

Zhi John Lu

List of Publications by Year in descending order

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Version: 2024-02-01

59
papers

5,675
citations

117453

34
h-index

138251

58
g-index

61
all docs

61
docs citations

61
times ranked

9064
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Integrative Analysis of the <i>Caenorhabditis elegans</i> Genome by the modENCODE Project. <i>Science</i> , 2010, 330, 1775-1787. | 6.0 | 912 |
| 2 | Divergent lncRNAs Regulate Gene Expression and Lineage Differentiation in Pluripotent Cells. <i>Cell Stem Cell</i> , 2016, 18, 637-652. | 5.2 | 358 |
| 3 | Comparative analysis of the transcriptome across distant species. <i>Nature</i> , 2014, 512, 445-448. | 13.7 | 289 |
| 4 | Recurrently deregulated lncRNAs in hepatocellular carcinoma. <i>Nature Communications</i> , 2017, 8, 14421. | 5.8 | 279 |
| 5 | Characterization of stress-responsive lncRNAs in <i>Arabidopsis thaliana</i> by integrating expression, epigenetic and structural features. <i>Plant Journal</i> , 2014, 80, 848-861. | 2.8 | 264 |
| 6 | Diverse transcription factor binding features revealed by genome-wide ChIP-seq in <i>C. elegans</i> . <i>Genome Research</i> , 2011, 21, 245-254. | 2.4 | 224 |
| 7 | CLIPdb: a CLIP-seq database for protein-RNA interactions. <i>BMC Genomics</i> , 2015, 16, 51. | 1.2 | 210 |
| 8 | Improved RNA secondary structure prediction by maximizing expected pair accuracy. <i>Rna</i> , 2009, 15, 1805-1813. | 1.6 | 194 |
| 9 | 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. | 1.5 | 165 |
| 10 | Critical roles of long noncoding RNAs in <i>Drosophila</i> spermatogenesis. <i>Genome Research</i> , 2016, 26, 1233-1244. | 2.4 | 164 |
| 11 | Microarray is an efficient tool for circRNA profiling. <i>Briefings in Bioinformatics</i> , 2019, 20, 1420-1433. | 3.2 | 161 |
| 12 | POSTAR2: deciphering the post-transcriptional regulatory logics. <i>Nucleic Acids Research</i> , 2019, 47, D203-D211. | 6.5 | 145 |
| 13 | Efficient siRNA selection using hybridization thermodynamics. <i>Nucleic Acids Research</i> , 2007, 36, 640-647. | 6.5 | 126 |
| 14 | A set of nearest neighbor parameters for predicting the enthalpy change of RNA secondary structure formation. <i>Nucleic Acids Research</i> , 2006, 34, 4912-4924. | 6.5 | 121 |
| 15 | POSTAR: a platform for exploring post-transcriptional regulation coordinated by RNA-binding proteins. <i>Nucleic Acids Research</i> , 2017, 45, D104-D114. | 6.5 | 115 |
| 16 | Systematic characterization of novel lncRNAs responding to phosphate starvation in <i>Arabidopsis thaliana</i> . <i>BMC Genomics</i> , 2016, 17, 655. | 1.2 | 113 |
| 17 | RNA Biomarkers: Frontier of Precision Medicine for Cancer. <i>Non-coding RNA</i> , 2017, 3, 9. | 1.3 | 106 |
| 18 | COME: a robust coding potential calculation tool for lncRNA identification and characterization based on multiple features. <i>Nucleic Acids Research</i> , 2017, 45, e2-e2. | 6.5 | 102 |

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|----|--|------|-----------|
| 19 | 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, 869-874. | 3.3 | 99 |
| 20 | OligoWalk: an online siRNA design tool utilizing hybridization thermodynamics. <i>Nucleic Acids Research</i> , 2008, 36, W104-W108. | 6.5 | 93 |
| 21 | Construction and Analysis of an Integrated Regulatory Network Derived from High-Throughput Sequencing Data. <i>PLoS Computational Biology</i> , 2011, 7, e1002190. | 1.5 | 92 |
| 22 | Pervasive and dynamic protein binding sites of the mRNA transcriptome in <i>Saccharomyces cerevisiae</i> . <i>Genome Biology</i> , 2013, 14, R13. | 13.9 | 91 |
| 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, 7247-7259. | 6.5 | 87 |
| 24 | Stress-responsive regulation of long non-coding RNA polyadenylation in <i>Oryza sativa</i> . <i>Plant Journal</i> , 2018, 93, 814-827. | 2.8 | 86 |
| 25 | 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, 7058-7076. | 6.5 | 81 |
| 26 | 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. | 1.6 | 75 |
| 27 | RISE: a database of RNA interactome from sequencing experiments. <i>Nucleic Acids Research</i> , 2018, 46, D194-D201. | 6.5 | 75 |
| 28 | POSTAR3: an updated platform for exploring post-transcriptional regulation coordinated by RNA-binding proteins. <i>Nucleic Acids Research</i> , 2022, 50, D287-D294. | 6.5 | 65 |
| 29 | A common set of distinct features that characterize noncoding RNAs across multiple species. <i>Nucleic Acids Research</i> , 2015, 43, 104-114. | 6.5 | 63 |
| 30 | 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, 276-285. | 2.4 | 60 |
| 31 | Tissue-specific transcription reprogramming promotes liver metastasis of colorectal cancer. <i>Cell Research</i> , 2020, 30, 34-49. | 5.7 | 60 |
| 32 | Mitochondrial Trafficking and Processing of Telomerase RNA TERC. <i>Cell Reports</i> , 2018, 24, 2589-2595. | 2.9 | 59 |
| 33 | Noncoding RNAs Serve as Diagnosis and Prognosis Biomarkers for Hepatocellular Carcinoma. <i>Clinical Chemistry</i> , 2019, 65, 905-915. | 1.5 | 57 |
| 34 | The phzA2-G2 Transcript Exhibits Direct RsmA-Mediated Activation in <i>Pseudomonas aeruginosa</i> M18. <i>PLoS ONE</i> , 2014, 9, e89653. | 1.1 | 48 |
| 35 | Identification of high-confidence RNA regulatory elements by combinatorial classification of RNA-protein binding sites. <i>Genome Biology</i> , 2017, 18, 169. | 3.8 | 42 |
| 36 | Integrative analysis of long extracellular RNAs reveals a detection panel of noncoding RNAs for liver cancer. <i>Theranostics</i> , 2021, 11, 181-193. | 4.6 | 41 |

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|----|---|-----|-----------|
| 37 | Selective translation by alternative bacterial ribosomes. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 19487-19496. | 3.3 | 38 |
| 38 | Mitochondrion-processed TERC regulates senescence without affecting telomerase activities. Protein and Cell, 2019, 10, 631-648. | 4.8 | 34 |
| 39 | Regulatory Feedback Loop of Two phz Gene Clusters through 5'â€²-Untranslated Regions in Pseudomonas sp. M18. PLoS ONE, 2011, 6, e19413. | 1.1 | 30 |
| 40 | Methylation of <i>TMEM176A</i> is an independent prognostic marker and is involved in human colorectal cancer development. Epigenetics, 2017, 12, 575-583. | 1.3 | 28 |
| 41 | Fundamental differences in the equilibrium considerations for siRNA and antisense oligodeoxynucleotide design. Nucleic Acids Research, 2008, 36, 3738-3745. | 6.5 | 25 |
| 42 | MiRmat: Mature microRNA Sequence Prediction. PLoS ONE, 2012, 7, e51673. | 1.1 | 24 |
| 43 | Cancer type classification using plasma cell-free RNAs derived from human and microbes. ELife, 0, 11, . | 2.8 | 23 |
| 44 | A comprehensive evaluation of connectivity methods for L1000 data. Briefings in Bioinformatics, 2020, 21, 2194-2205. | 3.2 | 22 |
| 45 | The THO/TREX Complex Active in miRNA Biogenesis Negatively Regulates Root-Associated Acid Phosphatase Activity Induced by Phosphate Starvation. Plant Physiology, 2016, 171, 2841-2853. | 2.3 | 16 |
| 46 | H3K18ac Primes Mesendodermal Differentiation upon Nodal Signaling. Stem Cell Reports, 2019, 13, 642-656. | 2.3 | 16 |
| 47 | Integrative genomic analysis of early neurogenesis reveals a temporal genetic program for differentiation and specification of preplate and Cajal-Retzius neurons. PLoS Genetics, 2021, 17, e1009355. | 1.5 | 15 |
| 48 | Arabidopsis exoribonuclease USB1 interacts with the PPR-domain protein SOAR1 to negatively regulate abscisic acid signaling. Journal of Experimental Botany, 2020, 71, 5837-5851. | 2.4 | 12 |
| 49 | RNAex: an RNA secondary structure prediction server enhanced by high-throughput structure-probing data. Nucleic Acids Research, 2016, 44, W294-W301. | 6.5 | 11 |
| 50 | Large-scale mapping of mammalian transcriptomes identifies conserved genes associated with different cell states. Nucleic Acids Research, 2017, 45, gkw1256. | 6.5 | 10 |
| 51 | Systematic study of novel lncRNAs in different gastrointestinal cancer cells. Discovery Medicine, 2016, 21, 159-71. | 0.5 | 9 |
| 52 | Global signatures of protein binding on structured RNAs in Saccharomyces cerevisiae. Science China Life Sciences, 2014, 57, 22-35. | 2.3 | 8 |
| 53 | CCG: an integrative resource of cancer protein-coding genes and long noncoding RNAs. Discovery Medicine, 2016, 22, 351-359. | 0.5 | 7 |
| 54 | A Nodal enhanced micropeptide NEMEP regulates glucose uptake during mesendoderm differentiation of embryonic stem cells. Nature Communications, 2022, 13, . | 5.8 | 7 |

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|----|--|-----|-----------|
| 55 | Analysis of sequencing data for probing RNA secondary structures and protein-RNA binding in studying posttranscriptional regulations. <i>Briefings in Bioinformatics</i> , 2015, 17, bbv106. | 3.2 | 6 |
| 56 | Computational identification of protein binding sites on RNAs using high-throughput RNA structure-probing data. <i>Bioinformatics</i> , 2014, 30, 1049-1055. | 1.8 | 5 |
| 57 | Methylome profiling identifies TCHH methylation in CfDNA as a noninvasive marker of liver metastasis in colorectal cancer. <i>FASEB Journal</i> , 2021, 35, e21720. | 0.2 | 4 |
| 58 | 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. | 8.3 | 2 |
| 59 | Decoding Plant RNA Structurome. <i>Molecular Plant</i> , 2018, 11, 521-522. | 3.9 | 1 |