

Sixue Chen

List of Publications by Year in descending order

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Version: 2024-02-01

226
papers

10,867
citations

32410

55
h-index

51423

90
g-index

234
all docs

234
docs citations

234
times ranked

13291
citing authors

#	ARTICLE	IF	CITATIONS
1	Mitogen-Activated Protein Kinase 4-Regulated Metabolic Networks. International Journal of Molecular Sciences, 2022, 23, 880.	1.8	5
2	Roles of E3 Ubiquitin Ligases in Plant Responses to Abiotic Stresses. International Journal of Molecular Sciences, 2022, 23, 2308.	1.8	18
3	Suppressing the activation of protein kinase A as a DNA damage-independent mechanistic lead for dihydromethysticin prophylaxis of NNK-induced lung carcinogenesis. Carcinogenesis, 2022, 43, 659-670.	1.3	4
4	PRP4KA phosphorylates SERRATE for degradation via 20 S proteasome to fine-tune miRNA production in Arabidopsis. Science Advances, 2022, 8, eabm8435.	4.7	16
5	Quantitative redox proteomics revealed molecular mechanisms of salt tolerance in the roots of sugar beet monomeric addition line M14. , 2022, 63, 5.		8
6	Inhibitors of ERp44, PDIA1, and AGR2 induce disulfide-mediated oligomerization of Death Receptors 4 and 5 and cancer cell death. Cancer Letters, 2022, 534, 215604.	3.2	4
7	Genome-wide identification of CBF genes and their responses to cold acclimation in Taraxacum kok-saghyz. PeerJ, 2022, 10, e13429.	0.9	8
8	Structural characterization and analysis of different epimers of neutral glycosphingolipid LcGg4 by ion mobility spectrometry-mass spectrometry. Analyst, The, 2022, 147, 3101-3108.	1.7	3
9	Advances in Plant Metabolomics and Its Applications in Stress and Single-Cell Biology. International Journal of Molecular Sciences, 2022, 23, 6985.	1.8	21
10	Overexpression of McHB7 Transcription Factor from Mesembryanthemum crystallinum Improves Plant Salt Tolerance. International Journal of Molecular Sciences, 2022, 23, 7879.	1.8	5
11	Advances and perspectives in the metabolomics of stomatal movement and the disease triangle. Plant Science, 2021, 302, 110697.	1.7	7
12	Comparative proteomics of Mesembryanthemum crystallinum guard cells and mesophyll cells in transition from C3 to CAM. Journal of Proteomics, 2021, 231, 104019.	1.2	10
13	Combined ultraviolet and darkness regulation of medicinal metabolites in Mahonia bealei revealed by proteomics and metabolomics. Journal of Proteomics, 2021, 233, 104081.	1.2	17
14	Protein complex formation in methionine chain-elongation and leucine biosynthesis. Scientific Reports, 2021, 11, 3524.	1.6	0
15	Investigating an increase in Florida manatee mortalities using a proteomic approach. Scientific Reports, 2021, 11, 4282.	1.6	6
16	Selection and Validation of Reference Genes for RT-qPCR Analysis in Spinacia oleracea under Abiotic Stress. BioMed Research International, 2021, 2021, 1-12.	0.9	6
17	Identification of physiological and morphological traits governing high water use efficiency in alfalfa. Journal of Agronomy and Crop Science, 2021, 207, 644-653.	1.7	4
18	Functional Characterization of a Sugar Beet BvbHLH93 Transcription Factor in Salt Stress Tolerance. International Journal of Molecular Sciences, 2021, 22, 3669.	1.8	27

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19	Three-in-One Simultaneous Extraction of Proteins, Metabolites and Lipids for Multi-Omics. <i>Frontiers in Genetics</i> , 2021, 12, 635971.	1.1	22
20	Guard cell redox proteomics reveals a role of lipid transfer protein in plant defense. <i>Journal of Proteomics</i> , 2021, 242, 104247.	1.2	10
21	Proteomics of Homeobox7 Enhanced Salt Tolerance in <i>Mesembryanthemum crystallinum</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 6390.	1.8	12
22	Carbon Starved Anther modulates sugar and ABA metabolism to protect rice seed germination and seedling fitness. <i>Plant Physiology</i> , 2021, 187, 2405-2418.	2.3	11
23	Integrative omic analysis reveals the improvement of alkaloid accumulation by ultraviolet-B radiation and its upstream regulation in <i>Catharanthus roseus</i> . <i>Industrial Crops and Products</i> , 2021, 166, 113448.	2.5	17
24	The Arabidopsis MIK2 receptor elicits immunity by sensing a conserved signature from phytocytokines and microbes. <i>Nature Communications</i> , 2021, 12, 5494.	5.8	54
25	Vision, challenges and opportunities for a Plant Cell Atlas. <i>ELife</i> , 2021, 10, .	2.8	31
26	Untargeted Metabolomics of Arabidopsis Stomatal Immunity. <i>Methods in Molecular Biology</i> , 2021, 2200, 413-424.	0.4	5
27	Multi-Omics Revealed Molecular Mechanisms Underlying Guard Cell Systemic Acquired Resistance. <i>International Journal of Molecular Sciences</i> , 2021, 22, 191.	1.8	15
28	Cys-SH based quantitative redox proteomics of salt induced response in sugar beet monosomic addition line M14. , 2021, 62, 16.		5
29	Integrative Proteomic and Phosphoproteomic Analyses of Pattern- and Effector-Triggered Immunity in Tomato. <i>Frontiers in Plant Science</i> , 2021, 12, 768693.	1.7	11
30	Identification of DIR1-Dependant Cellular Responses in Guard Cell Systemic Acquired Resistance. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 746523.	1.6	0
31	Plant Proteomic Research 4.0: Frontiers in Stress Resilience. <i>International Journal of Molecular Sciences</i> , 2021, 22, 13362.	1.8	0
32	Seaweed natural products modify the host inflammatory response via Nrf2 signaling and alter colon microbiota composition and gene expression. <i>Free Radical Biology and Medicine</i> , 2020, 146, 306-323.	1.3	13
33	Metabolomics of red light-induced stomatal opening in <i>Arabidopsis thaliana</i> : Coupling with abscisic acid and jasmonic acid metabolism. <i>Plant Journal</i> , 2020, 101, 1331-1348.	2.8	25
34	Proteomics data of SNF1-related protein kinase 2.4 interacting proteins revealed by immunoprecipitation-mass spectrometry. <i>Data in Brief</i> , 2020, 32, 106326.	0.5	1
35	Proteomics and phosphoproteomics revealed molecular networks of stomatal immune responses. <i>Planta</i> , 2020, 252, 66.	1.6	17
36	Na ₂ CO ₃ -responsive Photosynthetic and ROS Scavenging Mechanisms in Chloroplasts of Alkaligrass Revealed by Phosphoproteomics. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 271-288.	3.0	10

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37	Glucosinolate Biosynthesis and the Glucosinolate-Myrosinase System in Plant Defense. <i>Agronomy</i> , 2020, 10, 1786.	1.3	56
38	Identification of proteins associated with two diverse Caulobacter phicbkvirus particles. <i>Archives of Virology</i> , 2020, 165, 1995-2002.	0.9	0
39	Jasmonate induced alternative splicing responses in <i>Arabidopsis</i> . <i>Plant Direct</i> , 2020, 4, e00245.	0.8	11
40	Secretome Analysis of Inductive Signals for BM-MSC Transdifferentiation into Salivary Gland Progenitors. <i>International Journal of Molecular Sciences</i> , 2020, 21, 9055.	1.8	7
41	Molecular changes in <i>Mesembryanthemum crystallinum</i> guard cells underlying the C3 to CAM transition. <i>Plant Molecular Biology</i> , 2020, 103, 653-667.	2.0	14
42	Physiological Changes in <i>Mesembryanthemum crystallinum</i> During the C3 to CAM Transition Induced by Salt Stress. <i>Frontiers in Plant Science</i> , 2020, 11, 283.	1.7	26
43	S-Nitroso-Proteome Revealed in Stomatal Guard Cell Response to Flg22. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1688.	1.8	28
44	Hydrotropism in the primary roots of maize. <i>New Phytologist</i> , 2020, 226, 1796-1808.	3.5	11
45	Bisphenol A and bisphenol S disruptions of the mouse placenta and potential effects on the placenta-brain axis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 4642-4652.	3.3	92
46	Plant Chloroplast Stress Response: Insights from Thiol Redox Proteomics. <i>Antioxidants and Redox Signaling</i> , 2020, 33, 35-57.	2.5	29
47	Targeted Metabolomics of Plant Hormones and Redox Metabolites in Stomatal Immunity. <i>Methods in Molecular Biology</i> , 2020, 2085, 79-92.	0.4	19
48	Proteomic characterization of MPK4 signaling network and putative substrates. <i>Plant Molecular Biology</i> , 2019, 101, 325-339.	2.0	10
49	The Receptor Kinases BAK1/SERK4 Regulate Ca ²⁺ Channel-Mediated Cellular Homeostasis for Cell Death Containment. <i>Current Biology</i> , 2019, 29, 3778-3790.e8.	1.8	86
50	Advances in Understanding the Physiological and Molecular Responses of Sugar Beet to Salt Stress. <i>Frontiers in Plant Science</i> , 2019, 10, 1431.	1.7	59
51	UBASH3A Regulates the Synthesis and Dynamics of TCR-CD3 Complexes. <i>Journal of Immunology</i> , 2019, 203, 2827-2836.	0.4	32
52	Negative Regulation of Age-Related Developmental Leaf Senescence by the IAOx Pathway, PEN1, and PEN3. <i>Frontiers in Plant Science</i> , 2019, 10, 1202.	1.7	7
53	Carbohydrate, glutathione, and polyamine metabolism are central to <i>Aspergillus flavus</i> oxidative stress responses over time. <i>BMC Microbiology</i> , 2019, 19, 209.	1.3	18
54	Cardiac MLC2 kinase is localized to the Z-disc and interacts with β -actinin2. <i>Scientific Reports</i> , 2019, 9, 12580.	1.6	7

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55	Metabolite signatures of grasspea suspension-cultured cells illustrate the complexity of dehydration response. <i>Planta</i> , 2019, 250, 857-871.	1.6	7
56	Chemodiversity of the Glucosinolate-Myrosinase System at the Single Cell Type Resolution. <i>Frontiers in Plant Science</i> , 2019, 10, 618.	1.7	56
57	Overexpression of a S-Adenosylmethionine Decarboxylase from Sugar Beet M14 Increased Arabidopsis Salt Tolerance. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1990.	1.8	36
58	Directions for research and training in plant omics: Big Questions and Big Data. <i>Plant Direct</i> , 2019, 3, e00133.	0.8	47
59	Plant immune responses - from guard cells and local responses to systemic defense against bacterial pathogens. <i>Plant Signaling and Behavior</i> , 2019, 14, e1588667.	1.2	24
60	Arabidopsis bioinformatics resources: The current state, challenges, and priorities for the future. <i>Plant Direct</i> , 2019, 3, e00109.	0.8	14
61	Physiological and comparative proteomic analyses of saline-alkali NaHCO ₃ -responses in leaves of halophyte <i>Puccinellia tenuiflora</i> . <i>Plant and Soil</i> , 2019, 437, 137-158.	1.8	41
62	Comparative proteomics and metabolomics of JAZ7-mediated drought tolerance in Arabidopsis. <i>Journal of Proteomics</i> , 2019, 196, 81-91.	1.2	49
63	The C-terminal WD40 repeats on the TOPLESS co-repressor function as a protein-protein interaction surface. <i>Plant Molecular Biology</i> , 2019, 100, 47-58.	2.0	22
64	NaCl-responsive ROS scavenging and energy supply in alkaligrass callus revealed from proteomic analysis. <i>BMC Genomics</i> , 2019, 20, 990.	1.2	19
65	The guard cell ionome: Understanding the role of ions in guard cell functions. <i>Progress in Biophysics and Molecular Biology</i> , 2019, 146, 50-62.	1.4	18
66	MPK4 Phosphorylation Dynamics and Interacting Proteins in Plant Immunity. <i>Journal of Proteome Research</i> , 2019, 18, 826-840.	1.8	35
67	Deciphering drought-induced metabolic responses and regulation in developing maize kernels. <i>Plant Biotechnology Journal</i> , 2018, 16, 1616-1628.	4.1	70
68	Characterization of thiol-based redox modifications of Brassica napus SNF1-related protein kinase 2.6. <i>FEBS Open Bio</i> , 2018, 8, 628-645.	1.0	12
69	Regulation of Arabidopsis brassinosteroid receptor BRI1 endocytosis and degradation by plant U-box PUB12/PUB13-mediated ubiquitination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E1906-E1915.	3.3	134
70	A Phosphorylation Switch on Lon Protease Regulates Bacterial Type III Secretion System in Host. <i>MBio</i> , 2018, 9, .	1.8	37
71	Effects of overexpression of jasmonic acid biosynthesis genes on nicotine accumulation in tobacco. <i>Plant Direct</i> , 2018, 2, e00036.	0.8	11
72	Quantitative proteomics reveals a role of JAZ7 in plant defense response to <i>Pseudomonas syringae</i> DC3000. <i>Journal of Proteomics</i> , 2018, 175, 114-126.	1.2	13

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73	An <i>Erwinia amylovora</i> yjeK mutant exhibits reduced virulence, increased chemical sensitivity and numerous environmentally dependent proteomic alterations. <i>Molecular Plant Pathology</i> , 2018, 19, 1667-1678.	2.0	14
74	Proteome analysis of <i>Aspergillus flavus</i> isolate-specific responses to oxidative stress in relationship to aflatoxin production capability. <i>Scientific Reports</i> , 2018, 8, 3430.	1.6	45
75	A Robust Methodology for Assessing Differential Homeolog Contributions to the Transcriptomes of Allopolyploids. <i>Genetics</i> , 2018, 210, 883-894.	1.2	21
76	Proteomics dataset containing proteins that obscure identification of TOPLESS interactors in <i>Arabidopsis</i> . <i>Data in Brief</i> , 2018, 20, 909-916.	0.5	0
77	New functions of an old kinase MPK4 in guard cells. <i>Plant Signaling and Behavior</i> , 2018, 13, e1477908.	1.2	4
78	Metabolomics of Early Stage Plant Cell-Microbe Interaction Using Stable Isotope Labeling. <i>Frontiers in Plant Science</i> , 2018, 9, 760.	1.7	58
79	Proteomics and Phosphoproteomics of Heat Stress-Responsive Mechanisms in Spinach. <i>Frontiers in Plant Science</i> , 2018, 9, 800.	1.7	79
80	Stomata Tape-Peel: An Improved Method for Guard Cell Sample Preparation. <i>Journal of Visualized Experiments</i> , 2018, . .	0.2	15
81	Proteomic discovery of H ₂ O ₂ response in roots and functional characterization of PutGLP gene from alkaligrass. <i>Planta</i> , 2018, 248, 1079-1099.	1.6	18
82	Multiplex quantitative SILAC for analysis of archaeal proteomes: a case study of oxidative stress responses. <i>Environmental Microbiology</i> , 2018, 20, 385-401.	1.8	21
83	Identification of MAPK Substrates Using Quantitative Phosphoproteomics. <i>Methods in Molecular Biology</i> , 2017, 1578, 133-142.	0.4	18
84	Redox regulation of a guard cell SNF1-related protein kinase in <i>Brassica napus</i> , an oilseed crop. <i>Biochemical Journal</i> , 2017, 474, 2585-2599.	1.7	21
85	Bicarbonate Induced Redox Proteome Changes in <i>Arabidopsis</i> Suspension Cells. <i>Frontiers in Plant Science</i> , 2017, 8, 58.	1.7	36
86	Membrane Proteomics of <i>Arabidopsis</i> Glucosinolate Mutants cyp79B2/B3 and myb28/29. <i>Frontiers in Plant Science</i> , 2017, 8, 534.	1.7	5
87	Salinity-Induced Palmella Formation Mechanism in Halotolerant Algae <i>Dunaliella salina</i> Revealed by Quantitative Proteomics and Phosphoproteomics. <i>Frontiers in Plant Science</i> , 2017, 8, 810.	1.7	41
88	Overexpression of S-Adenosyl-L-Methionine Synthetase 2 from Sugar Beet M14 Increased <i>Arabidopsis</i> Tolerance to Salt and Oxidative Stress. <i>International Journal of Molecular Sciences</i> , 2017, 18, 847.	1.8	65
89	Hydrogen Peroxide Response in Leaves of Poplar (<i>Populus simonii</i> – <i>Populus nigra</i>) Revealed from Physiological and Proteomic Analyses. <i>International Journal of Molecular Sciences</i> , 2017, 18, 2085.	1.8	20
90	Salinity Response in Chloroplasts: Insights from Gene Characterization. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1011.	1.8	94

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91	Metabolomics and Proteomics of Brassica napus Guard Cells in Response to Low CO ₂ . <i>Frontiers in Molecular Biosciences</i> , 2017, 4, 51.	1.6	28
92	Proteomic Analysis Reveals the Leaf Color Regulation Mechanism in Chimera Hosta "Gold Standard" Leaves. <i>International Journal of Molecular Sciences</i> , 2016, 17, 346.	1.8	9
93	Protein Phosphorylation and Redox Modification in Stomatal Guard Cells. <i>Frontiers in Physiology</i> , 2016, 7, 26.	1.3	37
94	Editorial: Plant Single Cell Type Systems Biology. <i>Frontiers in Plant Science</i> , 2016, 7, 35.	1.7	7
95	Comparative Proteomic Analysis of Soybean Leaves and Roots by iTRAQ Provides Insights into Response Mechanisms to Short-Term Salt Stress. <i>Frontiers in Plant Science</i> , 2016, 7, 573.	1.7	89
96	Proteome targets of ubiquitin-like sanylation are associated with sulfur metabolism and oxidative stress in <i>Haloferax volcanii</i> . <i>Proteomics</i> , 2016, 16, 1100-1110.	1.3	16
97	Nitrogen starvation-induced accumulation of triacylglycerol in the green algae: evidence for a role for <i>ROC40</i> , a transcription factor involved in circadian rhythm. <i>Plant Journal</i> , 2016, 85, 743-757.	2.8	49
98	CUB domain-containing protein 1 and the epidermal growth factor receptor cooperate to induce cell detachment. <i>Breast Cancer Research</i> , 2016, 18, 80.	2.2	25
99	Ubiquitin-Like Proteasome System Represents a Eukaryotic-Like Pathway for Targeted Proteolysis in Archaea. <i>MBio</i> , 2016, 7, .	1.8	28
100	Chilling-responsive mechanisms in halophyte <i>Puccinellia tenuiflora</i> seedlings revealed from proteomics analysis. <i>Journal of Proteomics</i> , 2016, 143, 365-381.	1.2	28
101	Quantitative proteomics and phosphoproteomics of sugar beet monosomic addition line M14 in response to salt stress. <i>Journal of Proteomics</i> , 2016, 143, 286-297.	1.2	37
102	Jasmonate-mediated stomatal closure under elevated CO ₂ revealed by time-resolved metabolomics. <i>Plant Journal</i> , 2016, 88, 947-962.	2.8	87
103	Plant Response to Bacterial Pathogens: A Proteomics View. , 2016, , 203-225.		2
104	Metabolomic Responses of Arabidopsis Suspension Cells to Bicarbonate under Light and Dark Conditions. <i>Scientific Reports</i> , 2016, 6, 35778.	1.6	12
105	Critical Role of COI1-Dependent Jasmonate Pathway in AAL toxin induced PCD in Tomato Revealed by Comparative Proteomics. <i>Scientific Reports</i> , 2016, 6, 28451.	1.6	14
106	Na ₂ CO ₃ -responsive mechanisms in halophyte <i>Puccinellia tenuiflora</i> roots revealed by physiological and proteomic analyses. <i>Scientific Reports</i> , 2016, 6, 32717.	1.6	63
107	Regulation of BZR1 in fruit ripening revealed by iTRAQ proteomics analysis. <i>Scientific Reports</i> , 2016, 6, 33635.	1.6	26
108	PARylation of the forkhead-associated domain protein DAWDLE regulates plant immunity. <i>EMBO Reports</i> , 2016, 17, 1799-1813.	2.0	42

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109	Quantitative proteomics reveals an important role of GsCBRLK in salt stress response of soybean. <i>Plant and Soil</i> , 2016, 402, 159-178.	1.8	12
110	Protein-protein interactions in plant mitogen-activated protein kinase cascades. <i>Journal of Experimental Botany</i> , 2016, 67, 607-618.	2.4	35
111	Differential metabolomic responses of PAMP-triggered immunity and effector-triggered immunity in <i>Arabidopsis</i> suspension cells. <i>Metabolomics</i> , 2016, 12, 1.	1.4	23
112	Polyploidy and the proteome. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2016, 1864, 896-907.	1.1	39
113	Genome-wide identification and homeolog-specific expression analysis of the SnRK2 genes in <i>Brassica napus</i> guard cells. <i>Plant Molecular Biology</i> , 2016, 91, 211-227.	2.0	20
114	New nodes and edges in the glucosinolate molecular network revealed by proteomics and metabolomics of <i>Arabidopsis</i> myb28/29 and cyp79B2/B3 glucosinolate mutants. <i>Journal of Proteomics</i> , 2016, 138, 1-19.	1.2	45
115	Identification of thioredoxin targets in guard cell enriched epidermal peels using cystMT proteomics. <i>Journal of Proteomics</i> , 2016, 133, 48-53.	1.2	37
116	Preparation of Epidermal Peels and Guard Cell Protoplasts for Cellular, Electrophysiological, and -Omics Assays of Guard Cell Function. <i>Methods in Molecular Biology</i> , 2016, 1363, 89-121.	0.4	30
117	Proteomic Insight into the Response of <i>Arabidopsis</i> Chloroplasts to Darkness. <i>PLoS ONE</i> , 2016, 11, e0154235.	1.1	20
118	Redox proteomics of tomato in response to <i>Pseudomonas syringae</i> infection. <i>Horticulture Research</i> , 2015, 2, 15043.	2.9	30
119	Metabolomic Responses of Guard Cells and Mesophyll Cells to Bicarbonate. <i>PLoS ONE</i> , 2015, 10, e0144206.	1.1	38
120	Phosphoproteomics technologies and applications in plant biology research. <i>Frontiers in Plant Science</i> , 2015, 6, 430.	1.7	32
121	Cytological and proteomic analyses of horsetail (<i>Equisetum arvense</i> L.) spore germination. <i>Frontiers in Plant Science</i> , 2015, 6, 441.	1.7	11
122	cysTMTRAQ—An Integrative Method for Unbiased Thiol-based Redox Proteomics. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 237-242.	2.5	52
123	Gene-Expression Novelty in Allopolyploid Cotton: A Proteomic Perspective. <i>Genetics</i> , 2015, 200, 91-104.	1.2	37
124	Advances in understanding CO ₂ responsive plant metabolomes in the era of climate change. <i>Metabolomics</i> , 2015, 11, 1478-1491.	1.4	33
125	Dihydroxyacid dehydratase is important for gametophyte development and disruption causes increased susceptibility to salinity stress in <i>Arabidopsis</i> . <i>Journal of Experimental Botany</i> , 2015, 66, 879-888.	2.4	21
126	Distinct patterns of the histone marks associated with recruitment of the methionine chain-elongation pathway from leucine biosynthesis. <i>Journal of Experimental Botany</i> , 2015, 66, 805-812.	2.4	11

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127	Fern spore germination in response to environmental factors. <i>Frontiers in Biology</i> , 2015, 10, 358-376.	0.7	27
128	Cytological and Proteomic Analyses of <i>Osmunda cinnamomea</i> Germinating Spores Reveal Characteristics of Fern Spore Germination and Rhizoid Tip Growth*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2510-2534.	2.5	51
129	Comparative Proteomic Analysis of <i>Brassica napus</i> in Response to Drought Stress. <i>Journal of Proteome Research</i> , 2015, 14, 3068-3081.	1.8	90
130	Adaptive Engineering of Phytochelatin-based Heavy Metal Tolerance. <i>Journal of Biological Chemistry</i> , 2015, 290, 17321-17330.	1.6	26
131	Phosphorylation of Trihelix Transcriptional Repressor ASR3 by MAP KINASE4 Negatively Regulates Arabidopsis Immunity. <i>Plant Cell</i> , 2015, 27, 839-856.	3.1	109
132	Gold Nanoparticle-Enabled Blood Test for Early Stage Cancer Detection and Risk Assessment. <i>ACS Applied Materials & Interfaces</i> , 2015, 7, 6819-6827.	4.0	125
133	The guard cell metabolome: functions in stomatal movement and global food security. <i>Frontiers in Plant Science</i> , 2015, 6, 334.	1.7	71
134	Salt stress response of membrane proteome of sugar beet monosomic addition line M14. <i>Journal of Proteomics</i> , 2015, 127, 18-33.	1.2	25
135	Oxidation and phosphorylation of MAP kinase 4 cause protein aggregation. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015, 1854, 156-165.	1.1	23
136	Recent advances and challenges in plant phosphoproteomics. <i>Proteomics</i> , 2015, 15, 1127-1141.	1.3	112
137	HIV-Enhancing Factors Are Secreted by Reproductive Epithelia upon Inoculation with Bacterial Vaginosis-Associated Bacteria. <i>Protein and Peptide Letters</i> , 2015, 22, 672-680.	0.4	5
138	Proteomic Analysis of Arabidopsis Leaves Subjected to Mechanical Wounding. <i>Current Proteomics</i> , 2015, 12, 124-136.	0.1	1
139	Identification of Regulatory Factors for Mesenchymal Stem Cell-Derived Salivary Epithelial Cells in a Co-Culture System. <i>PLoS ONE</i> , 2014, 9, e112158.	1.1	18
140	Tyrosine phosphorylation of protein kinase complex BAK1/BIK1 mediates <i>Arabidopsis</i> innate immunity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 3632-3637.	3.3	151
141	Protein Profiles Reveal Diverse Responsive Signaling Pathways in Kernels of Two Maize Inbred Lines with Contrasting Drought Sensitivity. <i>International Journal of Molecular Sciences</i> , 2014, 15, 18892-18918.	1.8	31
142	A comparative glycoproteome study of developing endosperm in the hexose-deficient miniature1 (mn1) seed mutant and its wild type Mn1 in maize. <i>Frontiers in Plant Science</i> , 2014, 5, 63.	1.7	31
143	Thiol-based redox proteins in abscisic acid and methyl jasmonate signaling in <i>Brassica napus</i> guard cells. <i>Plant Journal</i> , 2014, 78, 491-515.	2.8	58
144	Modulation of RNA Polymerase II Phosphorylation Downstream of Pathogen Perception Orchestrates Plant Immunity. <i>Cell Host and Microbe</i> , 2014, 16, 748-758.	5.1	70

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145	Molecular Reprogramming of <i>Arabidopsis</i> in Response to Perturbation of Jasmonate Signaling. <i>Journal of Proteome Research</i> , 2014, 13, 5751-5766.	1.8	29
146	Ectopic expression of a <i>BZR1</i> transcription factor in brassinosteroid signalling enhances carotenoid accumulation and fruit quality attributes in tomato. <i>Plant Biotechnology Journal</i> , 2014, 12, 105-115.	4.1	135
147	Protein phosphorylation in stomatal movement. <i>Plant Signaling and Behavior</i> , 2014, 9, e972845.	1.2	65
148	Proteomics profiling of fiber development and domestication in upland cotton (<i>Gossypium hirsutum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.6	25
149	Abscisic Acid-Responsive Guard Cell Metabolomes of <i>Arabidopsis</i> Wild-Type and <i>gpa1</i> G-Protein Mutants. <i>Plant Cell</i> , 2014, 25, 4789-4811.	3.1	79
150	Plant single-cell and single-cell-type metabolomics. <i>Trends in Plant Science</i> , 2014, 19, 637-646.	4.3	110
151	Understanding Information Processes at the Proteomics Level. , 2014, , 57-72.		2
152	Proteomics-based investigation of salt-responsive mechanisms in plant roots. <i>Journal of Proteomics</i> , 2013, 82, 230-253.	1.2	150
153	Sugar beet M14 glyoxalase I gene can enhance plant tolerance to abiotic stresses. <i>Journal of Plant Research</i> , 2013, 126, 415-425.	1.2	56
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