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List of Publications by Year
in descending order

37 papers	815 citations	516710 16 h-index	580821 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. Cell Research, 2012, 22, 33-42.	12.0	110
2	APAtrap: identification and quantification of alternative polyadenylation sites from RNA-seq data. Bioinformatics, 2018, 34, 1841-1849.	4.1	91
3	Transcriptome profiling during mangrove viviparity in response to abscisic acid. Scientific Reports, 2018, 8, 770.	3.3	48
4	Recombinatorial Biases and Convergent Recombination Determine Interindividual TCRÎ² Sharing in Murine Thymocytes. Journal of Immunology, 2012, 189, 2404-2413.	0.8	42
5	detectMITE: A novel approach to detect miniature inverted repeat transposable elements in genomes. Scientific Reports, 2016, 6, 19688.	3.3	41
6	Role of alternative polyadenylation dynamics in acute myeloid leukaemia at single-cell resolution. RNA Biology, 2019, 16, 785-797.	3.1	40
7	Alternative polyadenylation is involved in auxinâ€based plant growth and development. Plant Journal, 2018, 93, 246-258.	5.7	38
8	Genome-wide alternative polyadenylation dynamics in response to biotic and abiotic stresses in rice. Ecotoxicology and Environmental Safety, 2019, 183, 109485.	6.0	35
9	Identification of putative key genes for coastal environments and cold adaptation in mangrove Kandelia obovata through transcriptome analysis. Science of the Total Environment, 2019, 681, 191-201.	8.0	33
10	A survey on identification and quantification of alternative polyadenylation sites from RNA-seq data. Briefings in Bioinformatics, 2020, 21, 1261-1276.	6.5	33
11	PlantAPAdb: A Comprehensive Database for Alternative Polyadenylation Sites in Plants. Plant Physiology, 2020, 182, 228-242.	4.8	30
12	Differential alternative polyadenylation contributes to the developmental divergence between two rice subspecies, <i>japonica</i> and <i>indica</i>. Plant Journal, 2019, 98, 260-276.	5.7	26
13	detectIR: A Novel Program for Detecting Perfect and Imperfect Inverted Repeats Using Complex Numbers and Vector Calculation. PLoS ONE, 2014, 9, e113349.	2.5	25
14	Root Hair Single Cell Type Specific Profiles of Gene Expression and Alternative Polyadenylation Under Cadmium Stress. Frontiers in Plant Science, 2019, 10, 589.	3.6	24
15	scDAPA: detection and visualization of dynamic alternative polyadenylation from single cell RNA-seq data. Bioinformatics, 2020, 36, 1262-1264.	4.1	24
16	scAPAtrap: identification and quantification of alternative polyadenylation sites from single-cell RNA-seq data. Briefings in Bioinformatics, 2021, 22, .	6.5	24
17	HDA6-dependent histone deacetylation regulates mRNA polyadenylation in <i>Arabidopsis</i>. Genome Research, 2020, 30, 1407-1417.	5.5	21
18	Genome-Wide Comparative Analysis of Miniature Inverted Repeat Transposable Elements in 19 Arabidopsis thaliana Ecotype Accessions. Scientific Reports, 2017, 7, 2634.	3.3	17

#	Article	IF	Citations
19	scHinter: imputing dropout events for single-cell RNA-seq data with limited sample size. Bioinformatics, 2020, 36, 789-797.	4.1	16
20	Intragenic heterochromatinâ€mediated alternative polyadenylation modulates miRNA and pollen development in rice. New Phytologist, 2021, 232, 835-852.	7.3	16
21	PlantOrDB: a genome-wide ortholog database for land plants and green algae. BMC Plant Biology, 2015, 15, 161.	3.6	12
22	Discovery of alternative polyadenylation dynamics from single cell types. Computational and Structural Biotechnology Journal, 2020, 18, 1012-1019.	4.1	9
23	TSAPA: identification of tissue-specific alternative polyadenylation sites in plants. Bioinformatics, 2018, 34, 2123-2125.	4.1	8
24	QuantifyPoly(A): reshaping alternative polyadenylation landscapes of eukaryotes with weighted density peak clustering. Briefings in Bioinformatics, 2021, 22, .	6.5	8
25	movAPA: modeling and visualization of dynamics of alternative polyadenylation across biological samples. Bioinformatics, 2021, 37, 2470-2472.	4.1	8
26	Alternative polyadenylated mRNAs behave as asynchronous rhythmic transcription in Arabidopsis. RNA Biology, 2021, 18, 2594-2604.	3.1	6
27	AEGS: identifying aberrantly expressed gene sets for differential variability analysis. Bioinformatics, 2018, 34, 881-883.	4.1	4
28	Modeling of Genome-Wide Polyadenylation Signals in Xenopus tropicalis. Frontiers in Genetics, 2019, 10, 647.	2.3	4
29	Multi-omics analyses on Kandelia obovata reveal its response to transplanting and genetic differentiation among populations. BMC Plant Biology, 2021, 21, 341.	3.6	4
30	PAcluster: Clustering polyadenylation site data using canonical correlation analysis. Journal of Bioinformatics and Computational Biology, 2017, 15, 1750018.	0.8	3
31	A Novel Method for Progressive Multiple Sequence Alignment Based on Lempel-Ziv. Lecture Notes in Computer Science, 2009, , 151-158.	1.3	3
32	LemK_MSA: A Multiple Sequence Alignment Method with Sequence Vectorization Based on Lempel-Ziv. Applied Mechanics and Materials, 0, 284-287, 3203-3207.	0.2	1
33	QPAT-seq, a rapid and deduplicatable method for quantification of poly(A) site usages. Methods in Enzymology, 2021, 655, 73-83.	1.0	1
34	Recent Advances in Mathematical Modeling and Simulation of DNA Replication Process.. Current Bioinformatics, 2013, 8, 591-602.	1.5	0
35	A multiple sequence alignment method with sequence vectorization. Engineering Computations, 2014, 31, 283-296.	1.4	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 *Kandelia obovata*. Tree Physiology, 0, , .	3.1	0