

Xiaohui Wu

List of Publications by Year in descending order

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Version: 2024-02-01

63
papers

1,614
citations

361045

20
h-index

329751

37
g-index

67
all docs

67
docs citations

67
times ranked

1461
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 1 | scAPAdb: a comprehensive database of alternative polyadenylation at single-cell resolution. <i>Nucleic Acids Research</i> , 2022, 50, D365-D370. | 6.5 | 12 |
| 2 | Regulatory network-based imputation of dropouts in single-cell RNA sequencing data. <i>PLoS Computational Biology</i> , 2022, 18, e1009849. | 1.5 | 5 |
| 3 | scAPAtrop: identification and quantification of alternative polyadenylation sites from single-cell RNA-seq data. <i>Briefings in Bioinformatics</i> , 2021, 22, . | 3.2 | 24 |
| 4 | QuantifyPoly(A): reshaping alternative polyadenylation landscapes of eukaryotes with weighted density peak clustering. <i>Briefings in Bioinformatics</i> , 2021, 22, . | 3.2 | 8 |
| 5 | scLINE: A multi-network integration framework based on network embedding for representation of single-cell RNA-seq data. <i>Journal of Biomedical Informatics</i> , 2021, 122, 103899. | 2.5 | 5 |
| 6 | movAPA: modeling and visualization of dynamics of alternative polyadenylation across biological samples. <i>Bioinformatics</i> , 2021, 37, 2470-2472. | 1.8 | 8 |
| 7 | scHinter: imputing dropout events for single-cell RNA-seq data with limited sample size. <i>Bioinformatics</i> , 2020, 36, 789-797. | 1.8 | 16 |
| 8 | A survey on identification and quantification of alternative polyadenylation sites from RNA-seq data. <i>Briefings in Bioinformatics</i> , 2020, 21, 1261-1276. | 3.2 | 33 |
| 9 | scDAPA: detection and visualization of dynamic alternative polyadenylation from single cell RNA-seq data. <i>Bioinformatics</i> , 2020, 36, 1262-1264. | 1.8 | 24 |
| 10 | Heat Shock Responsive Gene Expression Modulated by mRNA Poly(A) Tail Length. <i>Frontiers in Plant Science</i> , 2020, 11, 1255. | 1.7 | 17 |
| 11 | PlantAPAdb: A Comprehensive Database for Alternative Polyadenylation Sites in Plants. <i>Plant Physiology</i> , 2020, 182, 228-242. | 2.3 | 30 |
| 12 | The Full-Length Transcriptome of <i>Spartina alterniflora</i> Reveals the Complexity of High Salt Tolerance in Monocotyledonous Halophyte. <i>Plant and Cell Physiology</i> , 2020, 61, 882-896. | 1.5 | 25 |
| 13 | Modeling of Genome-Wide Polyadenylation Signals in <i>Xenopus tropicalis</i> . <i>Frontiers in Genetics</i> , 2019, 10, 647. | 1.1 | 4 |
| 14 | Genome-wide alternative polyadenylation dynamics in response to biotic and abiotic stresses in rice. <i>Ecotoxicology and Environmental Safety</i> , 2019, 183, 109485. | 2.9 | 35 |
| 15 | Low-Rank Tensor Completion by Sum of Tensor Nuclear Norm Minimization. <i>IEEE Access</i> , 2019, 7, 134943-134953. | 2.6 | 11 |
| 16 | Cluster analysis of replicated alternative polyadenylation data using canonical correlation analysis. <i>BMC Genomics</i> , 2019, 20, 75. | 1.2 | 0 |
| 17 | scNPF: an integrative framework assisted by network propagation and network fusion for preprocessing of single-cell RNA-seq data. <i>BMC Genomics</i> , 2019, 20, 347. | 1.2 | 11 |
| 18 | Distinct genome-wide alternative polyadenylation during the response to silicon availability in the marine diatom <i>Thalassiosira pseudonana</i> . <i>Plant Journal</i> , 2019, 99, 67-80. | 2.8 | 9 |

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|----|---|-----|-----------|
| 19 | Genome-Wide Comparative Analyses of Polyadenylation Signals in Eukaryotes Suggest a Possible Origin of the AAUAAA Signal. <i>International Journal of Molecular Sciences</i> , 2019, 20, 958. | 1.8 | 12 |
| 20 | Nonconvex Low Tubal Rank Tensor Minimization. <i>IEEE Access</i> , 2019, 7, 170831-170843. | 2.6 | 2 |
| 21 | Differential alternative polyadenylation contributes to the developmental divergence between two rice subspecies, <i>Oryza japonica</i> and <i>Oryza indica</i> . <i>Plant Journal</i> , 2019, 98, 260-276. | 2.8 | 26 |
| 22 | AStrap: identification of alternative splicing from transcript sequences without a reference genome. <i>Bioinformatics</i> , 2019, 35, 2654-2656. | 1.8 | 10 |
| 23 | TSAPA: identification of tissue-specific alternative polyadenylation sites in plants. <i>Bioinformatics</i> , 2018, 34, 2123-2125. | 1.8 | 8 |
| 24 | APAtrap: identification and quantification of alternative polyadenylation sites from RNA-seq data. <i>Bioinformatics</i> , 2018, 34, 1841-1849. | 1.8 | 91 |
| 25 | Alternative polyadenylation is involved in auxin-based plant growth and development. <i>Plant Journal</i> , 2018, 93, 246-258. | 2.8 | 38 |
| 26 | Role of cleavage and polyadenylation specificity factor 100: anchoring poly(A) sites and modulating transcription termination. <i>Plant Journal</i> , 2017, 91, 829-839. | 2.8 | 30 |
| 27 | PAcluster: Clustering polyadenylation site data using canonical correlation analysis. <i>Journal of Bioinformatics and Computational Biology</i> , 2017, 15, 1750018. | 0.3 | 3 |
| 28 | A two-layer model for gene clustering using poly(A) site data. , 2017, , . | | 0 |
| 29 | PlantAPA: A Portal for Visualization and Analysis of Alternative Polyadenylation in Plants. <i>Frontiers in Plant Science</i> , 2016, 7, 889. | 1.7 | 25 |
| 30 | Genome-wide dynamics of alternative polyadenylation in rice. <i>Genome Research</i> , 2016, 26, 1753-1760. | 2.4 | 65 |
| 31 | Genome-wide analysis of the associations between polyadenylation sites and repeated sequences in <i>Arabidopsis thaliana</i> . , 2015, , . | | 0 |
| 32 | PASPA: a web server for mRNA poly(A) site predictions in plants and algae. <i>Bioinformatics</i> , 2015, 31, 1671-1673. | 1.8 | 13 |
| 33 | Using consensus interval partial least square in near infrared spectra analysis. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2015, 144, 56-62. | 1.8 | 27 |
| 34 | Genome-wide characterization of intergenic polyadenylation sites redefines gene spaces in <i>Arabidopsis thaliana</i> . <i>BMC Genomics</i> , 2015, 16, 511. | 1.2 | 17 |
| 35 | VAAPA: A web platform for visualization and analysis of alternative polyadenylation. <i>Computers in Biology and Medicine</i> , 2015, 57, 20-25. | 3.9 | 0 |
| 36 | Genome-wide identification and predictive modeling of polyadenylation sites in eukaryotes. <i>Briefings in Bioinformatics</i> , 2015, 16, 304-313. | 3.2 | 39 |

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|----|--|-----|-----------|
| 37 | Computational Analysis of Plant Polyadenylation Signals. <i>Methods in Molecular Biology</i> , 2015, 1255, 3-11. | 0.4 | 5 |
| 38 | DNA/RNA Hybrid Primer Mediated Poly(A) Tag Library Construction for Illumina Sequencing. <i>Methods in Molecular Biology</i> , 2015, 1255, 175-184. | 0.4 | 3 |
| 39 | Prediction of Plant mRNA Polyadenylation Sites. <i>Methods in Molecular Biology</i> , 2015, 1255, 13-23. | 0.4 | 3 |
| 40 | Poly(A)-Tag Deep Sequencing Data Processing to Extract Poly(A) Sites. <i>Methods in Molecular Biology</i> , 2015, 1255, 39-48. | 0.4 | 6 |
| 41 | Characterization and prediction of mRNA alternative polyadenylation sites in rice genes. <i>Bio-Medical Materials and Engineering</i> , 2014, 24, 3779-3785. | 0.4 | 0 |
| 42 | Bioinformatics Analysis of Alternative Polyadenylation in Green Alga <i>Chlamydomonas reinhardtii</i> Using Transcriptome Sequences from Three Different Sequencing Platforms. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 871-883. | 0.8 | 25 |
| 43 | Genome-wide determination of poly(A) sites in <i>Medicago truncatula</i> : evolutionary conservation of alternative poly(A) site choice. <i>BMC Genomics</i> , 2014, 15, 615. | 1.2 | 30 |
| 44 | Genome-Wide Control of Polyadenylation Site Choice by CPSF30 in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2012, 24, 4376-4388. | 3.1 | 97 |
| 45 | High-throughput antibody sequence alignment based on GPU computing. , 2012, , . | | 0 |
| 46 | Recombinatorial Biases and Convergent Recombination Determine Interindividual TCR \hat{I}^2 Sharing in Murine Thymocytes. <i>Journal of Immunology</i> , 2012, 189, 2404-2413. | 0.4 | 42 |
| 47 | In silico prediction of mRNA poly(A) sites in <i>Chlamydomonas reinhardtii</i> . <i>Molecular Genetics and Genomics</i> , 2012, 287, 895-907. | 1.0 | 9 |
| 48 | PATMAP: Polyadenylation Site Identification from Next-Generation Sequencing Data. <i>Lecture Notes in Computer Science</i> , 2012, , 485-496. | 1.0 | 0 |
| 49 | Characterization and Recognition of mRNA Alternative Polyadenylation Signals. <i>Advanced Science Letters</i> , 2012, 9, 811-816. | 0.2 | 0 |
| 50 | Identification of mRNA poly(A) signal patterns. , 2011, , . | | 0 |
| 51 | Genome-wide landscape of polyadenylation in <i>Arabidopsis</i> provides evidence for extensive alternative polyadenylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 12533-12538. | 3.3 | 292 |
| 52 | Transcriptome dynamics through alternative polyadenylation in developmental and environmental responses in plants revealed by deep sequencing. <i>Genome Research</i> , 2011, 21, 1478-1486. | 2.4 | 117 |
| 53 | Identification of plant messenger RNA polyadenylation sites using length-variable second order Markov model. , 2011, , . | | 0 |
| 54 | Ratio-Based Analysis of Differential mRNA Processing and Expression of a Polyadenylation Factor Mutant <i>pcfs4</i> Using <i>Arabidopsis</i> Tiling Microarray. <i>PLoS ONE</i> , 2011, 6, e14719. | 1.1 | 5 |

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|----|---|-----|-----------|
| 55 | Implementation of a Classification-Based Prediction Model for Plant mRNA Poly(A) Sites. Journal of Computational and Theoretical Nanoscience, 2010, 7, 927-932. | 0.4 | 2 |
| 56 | A classification-based prediction model of messenger RNA polyadenylation sites. Journal of Theoretical Biology, 2010, 265, 287-296. | 0.8 | 37 |
| 57 | Messenger RNA Polyadenylation Site Recognition in Green Alga Chlamydomonas Reinhardtii. Lecture Notes in Computer Science, 2010, , 17-26. | 1.0 | 3 |
| 58 | Data Analysis of Arabidopsis Tiling Array. , 2009, , . | | 0 |
| 59 | PROBER: Segmentation and Differential Analysis Tool for Tiling Microarray Data. , 2009, , . | | 0 |
| 60 | Implementation of a classification-based prediction model for plant mRNA Poly(A) sites. , 2008, , . | | 28 |
| 61 | Genome level analysis of rice mRNA 3' end processing signals and alternative polyadenylation. Nucleic Acids Research, 2008, 36, 3150-3161. | 6.5 | 163 |
| 62 | Predictive modeling of plant messenger RNA polyadenylation sites. BMC Bioinformatics, 2007, 8, 43. | 1.2 | 52 |
| 63 | Modeling Plant mRNA Poly(A) Sites: Software Design and Implementation. Journal of Computational and Theoretical Nanoscience, 2007, 4, 1365-1368. | 0.4 | 7 |