

Congting Ye

List of Publications by Year in descending order

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Version: 2024-02-01

37
papers

815
citations

516561

16
h-index

580701

25
g-index

38
all docs

38
docs citations

38
times ranked

1183
citing authors

#	ARTICLE	IF	CITATIONS
1	Determinants of public T cell responses. <i>Cell Research</i> , 2012, 22, 33-42.	5.7	110
2	APAtrap: identification and quantification of alternative polyadenylation sites from RNA-seq data. <i>Bioinformatics</i> , 2018, 34, 1841-1849.	1.8	91
3	Transcriptome profiling during mangrove viviparity in response to abscisic acid. <i>Scientific Reports</i> , 2018, 8, 770.	1.6	48
4	Recombinatorial Biases and Convergent Recombination Determine Interindividual TCR $\hat{2}$ Sharing in Murine Thymocytes. <i>Journal of Immunology</i> , 2012, 189, 2404-2413.	0.4	42
5	detectMITE: A novel approach to detect miniature inverted repeat transposable elements in genomes. <i>Scientific Reports</i> , 2016, 6, 19688.	1.6	41
6	Role of alternative polyadenylation dynamics in acute myeloid leukaemia at single-cell resolution. <i>RNA Biology</i> , 2019, 16, 785-797.	1.5	40
7	Alternative polyadenylation is involved in auxin-based plant growth and development. <i>Plant Journal</i> , 2018, 93, 246-258.	2.8	38
8	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
9	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.	3.9	33
10	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
11	PlantAPAdb: A Comprehensive Database for Alternative Polyadenylation Sites in Plants. <i>Plant Physiology</i> , 2020, 182, 228-242.	2.3	30
12	Differential alternative polyadenylation contributes to the developmental divergence between two rice subspecies, <i>japonica</i> and <i>indica</i> . <i>Plant Journal</i> , 2019, 98, 260-276.	2.8	26
13	detectIR: A Novel Program for Detecting Perfect and Imperfect Inverted Repeats Using Complex Numbers and Vector Calculation. <i>PLoS ONE</i> , 2014, 9, e113349.	1.1	25
14	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.	1.7	24
15	scDAPA: detection and visualization of dynamic alternative polyadenylation from single cell RNA-seq data. <i>Bioinformatics</i> , 2020, 36, 1262-1264.	1.8	24
16	scAPAtrap: identification and quantification of alternative polyadenylation sites from single-cell RNA-seq data. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	24
17	HDA6-dependent histone deacetylation regulates mRNA polyadenylation in <i>Arabidopsis</i> . <i>Genome Research</i> , 2020, 30, 1407-1417.	2.4	21
18	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.	1.6	17

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19	scHinter: imputing dropout events for single-cell RNA-seq data with limited sample size. <i>Bioinformatics</i> , 2020, 36, 789-797.	1.8	16
20	Intragenic heterochromatin-mediated alternative polyadenylation modulates miRNA and pollen development in rice. <i>New Phytologist</i> , 2021, 232, 835-852.	3.5	16
21	PlantOrDB: a genome-wide ortholog database for land plants and green algae. <i>BMC Plant Biology</i> , 2015, 15, 161.	1.6	12
22	Discovery of alternative polyadenylation dynamics from single cell types. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 1012-1019.	1.9	9
23	TSAPA: identification of tissue-specific alternative polyadenylation sites in plants. <i>Bioinformatics</i> , 2018, 34, 2123-2125.	1.8	8
24	QuantifyPoly(A): reshaping alternative polyadenylation landscapes of eukaryotes with weighted density peak clustering. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	8
25	movAPA: modeling and visualization of dynamics of alternative polyadenylation across biological samples. <i>Bioinformatics</i> , 2021, 37, 2470-2472.	1.8	8
26	Alternative polyadenylated mRNAs behave as asynchronous rhythmic transcription in Arabidopsis. <i>RNA Biology</i> , 2021, 18, 2594-2604.	1.5	6
27	AECS: identifying aberrantly expressed gene sets for differential variability analysis. <i>Bioinformatics</i> , 2018, 34, 881-883.	1.8	4
28	Modeling of Genome-Wide Polyadenylation Signals in <i>Xenopus tropicalis</i> . <i>Frontiers in Genetics</i> , 2019, 10, 647.	1.1	4
29	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.	1.6	4
30	PAcluster: Clustering polyadenylation site data using canonical correlation analysis. <i>Journal of Bioinformatics and Computational Biology</i> , 2017, 15, 1750018.	0.3	3
31	A Novel Method for Progressive Multiple Sequence Alignment Based on Lempel-Ziv. <i>Lecture Notes in Computer Science</i> , 2009, , 151-158.	1.0	3
32	LemK_MSA: A Multiple Sequence Alignment Method with Sequence Vectorization Based on Lempel-Ziv. <i>Applied Mechanics and Materials</i> , 0, 284-287, 3203-3207.	0.2	1
33	QPAT-seq, a rapid and deduplicatable method for quantification of poly(A) site usages. <i>Methods in Enzymology</i> , 2021, 655, 73-83.	0.4	1
34	Recent Advances in Mathematical Modeling and Simulation of DNA Replication Process.. <i>Current Bioinformatics</i> , 2013, 8, 591-602.	0.7	0
35	A multiple sequence alignment method with sequence vectorization. <i>Engineering Computations</i> , 2014, 31, 283-296.	0.7	0
36	A two-layer model for gene clustering using poly(A) site data. , 2017, , .		0

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37	Plastid development of albino viviparous propagules in woody mangrove <i>Kandelia obovata</i>. Tree Physiology, 0, , .	1.4	0