

Xiaohui Wu

List of Publications by Year in descending order

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Version: 2024-02-01

63
papers

1,614
citations

361388

20
h-index

330122

37
g-index

67
all docs

67
docs citations

67
times ranked

1461
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	7.1	292
2	Genome level analysis of rice mRNA 3'-end processing signals and alternative polyadenylation. <i>Nucleic Acids Research</i> , 2008, 36, 3150-3161.	14.5	163
3	Transcriptome dynamics through alternative polyadenylation in developmental and environmental responses in plants revealed by deep sequencing. <i>Genome Research</i> , 2011, 21, 1478-1486.	5.5	117
4	Genome-Wide Control of Polyadenylation Site Choice by CPSF30 in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2012, 24, 4376-4388.	6.6	97
5	APATrap: identification and quantification of alternative polyadenylation sites from RNA-seq data. <i>Bioinformatics</i> , 2018, 34, 1841-1849.	4.1	91
6	Genome-wide dynamics of alternative polyadenylation in rice. <i>Genome Research</i> , 2016, 26, 1753-1760.	5.5	65
7	Predictive modeling of plant messenger RNA polyadenylation sites. <i>BMC Bioinformatics</i> , 2007, 8, 43.	2.6	52
8	Recombinatorial Biases and Convergent Recombination Determine Interindividual TCR $\hat{\rho}$ Sharing in Murine Thymocytes. <i>Journal of Immunology</i> , 2012, 189, 2404-2413.	0.8	42
9	Genome-wide identification and predictive modeling of polyadenylation sites in eukaryotes. <i>Briefings in Bioinformatics</i> , 2015, 16, 304-313.	6.5	39
10	Alternative polyadenylation is involved in auxin-based plant growth and development. <i>Plant Journal</i> , 2018, 93, 246-258.	5.7	38
11	A classification-based prediction model of messenger RNA polyadenylation sites. <i>Journal of Theoretical Biology</i> , 2010, 265, 287-296.	1.7	37
12	Genome-wide alternative polyadenylation dynamics in response to biotic and abiotic stresses in rice. <i>Ecotoxicology and Environmental Safety</i> , 2019, 183, 109485.	6.0	35
13	A survey on identification and quantification of alternative polyadenylation sites from RNA-seq data. <i>Briefings in Bioinformatics</i> , 2020, 21, 1261-1276.	6.5	33
14	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.	2.8	30
15	Role of cleavage and polyadenylation specificity factor 100: anchoring poly(A) sites and modulating transcription termination. <i>Plant Journal</i> , 2017, 91, 829-839.	5.7	30
16	PlantAPAdb: A Comprehensive Database for Alternative Polyadenylation Sites in Plants. <i>Plant Physiology</i> , 2020, 182, 228-242.	4.8	30
17	Implementation of a classification-based prediction model for plant mRNA Poly(A) sites. , 2008, , .		28
18	Using consensus interval partial least square in near infrared spectra analysis. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2015, 144, 56-62.	3.5	27

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19	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.	5.7	26
20	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.	1.8	25
21	PlantAPA: A Portal for Visualization and Analysis of Alternative Polyadenylation in Plants. <i>Frontiers in Plant Science</i> , 2016, 7, 889.	3.6	25
22	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.	3.1	25
23	scDAPA: detection and visualization of dynamic alternative polyadenylation from single cell RNA-seq data. <i>Bioinformatics</i> , 2020, 36, 1262-1264.	4.1	24
24	scAPAttrap: identification and quantification of alternative polyadenylation sites from single-cell RNA-seq data. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	24
25	Genome-wide characterization of intergenic polyadenylation sites redefines gene spaces in <i>Arabidopsis thaliana</i> . <i>BMC Genomics</i> , 2015, 16, 511.	2.8	17
26	Heat Shock Responsive Gene Expression Modulated by mRNA Poly(A) Tail Length. <i>Frontiers in Plant Science</i> , 2020, 11, 1255.	3.6	17
27	scHinter: imputing dropout events for single-cell RNA-seq data with limited sample size. <i>Bioinformatics</i> , 2020, 36, 789-797.	4.1	16
28	PASPA: a web server for mRNA poly(A) site predictions in plants and algae. <i>Bioinformatics</i> , 2015, 31, 1671-1673.	4.1	13
29	Genome-Wide Comparative Analyses of Polyadenylation Signals in Eukaryotes Suggest a Possible Origin of the AUA AAA Signal. <i>International Journal of Molecular Sciences</i> , 2019, 20, 958.	4.1	12
30	scAPAdb: a comprehensive database of alternative polyadenylation at single-cell resolution. <i>Nucleic Acids Research</i> , 2022, 50, D365-D370.	14.5	12
31	Low-Rank Tensor Completion by Sum of Tensor Nuclear Norm Minimization. <i>IEEE Access</i> , 2019, 7, 134943-134953.	4.2	11
32	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.	2.8	11
33	AStrAp: identification of alternative splicing from transcript sequences without a reference genome. <i>Bioinformatics</i> , 2019, 35, 2654-2656.	4.1	10
34	In silico prediction of mRNA poly(A) sites in <i>Chlamydomonas reinhardtii</i> . <i>Molecular Genetics and Genomics</i> , 2012, 287, 895-907.	2.1	9
35	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.	5.7	9
36	TSAPA: identification of tissue-specific alternative polyadenylation sites in plants. <i>Bioinformatics</i> , 2018, 34, 2123-2125.	4.1	8

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37	QuantifyPoly(A): reshaping alternative polyadenylation landscapes of eukaryotes with weighted density peak clustering. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	8
38	movAPA: modeling and visualization of dynamics of alternative polyadenylation across biological samples. <i>Bioinformatics</i> , 2021, 37, 2470-2472.	4.1	8
39	Modeling Plant mRNA Poly(A) Sites: Software Design and Implementation. <i>Journal of Computational and Theoretical Nanoscience</i> , 2007, 4, 1365-1368.	0.4	7
40	Poly(A)-Tag Deep Sequencing Data Processing to Extract Poly(A) Sites. <i>Methods in Molecular Biology</i> , 2015, 1255, 39-48.	0.9	6
41	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.	4.3	5
42	Computational Analysis of Plant Polyadenylation Signals. <i>Methods in Molecular Biology</i> , 2015, 1255, 3-11.	0.9	5
43	Ratio-Based Analysis of Differential mRNA Processing and Expression of a Polyadenylation Factor Mutant <i>pcfs4</i> Using Arabidopsis Tiling Microarray. <i>PLoS ONE</i> , 2011, 6, e14719.	2.5	5
44	Regulatory network-based imputation of dropouts in single-cell RNA sequencing data. <i>PLoS Computational Biology</i> , 2022, 18, e1009849.	3.2	5
45	Modeling of Genome-Wide Polyadenylation Signals in <i>Xenopus tropicalis</i> . <i>Frontiers in Genetics</i> , 2019, 10, 647.	2.3	4
46	PAcluster: Clustering polyadenylation site data using canonical correlation analysis. <i>Journal of Bioinformatics and Computational Biology</i> , 2017, 15, 1750018.	0.8	3
47	DNA/RNA Hybrid Primer Mediated Poly(A) Tag Library Construction for Illumina Sequencing. <i>Methods in Molecular Biology</i> , 2015, 1255, 175-184.	0.9	3
48	Prediction of Plant mRNA Polyadenylation Sites. <i>Methods in Molecular Biology</i> , 2015, 1255, 13-23.	0.9	3
49	Messenger RNA Polyadenylation Site Recognition in Green Alga <i>Chlamydomonas Reinhardtii</i> . <i>Lecture Notes in Computer Science</i> , 2010, , 17-26.	1.3	3
50	Implementation of a Classification-Based Prediction Model for Plant mRNA Poly(A) Sites. <i>Journal of Computational and Theoretical Nanoscience</i> , 2010, 7, 927-932.	0.4	2
51	Nonconvex Low Tubal Rank Tensor Minimization. <i>IEEE Access</i> , 2019, 7, 170831-170843.	4.2	2
52	Data Analysis of Arabidopsis Tiling Array. , 2009, , .		0
53	PROBER: Segmentation and Differential Analysis Tool for Tiling Microarray Data. , 2009, , .		0
54	Identification of mRNA poly(A) signal patterns. , 2011, , .		0

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55	Identification of plant messenger RNA polyadenylation sites using length-variable second order Markov model. , 2011, , .		0
56	High-throughput antibody sequence alignment based on GPU computing. , 2012, , .		0
57	Characterization and prediction of mRNA alternative polyadenylation sites in rice genes. Bio-Medical Materials and Engineering, 2014, 24, 3779-3785.	0.6	0
58	Genome-wide analysis of the associations between polyadenylation sites and repeated sequences in Arabidopsis thaliana. , 2015, , .		0
59	VAAPA: A web platform for visualization and analysis of alternative polyadenylation. Computers in Biology and Medicine, 2015, 57, 20-25.	7.0	0
60	A two-layer model for gene clustering using poly(A) site data. , 2017, , .		0
61	Cluster analysis of replicated alternative polyadenylation data using canonical correlation analysis. BMC Genomics, 2019, 20, 75.	2.8	0
62	PATMAP: Polyadenylation Site Identification from Next-Generation Sequencing Data. Lecture Notes in Computer Science, 2012, , 485-496.	1.3	0
63	Characterization and Recognition of <I>m</I>RNA Alternative Polyadenylation Signals. Advanced Science Letters, 2012, 9, 811-816.	0.2	0