Xiaohui Wu

List of Publications by Year
in descending order

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	Genome-wide landscape of polyadenylation in <i>Arabidopsis</i> provides evidence for extensive alternative polyadenylation. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 12533-12538.	3.3	292
2	Genome level analysis of rice mRNA 3â€²-end processing signals and alternative polyadenylation. Nucleic Acids Research, 2008, 36, 3150-3161.	6.5	163
3	Transcriptome dynamics through alternative polyadenylation in developmental and environmental responses in plants revealed by deep sequencing. Genome Research, 2011, 21, 1478-1486.	2.4	117
4	Genome-Wide Control of Polyadenylation Site Choice by CPSF30 in <i>Arabidopsis</i>. Plant Cell, 2012, 24, 4376-4388.	3.1	97
5	APAtrap: identification and quantification of alternative polyadenylation sites from RNA-seq data. Bioinformatics, 2018, 34, 1841-1849.	1.8	91
6	Genome-wide dynamics of alternative polyadenylation in rice. Genome Research, 2016, 26, 1753-1760.	2.4	65
7	Predictive modeling of plant messenger RNA polyadenylation sites. BMC Bioinformatics, 2007, 8, 43.	1.2	52
8	Recombinatorial Biases and Convergent Recombination Determine Interindividual TCRÎ² Sharing in Murine Thymocytes. Journal of Immunology, 2012, 189, 2404-2413.	0.4	42
9	Genome-wide identification and predictive modeling of polyadenylation sites in eukaryotes. Briefings in Bioinformatics, 2015, 16, 304-313.	3.2	39
10	Alternative polyadenylation is involved in auxinâ€based plant growth and development. Plant Journal, 2018, 93, 246-258.	2.8	38
11	A classification-based prediction model of messenger RNA polyadenylation sites. Journal of Theoretical Biology, 2010, 265, 287-296.	0.8	37
12	Genome-wide alternative polyadenylation dynamics in response to biotic and abiotic stresses in rice. Ecotoxicology and Environmental Safety, 2019, 183, 109485.	2.9	35
13	A survey on identification and quantification of alternative polyadenylation sites from RNA-seq data. Briefings in Bioinformatics, 2020, 21, 1261-1276.	3.2	33
14	Genome-wide determination of poly(A) sites in Medicago truncatula: evolutionary conservation of alternative poly(A) site choice. BMC Genomics, 2014, 15, 615.	1.2	30
15	Role of cleavage and polyadenylation specificity factor 100: anchoring poly(A) sites and modulating transcription termination. Plant Journal, 2017, 91, 829-839.	2.8	30
16	PlantAPAdb: A Comprehensive Database for Alternative Polyadenylation Sites in Plants. Plant Physiology, 2020, 182, 228-242.	2.3	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. Chemometrics and Intelligent Laboratory Systems, 2015, 144, 56-62.	1.8	27

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19	Differential alternative polyadenylation contributes to the developmental divergence between two rice subspecies, *japonica* and *indica*. Plant Journal, 2019, 98, 260-276.	2.8	26
20	Bioinformatics Analysis of Alternative Polyadenylation in Green Alga *Chlamydomonas reinhardtii* Using Transcriptome Sequences from Three Different Sequencing Platforms. G3: Genes, Genomes, Genetics, 2014, 4, 871-883.	0.8	25
21	PlantAPA: A Portal for Visualization and Analysis of Alternative Polyadenylation in Plants. Frontiers in Plant Science, 2016, 7, 889.	1.7	25
22	The Full-Length Transcriptome of Spartina alterniflora Reveals the Complexity of High Salt Tolerance in Monocotyledonous Halophyte. Plant and Cell Physiology, 2020, 61, 882-896.	1.5	25
23	scDAPA: detection and visualization of dynamic alternative polyadenylation from single cell RNA-seq data. Bioinformatics, 2020, 36, 1262-1264.	1.8	24
24	scAPAtrap: identification and quantification of alternative polyadenylation sites from single-cell RNA-seq data. Briefings in Bioinformatics, 2021, 22, .	3.2	24
25	Genome-wide characterization of intergenic polyadenylation sites redefines gene spaces in Arabidopsis thaliana. BMC Genomics, 2015, 16, 511.	1.2	17
26	Heat Shock Responsive Gene Expression Modulated by mRNA Poly(A) Tail Length. Frontiers in Plant Science, 2020, 11, 1255.	1.7	17
27	scHinter: imputing dropout events for single-cell RNA-seq data with limited sample size. Bioinformatics, 2020, 36, 789-797.	1.8	16
28	PASPA: a web server for mRNA poly(A) site predictions in plants and algae. Bioinformatics, 2015, 31, 1671-1673.	1.8	13
29	Genome-Wide Comparative Analyses of Polyadenylation Signals in Eukaryotes Suggest a Possible Origin of the AAUAAA Signal. International Journal of Molecular Sciences, 2019, 20, 958.	1.8	12
30	scAPAdb: a comprehensive database of alternative polyadenylation at single-cell resolution. Nucleic Acids Research, 2022, 50, D365-D370.	6.5	12
31	Low-Rank Tensor Completion by Sum of Tensor Nuclear Norm Minimization. IEEE Access, 2019, 7, 134943-134953.	2.6	11
32	scNPF: an integrative framework assisted by network propagation and network fusion for preprocessing of single-cell RNA-seq data. BMC Genomics, 2019, 20, 347.	1.2	11
33	AStrap: identification of alternative splicing from transcript sequences without a reference genome. Bioinformatics, 2019, 35, 2654-2656.	1.8	10
34	In silico prediction of mRNA poly(A) sites in Chlamydomonas reinhardtii. Molecular Genetics and Genomics, 2012, 287, 895-907.	1.0	9
35	Distinct genome-wide alternative polyadenylation during the response to silicon availability in the marine diatom *Thalassiosira pseudonana*. Plant Journal, 2019, 99, 67-80.	2.8	9
36	TSAPA: identification of tissue-specific alternative polyadenylation sites in plants. Bioinformatics, 2018, 34, 2123-2125.	1.8	8

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37	QuantifyPoly(A): reshaping alternative polyadenylation landscapes of eukaryotes with weighted density peak clustering. Briefings in Bioinformatics, 2021, 22, .	3.2	8
38	movAPA: modeling and visualization of dynamics of alternative polyadenylation across biological samples. Bioinformatics, 2021, 37, 2470-2472.	1.8	8
39	Modeling Plant mRNA Poly(A) Sites: Software Design and Implementation. Journal of Computational and Theoretical Nanoscience, 2007, 4, 1365-1368.	0.4	7
40	Poly(A)-Tag Deep Sequencing Data Processing to Extract Poly(A) Sites. Methods in Molecular Biology, 2015, 1255, 39-48.	0.4	6
41	scLINE: A multi-network integration framework based on network embedding for representation of single-cell RNA-seq data. Journal of Biomedical Informatics, 2021, 122, 103899.	2.5	5
42	Computational Analysis of Plant Polyadenylation Signals. Methods in Molecular Biology, 2015, 1255, 3-11.	0.4	5
43	Ratio-Based Analysis of Differential mRNA Processing and Expression of a Polyadenylation Factor Mutant pcfs4 Using Arabidopsis Tiling Microarray. PLoS ONE, 2011, 6, e14719.	1.1	5
44	Regulatory network-based imputation of dropouts in single-cell RNA sequencing data. PLoS Computational Biology, 2022, 18, e1009849.	1.5	5
45	Modeling of Genome-Wide Polyadenylation Signals in Xenopus tropicalis. Frontiers in Genetics, 2019, 10, 647.	1.1	4
46	PAcluster: Clustering polyadenylation site data using canonical correlation analysis. Journal of Bioinformatics and Computational Biology, 2017, 15, 1750018.	0.3	3
47	DNA/RNA Hybrid Primer Mediated Poly(A) Tag Library Construction for Illumina Sequencing. Methods in Molecular Biology, 2015, 1255, 175-184.	0.4	3
48	Prediction of Plant mRNA Polyadenylation Sites. Methods in Molecular Biology, 2015, 1255, 13-23.	0.4	3
49	Messenger RNA Polyadenylation Site Recognition in Green Alga Chlamydomonas Reinhardtii. Lecture Notes in Computer Science, 2010, , 17-26.	1.0	3
50	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
51	Nonconvex Low Tubal Rank Tensor Minimization. IEEE Access, 2019, 7, 170831-170843.	2.6	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.	0.4	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.	3.9	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.	1.2	0
62	PATMAP: Polyadenylation Site Identification from Next-Generation Sequencing Data. Lecture Notes in Computer Science, 2012, , 485-496.	1.0	0
63	Characterization and Recognition of <I>m</I>RNA Alternative Polyadenylation Signals. Advanced Science Letters, 2012, 9, 811-816.	0.2	0