

Liang-Hu Qu

List of Publications by Year in descending order

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69
papers

9,903
citations

196777

29
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107981

68
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74
all docs

74
docs citations

74
times ranked

13836
citing authors

#	ARTICLE	IF	CITATIONS
1	tsRFun: a comprehensive platform for decoding human tsRNA expression, functions and prognostic value by high-throughput small RNA-Seq and CLIP-Seq data. <i>Nucleic Acids Research</i> , 2022, 50, D421-D431.	6.5	26
2	Pol3Base: a resource for decoding the interactome, expression, evolution, epitranscriptome and disease variations of Pol III-transcribed ncRNAs. <i>Nucleic Acids Research</i> , 2022, 50, D279-D286.	6.5	6
3	Integrated Analysis Reveals the Characteristics and Effects of SARS-CoV-2 Maternal-Fetal Transmission. <i>Frontiers in Microbiology</i> , 2022, 13, 813187.	1.5	3
4	SARS-CoV-2 causes a significant stress response mediated by small RNAs in the blood of COVID-19 patients. <i>Molecular Therapy - Nucleic Acids</i> , 2022, 27, 751-762.	2.3	12
5	TP53-inducible putative long noncoding RNAs encode functional polypeptides that suppress cell proliferation. <i>Genome Research</i> , 2022, 32, 1026-1041.	2.4	11
6	ColorCells: a database of expression, classification and functions of lncRNAs in single cells. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	8
7	deepBase v3.0: expression atlas and interactive analysis of ncRNAs from thousands of deep-sequencing data. <i>Nucleic Acids Research</i> , 2021, 49, D877-D883.	6.5	29
8	The functional analysis of transiently upregulated miR-101 suggests a "braking" regulatory mechanism during myogenesis. <i>Science China Life Sciences</i> , 2021, 64, 1612-1623.	2.3	7
9	PERK Signaling Controls Myoblast Differentiation by Regulating MicroRNA Networks. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 670435.	1.8	11
10	The cardiac translational landscape reveals that micropeptides are new players involved in cardiomyocyte hypertrophy. <i>Molecular Therapy</i> , 2021, 29, 2253-2267.	3.7	24
11	Genome-wide identification of microRNA targets reveals positive regulation of the Hippo pathway by miR-122 during liver development. <i>Cell Death and Disease</i> , 2021, 12, 1161.	2.7	7
12	Ribosome profiling analysis identified a KRAS-interacting microprotein that represses oncogenic signaling in hepatocellular carcinoma cells. <i>Science China Life Sciences</i> , 2020, 63, 529-542.	2.3	36
13	Novel organization of mitochondrial minicircles and guide RNAs in the zoonotic pathogen <i>Trypanosoma lewisi</i> . <i>Nucleic Acids Research</i> , 2020, 48, 9747-9761.	6.5	10
14	Classification and function of <sc>RNA</sc>-protein interactions. <i>Wiley Interdisciplinary Reviews RNA</i> , 2020, 11, e1601.	3.2	26
15	Noncoding RNA: from dark matter to bright star. <i>Science China Life Sciences</i> , 2020, 63, 463-468.	2.3	32
16	Differential impacts of charcoal-stripped fetal bovine serum on c-Myc among distinct subtypes of breast cancer cell lines. <i>Biochemical and Biophysical Research Communications</i> , 2020, 526, 267-272.	1.0	7
17	Histone H3 trimethylation at lysine 36 guides m6A RNA modification co-transcriptionally. <i>Nature</i> , 2019, 567, 414-419.	13.7	452
18	An <sc>LTR</sc> retrotransposon-derived lncRNA interacts with <sc>RNF</sc> 169 to promote homologous recombination. <i>EMBO Reports</i> , 2019, 20, e47650.	2.0	28

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19	MicroRNA-122 supports robust innate immunity in hepatocytes by targeting the RTKs/STAT3 signaling pathway. <i>ELife</i> , 2019, 8, .	2.8	32
20	Recognition of RNA N6-methyladenosine by IGF2BP proteins enhances mRNA stability and translation. <i>Nature Cell Biology</i> , 2018, 20, 285-295.	4.6	1,650
21	A group of tissue-specific microRNAs contribute to the silencing of CLUX1 in different cell lineages during development. <i>Journal of Cellular Biochemistry</i> , 2018, 119, 6238-6248.	1.2	5
22	Inhibition of the JNK/MAPK signaling pathway by myogenesis-associated miRNAs is required for skeletal muscle development. <i>Cell Death and Differentiation</i> , 2018, 25, 1581-1597.	5.0	79
23	Comprehensive Genomic Characterization of RNA-Binding Proteins across Human Cancers. <i>Cell Reports</i> , 2018, 22, 286-298.	2.9	166
24	dreamBase: DNA modification, RNA regulation and protein binding of expressed pseudogenes in human health and disease. <i>Nucleic Acids Research</i> , 2018, 46, D85-D91.	6.5	62
25	RMBase v2.0: deciphering the map of RNA modifications from epitranscriptome sequencing data. <i>Nucleic Acids Research</i> , 2018, 46, D327-D334.	6.5	327
26	miR-372 and miR-373 enhance the stemness of colorectal cancer cells by repressing differentiation signaling pathways. <i>Molecular Oncology</i> , 2018, 12, 1949-1964.	2.1	62
27	Cryptotanshinone suppresses key onco-proliferative and drug-resistant pathways of chronic myeloid leukemia by targeting STAT5 and STAT3 phosphorylation. <i>Science China Life Sciences</i> , 2018, 61, 999-1009.	2.3	30
28	Applications of RNA Indexes for Precision Oncology in Breast Cancer. <i>Genomics, Proteomics and Bioinformatics</i> , 2018, 16, 108-119.	3.0	16
29	Oridonin Triggers Chaperon-mediated Proteasomal Degradation of BCR-ABL in Leukemia. <i>Scientific Reports</i> , 2017, 7, 41525.	1.6	44
30	Oridonin induces autophagy via inhibition of glucose metabolism in p53-mutated colorectal cancer cells. <i>Cell Death and Disease</i> , 2017, 8, e2633-e2633.	2.7	91
31	ChIPBase v2.0: decoding transcriptional regulatory networks of non-coding RNAs and protein-coding genes from ChIP-seq data. <i>Nucleic Acids Research</i> , 2017, 45, D43-D50.	6.5	228
32	Computational Approaches to tRNA-Derived Small RNAs. <i>Non-coding RNA</i> , 2017, 3, 2.	1.3	20
33	Exo-miRExplorer: A Comprehensive Resource for Exploring and Comparatively Analyzing Exogenous MicroRNAs. <i>Frontiers in Microbiology</i> , 2017, 8, 126.	1.5	6
34	tRF2Cancer: A web server to detect tRNA-derived small RNA fragments (tRFs) and their expression in multiple cancers. <i>Nucleic Acids Research</i> , 2016, 44, W185-W193.	6.5	113
35	Long non-coding RNAs link extracellular matrix gene expression to ischemic cardiomyopathy. <i>Cardiovascular Research</i> , 2016, 112, 543-554.	1.8	64
36	27-Hydroxycholesterol increases Myc protein stability via suppressing PP2A, SCP1 and FBW7 transcription in MCF-7 breast cancer cells. <i>Biochemical and Biophysical Research Communications</i> , 2016, 480, 328-333.	1.0	13

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37	deepBase v2.0: identification, expression, evolution and function of small RNAs, lncRNAs and circular RNAs from deep-sequencing data. <i>Nucleic Acids Research</i> , 2016, 44, D196-D202.	6.5	203
38	RMBase: a resource for decoding the landscape of RNA modifications from high-throughput sequencing data. <i>Nucleic Acids Research</i> , 2016, 44, D259-D265.	6.5	166
39	Integrative analysis reveals clinical phenotypes and oncogenic potentials of long non-coding RNAs across 15 cancer types. <i>Oncotarget</i> , 2016, 7, 35044-35055.	0.8	17
40	CLIP: viewing the RNA world from an RNA-protein interactome perspective. <i>Science China Life Sciences</i> , 2015, 58, 75-88.	2.3	12
41	Cancer in the parasitic protozoans <i>Trypanosoma brucei</i> and <i>Toxoplasma gondii</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 8835-8842.	3.3	42
42	StarScan: a web server for scanning small RNA targets from degradome sequencing data. <i>Nucleic Acids Research</i> , 2015, 43, W480-W486.	6.5	36
43	Conservation and divergence of transcriptional coregulations between box C/D snoRNA and ribosomal protein genes in Ascomycota. <i>Rna</i> , 2014, 20, 1376-1385.	1.6	6
44	Pachytene piRNAs instruct massive mRNA elimination during late spermiogenesis. <i>Cell Research</i> , 2014, 24, 680-700.	5.7	344
45	Inhibition of miR-17 and miR-20a by Oridonin Triggers Apoptosis and Reverses Chemoresistance by Derepressing BIM-S. <i>Cancer Research</i> , 2014, 74, 4409-4419.	0.4	69
46	The ribosomal protein rpl26 promoter is required for its 3' sense terminus ncRNA transcription in <i>Schizosaccharomyces pombe</i> , implicating a new transcriptional mechanism for ncRNAs. <i>Biochemical and Biophysical Research Communications</i> , 2014, 444, 86-91.	1.0	4
47	starBase v2.0: decoding miRNA-ceRNA, miRNA-ncRNA and protein-RNA interaction networks from large-scale CLIP-Seq data. <i>Nucleic Acids Research</i> , 2014, 42, D92-D97.	6.5	4,113
48	Both endo-siRNAs and tRNA-derived small RNAs are involved in the differentiation of primitive eukaryote <i>Giardia lamblia</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 14159-14164.	3.3	37
49	Discovery of Protein-lncRNA Interactions by Integrating Large-Scale CLIP-Seq and RNA-Seq Datasets. <i>Frontiers in Bioengineering and Biotechnology</i> , 2014, 2, 88.	2.0	73
50	A Contig-Based Strategy for the Genome-Wide Discovery of MicroRNAs without Complete Genome Resources. <i>PLoS ONE</i> , 2014, 9, e88179.	1.1	11
51	Rapid Birth-and-Death Evolution of Imprinted snoRNAs in the Prader-Willi Syndrome Locus: Implications for Neural Development in Euarchontoglires. <i>PLoS ONE</i> , 2014, 9, e100329.	1.1	19
52	Non-coding RNA annotation: Deciphering the second genetic code. <i>Science China Life Sciences</i> , 2013, 56, 865-866.	2.3	1
53	A Helm model for microRNA regulation in cell fate decision and conversion. <i>Science China Life Sciences</i> , 2013, 56, 897-906.	2.3	14
54	miR-125b, a Target of CDX2, Regulates Cell Differentiation through Repression of the Core Binding Factor in Hematopoietic Malignancies. <i>Journal of Biological Chemistry</i> , 2011, 286, 38253-38263.	1.6	63

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55	Molecular phylogeny of the entomopathogenic fungi of the genus <i>Cordyceps</i> (Ascomycota: Tj ETQq1 1 0.784314 rgBT /Overlock 10 435-444.	1.6	8
56	Liver-enriched transcription factors regulate MicroRNA-122 that targets CUTL1 during liver development. <i>Hepatology</i> , 2010, 52, 1431-1442.	3.6	246
57	Deep Sequencing of Human Nuclear and Cytoplasmic Small RNAs Reveals an Unexpectedly Complex Subcellular Distribution of miRNAs and tRNA 3' Trainers. <i>PLoS ONE</i> , 2010, 5, e10563.	1.1	265
58	Identification and evolutionary implication of four novel box H/ACA snoRNAs from <i>Giardia lamblia</i> . <i>Science Bulletin</i> , 2006, 51, 2451-2456.	1.7	5
59	Identification of three novel noncoding RNAs from <i>Drosophila melanogaster</i> . <i>Science Bulletin</i> , 2006, 51, 2737-2742.	1.7	6
60	Isolation of a Tomato Protease that May Be Involved in Proteolysis of 1-Aminocyclopropane-1-Carboxylate Synthase. <i>Journal of Integrative Plant Biology</i> , 2005, 47, 1220-1227.	4.1	2
61	Cleavage of the Carboxyl-Terminus of LEACS2, a Tomato 1-Aminocyclopropane-1-Carboxylic Acid Synthase Isomer, by a 64-kDa Tomato Metalloprotease Produces a Truncated but Active Enzyme. <i>Journal of Integrative Plant Biology</i> , 2005, 47, 1352-1363.	4.1	5
62	Identification of 20 microRNAs from <i>Oryza sativa</i> . <i>Nucleic Acids Research</i> , 2004, 32, 1688-1695.	6.5	154
63	Identification and functional analysis of a novel box C/D snoRNA from <i>Schizosaccharomyces pombe</i> . <i>Science Bulletin</i> , 2004, 49, 1929-1936.	1.7	0
64	Genetic variability in Gymnodiniaceae ITS regions: implications for species identification and phylogenetic analysis. <i>Marine Biology</i> , 2004, 144, 215-224.	0.7	31
65	Phylogenetic diversity of Archaea in prawn farm sediment. <i>Marine Biology</i> , 2004, 146, 133-142.	0.7	11
66	Synthesis, DNA-binding and cleavage studies of macrocyclic copper(II) complexes. <i>Transition Metal Chemistry</i> , 2003, 28, 116-121.	0.7	58
67	Title is missing!. <i>Transition Metal Chemistry</i> , 2002, 27, 686-690.	0.7	26
68	Diversity and structure of the archaeal community in the leachate of a full-scale recirculating landfill as examined by direct 16S rRNA gene sequence retrieval. , 0, .		1
69	Wnt/ β -catenin pathway transactivates microRNA-150 that promotes EMT of colorectal cancer cells by suppressing CREB signaling. <i>Oncotarget</i> , 0, 7, 42513-42526.	0.8	55