

Zhi John Lu

List of Publications by Citations

Source: <https://exaly.com/author-pdf/9456249/zhi-john-lu-publications-by-citations.pdf>

Version: 2024-04-26

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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 | Integrative analysis of the <i>Caenorhabditis elegans</i> genome by the modENCODE project. <i>Science</i> , 2010 , 330, 1775-87 | 33.3 | 744 |
| 56 | Divergent lncRNAs Regulate Gene Expression and Lineage Differentiation in Pluripotent Cells. <i>Cell Stem Cell</i> , 2016 , 18, 637-52 | 18 | 255 |
| 55 | Comparative analysis of the transcriptome across distant species. <i>Nature</i> , 2014 , 512, 445-8 | 50.4 | 207 |
| 54 | Recurrently deregulated lncRNAs in hepatocellular carcinoma. <i>Nature Communications</i> , 2017 , 8, 14421 | 17.4 | 196 |
| 53 | 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 |
| 52 | 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 |
| 51 | CLIPdb: a CLIP-seq database for protein-RNA interactions. <i>BMC Genomics</i> , 2015 , 16, 51 | 4.5 | 147 |
| 50 | Improved RNA secondary structure prediction by maximizing expected pair accuracy. <i>Rna</i> , 2009 , 15, 1805-13 | 5.83 | 146 |
| 49 | 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 |
| 48 | Efficient siRNA selection using hybridization thermodynamics. <i>Nucleic Acids Research</i> , 2008 , 36, 640-7 | 20.1 | 105 |
| 47 | A set of nearest neighbor parameters for predicting the enthalpy change of RNA secondary structure formation. <i>Nucleic Acids Research</i> , 2006 , 34, 4912-24 | 20.1 | 100 |
| 46 | Critical roles of long noncoding RNAs in <i>Drosophila</i> spermatogenesis. <i>Genome Research</i> , 2016 , 26, 1233-47 | 14.7 | 97 |
| 45 | Microarray is an efficient tool for circRNA profiling. <i>Briefings in Bioinformatics</i> , 2019 , 20, 1420-1433 | 13.4 | 88 |
| 44 | POSTAR2: deciphering the post-transcriptional regulatory logics. <i>Nucleic Acids Research</i> , 2019 , 47, D203-D211 | 11.1 | 80 |
| 43 | 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 |
| 42 | RNA Biomarkers: Frontier of Precision Medicine for Cancer. <i>Non-coding RNA</i> , 2017 , 3, | 7.1 | 73 |
| 41 | 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 |

| | | | |
|----|---|------|----|
| 40 | Construction and analysis of an integrated regulatory network derived from high-throughput sequencing data. <i>PLoS Computational Biology</i> , 2011 , 7, e1002190 | 5 | 69 |
| 39 | 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 |
| 38 | OligoWalk: an online siRNA design tool utilizing hybridization thermodynamics. <i>Nucleic Acids Research</i> , 2008 , 36, W104-8 | 20.1 | 66 |
| 37 | 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 |
| 36 | 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 |
| 35 | 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 |
| 34 | 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 |
| 33 | Systematic characterization of novel lncRNAs responding to phosphate starvation in <i>Arabidopsis thaliana</i> . <i>BMC Genomics</i> , 2016 , 17, 655 | 4.5 | 52 |
| 32 | 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 |
| 31 | 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 |
| 30 | RISE: a database of RNA interactome from sequencing experiments. <i>Nucleic Acids Research</i> , 2018 , 46, D194-D201 | 20.1 | 42 |
| 29 | Mitochondrial Trafficking and Processing of Telomerase RNA TERC. <i>Cell Reports</i> , 2018 , 24, 2589-2595 | 10.6 | 39 |
| 28 | Noncoding RNAs Serve as Diagnosis and Prognosis Biomarkers for Hepatocellular Carcinoma. <i>Clinical Chemistry</i> , 2019 , 65, 905-915 | 5.5 | 34 |
| 27 | 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 |
| 26 | 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 |
| 25 | 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 |
| 24 | 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 |
| 23 | MiRmat: mature microRNA sequence prediction. <i>PLoS ONE</i> , 2012 , 7, e51673 | 3.7 | 21 |

| | | | |
|----|--|------|----|
| 22 | Tissue-specific transcription reprogramming promotes liver metastasis of colorectal cancer. <i>Cell Research</i> , 2020 , 30, 34-49 | 24.7 | 21 |
| 21 | Fundamental differences in the equilibrium considerations for siRNA and antisense oligodeoxynucleotide design. <i>Nucleic Acids Research</i> , 2008 , 36, 3738-45 | 20.1 | 20 |
| 20 | Mitochondrion-processed TERC regulates senescence without affecting telomerase activities. <i>Protein and Cell</i> , 2019 , 10, 631-648 | 7.2 | 20 |
| 19 | 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 |
| 18 | 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 |
| 17 | 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 |
| 16 | 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 |
| 15 | Systematic study of novel lncRNAs in different gastrointestinal cancer cells. <i>Discovery Medicine</i> , 2016 , 21, 159-71 | 2.5 | 9 |
| 14 | 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 |
| 13 | 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 |
| 12 | CCG: an integrative resource of cancer protein-coding genes and long noncoding RNAs. <i>Discovery Medicine</i> , 2016 , 22, 351-359 | 2.5 | 7 |
| 11 | 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 |
| 10 | 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 |
| 9 | 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 |
| 8 | H3K18ac Primes Mesendodermal Differentiation upon Nodal Signaling. <i>Stem Cell Reports</i> , 2019 , 13, 642-656 | 8.5 | 4 |
| 7 | A comprehensive evaluation of connectivity methods for L1000 data. <i>Briefings in Bioinformatics</i> , 2020 , 21, 2194-2205 | 13.4 | 4 |
| 6 | POSTAR3: an updated platform for exploring post-transcriptional regulation coordinated by RNA-binding proteins. <i>Nucleic Acids Research</i> , 2021 , | 20.1 | 3 |
| 5 | 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 |

| | | | |
|---|--|------|---|
| 4 | Decoding Plant RNA Structurome. <i>Molecular Plant</i> , 2018 , 11, 521-522 | 14.4 | 1 |
| 3 | 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 |
| 2 | 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 |
| 1 | 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 |