

Xiang Jin

List of Publications by Year in descending order

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972
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#	ARTICLE	IF	CITATIONS
1	MS4A15 drives ferroptosis resistance through calcium-restricted lipid remodeling. <i>Cell Death and Differentiation</i> , 2022, 29, 670-686.	11.2	35
2	Expression profiling of the mitogen-activated protein kinase gene family reveals their diverse response pattern in two different salt-tolerant <i>Glycyrrhiza</i> species. <i>Genes and Genomics</i> , 2022, , 1.	1.4	0
3	Evolutionary and functional analyses demonstrate conserved ferroptosis protection by Arabidopsis GPXs in mammalian cells. <i>FASEB Journal</i> , 2021, 35, e21550.	0.5	5
4	Transcriptome analysis of <i>Sonneratia caseolaris</i> seedlings under chilling stress. <i>PeerJ</i> , 2021, 9, e11506.	2.0	10
5	Genome-Wide Analysis of MDHAR Gene Family in Four Cotton Species Provides Insights into Fiber Development via Regulating AsA Redox Homeostasis. <i>Plants</i> , 2021, 10, 227.	3.5	9
6	Selection of the reference genes for quantitative gene expression by RT-qPCR in the desert plant <i>Stipagrostis pennata</i> . <i>Scientific Reports</i> , 2021, 11, 21711.	3.3	12
7	Evolutionary Analysis of Calcium-Dependent Protein Kinase in Five Asteraceae Species. <i>Plants</i> , 2020, 9, 32.	3.5	3
8	The first complete chloroplast genome of a mangrove fern, <i>Acrostichum speciosum</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1413-1414.	0.4	2
9	The complete chloroplast genome of <i>Bougainvillea glabra</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 889-890.	0.4	5
10	Comparative Proteomic Analysis of Molecular Differences between Leaves of Wild-Type Upland Cotton and Its Fuzzless-Lintless Mutant. <i>Molecules</i> , 2019, 24, 3769.	3.8	1
11	GhVTC1, the Key Gene for Ascorbate Biosynthesis in <i>Gossypium hirsutum</i> , Involves in Cell Elongation Under Control of Ethylene. <i>Cells</i> , 2019, 8, 1039.	4.1	14
12	Calcium-Dependent Protein Kinase Genes in <i>Glycyrrhiza uralensis</i> Appear to be Involved in Promoting the Biosynthesis of Glycyrrhizic Acid and Flavonoids under Salt Stress. <i>Molecules</i> , 2019, 24, 1837.	3.8	16
13	An improved protein extraction method applied to cotton leaves is compatible with 2-DE and LC-MS. <i>BMC Genomics</i> , 2019, 20, 285.	2.8	7
14	A Cotton (<i>Gossypium hirsutum</i>) Myo-Inositol-1-Phosphate Synthase (GhMIPS1D) Gene Promotes Root Cell Elongation in Arabidopsis. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1224.	4.1	13
15	Genome-Wide Identification and Expression Analysis of the Ascorbate Oxidase Gene Family in <i>Gossypium hirsutum</i> Reveals the Critical Role of GhAO1A in Delaying Dark-Induced Leaf Senescence. <i>International Journal of Molecular Sciences</i> , 2019, 20, 6167.	4.1	11
16	Genome-wide investigation and expression profiling of APX gene family in <i>Gossypium hirsutum</i> provide new insights in redox homeostasis maintenance during different fiber development stages. <i>Molecular Genetics and Genomics</i> , 2018, 293, 685-697.	2.1	47
17	Calcium-Dependent Protein Kinase Family Genes Involved in Ethylene-Induced Natural Rubber Production in Different <i>Hevea brasiliensis</i> Cultivars. <i>International Journal of Molecular Sciences</i> , 2018, 19, 947.	4.1	11
18	Subcellular proteome profiles of different latex fractions revealed washed solutions from rubber particles contain crucial enzymes for natural rubber biosynthesis. <i>Journal of Proteomics</i> , 2018, 182, 53-64.	2.4	17

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19	Proteomic analysis of phytase transgenic and non-transgenic maize seeds. <i>Scientific Reports</i> , 2017, 7, 9246.	3.3	18
20	Expression Profiling of Mitogen-Activated Protein Kinase Genes Reveals Their Evolutionary and Functional Diversity in Different Rubber Tree (<i>Hevea brasiliensis</i>) Cultivars. <i>Genes</i> , 2017, 8, 261.	2.4	23
21	Cotton Ascorbate Oxidase Promotes Cell Growth in Cultured Tobacco Bright Yellow-2 Cells through Generation of Apoplast Oxidation. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1346.	4.1	26
22	Proteomics Profiling Reveals Carbohydrate Metabolic Enzymes and 14-3-3 Proteins Play Important Roles for Starch Accumulation during Cassava Root Tuberization. <i>Scientific Reports</i> , 2016, 6, 19643.	3.3	47
23	Comparative Proteomics Reveals that Phosphorylation of β Carbonic Anhydrase 1 Might be Important for Adaptation to Drought Stress in <i>Brassica napus</i> . <i>Scientific Reports</i> , 2016, 6, 39024.	3.3	37
24	Two-dimensional gel electrophoresis-based analysis provides global insights into the cotton ovule and fiber proteomes. <i>Science China Life Sciences</i> , 2016, 59, 154-163.	4.9	16
25	Two-Dimensional Gel Electrophoresis-Based Proteomic Analysis Reveals N-terminal Truncation of the Hsc70 Protein in Cotton Fibers In Vivo. <i>Scientific Reports</i> , 2016, 6, 36961.	3.3	7
26	Comprehensive Proteomics Analysis of Laticifer Latex Reveals New Insights into Ethylene Stimulation of Natural Rubber Production. <i>Scientific Reports</i> , 2015, 5, 13778.	3.3	66
27	Comparative proteomics of Bt-transgenic and non-transgenic cotton leaves. <i>Proteome Science</i> , 2015, 13, 15.	1.7	41
28	The beta subunit of glyceraldehyde 3-phosphate dehydrogenase is an important factor for maintaining photosynthesis and plant development under salt stress—Based on an integrative analysis of the structural, physiological and proteomic changes in chloroplasts in <i>Thellungiella halophila</i> . <i>Plant Science</i> , 2015, 236, 223-238.	3.6	40
29	Quantitative proteomics and transcriptomics reveal key metabolic processes associated with cotton fiber initiation. <i>Journal of Proteomics</i> , 2015, 114, 16-27.	2.4	35
30	Quantitative proteomics of <i>Sesuvium portulacastrum</i> leaves revealed that ion transportation by V-ATPase and sugar accumulation in chloroplast played crucial roles in halophyte salt tolerance. <i>Journal of Proteomics</i> , 2014, 99, 84-100.	2.4	52
31	Proteomics of <i>Fusarium oxysporum</i> Race 1 and Race 4 Reveals Enzymes Involved in Carbohydrate Metabolism and Ion Transport That Might Play Important Roles in Banana Fusarium Wilt. <i>PLoS ONE</i> , 2014, 9, e113818.	2.5	31
32	Using Genome-Referenced Expressed Sequence Tag Assembly to Analyze the Origin and Expression Patterns of <i>Gossypium hirsutum</i> Transcripts. <i>Journal of Integrative Plant Biology</i> , 2013, 55, 576-585.	8.5	17
33	A Potential Role for CHH DNA Methylation in Cotton Fiber Growth Patterns. <i>PLoS ONE</i> , 2013, 8, e60547.	2.5	28
34	Identification and Analyses of miRNA Genes in Allotetraploid <i>Gossypium hirsutum</i> Fiber Cells Based on the Sequenced Diploid <i>G. Araimondii</i> Genome. <i>Journal of Genetics and Genomics</i> , 2012, 39, 351-360.	3.9	31