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List of Publications by Year in descending order

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37
papers

815
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516710

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1183
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#	ARTICLE	IF	CITATIONS
1	scAPATrap: identification and quantification of alternative polyadenylation sites from single-cell RNA-seq data. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	24
2	QPAT-seq, a rapid and deduplicatable method for quantification of poly(A) site usages. <i>Methods in Enzymology</i> , 2021, 655, 73-83.	1.0	1
3	Alternative polyadenylated mRNAs behave as asynchronous rhythmic transcription in <i>Arabidopsis</i> . <i>RNA Biology</i> , 2021, 18, 2594-2604.	3.1	6
4	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.	3.6	4
5	QuantifyPoly(A): reshaping alternative polyadenylation landscapes of eukaryotes with weighted density peak clustering. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	8
6	Intragenic heterochromatin-mediated alternative polyadenylation modulates miRNA and pollen development in rice. <i>New Phytologist</i> , 2021, 232, 835-852.	7.3	16
7	movAPA: modeling and visualization of dynamics of alternative polyadenylation across biological samples. <i>Bioinformatics</i> , 2021, 37, 2470-2472.	4.1	8
8	scHinter: imputing dropout events for single-cell RNA-seq data with limited sample size. <i>Bioinformatics</i> , 2020, 36, 789-797.	4.1	16
9	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
10	scDAPA: detection and visualization of dynamic alternative polyadenylation from single cell RNA-seq data. <i>Bioinformatics</i> , 2020, 36, 1262-1264.	4.1	24
11	HDA6-dependent histone deacetylation regulates mRNA polyadenylation in <i>Arabidopsis</i> . <i>Genome Research</i> , 2020, 30, 1407-1417.	5.5	21
12	Discovery of alternative polyadenylation dynamics from single cell types. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 1012-1019.	4.1	9
13	PlantAPAdb: A Comprehensive Database for Alternative Polyadenylation Sites in Plants. <i>Plant Physiology</i> , 2020, 182, 228-242.	4.8	30
14	Modeling of Genome-Wide Polyadenylation Signals in <i>Xenopus tropicalis</i> . <i>Frontiers in Genetics</i> , 2019, 10, 647.	2.3	4
15	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
16	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.	8.0	33
17	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.	3.6	24
18	Role of alternative polyadenylation dynamics in acute myeloid leukaemia at single-cell resolution. <i>RNA Biology</i> , 2019, 16, 785-797.	3.1	40

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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	TSAPA: identification of tissue-specific alternative polyadenylation sites in plants. <i>Bioinformatics</i> , 2018, 34, 2123-2125.	4.1	8
21	APAttrap: identification and quantification of alternative polyadenylation sites from RNA-seq data. <i>Bioinformatics</i> , 2018, 34, 1841-1849.	4.1	91
22	Transcriptome profiling during mangrove viviparity in response to abscisic acid. <i>Scientific Reports</i> , 2018, 8, 770.	3.3	48
23	AECS: identifying aberrantly expressed gene sets for differential variability analysis. <i>Bioinformatics</i> , 2018, 34, 881-883.	4.1	4
24	Alternative polyadenylation is involved in auxin-based plant growth and development. <i>Plant Journal</i> , 2018, 93, 246-258.	5.7	38
25	PAcluster: Clustering polyadenylation site data using canonical correlation analysis. <i>Journal of Bioinformatics and Computational Biology</i> , 2017, 15, 1750018.	0.8	3
26	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.	3.3	17
27	A two-layer model for gene clustering using poly(A) site data. , 2017, , .		0
28	detectMITE: A novel approach to detect miniature inverted repeat transposable elements in genomes. <i>Scientific Reports</i> , 2016, 6, 19688.	3.3	41
29	PlantOrDB: a genome-wide ortholog database for land plants and green algae. <i>BMC Plant Biology</i> , 2015, 15, 161.	3.6	12
30	A multiple sequence alignment method with sequence vectorization. <i>Engineering Computations</i> , 2014, 31, 283-296.	1.4	0
31	detectIR: A Novel Program for Detecting Perfect and Imperfect Inverted Repeats Using Complex Numbers and Vector Calculation. <i>PLoS ONE</i> , 2014, 9, e113349.	2.5	25
32	Recent Advances in Mathematical Modeling and Simulation of DNA Replication Process.. <i>Current Bioinformatics</i> , 2013, 8, 591-602.	1.5	0
33	Recombinatorial Biases and Convergent Recombination Determine Interindividual TCR β Sharing in Murine Thymocytes. <i>Journal of Immunology</i> , 2012, 189, 2404-2413.	0.8	42
34	Determinants of public T cell responses. <i>Cell Research</i> , 2012, 22, 33-42.	12.0	110
35	A Novel Method for Progressive Multiple Sequence Alignment Based on Lempel-Ziv. <i>Lecture Notes in Computer Science</i> , 2009, , 151-158.	1.3	3
36	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

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37	Plastid development of albino viviparous propagules in woody mangrove <i>Kandelia obovata</i>. Tree Physiology, 0, , .	3.1	0