

Fu-Yuan Zhu

List of Publications by Year in descending order

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36
papers

1,055
citations

430874

18
h-index

434195

31
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39
all docs

39
docs citations

39
times ranked

1147
citing authors

#	ARTICLE	IF	CITATIONS
1	Proteogenomic analysis reveals alternative splicing and translation as part of the abscisic acid response in Arabidopsis seedlings. <i>Plant Journal</i> , 2017, 91, 518-533.	5.7	156
2	Comparative performance of the BGISEQ-500 and Illumina HiSeq4000 sequencing platforms for transcriptome analysis in plants. <i>Plant Methods</i> , 2018, 14, 69.	4.3	128
3	Rhizosheath formation and involvement in foxtail millet (<i>Setaria italica</i>) root growth under drought stress. <i>Journal of Integrative Plant Biology</i> , 2019, 61, 449-462.	8.5	58
4	Full-Length Transcript-Based Proteogenomics of Rice Improves Its Genome and Proteome Annotation. <i>Plant Physiology</i> , 2020, 182, 1510-1526.	4.8	53
5	Alternative splicing and translation play important roles in hypoxic germination in rice. <i>Journal of Experimental Botany</i> , 2019, 70, 817-833.	4.8	51
6	Flavonoids are indispensable for complete male fertility in rice. <i>Journal of Experimental Botany</i> , 2020, 71, 4715-4728.	4.8	48
7	Natural variation in the promoter of rice calcineurin-like protein 10 (<i>OscBL10</i>) affects flooding tolerance during seed germination among rice subspecies. <i>Plant Journal</i> , 2018, 94, 612-625.	5.7	42
8	Recruitment of specific flavonoid ring hydroxylases for two independent biosynthesis pathways of flavone-derived metabolites in grasses. <i>New Phytologist</i> , 2019, 223, 204-219.	7.3	38
9	SWATH-MS-Based Proteomics: Strategies and Applications in Plants. <i>Trends in Biotechnology</i> , 2021, 39, 433-437.	9.3	38
10	SWATH-MS Quantitative Proteomic Investigation Reveals a Role of Jasmonic Acid during Lead Response in <i>Arabidopsis</i> . <i>Journal of Proteome Research</i> , 2016, 15, 3528-3539.	3.7	33
11	SWATH-MS quantitative proteomic investigation of nitrogen starvation in <i>Arabidopsis</i> reveals new aspects of plant nitrogen stress responses. <i>Journal of Proteomics</i> , 2018, 187, 161-170.	2.4	32
12	Sorghum Extracellular Leucine-Rich Repeat Protein SbLRR2 Mediates Lead Tolerance in Transgenic <i>Arabidopsis</i> . <i>Plant and Cell Physiology</i> , 2013, 54, 1549-1559.	3.1	31
13	Comparative metabolite profiling of two switchgrass ecotypes reveals differences in drought stress responses and rhizosheath weight. <i>Planta</i> , 2019, 250, 1355-1369.	3.2	31
14	Alternative splicing and its regulatory role in woody plants. <i>Tree Physiology</i> , 2020, 40, 1475-1486.	3.1	31
15	Phylogenetic comparison of 5' splice site determination in central spliceosomal proteins of the <i>U1</i> gene family, in response to developmental cues and stress conditions. <i>Plant Journal</i> , 2020, 103, 357-378.	5.7	30
16	A Phylogenetically Informed Comparison of GH1 Hydrolases between <i>Arabidopsis</i> and Rice Response to Stressors. <i>Frontiers in Plant Science</i> , 2017, 8, 350.	3.6	27
17	SWATH-MS-facilitated proteomic profiling of fruit skin between Fuji apple and a red skin bud sport mutant. <i>BMC Plant Biology</i> , 2019, 19, 445.	3.6	23
18	Global proteome response to Pb(II) toxicity in poplar using SWATH-MS-based quantitative proteomics investigation. <i>Ecotoxicology and Environmental Safety</i> , 2021, 220, 112410.	6.0	23

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19	ABA Mediates Plant Development and Abiotic Stress via Alternative Splicing. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3796.	4.1	22
20	Alternative Splicing and Its Roles in Plant Metabolism. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7355.	4.1	20
21	Emerging Functions of Plant Serine/Arginine-Rich (SR) Proteins: Lessons from Animals. <i>Critical Reviews in Plant Sciences</i> , 2020, 39, 173-194.	5.7	19
22	Alternative splicing is a <i>Sorghum bicolor</i> defense response to fungal infection. <i>Planta</i> , 2020, 251, 14.	3.2	18
23	Deficiency in flavonoid biosynthesis genes <i>CHS</i> , <i>CHI</i> , and <i>CHIL</i> alters rice flavonoid and lignin profiles. <i>Plant Physiology</i> , 2022, 188, 1993-2011.	4.8	18
24	Phosphoproteomic analysis of the non-seed vascular plant model <i>Selaginella moellendorffii</i> . <i>Proteome Science</i> , 2014, 12, 16.	1.7	16
25	SWATH-MS Quantitative Analysis of Proteins in the Rice Inferior and Superior Spikelets during Grain Filling. <i>Frontiers in Plant Science</i> , 2016, 7, 1926.	3.6	15
26	Evolution by duplication: paleopolyploidy events in plants reconstructed by deciphering the evolutionary history of VOZ transcription factors. <i>BMC Plant Biology</i> , 2018, 18, 256.	3.6	13
27	Quantifying Plant Dynamic Proteomes by SWATH-based Mass Spectrometry. <i>Trends in Plant Science</i> , 2020, 25, 1171-1172.	8.8	11
28	Comparative transcriptome analysis of coleorhiza development in japonica and Indica rice. <i>BMC Plant Biology</i> , 2021, 21, 514.	3.6	7
29	Effect of Alternate Wetting and Drying Irrigation on the Nutritional Qualities of Milled Rice. <i>Frontiers in Plant Science</i> , 2021, 12, 721160.	3.6	6
30	Systematic characterization of the branch point binding protein, splicing factor 1, gene family in plant development and stress responses. <i>BMC Plant Biology</i> , 2020, 20, 379.	3.6	5
31	High-Throughput Sequencing Reveals the Regulatory Networks of Transcriptome and Small RNAs During the Defense Against <i>Marssonina brunnea</i> in Poplar. <i>Frontiers in Plant Science</i> , 2021, 12, 719549.	3.6	5
32	iTRAQ-based quantitative proteomic analysis in vernalization-treated faba bean (<i>Vicia faba</i> L.). <i>PLoS ONE</i> , 2017, 12, e0187436.	2.5	3
33	Transcriptome changes in seeds during coleorhiza hair formation in rice. <i>Crop Journal</i> , 2021, , .	5.2	2
34	Phylogenetic Comparison and Splicing Analysis of the U1 snRNP-specific Protein U1C in Eukaryotes. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 696319.	3.5	1
35	SWATH-MS based quantitative proteomics reveal regulatory metabolism and networks of androdioecy breeding system in <i>Osmanthus fragrans</i> . <i>BMC Plant Biology</i> , 2021, 21, 468.	3.6	1
36	SWATH-MS Approach to Discover Novel Protein Targets and Pathways in Response to Abscisic. <i>Methods in Molecular Biology</i> , 2022, 2462, 191-200.	0.9	0