Xiang Jin

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/10641464/publications.pdf

Version: 2024-02-01

516710 552781 34 733 16 26 citations h-index g-index papers 34 34 34 972 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Comprehensive Proteomics Analysis of Laticifer Latex Reveals New Insights into Ethylene Stimulation of Natural Rubber Production. Scientific Reports, 2015, 5, 13778.	3.3	66
2	Quantitative proteomics of Sesuvium portulacastrum leaves revealed that ion transportation by V-ATPase and sugar accumulation in chloroplast played crucial roles in halophyte salt tolerance. Journal of Proteomics, 2014, 99, 84-100.	2.4	52
3	Proteomics Profiling Reveals Carbohydrate Metabolic Enzymes and 14-3-3 Proteins Play Important Roles for Starch Accumulation during Cassava Root Tuberization. Scientific Reports, 2016, 6, 19643.	3.3	47
4	Genome-wide investigation and expression profiling of APX gene family in Gossypium hirsutum provide new insights in redox homeostasis maintenance during different fiber development stages. Molecular Genetics and Genomics, 2018, 293, 685-697.	2.1	47
5	Comparative proteomics of Bt-transgenic and non-transgenic cotton leaves. Proteome Science, 2015, 13, 15.	1.7	41
6	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 Thellungiella halophila. Plant Science, 2015, 236, 223-238.	3.6	40
7	Comparative Proteomics Reveals that Phosphorylation of \hat{l}^2 Carbonic Anhydrase 1 Might be Important for Adaptation to Drought Stress in Brassica napus. Scientific Reports, 2016, 6, 39024.	3.3	37
8	Quantitative proteomics and transcriptomics reveal key metabolic processes associated with cotton fiber initiation. Journal of Proteomics, 2015, 114, 16-27.	2.4	35
9	MS4A15 drives ferroptosis resistance through calcium-restricted lipid remodeling. Cell Death and Differentiation, 2022, 29, 670-686.	11.2	35
10	Identification and Analyses of miRNA Genes in Allotetraploid Gossypium hirsutum Fiber Cells Based on the Sequenced Diploid G.Âraimondii Genome. Journal of Genetics and Genomics, 2012, 39, 351-360.	3.9	31
11	Proteomics of Fusarium oxysporum Race 1 and Race 4 Reveals Enzymes Involved in Carbohydrate Metabolism and Ion Transport That Might Play Important Roles in Banana Fusarium Wilt. PLoS ONE, 2014, 9, e113818.	2.5	31
12	A Potential Role for CHH DNA Methylation in Cotton Fiber Growth Patterns. PLoS ONE, 2013, 8, e60547.	2.5	28
13	Cotton Ascorbate Oxidase Promotes Cell Growth in Cultured Tobacco Bright Yellow-2 Cells through Generation of Apoplast Oxidation. International Journal of Molecular Sciences, 2017, 18, 1346.	4.1	26
14	Expression Profiling of Mitogen-Activated Protein Kinase Genes Reveals Their Evolutionary and Functional Diversity in Different Rubber Tree (Hevea brasiliensis) Cultivars. Genes, 2017, 8, 261.	2.4	23
15	Proteomic analysis of phytase transgenic and non-transgenic maize seeds. Scientific Reports, 2017, 7, 9246.	3.3	18
16	Using Genomeâ€ <scp>R</scp> eferenced Expressed Sequence Tag Assembly to Analyze the Origin and Expression Patterns of <i>Gossypium hirsutum</i> Transcripts. Journal of Integrative Plant Biology, 2013, 55, 576-585.	8.5	17
17	Subcellular proteome profiles of different latex fractions revealed washed solutions from rubber particles contain crucial enzymes for natural rubber biosynthesis. Journal of Proteomics, 2018, 182, 53-64.	2.4	17
18	Two-dimensional gel electrophoresis-based analysis provides global insights into the cotton ovule and fiber proteomes. Science China Life Sciences, 2016, 59, 154-163.	4.9	16

#	Article	IF	CITATIONS
19	Calcium-Dependent Protein Kinase Genes in Glycyrrhiza Uralensis Appear to be Involved in Promoting the Biosynthesis of Glycyrrhizic Acid and Flavonoids under Salt Stress. Molecules, 2019, 24, 1837.	3.8	16
20	GhVTC1, the Key Gene for Ascorbate Biosynthesis in Gossypium hirsutum, Involves in Cell Elongation Under Control of Ethylene. Cells, 2019, 8, 1039.	4.1	14
21	A Cotton (Gossypium hirsutum) Myo-Inositol-1-Phosphate Synthase (GhMIPS1D) Gene Promotes Root Cell Elongation in Arabidopsis. International Journal of Molecular Sciences, 2019, 20, 1224.	4.1	13
22	Selection of the reference genes for quantitative gene expression by RT-qPCR in the desert plant Stipagrostis pennata. Scientific Reports, 2021, 11, 21711.	3.3	12
23	Calcium-Dependent Protein Kinase Family Genes Involved in Ethylene-Induced Natural Rubber Production in Different Hevea brasiliensis Cultivars. International Journal of Molecular Sciences, 2018, 19, 947.	4.1	11
24	Genome-Wide Identification and Expression Analysis of the Ascorbate Oxidase Gene Family in Gossypium hirsutum Reveals the Critical Role of GhAO1A in Delaying Dark-Induced Leaf Senescence. International Journal of Molecular Sciences, 2019, 20, 6167.	4.1	11
25	Transcriptome analysis of <i>Sonneratia caseolaris</i> seedlings under chilling stress. PeerJ, 2021, 9, e11506.	2.0	10
26	Genome-Wide Analysis of MDHAR Gene Family in Four Cotton Species Provides Insights into Fiber Development via Regulating AsA Redox Homeostasis. Plants, 2021, 10, 227.	3.5	9
27	Two-Dimensional Gel Electrophoresis-Based Proteomic Analysis Reveals N-terminal Truncation of the Hsc70 Protein in Cotton Fibers In Vivo. Scientific Reports, 2016, 6, 36961.	3.3	7
28	An improved protein extraction method applied to cotton leaves is compatible with 2-DE and LC-MS. BMC Genomics, 2019, 20, 285.	2.8	7
29	The complete chloroplast genome of <i>Bougainvillea glabra</i> . Mitochondrial DNA Part B: Resources, 2020, 5, 889-890.	0.4	5
30	Evolutionary and functional analyses demonstrate conserved ferroptosis protection by Arabidopsis GPXs in mammalian cells. FASEB Journal, 2021, 35, e21550.	0.5	5
31	Evolutionary Analysis of Calcium-Dependent Protein Kinase in Five Asteraceae Species. Plants, 2020, 9, 32.	3.5	3
32	The first complete chloroplast genome of a mangrove fern, Acrostichum speciosum. Mitochondrial DNA Part B: Resources, 2020, 5, 1413-1414.	0.4	2
33	Comparative Proteomic Analysis of Molecular Differences between Leaves of Wild-Type Upland Cotton and Its Fuzzless-Lintless Mutant. Molecules, 2019, 24, 3769.	3.8	1
34	Expression profiling of the mitogen-activated protein kinase gene family reveals their diverse response pattern in two different salt-tolerant Glycyrrhiza species. Genes and Genomics, 2022, , 1.	1.4	0