

Zhi John Lu

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

57
papers

3,876
citations

30
h-index

61
g-index

61
ext. papers

5,020
ext. citations

12.6
avg, IF

5.01
L-index

#	Paper	IF	Citations
57	A deep learning method for recovering missing signals in transcriptome-wide RNA structure profiles from probing experiments. <i>Nature Machine Intelligence</i> , 2021 , 3, 995-1006	22.5	1
56	Methylome profiling identifies TCHH methylation in CfDNA as a noninvasive marker of liver metastasis in colorectal cancer. <i>FASEB Journal</i> , 2021 , 35, e21720	0.9	1
55	Integrative analysis of long extracellular RNAs reveals a detection panel of noncoding RNAs for liver cancer. <i>Theranostics</i> , 2021 , 11, 181-193	12.1	5
54	Integrative genomic analysis of early neurogenesis reveals a temporal genetic program for differentiation and specification of preplate and Cajal-Retzius neurons. <i>PLoS Genetics</i> , 2021 , 17, e1009355	6	1
53	POSTAR3: an updated platform for exploring post-transcriptional regulation coordinated by RNA-binding proteins. <i>Nucleic Acids Research</i> , 2021 ,	20.1	3
52	Tissue-specific transcription reprogramming promotes liver metastasis of colorectal cancer. <i>Cell Research</i> , 2020 , 30, 34-49	24.7	21
51	A comprehensive evaluation of connectivity methods for L1000 data. <i>Briefings in Bioinformatics</i> , 2020 , 21, 2194-2205	13.4	4
50	Selective translation by alternative bacterial ribosomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 19487-19496	11.5	18
49	Arabidopsis exoribonuclease USB1 interacts with the PPR-domain protein SOAR1 to negatively regulate abscisic acid signaling. <i>Journal of Experimental Botany</i> , 2020 , 71, 5837-5851	7	2
48	H3K18ac Primes Mesendodermal Differentiation upon Nodal Signaling. <i>Stem Cell Reports</i> , 2019 , 13, 642-656	8.56	4
47	Noncoding RNAs Serve as Diagnosis and Prognosis Biomarkers for Hepatocellular Carcinoma. <i>Clinical Chemistry</i> , 2019 , 65, 905-915	5.5	34
46	Mitochondrion-processed TERC regulates senescence without affecting telomerase activities. <i>Protein and Cell</i> , 2019 , 10, 631-648	7.2	20
45	POSTAR2: deciphering the post-transcriptional regulatory logics. <i>Nucleic Acids Research</i> , 2019 , 47, D203-D211	21	80
44	Microarray is an efficient tool for circRNA profiling. <i>Briefings in Bioinformatics</i> , 2019 , 20, 1420-1433	13.4	88
43	Stress-responsive regulation of long non-coding RNA polyadenylation in <i>Oryza sativa</i> . <i>Plant Journal</i> , 2018 , 93, 814-827	6.9	48
42	Decoding Plant RNA Structurome. <i>Molecular Plant</i> , 2018 , 11, 521-522	14.4	1
41	Mitochondrial Trafficking and Processing of Telomerase RNA TERC. <i>Cell Reports</i> , 2018 , 24, 2589-2595	10.6	39

40	RISE: a database of RNA interactome from sequencing experiments. <i>Nucleic Acids Research</i> , 2018 , 46, D194-D201	20.1	42
39	Comprehensive analysis of long non-coding RNAs highlights their spatio-temporal expression patterns and evolutionary conservation in <i>Sus scrofa</i> . <i>Scientific Reports</i> , 2017 , 7, 43166	4.9	48
38	Recurrently deregulated lncRNAs in hepatocellular carcinoma. <i>Nature Communications</i> , 2017 , 8, 14421	17.4	196
37	Methylation of TMEM176A is an independent prognostic marker and is involved in human colorectal cancer development. <i>Epigenetics</i> , 2017 , 12, 575-583	5.7	15
36	COME: a robust coding potential calculation tool for lncRNA identification and characterization based on multiple features. <i>Nucleic Acids Research</i> , 2017 , 45, e2	20.1	67
35	POSTAR: a platform for exploring post-transcriptional regulation coordinated by RNA-binding proteins. <i>Nucleic Acids Research</i> , 2017 , 45, D104-D114	20.1	57
34	Identification of high-confidence RNA regulatory elements by combinatorial classification of RNA-protein binding sites. <i>Genome Biology</i> , 2017 , 18, 169	18.3	27
33	RNA Biomarkers: Frontier of Precision Medicine for Cancer. <i>Non-coding RNA</i> , 2017 , 3,	7.1	73
32	Large-scale mapping of mammalian transcriptomes identifies conserved genes associated with different cell states. <i>Nucleic Acids Research</i> , 2017 , 45, 1657-1672	20.1	7
31	Systematic characterization of novel lncRNAs responding to phosphate starvation in <i>Arabidopsis thaliana</i> . <i>BMC Genomics</i> , 2016 , 17, 655	4.5	52
30	RNAex: an RNA secondary structure prediction server enhanced by high-throughput structure-probing data. <i>Nucleic Acids Research</i> , 2016 , 44, W294-301	20.1	9
29	The THO/TREX Complex Active in miRNA Biogenesis Negatively Regulates Root-Associated Acid Phosphatase Activity Induced by Phosphate Starvation. <i>Plant Physiology</i> , 2016 , 171, 2841-53	6.6	12
28	Divergent lncRNAs Regulate Gene Expression and Lineage Differentiation in Pluripotent Cells. <i>Cell Stem Cell</i> , 2016 , 18, 637-52	18	255
27	Analysis of sequencing data for probing RNA secondary structures and protein-RNA binding in studying posttranscriptional regulations. <i>Briefings in Bioinformatics</i> , 2016 , 17, 1032-1043	13.4	6
26	Critical roles of long noncoding RNAs in <i>Drosophila</i> spermatogenesis. <i>Genome Research</i> , 2016 , 26, 1233-47	4.7	97
25	Systematic study of novel lncRNAs in different gastrointestinal cancer cells. <i>Discovery Medicine</i> , 2016 , 21, 159-71	2.5	9
24	CCG: an integrative resource of cancer protein-coding genes and long noncoding RNAs. <i>Discovery Medicine</i> , 2016 , 22, 351-359	2.5	7
23	Improved prediction of RNA secondary structure by integrating the free energy model with restraints derived from experimental probing data. <i>Nucleic Acids Research</i> , 2015 , 43, 7247-59	20.1	55

22	CLIPdb: a CLIP-seq database for protein-RNA interactions. <i>BMC Genomics</i> , 2015 , 16, 51	4.5	147
21	A common set of distinct features that characterize noncoding RNAs across multiple species. <i>Nucleic Acids Research</i> , 2015 , 43, 104-14	20.1	27
20	Comparative analysis of the transcriptome across distant species. <i>Nature</i> , 2014 , 512, 445-8	50.4	207
19	Characterization of stress-responsive lncRNAs in <i>Arabidopsis thaliana</i> by integrating expression, epigenetic and structural features. <i>Plant Journal</i> , 2014 , 80, 848-61	6.9	192
18	The phzA2-G2 transcript exhibits direct RsmA-mediated activation in <i>Pseudomonas aeruginosa</i> M18. <i>PLoS ONE</i> , 2014 , 9, e89653	3.7	29
17	Computational identification of protein binding sites on RNAs using high-throughput RNA structure-probing data. <i>Bioinformatics</i> , 2014 , 30, 1049-1055	7.2	5
16	Global signatures of protein binding on structured RNAs in <i>Saccharomyces cerevisiae</i> . <i>Science China Life Sciences</i> , 2014 , 57, 22-35	8.5	7
15	Pervasive and dynamic protein binding sites of the mRNA transcriptome in <i>Saccharomyces cerevisiae</i> . <i>Genome Biology</i> , 2013 , 14, R13	18.3	71
14	Tiling genomes of pathogenic viruses identifies potent antiviral shRNAs and reveals a role for secondary structure in shRNA efficacy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 869-74	11.5	78
13	MiRmat: mature microRNA sequence prediction. <i>PLoS ONE</i> , 2012 , 7, e51673	3.7	21
12	Regulatory feedback loop of two phz gene clusters through 5' untranslated regions in <i>Pseudomonas</i> sp. M18. <i>PLoS ONE</i> , 2011 , 6, e19413	3.7	26
11	Diverse transcription factor binding features revealed by genome-wide ChIP-seq in <i>C. elegans</i> . <i>Genome Research</i> , 2011 , 21, 245-54	9.7	167
10	Analysis of genomic variation in non-coding elements using population-scale sequencing data from the 1000 Genomes Project. <i>Nucleic Acids Research</i> , 2011 , 39, 7058-76	20.1	58
9	Prediction and characterization of noncoding RNAs in <i>C. elegans</i> by integrating conservation, secondary structure, and high-throughput sequencing and array data. <i>Genome Research</i> , 2011 , 21, 276-85	9.7	55
8	Construction and analysis of an integrated regulatory network derived from high-throughput sequencing data. <i>PLoS Computational Biology</i> , 2011 , 7, e1002190	5	69
7	Genome-wide identification of binding sites defines distinct functions for <i>Caenorhabditis elegans</i> PHA-4/FOXA in development and environmental response. <i>PLoS Genetics</i> , 2010 , 6, e1000848	6	132
6	Integrative analysis of the <i>Caenorhabditis elegans</i> genome by the modENCODE project. <i>Science</i> , 2010 , 330, 1775-87	33.3	744
5	Improved RNA secondary structure prediction by maximizing expected pair accuracy. <i>Rna</i> , 2009 , 15, 1805-13	5.83	146

- 4 OligoWalk: an online siRNA design tool utilizing hybridization thermodynamics. *Nucleic Acids Research*, **2008**, 36, W104-8 20.1 66
- 3 Fundamental differences in the equilibrium considerations for siRNA and antisense oligodeoxynucleotide design. *Nucleic Acids Research*, **2008**, 36, 3738-45 20.1 20
- 2 Efficient siRNA selection using hybridization thermodynamics. *Nucleic Acids Research*, **2008**, 36, 640-7 20.1 105
- 1 A set of nearest neighbor parameters for predicting the enthalpy change of RNA secondary structure formation. *Nucleic Acids Research*, **2006**, 34, 4912-24 20.1 100