Sixue Chen

List of Publications by Citations

216 papers	8,004 citations	48 h-index	79 g-index
234 ext. papers	9,800 ext. citations	5.6 avg, IF	6.15 L-index

#	Paper	IF	Citations
216	Mechanisms of plant salt response: insights from proteomics. *Journal of Proteome Research*, **2012**, 11, 49-67	5.6	276
215	Transcriptome analysis of root transporters reveals participation of multiple gene families in the response to cation stress. *Plant Journal*, **2003**, 35, 675-92	6.9	265
214	Comparative proteomics of salt tolerance in Arabidopsis thaliana and Thellungiella halophila. *Journal of Proteome Research*, **2010**, 9, 2584-99	5.6	227
213	Bifurcation of Arabidopsis NLR immune signaling via Ca□+-dependent protein kinases. *PLoS Pathogens*, **2013**, 9, e1003127	7.6	193
212	Composition and content of glucosinolates in developing Arabidopsis thaliana. *Planta*, **2002**, 214, 562-71	4.7	190
211	Advances in plant proteomics. *Proteomics*, **2006**, 6, 5504-16	4.8	188
210	Regulation of plant glucosinolate metabolism. *Planta*, **2007**, 226, 1343-52	4.7	185
209	CYP79F1 and CYP79F2 have distinct functions in the biosynthesis of aliphatic glucosinolates in Arabidopsis. *Plant Journal*, **2003**, 33, 923-37	6.9	183
208	Cell wall proteome in the maize primary root elongation zone. II. Region-specific changes in water soluble and lightly ionically bound proteins under water deficit. *Plant Physiology*, **2007**, 145, 1533-48	6.6	168
207	Ubiquitin-like small archaeal modifier proteins (SAMPs) in Haloferax volcanii. *Nature*, **2010**, 463, 54-60	50.4	147
206	Physiological and proteomic analysis of salinity tolerance in Puccinellia tenuiflora. *Journal of Proteome Research*, **2011**, 10, 3852-70	5.6	145
205	Rapid protein identification using direct infusion nanoelectrospray ionization mass spectrometry. *Proteomics*, **2006**, 6, 16-25	4.8	145
204	Long-distance phloem transport of glucosinolates in Arabidopsis. *Plant Physiology*, **2001**, 127, 194-201	6.6	134
203	Cell wall proteome in the maize primary root elongation zone. I. Extraction and identification of water-soluble and lightly ionically bound proteins. *Plant Physiology*, **2006**, 140, 311-25	6.6	127
202	Update on glucosinolate metabolism and transport. *Plant Physiology and Biochemistry*, **2001**, 39, 743-758	5.4	126
201	Proteomics-based investigation of salt-responsive mechanisms in plant roots. *Journal of Proteomics* , **2013**, 82, 230-53	3.9	124
200	Tyrosine phosphorylation of protein kinase complex BAK1/BIK1 mediates Arabidopsis innate immunity. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 3632-7	11.5	120

199	Arabidopsis thaliana glutamate-cysteine ligase: functional properties, kinetic mechanism, and regulation of activity. *Journal of Biological Chemistry*, **2004**, 279, 33463-70	5.4	112
198	Additional freeze hardiness in wheat acquired by exposure to -3 degreesC is associated with extensive physiological, morphological, and molecular changes. *Journal of Experimental Botany*, **2006**, 57, 3601-18	7	103
197	Gold nanoparticle-enabled blood test for early stage cancer detection and risk assessment. *ACS Applied Materials & Interfaces*, **2015**, 7, 6819-27	9.5	99
196	Functional differentiation of Brassica napus guard cells and mesophyll cells revealed by comparative proteomics. *Molecular and Cellular Proteomics*, **2009**, 8, 752-66	7.6	98
195	Desiccation tolerance mechanism in resurrection fern-ally Selaginella tamariscina revealed by physiological and proteomic analysis. *Journal of Proteome Research*, **2010**, 9, 6561-77	5.6	91
194	Characterization of the maize xylem sap proteome. *Journal of Proteome Research*, **2006**, 5, 963-72	5.6	90
193	The cassava (Manihot esculenta Crantz) root proteome: protein identification and differential expression. *Proteomics*, **2006**, 6, 1588-98	4.8	88
192	Plant single-cell and single-cell-type metabolomics. *Trends in Plant Science*, **2014**, 19, 637-46	13.1	84
191	Recent advances and challenges in plant phosphoproteomics. *Proteomics*, **2015**, 15, 1127-41	4.8	77
190	Ectopic expression of a BZR1-1D transcription factor in brassinosteroid signalling enhances carotenoid accumulation and fruit quality attributes in tomato. *Plant Biotechnology Journal*, **2014**, 12, 105-15	11.6	77
189	Salt stress induced proteome and transcriptome changes in sugar beet monosomic addition line M14. *Journal of Plant Physiology*, **2012**, 169, 839-50	3.6	75
188	A redox-active isopropylmalate dehydrogenase functions in the biosynthesis of glucosinolates and leucine in Arabidopsis. *Plant Journal*, **2009**, 60, 679-90	6.9	75
187	Proteomic identification of differentially expressed proteins in Arabidopsis in response to methyl jasmonate. *Journal of Plant Physiology*, **2011**, 168, 995-1008	3.6	72
186	Functional characterization of AtATM1, AtATM2, and AtATM3, a subfamily of Arabidopsis half-molecule ATP-binding cassette transporters implicated in iron homeostasis. *Journal of Biological Chemistry*, **2007**, 282, 21561-71	5.4	70
185	Phosphorylation of trihelix transcriptional repressor ASR3 by MAP KINASE4 negatively regulates Arabidopsis immunity. *Plant Cell*, **2015**, 27, 839-56	11.6	69
184	Regulation of brassinosteroid receptor BRI1 endocytosis and degradation by plant U-box PUB12/PUB13-mediated ubiquitination. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, E1906-E1915	11.5	68
183	Comparative proteomics of the recently and recurrently formed natural allopolyploid Tragopogon mirus (Asteraceae) and its parents. *New Phytologist*, **2012**, 196, 292-305	9.8	67
182	Comparative Proteomic Analysis of Brassica napus in Response to Drought Stress. *Journal of Proteome Research*, **2015**, 14, 3068-81	5.6	63

181	Proteomic profiling of developing cotton fibers from wild and domesticated Gossypium barbadense. *New Phytologist*, **2013**, 200, 570-582	9.8	63
180	Comparative Proteomic Analysis of Soybean Leaves and Roots by iTRAQ Provides Insights into Response Mechanisms to Short-Term Salt Stress. *Frontiers in Plant Science*, **2016**, 7, 573	6.2	62
179	Abscisic acid-responsive guard cell metabolomes of Arabidopsis wild-type and gpa1 G-protein mutants. *Plant Cell*, **2013**, 25, 4789-811	11.6	59
178	TILLING for allergen reduction and improvement of quality traits in peanut (Arachis hypogaea L.). *BMC Plant Biology*, **2011**, 11, 81	5.3	59
177	Exoproteome of Staphylococcus aureus reveals putative determinants of nasal carriage. *Journal of Proteome Research*, **2011**, 10, 2064-78	5.6	56
176	Analysis of abscisic acid responsive proteins in Brassica napus guard cells by multiplexed isobaric tagging. *Journal of Proteomics*, **2010**, 73, 790-805	3.9	56
175	Jasmonate-mediated stomatal closure under elevated CO revealed by time-resolved metabolomics. *Plant Journal*, **2016**, 88, 947-962	6.9	56
174	Salinity Response in Chloroplasts: Insights from Gene Characterization. *International Journal of Molecular Sciences*, **2017**, 18,	6.3	55
173	The guard cell metabolome: functions in stomatal movement and global food security. *Frontiers in Plant Science*, **2015**, 6, 334	6.2	54
172	Proteomics of Arabidopsis redox proteins in response to methyl jasmonate. *Journal of Proteomics*, **2009**, 73, 30-40	3.9	54
171	Protein phosphorylation in stomatal movement. *Plant Signaling and Behavior*, **2014**, 9, e972845	2.5	52
170	Thiol-based redox proteins in abscisic acid and methyl jasmonate signaling in Brassica napus guard cells. *Plant Journal*, **2014**, 78, 491-515	6.9	50
169	Proteomic insights into seed germination in response to environmental factors. *Proteomics*, **2013**, 13, 1850-70	4.8	50
168	The Receptor Kinases BAK1/SERK4 Regulate Ca Channel-Mediated Cellular Homeostasis for Cell Death Containment. *Current Biology*, **2019**, 29, 3778-3790.e8	6.3	48
167	Comparative proteomic analysis of Puccinellia tenuiflora leaves under Na2CO3 stress. *International Journal of Molecular Sciences*, **2013**, 14, 1740-62	6.3	48
166	Nuclear localization of NPR1 is required for regulation of salicylate tolerance, isochorismate synthase 1 expression and salicylate accumulation in Arabidopsis. *Journal of Plant Physiology*, **2010**, 167, 144-8	3.6	48
165	Plant Vacuolar ATP-binding Cassette Transporters That Translocate Folates and Antifolates in Vitro and Contribute to Antifolate Tolerance in Vivo. *Journal of Biological Chemistry*, **2009**, 284, 8449-60	5.4	48
164	Modulation of RNA polymerase II phosphorylation downstream of pathogen perception orchestrates plant immunity. *Cell Host and Microbe*, **2014**, 16, 748-58	23.4	47

163	Deciphering drought-induced metabolic responses and regulation in developing maize kernels. *Plant Biotechnology Journal*, **2018**, 16, 1616	11.6	45
162	Sugar beet M14 glyoxalase I gene can enhance plant tolerance to abiotic stresses. *Journal of Plant Research*, **2013**, 126, 415-25	2.6	45
161	Proteomics and Phosphoproteomics of Heat Stress-Responsive Mechanisms in Spinach. *Frontiers in Plant Science*, **2018**, 9, 800	6.2	44
160	Bisphenol A and bisphenol S disruptions of the mouse placenta and potential effects on the placenta-brain axis. *Proceedings of the National Academy of Sciences of the United States of America*, **2020**, 117, 4642-4652	11.5	41
159	Proteomic analysis of salt tolerance in sugar beet monosomic addition line M14. *Journal of Proteome Research*, **2013**, 12, 4931-50	5.6	39
158	Proteomics and metabolomics of Arabidopsis responses to perturbation of glucosinolate biosynthesis. *Molecular Plant*, **2012**, 5, 1138-50	14.4	39
157	Functional expression and characterization of the myrosinase MYR1 from Brassica napus in Saccharomyces cerevisiae. *Protein Expression and Purification*, **1999**, 17, 414-20	2	39
156	Na2CO3-responsive mechanisms in halophyte Puccinellia tenuiflora roots revealed by physiological and proteomic analyses. *Scientific Reports*, **2016**, 6, 32717	4.9	38
155	Proteome analysis of Aspergillus flavus isolate-specific responses to oxidative stress in relationship to aflatoxin production capability. *Scientific Reports*, **2018**, 8, 3430	4.9	37
154	Overexpression of S-Adenosyl-l-Methionine Synthetase 2 from Sugar Beet M14 Increased Arabidopsis Tolerance to Salt and Oxidative Stress. *International Journal of Molecular Sciences*, **2017**, 18,	6.3	37
153	Methyl jasmonate responsive proteins in Brassica napus guard cells revealed by iTRAQ-based quantitative proteomics. *Journal of Proteome Research*, **2012**, 11, 3728-42	5.6	37
152	Archaeal JAB1/MPN/MOV34 metalloenzyme (HvJAMM1) cleaves ubiquitin-like small archaeal modifier proteins (SAMPs) from protein-conjugates. *Molecular Microbiology*, **2012**, 86, 971-87	4.1	36
151	Characterization of glucosinolate uptake by leaf protoplasts of Brassica napus. *Journal of Biological Chemistry*, **2000**, 275, 22955-60	5.4	36
150	Quantitative proteomics of tomato defense against Pseudomonas syringae infection. *Proteomics*, **2013**, 13, 1934-46	4.8	35
149	Comparative interactomics: analysis of arabidopsis 14-3-3 complexes reveals highly conserved 14-3-3 interactions between humans and plants. *Journal of Proteome Research*, **2009**, 8, 1913-24	5.6	35
148	Nitrogen starvation-induced accumulation of triacylglycerol in the green algae: evidence for a role for ROC40, a transcription factor involved in circadian rhythm. *Plant Journal*, **2016**, 85, 743-57	6.9	35
147	Proteomics of pollen development and germination. *Journal of Proteome Research*, **2007**, 6, 4556-63	5.6	34
146	Isobaric tags for relative and absolute quantification- based comparative proteomics reveals the features of plasma membrane-associated proteomes of pollen grains and pollen tubes from Lilium davidii. *Journal of Integrative Plant Biology*, **2010**, 52, 1043-58	8.3	33

145	Cytological and Proteomic Analyses of Osmunda cinnamomea Germinating Spores Reveal Characteristics of Fern Spore Germination and Rhizoid Tip Growth. *Molecular and Cellular Proteomics*, **2015**, 14, 2510-34	7.6	32
144	Single-cell-type proteomics: toward a holistic understanding of plant function. *Molecular and Cellular Proteomics*, **2012**, 11, 1622-30	7.6	32
143	Physiological and comparative proteomic analyses of saline-alkali NaHCO3-responses in leaves of halophyte Puccinellia tenuiflora. *Plant and Soil*, **2019**, 437, 137-158	4.2	30
142	cysTMTRAQ-An integrative method for unbiased thiol-based redox proteomics. *Molecular and Cellular Proteomics*, **2015**, 14, 237-42	7.6	30
141	Functional specification of Arabidopsis isopropylmalate isomerases in glucosinolate and leucine biosynthesis. *Plant and Cell Physiology*, **2010**, 51, 1480-7	4.9	30
140	The □-subunit of the SnRK1 complex is phosphorylated by the plant cell death suppressor Adi3. *Plant Physiology*, **2012**, 159, 1277-90	6.6	30
139	Quantitative proteomics and phosphoproteomics of sugar beet monosomic addition line M14 in response to salt stress. *Journal of Proteomics*, **2016**, 143, 286-297	3.9	29
138	Protein-protein interactions in plant mitogen-activated protein kinase cascades. *Journal of Experimental Botany*, **2016**, 67, 607-18	7	28
137	Salinity-Induced Palmella Formation Mechanism in Halotolerant Algae Revealed by Quantitative Proteomics and Phosphoproteomics. *Frontiers in Plant Science*, **2017**, 8, 810	6.2	28
136	Effect of salt treatment on the glucosinolate-myrosinase system in Thellungiella salsuginea. *Plant and Soil*, **2012**, 355, 363-374	4.2	28
135	Analysis of the vacuolar luminal proteome of Saccharomyces cerevisiae. *FEBS Journal*, **2007**, 274, 4287-305	3.7	28
134	PARylation of the forkhead-associated domain protein DAWDLE regulates plant immunity. *EMBO Reports*, **2016**, 17, 1799-1813	6.5	27
133	Gene-expression novelty in allopolyploid cotton: a proteomic perspective. *Genetics*, **2015**, 200, 91-104	4	27
132	Structural and functional evolution of isopropylmalate dehydrogenases in the leucine and glucosinolate pathways of Arabidopsis thaliana. *Journal of Biological Chemistry*, **2011**, 286, 28794-28801	5.4	27
131	Protein profiles reveal diverse responsive signaling pathways in kernels of two maize inbred lines with contrasting drought sensitivity. *International Journal of Molecular Sciences*, **2014**, 15, 18892-918	6.3	26
130	Cloning of a cystatin gene from sugar beet M14 that can enhance plant salt tolerance. *Plant Science* , **2012**, 191-192, 93-9	5.3	26
129	Functional characterization of Arabidopsis thaliana isopropylmalate dehydrogenases reveals their important roles in gametophyte development. *New Phytologist*, **2011**, 189, 160-75	9.8	26
128	Chemodiversity of the Glucosinolate-Myrosinase System at the Single Cell Type Resolution. *Frontiers in Plant Science*, **2019**, 10, 618	6.2	25

127	Polyploidy and the proteome. *Biochimica Et Biophysica Acta - Proteins and Proteomics*, **2016**, 1864, 896-907	4	25
126	Advances in understanding CO2 responsive plant metabolomes in the era of climate change. *Metabolomics*, **2015**, 11, 1478-1491	4.7	25
125	Comparative investigations of the glucosinolate-myrosinase system in Arabidopsis suspension cells and hypocotyls. *Plant and Cell Physiology*, **2008**, 49, 324-33	4.9	25
124	Protein Phosphorylation and Redox Modification in Stomatal Guard Cells. *Frontiers in Physiology*, **2016**, 7, 26	4.6	25
123	Advances in Understanding the Physiological and Molecular Responses of Sugar Beet to Salt Stress. *Frontiers in Plant Science*, **2019**, 10, 1431	6.2	24
122	Metabolomic Responses of Guard Cells and Mesophyll Cells to Bicarbonate. *PLoS ONE*, **2015**, 10, e0144206	3.7	24
121	Molecular reprogramming of Arabidopsis in response to perturbation of jasmonate signaling. *Journal of Proteome Research*, **2014**, 13, 5751-66	5.6	24
120	Adaptive Engineering of Phytochelatin-based Heavy Metal Tolerance. *Journal of Biological Chemistry*, **2015**, 290, 17321-30	5.4	23
119	Salt stress response of membrane proteome of sugar beet monosomic addition line M14. *Journal of Proteomics*, **2015**, 127, 18-33	3.9	23
118	Identification of thioredoxin targets in guard cell enriched epidermal peels using cysTMT proteomics. *Journal of Proteomics*, **2016**, 133, 48-53	3.9	23
117	Proteomics profiling of fiber development and domestication in upland cotton (Gossypium hirsutum L.). *Planta*, **2014**, 240, 1237-51	4.7	23
116	Bicarbonate Induced Redox Proteome Changes in Arabidopsis Suspension Cells. *Frontiers in Plant Science*, **2017**, 8, 58	6.2	23
115	Redox proteomics of tomato in response to Pseudomonas syringae infection. *Horticulture Research*, **2015**, 2, 15043	7.7	23
114	Phosphoproteomics technologies and applications in plant biology research. *Frontiers in Plant Science*, **2015**, 6, 430	6.2	23
113	Chilling-responsive mechanisms in halophyte Puccinellia tenuiflora seedlings revealed from proteomics analysis. *Journal of Proteomics*, **2016**, 143, 365-381	3.9	23
112	Oxidation and phosphorylation of MAP kinase 4 cause protein aggregation. *Biochimica Et Biophysica Acta - Proteins and Proteomics*, **2015**, 1854, 156-65	4	22
111	Metabolomics and Proteomics of Guard Cells in Response to Low CO. *Frontiers in Molecular Biosciences*, **2017**, 4, 51	5.6	22
110	Fern spore germination in response to environmental factors. *Frontiers in Biology*, **2015**, 10, 358-376		22

109	Characterization of glucosinolate--myrosinase system in developing salt cress Thellungiella halophila. *Physiologia Plantarum*, **2009**, 136, 1-9	4.6	22
108	Comparative proteomics and metabolomics of JAZ7-mediated drought tolerance in Arabidopsis. *Journal of Proteomics*, **2019**, 196, 81-91	3.9	21
107	New nodes and edges in the glucosinolate molecular network revealed by proteomics and metabolomics of Arabidopsis myb28/29 and cyp79B2/B3 glucosinolate mutants. *Journal of Proteomics*, **2016**, 138, 1-19	3.9	21
106	Glucosinolate Biosynthesis and the Glucosinolate-Myrosinase System in Plant Defense. *Agronomy*, **2020**, 10, 1786	3.6	21
105	Metabolomics of Early Stage Plant Cell-Microbe Interaction Using Stable Isotope Labeling. *Frontiers in Plant Science*, **2018**, 9, 760	6.2	20
104	The stomata frontline of plant interaction with the environment-perspectives from hormone regulation. *Frontiers in Biology*, **2012**, 7, 96-112		20
103	Bioinformatic analysis of molecular network of glucosinolate biosynthesis. *Computational Biology and Chemistry*, **2011**, 35, 10-8	3.6	20
102	Ubiquitin-Like Proteasome System Represents a Eukaryotic-Like Pathway for Targeted Proteolysis in Archaea. *MBio*, **2016**, 7,	7.8	20
101	Integrated proteomics and metabolomics of Arabidopsis acclimation to gene-dosage dependent perturbation of isopropylmalate dehydrogenases. *PLoS ONE*, **2013**, 8, e57118	3.7	19
100	Profiling thiol redox proteome using isotope tagging mass spectrometry. *Journal of Visualized Experiments*, **2012**,	1.6	19
99	Proteomics characteristics of rice leaves in response to environmental factors. *Frontiers in Biology*, **2010**, 5, 246-254		19
98	CUB domain-containing protein 1 and the epidermal growth factor receptor cooperate to induce cell detachment. *Breast Cancer Research*, **2016**, 18, 80	8.3	19
97	A comparative glycoproteome study of developing endosperm in the hexose-deficient miniature1 (mn1) seed mutant and its wild type Mn1 in maize. *Frontiers in Plant Science*, **2014**, 5, 63	6.2	18
96	Proteomic analysis of sugar beet apomictic monosomic addition line M14. *Journal of Proteomics*, **2009**, 73, 297-308	3.9	18
95	Dihydroxyacid dehydratase is important for gametophyte development and disruption causes increased susceptibility to salinity stress in Arabidopsis. *Journal of Experimental Botany*, **2015**, 66, 879-88	7	17
94	Preparation of Epidermal Peels and Guard Cell Protoplasts for Cellular, Electrophysiological, and -Omics Assays of Guard Cell Function. *Methods in Molecular Biology*, **2016**, 1363, 89-121	1.4	17
93	MPK4 Phosphorylation Dynamics and Interacting Proteins in Plant Immunity. *Journal of Proteome Research*, **2019**, 18, 826-840	5.6	17
92	Directions for research and training in plant omics: Big Questions and Big Data. *Plant Direct*, **2019**, 3, e00133	3.3	16

91	Regulation of BZR1 in fruit ripening revealed by iTRAQ proteomics analysis. *Scientific Reports*, **2016**, 6, 33635	4.9	16
90	Genome-wide identification and homeolog-specific expression analysis of the SnRK2 genes in Brassica napus guard cells. *Plant Molecular Biology*, **2016**, 91, 211-27	4.6	16
89	Treatment with the proteasome inhibitor MG132 during the end of oocyte maturation improves oocyte competence for development after fertilization in cattle. *PLoS ONE*, **2012**, 7, e48613	3.7	16
88	A Phosphorylation Switch on Lon Protease Regulates Bacterial Type III Secretion System in Host. *MBio*, **2018**, 9,	7.8	15
87	Proteomic comparison of basal endosperm in maize miniature1 mutant and its wild-type Mn1. *Frontiers in Plant Science*, **2013**, 4, 211	6.2	15
86	Multiplex quantitative SILAC for analysis of archaeal proteomes: a case study of oxidative stress responses. *Environmental Microbiology*, **2018**, 20, 385-401	5.2	15
85	The Arabidopsis MIK2 receptor elicits immunity by sensing a conserved signature from phytocytokines and microbes. *Nature Communications*, **2021**, 12, 5494	17.4	15
84	S-Nitroso-Proteome Revealed in Stomatal Guard Cell Response to Flg22. *International Journal of Molecular Sciences*, **2020**, 21,	6.3	14
83	Plant Chloroplast Stress Response: Insights from Thiol Redox Proteomics. *Antioxidants and Redox Signaling*, **2020**, 33, 35-57	8.4	14
82	Critical Role of COI1-Dependent Jasmonate Pathway in AAL toxin induced PCD in Tomato Revealed by Comparative Proteomics. *Scientific Reports*, **2016**, 6, 28451	4.9	14
81	Proteomic discovery of HO response in roots and functional characterization of PutGLP gene from alkaligrass. *Planta*, **2018**, 248, 1079-1099	4.7	14
80	Identification of regulatory factors for mesenchymal stem cell-derived salivary epithelial cells in a co-culture system. *PLoS ONE*, **2014**, 9, e112158	3.7	14
79	C4 photosynthetic machinery: insights from maize chloroplast proteomics. *Frontiers in Plant Science* , **2013**, 4, 85	6.2	14
78	Determination of in vivo disulfide-bonded proteins in Arabidopsis. *Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences*, **2009**, 877, 101-4	3.2	14
77	Proteomic Insight into the Response of Arabidopsis Chloroplasts to Darkness. *PLoS ONE*, **2016**, 11, e0154235	3.7	14
76	The C-terminal WD40 repeats on the TOPLESS co-repressor function as a protein-protein interaction surface. *Plant Molecular Biology*, **2019**, 100, 47-58	4.6	14
75	Arabidopsis bioinformatics resources: The current state, challenges, and priorities for the future. *Plant Direct*, **2019**, 3, e00109	3.3	13
74	Hydrogen Peroxide Response in Leaves of Poplar (Populus simonii □Populus nigra) Revealed from Physiological and Proteomic Analyses. *International Journal of Molecular Sciences*, **2017**, 18,	6.3	13

73	Proteome targets of ubiquitin-like samp1ylation are associated with sulfur metabolism and oxidative stress in Haloferax volcanii. *Proteomics*, **2016**, 16, 1100-10	4.8	13
72	Physiological Changes in During the C to CAM Transition Induced by Salt Stress. *Frontiers in Plant Science*, **2020**, 11, 283	6.2	12
71	Differential metabolomic responses of PAMP-triggered immunity and effector-triggered immunity in Arabidopsis suspension cells. *Metabolomics*, **2016**, 12, 1	4.7	12
70	UBASH3A Regulates the Synthesis and Dynamics of TCR-CD3 Complexes. *Journal of Immunology*, **2019**, 203, 2827-2836	5.3	12
69	NaCl-responsive ROS scavenging and energy supply in alkaligrass callus revealed from proteomic analysis. *BMC Genomics*, **2019**, 20, 990	4.5	12
68	Overexpression of a -Adenosylmethionine Decarboxylase from Sugar Beet M14 Increased Salt Tolerance. *International Journal of Molecular Sciences*, **2019**, 20,	6.3	11
67	Quantitative proteomics reveals a role of JAZ7 in plant defense response to Pseudomonas syringae DC3000. *Journal of Proteomics*, **2018**, 175, 114-126	3.9	11
66	Redox regulation of a guard cell SNF1-related protein kinase in , an oilseed crop. *Biochemical Journal*, **2017**, 474, 2585-2599	3.8	11
65	Distinct patterns of the histone marks associated with recruitment of the methionine chain-elongation pathway from leucine biosynthesis. *Journal of Experimental Botany*, **2015**, 66, 805-12	7	11
64	Proteomics and phosphoproteomics revealed molecular networks of stomatal immune responses. *Planta*, **2020**, 252, 66	4.7	11
63	A Robust Methodology for Assessing Differential Homeolog Contributions to the Transcriptomes of Allopolyploids. *Genetics*, **2018**, 210, 883-894	4	11
62	Plant immune responses - from guard cells and local responses to systemic defense against bacterial pathogens. *Plant Signaling and Behavior*, **2019**, 14, e1588667	2.5	10
61	An Erwinia amylovora yjeK mutant exhibits reduced virulence, increased chemical sensitivity and numerous environmentally dependent proteomic alterations. *Molecular Plant Pathology*, **2018**, 19, 1667-1678	5.7	10
60	Stomata Tape-Peel: An Improved Method for Guard Cell Sample Preparation. *Journal of Visualized Experiments*, **2018**,	1.6	10
59	In vivo synthesis and purification of radioactive p-hydroxybenzylglucosinolate in Sinapis alba L. **2000**, 11, 174-178		10
58	Identification of MAPK Substrates Using Quantitative Phosphoproteomics. *Methods in Molecular Biology*, **2017**, 1578, 133-142	1.4	9
57	Characterization of thiol-based redox modifications of SNF1-related protein kinase 2.6-2C. *FEBS Open Bio*, **2018**, 8, 628-645	2.7	9
56	Quantitative proteomics reveals an important role of GsCBRLK in salt stress response of soybean. *Plant and Soil*, **2016**, 402, 159-178	4.2	9

55	Cytological and proteomic analyses of horsetail (Equisetum arvense L.) spore germination. *Frontiers in Plant Science*, **2015**, 6, 441	6.2	9
54	Boosting the globalization of plant proteomics through INPPO: current developments and future prospects. *Proteomics*, **2012**, 12, 359-68	4.8	9
53	Metabolomics of red-light-induced stomatal opening in Arabidopsis thaliana: Coupling with abscisic acid and jasmonic acid metabolism. *Plant Journal*, **2020**, 101, 1331-1348	6.9	8
52	Seaweed natural products modify the host inflammatory response via Nrf2 signaling and alter colon microbiota composition and gene expression. *Free Radical Biology and Medicine*, **2020**, 146, 306-323	7.8	8
51	Integrative omic analysis reveals the improvement of alkaloid accumulation by ultraviolet-B radiation and its upstream regulation in Catharanthus roseus. *Industrial Crops and Products*, **2021**, 166, 113448	5.9	8
50	Vision, challenges and opportunities for a Plant Cell Atlas. *ELife*, **2021**, 10,	8.9	8
49	Targeted Metabolomics of Plant Hormones and Redox Metabolites in Stomatal Immunity. *Methods in Molecular Biology*, **2020**, 2085, 79-92	1.4	8
48	Metabolomic Responses of Arabidopsis Suspension Cells to Bicarbonate under Light and Dark Conditions. *Scientific Reports*, **2016**, 6, 35778	4.9	7
47	Identification of a sugar beet BvM14-MADS box gene through differential gene expression analysis of monosomic addition line M14. *Journal of Plant Physiology*, **2011**, 168, 1980-6	3.6	7
46	The guard cell ionome: Understanding the role of ions in guard cell functions. *Progress in Biophysics and Molecular Biology*, **2019**, 146, 50-62	4.7	7
45	Combined ultraviolet and darkness regulation of medicinal metabolites in Mahonia bealei revealed by proteomics and metabolomics. *Journal of Proteomics*, **2021**, 233, 104081	3.9	7
44	Advances in quantitative proteomics. *Frontiers in Biology*, **2010**, 5, 195-203		6
43	Multi-Omics Revealed Molecular Mechanisms Underlying Guard Cell Systemic Acquired Resistance. *International Journal of Molecular Sciences*, **2020**, 22,	6.3	6
42	Proteomic Analysis Reveals the Leaf Color Regulation Mechanism in Chimera Hosta "Gold Standard" Leaves. *International Journal of Molecular Sciences*, **2016**, 17, 346	6.3	6
41	Advances and perspectives in the metabolomics of stomatal movement and the disease triangle. *Plant Science*, **2021**, 302, 110697	5.3	6
40	Effects of overexpression of jasmonic acid biosynthesis genes on nicotine accumulation in tobacco. *Plant Direct*, **2018**, 2, e00036	3.3	5
39	Proteomic characterization of MPK4 signaling network and putative substrates. *Plant Molecular Biology*, **2019**, 101, 325-339	4.6	5
38	HIV-Enhancing Factors Are Secreted by Reproductive Epithelia upon Inoculation with Bacterial Vaginosis-Associated Bacteria. *Protein and Peptide Letters*, **2015**, 22, 672-80	1.9	5

37	Comparative proteomics of Mesembryanthemum crystallinum guard cells and mesophyll cells in transition from C to CAM. *Journal of Proteomics*, **2021**, 231, 104019	3.9	5
36	Carbohydrate, glutathione, and polyamine metabolism are central to Aspergillus flavus oxidative stress responses over time. *BMC Microbiology*, **2019**, 19, 209	4.5	4
35	Metabolite signatures of grasspea suspension-cultured cells illustrate the complexity of dehydration response. *Planta*, **2019**, 250, 857-871	4.7	4
34	Molecular changes in Mesembryanthemum crystallinum guard cells underlying the C to CAM transition. *Plant Molecular Biology*, **2020**, 103, 653-667	4.6	4
33	Developing a new interdisciplinary lab course for undergraduate and graduate students: Plant cells and proteins. *Biochemistry and Molecular Biology Education*, **2007**, 35, 410-5	1.3	4
32	Functional Characterization of a Sugar Beet Transcription Factor in Salt Stress Tolerance. *International Journal of Molecular Sciences*, **2021**, 22,	6.3	4
31	Three-in-One Simultaneous Extraction of Proteins, Metabolites and Lipids for Multi-Omics. *Frontiers in Genetics*, **2021**, 12, 635971	4.5	4
30	Cardiac MLC2 kinase is localized to the Z-disc and interacts with □actinin2. *Scientific Reports*, **2019**, 9, 12580	4.9	3
29	NaCO-responsive Photosynthetic and ROS Scavenging Mechanisms in Chloroplasts of Alkaligrass Revealed by Phosphoproteomics. *Genomics, Proteomics and Bioinformatics*, **2020**, 18, 271-288	6.5	3
28	Jasmonate induced alternative splicing responses in. *Plant Direct*, **2020**, 4, e00245	3.3	3
27	Hydrotropism in the primary roots of maize. *New Phytologist*, **2020**, 226, 1796-1808	9.8	2
26	Plant Response to Bacterial Pathogens: A Proteomics View **2016**, 203-225		2
25	Negative Regulation of Age-Related Developmental Leaf Senescence by the IAOx Pathway, PEN1, and PEN3. *Frontiers in Plant Science*, **2019**, 10, 1202	6.2	2
24	Membrane Proteomics of Arabidopsis Glucosinolate Mutants and. *Frontiers in Plant Science*, **2017**, 8, 534	6.2	2
23	Integrative Proteomic and Phosphoproteomic Analyses of Pattern- and Effector-Triggered Immunity in Tomato.. *Frontiers in Plant Science*, **2021**, 12, 768693	6.2	2
22	Understanding Information Processes at the Proteomics Level **2014**, 57-72		2
21	Na2CO3-Responsive Photosynthetic and ROS Scavenging Mechanisms in Chloroplasts of Alkaligrass Revealed by Phosphoproteomics		2
20	Guard cell redox proteomics reveals a role of lipid transfer protein in plant defense. *Journal of Proteomics*, **2021**, 242, 104247	3.9	2

19	Untargeted Metabolomics of Arabidopsis Stomatal Immunity. *Methods in Molecular Biology*, **2021**, 2200, 413-424	1.4	2
18	Genome-wide identification of genes and their responses to cold acclimation in .. *PeerJ*, **2022**, 10, e13429	3.1	2
17	Proteomics in the Classroom: An Investigative Study of Proteins in Microorganisms. *American Biology Teacher*, **2012**, 74, 237-243	0.3	1
16	Cys-SH based quantitative redox proteomics of salt induced response in sugar beet monosomic addition line M14. *Botanical Studies*, **2021**, 62, 16	2.3	1
15	Investigating an increase in Florida manatee mortalities using a proteomic approach. *Scientific Reports*, **2021**, 11, 4282	4.9	1
14	New functions of an old kinase MPK4 in guard cells. *Plant Signaling and Behavior*, **2018**, 13, e1477908	2.5	1
13	Carbon Starved Anther modulates sugar and ABA metabolism to protect rice seed germination and seedling fitness. *Plant Physiology*, **2021**, 187, 2405-2418	6.6	1
12	PRP4KA phosphorylates SERRATE for degradation via 20 proteasome to fine-tune miRNA production in .. *Science Advances*, **2022**, 8, eabm8435	14.3	1
11	Proteomic profiling of developing cotton fibers from wild and domesticated Gossypium barbadense **2013**, 200, 570		0
10	Proteomics data of SNF1-related protein kinase 2.4 interacting proteins revealed by immunoprecipitation-mass spectrometry. *Data in Brief*, **2020**, 32, 106326	1.2	0
9	Identification of physiological and morphological traits governing high water use efficiency in alfalfa. *Journal of Agronomy and Crop Science*, **2021**, 207, 644-653	3.9	0
8	Selection and Validation of Reference Genes for RT-qPCR Analysis in under Abiotic Stress. *BioMed Research International*, **2021**, 2021, 4853632	3	0
7	Quantitative redox proteomics revealed molecular mechanisms of salt tolerance in the roots of sugar beet monomeric addition line M14.. *Botanical Studies*, **2022**, 63, 5	2.3	0
6	Inhibitors of ERp44, PDIA1, and AGR2 induce disulfide-mediated oligomerization of Death Receptors 4 and 5 and cancer cell death.. *Cancer Letters*, **2022**, 215604	9.9	0
5	INPPO Actions and Recognition as a Driving Force for Progress in Plant Proteomics: Change of Guard, INPPO Update, and Upcoming Activities. *Proteomics*, **2013**, 13, 3093-3100	4.8	
4	Identification of proteins associated with two diverse Caulobacter phicbkvirus particles. *Archives of Virology*, **2020**, 165, 1995-2002	2.6	
3	Protein complex formation in methionine chain-elongation and leucine biosynthesis. *Scientific Reports*, **2021**, 11, 3524	4.9	
2	Proteomics dataset containing proteins that obscure identification of TOPLESS interactors in. *Data in Brief*, **2018**, 20, 909-916	1.2	

1	Identification of DIR1-Dependant Cellular Responses in Guard Cell Systemic Acquired Resistance.. *Frontiers in Molecular Biosciences*, **2021**, 8, 746523	5.6