

Congting Ye

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

35
papers

389
citations

12
h-index

19
g-index

38
ext. papers

649
ext. citations

6.5
avg, IF

3.84
L-index

#	Paper	IF	Citations
35	movAPA: modeling and visualization of dynamics of alternative polyadenylation across biological samples. <i>Bioinformatics</i> , 2021 , 37, 2470-2472	7.2	1
34	scAPATrap: identification and quantification of alternative polyadenylation sites from single-cell RNA-seq data. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	4
33	Alternative polyadenylated mRNAs behave as asynchronous rhythmic transcription in. <i>RNA Biology</i> , 2021 , 18, 2594-2604	4.8	1
32	Multi-omics analyses on <i>Kandelia obovata</i> reveal its response to transplanting and genetic differentiation among populations. <i>BMC Plant Biology</i> , 2021 , 21, 341	5.3	
31	QPAT-seq, a rapid and deduplicatable method for quantification of poly(A) site usages. <i>Methods in Enzymology</i> , 2021 , 655, 73-83	1.7	
30	Intragenic heterochromatin-mediated alternative polyadenylation modulates miRNA and pollen development in rice. <i>New Phytologist</i> , 2021 , 232, 835-852	9.8	0
29	Discovery of alternative polyadenylation dynamics from single cell types. <i>Computational and Structural Biotechnology Journal</i> , 2020 , 18, 1012-1019	6.8	1
28	PlantAPAdb: A Comprehensive Database for Alternative Polyadenylation Sites in Plants. <i>Plant Physiology</i> , 2020 , 182, 228-242	6.6	13
27	scHinter: imputing dropout events for single-cell RNA-seq data with limited sample size. <i>Bioinformatics</i> , 2020 , 36, 789-797	7.2	2
26	scDAPA: detection and visualization of dynamic alternative polyadenylation from single cell RNA-seq data. <i>Bioinformatics</i> , 2020 , 36, 1262-1264	7.2	9
25	HDA6-dependent histone deacetylation regulates mRNA polyadenylation in. <i>Genome Research</i> , 2020 , 30, 1407-1417	9.7	11
24	A survey on identification and quantification of alternative polyadenylation sites from RNA-seq data. <i>Briefings in Bioinformatics</i> , 2020 , 21, 1261-1276	13.4	12
23	Identification of putative key genes for coastal environments and cold adaptation in mangrove <i>Kandelia obovata</i> through transcriptome analysis. <i>Science of the Total Environment</i> , 2019 , 681, 191-201	10.2	12
22	Root Hair Single Cell Type Specific Profiles of Gene Expression and Alternative Polyadenylation Under Cadmium Stress. <i>Frontiers in Plant Science</i> , 2019 , 10, 589	6.2	12
21	Role of alternative polyadenylation dynamics in acute myeloid leukaemia at single-cell resolution. <i>RNA Biology</i> , 2019 , 16, 785-797	4.8	18
20	Modeling of Genome-Wide Polyadenylation Signals in. <i>Frontiers in Genetics</i> , 2019 , 10, 647	4.5	2
19	Genome-wide alternative polyadenylation dynamics in response to biotic and abiotic stresses in rice. <i>Ecotoxicology and Environmental Safety</i> , 2019 , 183, 109485	7	16

18	Differential alternative polyadenylation contributes to the developmental divergence between two rice subspecies, japonica and indica. <i>Plant Journal</i> , 2019 , 98, 260-276	6.9	12
17	TSAPA: identification of tissue-specific alternative polyadenylation sites in plants. <i>Bioinformatics</i> , 2018 , 34, 2123-2125	7.2	4
16	APATrap: identification and quantification of alternative polyadenylation sites from RNA-seq data. <i>Bioinformatics</i> , 2018 , 34, 1841-1849	7.2	46
15	Transcriptome profiling during mangrove viviparity in response to abscisic acid. <i>Scientific Reports</i> , 2018 , 8, 770	4.9	7
14	AECS: identifying aberrantly expressed gene sets for differential variability analysis. <i>Bioinformatics</i> , 2018 , 34, 881-883	7.2	3
13	Alternative polyadenylation is involved in auxin-based plant growth and development. <i>Plant Journal</i> , 2018 , 93, 246-258	6.9	21
12	PAcluster: Clustering polyadenylation site data using canonical correlation analysis. <i>Journal of Bioinformatics and Computational Biology</i> , 2017 , 15, 1750018	1	2
11	Genome-Wide Comparative Analysis of Miniature Inverted Repeat Transposable Elements in 19 <i>Arabidopsis thaliana</i> Ecotype Accessions. <i>Scientific Reports</i> , 2017 , 7, 2634	4.9	10
10	detectMITE: A novel approach to detect miniature inverted repeat transposable elements in genomes. <i>Scientific Reports</i> , 2016 , 6, 19688	4.9	27
9	PlantOrDB: a genome-wide ortholog database for land plants and green algae. <i>BMC Plant Biology</i> , 2015 , 15, 161	5.3	10
8	A multiple sequence alignment method with sequence vectorization. <i>Engineering Computations</i> , 2014 , 31, 283-296	1.4	
7	detectIR: a novel program for detecting perfect and imperfect inverted repeats using complex numbers and vector calculation. <i>PLoS ONE</i> , 2014 , 9, e113349	3.7	15
6	LemK_MSA: A Multiple Sequence Alignment Method with Sequence Vectorization Based on Lempel-Ziv. <i>Applied Mechanics and Materials</i> , 2013 , 284-287, 3203-3207	0.3	1
5	Recent Advances in Mathematical Modeling and Simulation of DNA Replication Process.. <i>Current Bioinformatics</i> , 2013 , 8, 591-602	4.7	
4	Determinants of public T cell responses. <i>Cell Research</i> , 2012 , 22, 33-42	24.7	78
3	Recombinatorial biases and convergent recombination determine interindividual TCR β sharing in murine thymocytes. <i>Journal of Immunology</i> , 2012 , 189, 2404-13	5.3	35
2	A Novel Method for Progressive Multiple Sequence Alignment Based on Lempel-Ziv. <i>Lecture Notes in Computer Science</i> , 2009 , 151-158	0.9	2
1	The genomic and transcriptomic foundations of viviparous seed development in mangroves		2

