

# Runxuan Zhang

## List of Publications by Year in descending order

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Version: 2024-02-01

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	Rapid and Dynamic Alternative Splicing Impacts the Arabidopsis Cold Response Transcriptome. <i>Plant Cell</i> , 2018, 30, 1424-1444.	6.6	294
2	A high quality Arabidopsis transcriptome for accurate transcript-level analysis of alternative splicing. <i>Nucleic Acids Research</i> , 2017, 45, 5061-5073.	14.5	262
3	Multicategory Classification Using An Extreme Learning Machine for Microarray Gene Expression Cancer Diagnosis. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2007, 4, 485-495.	3.0	202
4	Physiological, biochemical and molecular responses of the potato ( <i>Solanum tuberosum</i> ) to late blight. <i>Plant, Cell &amp; Environment</i> , 2014, 37, 439-450.	5.7	196
5	Deterministic protein inference for shotgun proteomics data provides new insights into Arabidopsis pollen development and function. <i>Genome Research</i> , 2009, 19, 1786-1800.	5.5	151
6	Identification and Characterization of miRNA Transcriptome in Potato by High-Throughput Sequencing. <i>PLoS ONE</i> , 2013, 8, e57233.	2.5	119
7	Phytophthora capsici-tomato interaction features dramatic shifts in gene expression associated with a hemi-biotrophic lifestyle. <i>Genome Biology</i> , 2013, 14, R63.	8.8	113
8	Illuminating the dark side of the human transcriptome with long read transcript sequencing. <i>BMC Genomics</i> , 2020, 21, 751.	2.8	97
9	Alignment of LC-MS images, with applications to biomarker discovery and protein identification. <i>Proteomics</i> , 2008, 8, 650-672.	2.2	92
10	Barley SIX-ROWED SPIKE3 encodes a putative Jumonji C-type H3K9me2/me3 demethylase that represses lateral spikelet fertility. <i>Nature Communications</i> , 2017, 8, 936.	12.8	78
11	Cold-Dependent Expression and Alternative Splicing of Arabidopsis Long Non-coding RNAs. <i>Frontiers in Plant Science</i> , 2019, 10, 235.	3.6	70
12	TSIS: an R package to infer alternative splicing isoform switches for time-series data. <i>Bioinformatics</i> , 2017, 33, 3308-3310.	4.1	58
13	3D RNA-seq: a powerful and flexible tool for rapid and accurate differential expression and alternative splicing analysis of RNA-seq data for biologists. <i>RNA Biology</i> , 2021, 18, 1574-1587.	3.1	58
14	At RTD: a comprehensive reference transcript dataset resource for accurate quantification of transcript-specific expression in Arabidopsis thaliana. <i>New Phytologist</i> , 2015, 208, 96-101.	7.3	50
15	BaRTv1.0: an improved barley reference transcript dataset to determine accurate changes in the barley transcriptome using RNA-seq. <i>BMC Genomics</i> , 2019, 20, 968.	2.8	50
16	Potato miR828 Is Associated With Purple Tuber Skin and Flesh Color. <i>Frontiers in Plant Science</i> , 2018, 9, 1742.	3.6	49
17	The Dynamics of Transcript Abundance during Cellularization of Developing Barley Endosperm. <i>Plant Physiology</i> , 2016, 170, 1549-1565.	4.8	47
18	Insight on Genes Affecting Tuber Development in Potato upon Potato spindle tuber viroid (PSTVd) Infection. <i>PLoS ONE</i> , 2016, 11, e0150711.	2.5	43

#	ARTICLE	IF	CITATIONS
19	Nonsense-Mediated RNA Decay Factor UPF1 Is Critical for Posttranscriptional and Translational Gene Regulation in Arabidopsis. <i>Plant Cell</i> , 2020, 32, 2725-2741.	6.6	42
20	High-quality reference transcript datasets hold the key to transcript-specific RNA-seq analysis in plants. <i>New Phytologist</i> , 2017, 213, 525-530.	7.3	35
21	A high-resolution single-molecule sequencing-based Arabidopsis transcriptome using novel methods of Iso-seq analysis. <i>Genome Biology</i> , 2022, 23, .	8.8	35
22	Downy Mildew effector HaRxL21 interacts with the transcriptional repressor TOPLESS to promote pathogen susceptibility. <i>PLoS Pathogens</i> , 2020, 16, e1008835.	4.7	34
23	Improved GAP-RBF network for classification problems. <i>Neurocomputing</i> , 2007, 70, 3011-3018.	5.9	32
24	Comprehensive proteome analysis of <i>Mycobacterium ulcerans</i> and quantitative comparison of mycolactone biosynthesis. <i>Proteomics</i> , 2008, 8, 3124-3138.	2.2	26
25	How does temperature affect splicing events? Isoform switching of splicing factors regulates splicing of <i>LATE ELONGATED HYPOCOTYL</i> ( <i>LHY</i> ). <i>Plant, Cell and Environment</i> , 2018, 41, 1539-1550.	5.7	25
26	Evaluation for computational platforms of LC-MS based label-free quantitative proteomics: A global view. <i>Journal of Proteomics and Bioinformatics</i> , 2010, 03, 260-265.	0.4	25
27	Differential nucleosome occupancy modulates alternative splicing in <i>Arabidopsis thaliana</i> . <i>New Phytologist</i> , 2021, 229, 1937-1945.	7.3	19
28	<i>BaRTv2</i> : a highly resolved barley reference transcriptome for accurate transcript-specific RNA-seq quantification. <i>Plant Journal</i> , 2022, 111, 1183-1202.	5.7	17
29	Evaluation and improvement of the regulatory inference for large co-expression networks with limited sample size. <i>BMC Systems Biology</i> , 2017, 11, 62.	3.0	14
30	Chromatin accessibility landscapes activated by cell-surface and intracellular immune receptors. <i>Journal of Experimental Botany</i> , 2021, 72, 7927-7941.	4.8	14
31	Application of a Sensitive and Reproducible Label-Free Proteomic Approach to Explore the Proteome of Individual Meiotic-Phase Barley Anthers. <i>Frontiers in Plant Science</i> , 2019, 10, 393.	3.6	12
32	The proteome of developing barley anthers during meiotic prophase I. <i>Journal of Experimental Botany</i> , 2022, 73, 1464-1482.	4.8	3
33	Experimental Design for Time-Series RNA-Seq Analysis of Gene Expression and Alternative Splicing. <i>Methods in Molecular Biology</i> , 2022, 2398, 173-188.	0.9	2
34	The value of genotype-specific reference for transcriptome analyses in barley. <i>Life Science Alliance</i> , 2022, 5, e202101255.	2.8	2
35	In silico identification and characterization of conserved plant microRNAs in barley. <i>Open Life Sciences</i> , 2014, 9, 841-852.	1.4	1
36	The Expressed Portion of the Barley Genome. <i>Compendium of Plant Genomes</i> , 2018, , 89-107.	0.5	0