

Lei Li

List of Publications by Year in descending order

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Version: 2024-02-01

27
papers

1,809
citations

361388

20
h-index

580810

25
g-index

31
all docs

31
docs citations

31
times ranked

2365
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Using population-scale transcriptomic and genomic data to map 3' UTR alternative polyadenylation quantitative trait loci. STAR Protocols, 2022, 3, 101566. | 1.2 | 2 |
| 2 | An atlas of alternative polyadenylation quantitative trait loci contributing to complex trait and disease heritability. Nature Genetics, 2021, 53, 994-1005. | 21.4 | 85 |
| 3 | A critical role of nuclear m6A reader YTHDC1 in leukemogenesis by regulating MCM complex-mediated DNA replication. Blood, 2021, 138, 2838-2852. | 1.4 | 83 |
| 4 | A global data-driven census of <i>Salmonella</i> small proteins and their potential functions in bacterial virulence. MicroLife, 2020, 1, . | 2.1 | 34 |
| 5 | A Cancer-Specific Ubiquitin Ligase Drives mRNA Alternative Polyadenylation by Ubiquitinating the mRNA 3' End Processing Complex. Molecular Cell, 2020, 77, 1206-1221.e7. | 9.7 | 52 |
| 6 | Nudt21 regulates the alternative polyadenylation of Pak1 and is predictive in the prognosis of glioblastoma patients. Oncogene, 2019, 38, 4154-4168. | 5.9 | 54 |
| 7 | Cleavage factor 25 deregulation contributes to pulmonary fibrosis through alternative polyadenylation. Journal of Clinical Investigation, 2019, 129, 1984-1999. | 8.2 | 47 |
| 8 | TC3A: The Cancer 3' UTR Atlas. Nucleic Acids Research, 2018, 46, D1027-D1030. | 14.5 | 79 |
| 9 | 3' UTR shortening represses tumor-suppressor genes in trans by disrupting ceRNA crosstalk. Nature Genetics, 2018, 50, 783-789. | 21.4 | 148 |
| 10 | Global Maps of ProQ Binding In Vivo Reveal Target Recognition via RNA Structure and Stability Control at mRNA 3' Ends. Molecular Cell, 2018, 70, 971-982.e6. | 9.7 | 129 |
| 11 | In Vivo Cleavage Map Illuminates the Central Role of RNase E in Coding and Non-coding RNA Pathways. Molecular Cell, 2017, 65, 39-51. | 9.7 | 250 |
| 12 | Malonylome of the plant growth promoting rhizobacterium with potent biocontrol activity, <i>Bacillus amyloliquefaciens</i> FZB42. Data in Brief, 2017, 10, 548-550. | 1.0 | 4 |
| 13 | The primary transcriptome of <i>Neisseria meningitidis</i> and its interaction with the RNA chaperone Hfq. Nucleic Acids Research, 2017, 45, 6147-6167. | 14.5 | 67 |
| 14 | Malonylome analysis of rhizobacterium <i>Bacillus amyloliquefaciens</i> FZB42 reveals involvement of lysine malonylation in polyketide synthesis and plant-bacteria interactions. Journal of Proteomics, 2017, 154, 1-12. | 2.4 | 51 |
| 15 | Single-cell RNA-seq ties macrophage polarization to growth rate of intracellular <i>Salmonella</i> . Nature Microbiology, 2017, 2, 16206. | 13.3 | 159 |
| 16 | Global RNA recognition patterns of post-transcriptional regulators Hfq and CsrA revealed by UV crosslinking in vivo. EMBO Journal, 2016, 35, 991-1011. | 7.8 | 296 |
| 17 | Genetic diversity and population structure of Chinese <i>Lentinula edodes</i> revealed by InDel and SSR markers. Mycological Progress, 2016, 15, 1. | 1.4 | 25 |
| 18 | Genetic dissection of fruiting body-related traits using quantitative trait loci mapping in <i>Lentinula edodes</i> . Applied Microbiology and Biotechnology, 2016, 100, 5437-5452. | 3.6 | 22 |

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|----|--|------|-----------|
| 19 | dRNA-Seq Reveals Genomewide TSSs and Noncoding RNAs of Plant Beneficial Rhizobacterium <i>Bacillus amyloliquefaciens</i> FZB42. <i>PLoS ONE</i> , 2015, 10, e0142002. | 2.5 | 24 |
| 20 | Comparative genomic analysis of clinical and environmental strains provides insight into the pathogenicity and evolution of <i>Vibrio parahaemolyticus</i> . <i>BMC Genomics</i> , 2014, 15, 1135. | 2.8 | 19 |
| 21 | Human Proteins with Target Sites of Multiple Post-Translational Modification Types Are More Prone to Be Involved in Disease. <i>Journal of Proteome Research</i> , 2014, 13, 2735-2748. | 3.7 | 31 |
| 22 | RNA Sequencing Analysis of the Broad-Host-Range Strain <i>Sinorhizobium fredii</i> NGR234 Identifies a Large Set of Genes Linked to Quorum Sensing-Dependent Regulation in the Background of a <i>tral</i> and <i>ngrl</i> Deletion Mutant. <i>Applied and Environmental Microbiology</i> , 2014, 80, 5655-5671. | 3.1 | 28 |
| 23 | Genome Sequences of <i>Salmonella enterica</i> Serotype Typhimurium Blood Clinical Isolate ST4848/06 and Stool Isolate ST1489/06. <i>Genome Announcements</i> , 2013, 1, . | 0.8 | 0 |
| 24 | BSRD: a repository for bacterial small regulatory RNA. <i>Nucleic Acids Research</i> , 2013, 41, D233-D238. | 14.5 | 104 |
| 25 | Draft Genome Sequence of <i>Salmonella enterica</i> Serovar Typhimurium ST1660/06, a Multidrug-Resistant Clinical Strain Isolated from a Diarrheic Patient. <i>Journal of Bacteriology</i> , 2012, 194, 6319-6320. | 2.2 | 3 |
| 26 | Genome sequence and genetic linkage analysis of Shiitake mushroom <i>Lentinula edodes</i> . <i>Nature Precedings</i> , 2012, . . | 0.1 | 6 |
| 27 | A cost-effective and universal strategy for complete prokaryotic genomic sequencing proposed by computer simulation. <i>BMC Research Notes</i> , 2012, 5, 80. | 1.4 | 4 |