from deep-sequencing data. Nucleic Acids Research, 2016, 44, D196-D202.	14.5	203
11	Capturing the interactome of newly transcribed RNA. Nature Methods, 2018, 15, 213-220.	19.0	170
12	RMBase: a resource for decoding the landscape of RNA modifications from high-throughput sequencing data. Nucleic Acids Research, 2016, 44, D259-D265.	14.5	166
13	Comprehensive Genomic Characterization of RNA-Binding Proteins across Human Cancers. Cell Reports, 2018, 22, 286-298.	6.4	166
14	Prognostic Value of a Long Non-coding RNA Signature in Localized Clear Cell Renal Cell Carcinoma. European Urology, 2018, 74, 756-763.	1.9	144
15	deepBase: a database for deeply annotating and mining deep sequencing data. Nucleic Acids Research, 2010, 38, D123-D130.	14.5	141
16	tRF2Cancer: A web server to detect tRNA-derived small RNA fragments (tRFs) and their expression in multiple cancers. Nucleic Acids Research, 2016, 44, W185-W193.	14.5	113
17	snoSeeker: an advanced computational package for screening of guide and orphan snoRNA genes in the human genome. Nucleic Acids Research, 2006, 34, 5112-5123.	14.5	112
18	Oridonin induces autophagy via inhibition of glucose metabolism in p53-mutated colorectal cancer cells. Cell Death and Disease, 2017, 8, e2633-e2633.	6.3	91

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19	Pathophysiological Responses in Rat and Mouse Models of Radiation-Induced Brain Injury. Molecular Neurobiology, 2017, 54, 1022-1032.	4.0	86
20	Interplay of m^{6}A and H3K27 trimethylation restrains inflammation during bacterial infection. Science Advances, 2020, 6, eaba0647.	10.3	85
21	Inhibition of the JNK/MAPK signaling pathway by myogenesis-associated miRNAs is required for skeletal muscle development. Cell Death and Differentiation, 2018, 25, 1581-1597.	11.2	79
22	Discovery of ProteinÃ¢â¬â€œlncRNA Interactions by Integrating Large-Scale CLIP-Seq and RNA-Seq Datasets. Frontiers in Bioengineering and Biotechnology, 2014, 2, 88.	4.1	73
23	Long non-coding RNAs link extracellular matrix gene expression to ischemic cardiomyopathy. Cardiovascular Research, 2016, 112, 543-554.	3.8	64
24	dreamBase: DNA modification, RNA regulation and protein binding of expressed pseudogenes in human health and disease. Nucleic Acids Research, 2018, 46, D85-D91.	14.5	62
25	miRâ€372 and miRâ€373 enhance the stemness of colorectal cancer cells by repressing differentiation signaling pathways. Molecular Oncology, 2018, 12, 1949-1964.	4.6	62
26	Insufficient Radiofrequency Ablation Promotes Hepatocellular Carcinoma Metastasis Through N6â€Methyladenosine mRNA Methylationâ€Dependent Mechanism. Hepatology, 2021, 74, 1339-1356.	7.3	62
27	Wnt/Î²-catenin pathway transactivates microRNA-150 that promotes EMT of colorectal cancer cells by suppressing CREB signaling. Oncotarget, 0, 7, 42513-42526.	1.8	55
28	Systematic calibration of epitranscriptomic maps using a synthetic modification-free RNA library. Nature Methods, 2021, 18, 1213-1222.	19.0	44
29	LARP7-Mediated U6 snRNA Modification Ensures Splicing Fidelity and Spermatogenesis in Mice. Molecular Cell, 2020, 77, 999-1013.e6.	9.7	41
30	StarScan: a web server for scanning small RNA targets from degradome sequencing data. Nucleic Acids Research, 2015, 43, W480-W486.	14.5	36
31	Ribosome profiling analysis identified a KRAS-interacting microprotein that represses oncogenic signaling in hepatocellular carcinoma cells. Science China Life Sciences, 2020, 63, 529-542.	4.9	36
32	IL-37 Is a Novel Proangiogenic Factor of Developmental and Pathological Angiogenesis. Arteriosclerosis, Thrombosis, and Vascular Biology, 2015, 35, 2638-2646.	2.4	35
33	MicroRNA-122 supports robust innate immunity in hepatocytes by targeting the RTKs/STAT3 signaling pathway. ELife, 2019, 8, .	6.0	32
34	Cryptotanshinone suppresses key onco-proliferative and drug-resistant pathways of chronic myeloid leukemia by targeting STAT5 and STAT3 phosphorylation. Science China Life Sciences, 2018, 61, 999-1009.	4.9	30
35	deepBase v3.0: expression atlas and interactive analysis of ncRNAs from thousands of deep-sequencing data. Nucleic Acids Research, 2021, 49, D877-D883.	14.5	29
36	An LTR retrotransposonâ€derived lnc RNA interacts with RNF169 to promote homologous recombination. EMBO Reports, 2019, 20, e47650.	4.5	28

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37	Classification and function of <scp>RNA</scp>â€"protein interactions. Wiley Interdisciplinary Reviews RNA, 2020, 11, e1601.	6.4	26
38	tsRFun: a comprehensive platform for decoding human tsRNA expression, functions and prognostic value by high-throughput small RNA-Seq and CLIP-Seq data. Nucleic Acids Research, 2022, 50, D421-D431.	14.5	26
39	The cardiac translational landscape reveals that micropeptides are new players involved in cardiomyocyte hypertrophy. Molecular Therapy, 2021, 29, 2253-2267.	8.2	24
40	MtiBase: a database for decoding microRNA target sites located within CDS and 5â€²UTR regions from CLIP-Seq and expression profile datasets. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav102.	3.0	23
41	Discovering circRNA-microRNA Interactions from CLIP-Seq Data. Methods in Molecular Biology, 2018, 1724, 193-207.	0.9	23
42	deepBase: Annotation and Discovery of MicroRNAs and Other Noncoding RNAs from Deep-Sequencing Data. Methods in Molecular Biology, 2012, 822, 233-248.	0.9	21
43	Spatial-temporal transcriptional dynamics of long non-coding RNAs in human brain. Human Molecular Genetics, 2017, 26, 3202-3211.	2.9	20
44	Rapid Birth-and-Death Evolution of Imprinted snoRNAs in the Prader-Willi Syndrome Locus: Implications for Neural Development in Euarchontoglires. PLoS ONE, 2014, 9, e100329.	2.5	19
45	CREB1 contributes colorectal cancer cell plasticity by regulating lncRNA CCAT1 and NF-Î°B pathways. Science China Life Sciences, 2022, 65, 1481-1497.	4.9	18
46	Integrative analysis reveals clinical phenotypes and oncogenic potentials of long non-coding RNAs across 15 cancer types. Oncotarget, 2016, 7, 35044-35055.	1.8	17
47	Epitranscriptomic technologies and analyses. Science China Life Sciences, 2020, 63, 501-515.	4.9	12
48	A Contig-Based Strategy for the Genome-Wide Discovery of MicroRNAs without Complete Genome Resources. PLoS ONE, 2014, 9, e88179.	2.5	11
49	TP53-inducible putative long noncoding RNAs encode functional polypeptides that suppress cell proliferation. Genome Research, 2022, 32, 1026-1041.	5.5	11
50	ColorCells: a database of expression, classification and functions of lncRNAs in single cells. Briefings in Bioinformatics, 2021, 22, .	6.5	8
51	The functional analysis of transiently upregulated miR-101 suggests a â€œbrakingâ€•regulatory mechanism during myogenesis. Science China Life Sciences, 2021, 64, 1612-1623.	4.9	7
52	Genome-wide identification of microRNA targets reveals positive regulation of the Hippo pathway by miR-122 during liver development. Cell Death and Disease, 2021, 12, 1161.	6.3	7
53	Exo-miRExplorer: A Comprehensive Resource for Exploring and Comparatively Analyzing Exogenous MicroRNAs. Frontiers in Microbiology, 2017, 8, 126.	3.5	6
54	Decoding the Atlas of RNA Modifications from Epitranscriptome Sequencing Data. Methods in Molecular Biology, 2019, 1870, 107-124.	0.9	6

#	Article	IF	Citations
55	Pol3Base: a resource for decoding the interactome, expression, evolution, epitranscriptome and disease variations of Pol III-transcribed ncRNAs. Nucleic Acids Research, 2022, 50, D279-D286.	14.5	6
56	oncoNcRNA: A Web Portal for Exploring the Non-Coding RNAs with Oncogenic Potentials in Human Cancers. Non-coding RNA, 2017, 3, 7.	2.6	4