

Lili Chang

List of Publications by Year in descending order

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16
papers

524
citations

759233

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716
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#	ARTICLE	IF	CITATIONS
1	Comparative Proteomics of <i>Theilungiella halophila</i> Leaves from Plants Subjected to Salinity Reveals the Importance of Chloroplastic Starch and Soluble Sugars in Halophyte Salt Tolerance. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2174-2195.	3.8	136
2	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
3	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
4	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
5	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>Theilungiella halophila</i> . <i>Plant Science</i> , 2015, 236, 223-238.	3.6	40
6	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
7	Systematic comparison of technical details in CBB methods and development of a sensitive GAP stain for comparative proteomic analysis. <i>Electrophoresis</i> , 2012, 33, 296-306.	2.4	26
8	Comparative physiological and proteomic analyses of the chloroplasts in halophyte <i>Sesuvium portulacastrum</i> under differential salt conditions. <i>Journal of Plant Physiology</i> , 2019, 232, 141-150.	3.5	24
9	The chloroplast proteome response to drought stress in cassava leaves. <i>Plant Physiology and Biochemistry</i> , 2019, 142, 351-362.	5.8	23
10	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
11	Comparative Proteomics of Phytase-transgenic Maize Seeds Indicates Environmental Influence is More Important than that of Gene Insertion. <i>Scientific Reports</i> , 2019, 9, 8219.	3.3	16
12	A protein extraction method for low protein concentration solutions compatible with the proteomic analysis of rubber particles. <i>Electrophoresis</i> , 2016, 37, 2930-2939.	2.4	15
13	Secretome Analysis of the Banana Fusarium Wilt Fungi Foc R1 and Foc TR4 Reveals a New Effector OASTL Required for Full Pathogenicity of Foc TR4 in Banana. <i>Biomolecules</i> , 2020, 10, 1430.	4.0	10
14	Proteomic Landscape Has Revealed Small Rubber Particles Are Crucial Rubber Biosynthetic Machines for Ethylene-Stimulation in Natural Rubber Production. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5082.	4.1	9
15	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
16	Genome-wide analysis and phosphorylation sites identification of the <i>14-3-3</i> gene family and functional characterization of <i>MeGRF3</i> in cassava. <i>Physiologia Plantarum</i> , 2020, 169, 244-257.	5.2	5