Runxuan Zhang

List of Publications by Year
in descending order

36 papers	2,428 citations	279798 23 h-index	361022 35 g-index
50 all docs	50 docs citations	50 times ranked	3269 citing authors

#	Article	IF	Citations
1	Experimental Design for Time-Series RNA-Seq Analysis of Gene Expression and Alternative Splicing. Methods in Molecular Biology, 2022, 2398, 173-188.	0.9	2
2	The proteome of developing barley anthers during meiotic prophase I. Journal of Experimental Botany, 2022, 73, 1464-1482.	4.8	3
3	The value of genotype-specific reference for transcriptome analyses in barley. Life Science Alliance, 2022, 5, e202101255.	2.8	2
4	<scp>BaRTv2</scp>: a highly resolved barley reference transcriptome for accurate transcript€specific <scp>RNA</scp>€seq quantification. Plant Journal, 2022, 111, 1183-1202.	5.7	17
5	A high-resolution single-molecule sequencing-based Arabidopsis transcriptome using novel methods of Iso-seq analysis. Genome Biology, 2022, 23, .	8.8	35
6	3D RNA-seq: a powerful and flexible tool for rapid and accurate differential expression and alternative splicing analysis of RNA-seq data for biologists. RNA Biology, 2021, 18, 1574-1587.	3.1	58
7	Differential nucleosome occupancy modulates alternative splicing in <i>Arabidopsis thaliana</i>. New Phytologist, 2021, 229, 1937-1945.	7.3	19
8	Chromatin accessibility landscapes activated by cell-surface and intracellular immune receptors. Journal of Experimental Botany, 2021, 72, 7927-7941.	4.8	14
9	Nonsense-Mediated RNA Decay Factor UPF1 Is Critical for Posttranscriptional and Translational Gene Regulation in Arabidopsis. Plant Cell, 2020, 32, 2725-2741.	6.6	42
10	Downy Mildew effector HaRxL21 interacts with the transcriptional repressor TOPLESS to promote pathogen susceptibility. PLoS Pathogens, 2020, 16, e1008835.	4.7	34
11	Illuminating the dark side of the human transcriptome with long read transcript sequencing. BMC Genomics, 2020, 21, 751.	2.8	97
12	Application of a Sensitive and Reproducible Label-Free Proteomic Approach to Explore the Proteome of Individual Meiotic-Phase Barley Anthers. Frontiers in Plant Science, 2019, 10, 393.	3.6	12
13	Cold-Dependent Expression and Alternative Splicing of Arabidopsis Long Non-coding RNAs. Frontiers in Plant Science, 2019, 10, 235.	3.6	70
14	BaRTv1.0: an improved barley reference transcript dataset to determine accurate changes in the barley transcriptome using RNA-seq. BMC Genomics, 2019, 20, 968.	2.8	50
15	How does temperature affect splicing events? Isoform switching of splicing factors regulates splicing of <i>LATE ELONGATED HYPOCOTYL</i> (<i>LHY</i>). Plant, Cell and Environment, 2018, 41, 1539-1550.	5.7	25
16	Potato miR828 Is Associated With Purple Tuber Skin and Flesh Color. Frontiers in Plant Science, 2018, 9, 1742.	3.6	49
17	Rapid and Dynamic Alternative Splicing Impacts the Arabidopsis Cold Response Transcriptome. Plant Cell, 2018, 30, 1424-1444.	6.6	294
18	The Expressed Portion of the Barley Genome. Compendium of Plant Genomes, 2018, , 89-107.	0.5	0

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19	A high quality Arabidopsis transcriptome for accurate transcript-level analysis of alternative splicing. Nucleic Acids Research, 2017, 45, 5061-5073.	14.5	262
20	Barley SIX-ROWED SPIKE3 encodes a putative Jumonji C-type H3K9me2/me3 demethylase that represses lateral spikelet fertility. Nature Communications, 2017, 8, 936.	12.8	78
21	TSIS: an R package to infer alternative splicing isoform switches for time-series data. Bioinformatics, 2017, 33, 3308-3310.	4.1	58
22	Evaluation and improvement of the regulatory inference for large co-expression networks with limited sample size. BMC Systems Biology, 2017, 11, 62.	3.0	14
23	Highâ€quality reference transcript datasets hold the key to transcriptâ€specific RNAâ€sequencing analysis in plants. New Phytologist, 2017, 213, 525-530.	7.3	35
24	The Dynamics of Transcript Abundance during Cellularization of Developing Barley Endosperm. Plant Physiology, 2016, 170, 1549-1565.	4.8	47
25	Insight on Genes Affecting Tuber Development in Potato upon Potato spindle tuber viroid (PSTVd) Infection. PLoS ONE, 2016, 11, e0150711.	2.5	43
26	At RTD â€" a comprehensive reference transcript dataset resource forÂaccurate quantification of transcriptâ€specific expression in Arabidopsis thaliana. New Phytologist, 2015, 208, 96-101.	7.3	50
27	Physiological, biochemical and molecular responses of the potato (<i><scp>S</scp>olanum) Tj ETQq1 1 0.784314 rgBT /Overlock 10 2014, 37, 439-450.	5.7	196
28	In silico identification and characterization of conserved plant microRNAs in barley. Open Life Sciences, 2014, 9, 841-852.	1.4	1
29	Phytophthora capsici-tomato interaction features dramatic shifts in gene expression associated with a hemi-biotrophic lifestyle. Genome Biology, 2013, 14, R63.	8.8	113
30	Identification and Characterization of miRNA Transcriptome in Potato by High-Throughput Sequencing. PLoS ONE, 2013, 8, e57233.	2.5	119
31	Evaluation for computational platforms of LC-MS based label-free quantitative proteomics: A global view. Journal of Proteomics and Bioinformatics, 2010, 03, 260-265.	0.4	25
32	Deterministic protein inference for shotgun proteomics data provides new insights into Arabidopsis pollen development and function. Genome Research, 2009, 19, 1786-1800.	5.5	151
33	Alignment of LCâ€MS images, with applications to biomarker discovery and protein identification. Proteomics, 2008, 8, 650-672.	2.2	92
34	Comprehensive proteome analysis of <i>Mycobacterium ulcerans</i> and quantitative comparison of mycolactone biosynthesis. Proteomics, 2008, 8, 3124-3138.	2.2	26
35	Multicategory Classification Using An Extreme Learning Machine for Microarray Gene Expression Cancer Diagnosis. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2007, 4, 485-495.	3.0	202
36	Improved GAP-RBF network for classification problems. Neurocomputing, 2007, 70, 3011-3018.	5.9	32