

Sixue Chen

List of Publications by Year in descending order

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226
papers

10,867
citations

28274

55
h-index

45317

90
g-index

234
all docs

234
docs citations

234
times ranked

11968
citing authors

#	ARTICLE	IF	CITATIONS
1	Mechanisms of Plant Salt Response: Insights from Proteomics. <i>Journal of Proteome Research</i> , 2012, 11, 49-67.	3.7	340
2	Transcriptome analysis of root transporters reveals participation of multiple gene families in the response to cation stress. <i>Plant Journal</i> , 2003, 35, 675-692.	5.7	286
3	Comparative Proteomics of Salt Tolerance in <i>Arabidopsis thaliana</i> and <i>Thellungiella halophila</i> . <i>Journal of Proteome Research</i> , 2010, 9, 2584-2599.	3.7	266
4	Bifurcation of Arabidopsis NLR Immune Signaling via Ca ²⁺ -Dependent Protein Kinases. <i>PLoS Pathogens</i> , 2013, 9, e1003127.	4.7	257
5	CYP79F1 and CYP79F2 have distinct functions in the biosynthesis of aliphatic glucosinolates in Arabidopsis. <i>Plant Journal</i> , 2003, 33, 923-937.	5.7	238
6	Advances in plant proteomics. <i>Proteomics</i> , 2006, 6, 5504-5516.	2.2	229
7	Regulation of plant glucosinolate metabolism. <i>Planta</i> , 2007, 226, 1343-1352.	3.2	223
8	Composition and content of glucosinolates in developing Arabidopsis thaliana. <i>Planta</i> , 2002, 214, 562-571.	3.2	219
9	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. <i>Plant Physiology</i> , 2007, 145, 1533-1548.	4.8	196
10	Physiological and Proteomic Analysis of Salinity Tolerance in <i>Puccinellia tenuiflora</i> . <i>Journal of Proteome Research</i> , 2011, 10, 3852-3870.	3.7	187
11	Ubiquitin-like small archaeal modifier proteins (SAMPs) in <i>Haloferax volcanii</i> . <i>Nature</i> , 2010, 463, 54-60.	27.8	170
12	Update on glucosinolate metabolism and transport. <i>Plant Physiology and Biochemistry</i> , 2001, 39, 743-758.	5.8	155
13	Rapid protein identification using direct infusion nanoelectrospray ionization mass spectrometry. <i>Proteomics</i> , 2006, 6, 16-25.	2.2	155
14	Long-Distance Phloem Transport of Glucosinolates in Arabidopsis. <i>Plant Physiology</i> , 2001, 127, 194-201.	4.8	153
15	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.	7.1	151
16	Proteomics-based investigation of salt-responsive mechanisms in plant roots. <i>Journal of Proteomics</i> , 2013, 82, 230-253.	2.4	150
17	Cell Wall Proteome in the Maize Primary Root Elongation Zone. I. Extraction and Identification of Water-Soluble and Lightly Ionically Bound Proteins. <i>Plant Physiology</i> , 2006, 140, 311-325.	4.8	140
18	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.	8.3	135

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19	Regulation of <i>Arabidopsis</i> 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.	7.1	134
20	<i>Arabidopsis thaliana</i> Glutamate-Cysteine Ligase. Journal of Biological Chemistry, 2004, 279, 33463-33470.	3.4	126
21	Gold Nanoparticle-Enabled Blood Test for Early Stage Cancer Detection and Risk Assessment. ACS Applied Materials & Interfaces, 2015, 7, 6819-6827.	8.0	125
22	Desiccation Tolerance Mechanism in Resurrection Fern-Ally <i>Selaginella tamariscina</i> Revealed by Physiological and Proteomic Analysis. Journal of Proteome Research, 2010, 9, 6561-6577.	3.7	116
23	Additional freeze hardiness in wheat acquired by exposure to $\sim 3\text{ }^{\circ}\text{C}$ is associated with extensive physiological, morphological, and molecular changes. Journal of Experimental Botany, 2006, 57, 3601-3618.	4.8	115
24	Recent advances and challenges in plant phosphoproteomics. Proteomics, 2015, 15, 1127-1141.	2.2	112
25	Plant single-cell and single-cell-type metabolomics. Trends in Plant Science, 2014, 19, 637-646.	8.8	110
26	Phosphorylation of Trihelix Transcriptional Repressor ASR3 by MAP KINASE4 Negatively Regulates <i>Arabidopsis</i> Immunity. Plant Cell, 2015, 27, 839-856.	6.6	109
27	Functional Differentiation of <i>Brassica napus</i> Guard Cells and Mesophyll Cells Revealed by Comparative Proteomics. Molecular and Cellular Proteomics, 2009, 8, 752-766.	3.8	106
28	A redox-active isopropylmalate dehydrogenase functions in the biosynthesis of glucosinolates and leucine in <i>Arabidopsis</i> . Plant Journal, 2009, 60, 679-690.	5.7	102
29	Salt stress induced proteome and transcriptome changes in sugar beet monosomic addition line M14. Journal of Plant Physiology, 2012, 169, 839-850.	3.5	101
30	Characterization of the Maize Xylem Sap Proteome. Journal of Proteome Research, 2006, 5, 963-972.	3.7	100
31	Salinity Response in Chloroplasts: Insights from Gene Characterization. International Journal of Molecular Sciences, 2017, 18, 1011.	4.1	94
32	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.	7.1	92
33	The cassava (<i>Manihot esculenta</i> Crantz) root proteome: Protein identification and differential expression. Proteomics, 2006, 6, 1588-1598.	2.2	91
34	Comparative Proteomic Analysis of <i>Brassica napus</i> in Response to Drought Stress. Journal of Proteome Research, 2015, 14, 3068-3081.	3.7	90
35	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.	3.6	89
36	Jasmonate-mediated stomatal closure under elevated CO_2 revealed by time-resolved metabolomics. Plant Journal, 2016, 88, 947-962.	5.7	87

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37	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.	3.9	86
38	TILLING for allergen reduction and improvement of quality traits in peanut (<i>Arachis hypogaea</i> L.). <i>BMC Plant Biology</i> , 2011, 11, 81.	3.6	80
39	Comparative proteomics of the recently and recurrently formed natural allopolyploid <i>Tragopogon mirus</i> (Asteraceae) and its parents. <i>New Phytologist</i> , 2012, 196, 292-305.	7.3	79
40	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.	6.6	79
41	Proteomics and Phosphoproteomics of Heat Stress-Responsive Mechanisms in Spinach. <i>Frontiers in Plant Science</i> , 2018, 9, 800.	3.6	79
42	Proteomic identification of differentially expressed proteins in <i>Arabidopsis</i> in response to methyl jasmonate. <i>Journal of Plant Physiology</i> , 2011, 168, 995-1008.	3.5	78
43	Functional Characterization of AtATM1, AtATM2, and AtATM3, a Subfamily of <i>Arabidopsis</i> Half-molecule ATP-binding Cassette Transporters Implicated in Iron Homeostasis. <i>Journal of Biological Chemistry</i> , 2007, 282, 21561-21571.	3.4	76
44	Proteomic profiling of developing cotton fibers from wild and domesticated <i>Gossypium barbadense</i> . <i>New Phytologist</i> , 2013, 200, 570-582.	7.3	72
45	The guard cell metabolome: functions in stomatal movement and global food security. <i>Frontiers in Plant Science</i> , 2015, 6, 334.	3.6	71
46	Modulation of RNA Polymerase II Phosphorylation Downstream of Pathogen Perception Orchestrates Plant Immunity. <i>Cell Host and Microbe</i> , 2014, 16, 748-758.	11.0	70
47	Deciphering drought-induced metabolic responses and regulation in developing maize kernels. <i>Plant Biotechnology Journal</i> , 2018, 16, 1616-1628.	8.3	70
48	Nuclear localization of NPR1 is required for regulation of salicylate tolerance, isochorismate synthase 1 expression and salicylate accumulation in <i>Arabidopsis</i> . <i>Journal of Plant Physiology</i> , 2010, 167, 144-148.	3.5	66
49	Protein phosphorylation in stomatal movement. <i>Plant Signaling and Behavior</i> , 2014, 9, e972845.	2.4	65
50	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.	4.1	65
51	Proteomic insights into seed germination in response to environmental factors. <i>Proteomics</i> , 2013, 13, 1850-1870.	2.2	63
52	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.	3.3	63
53	Analysis of abscisic acid responsive proteins in <i>Brassica napus</i> guard cells by multiplexed isobaric tagging. <i>Journal of Proteomics</i> , 2010, 73, 790-805.	2.4	60
54	Exoproteome of <i>Staphylococcus aureus</i> Reveals Putative Determinants of Nasal Carriage. <i>Journal of Proteome Research</i> , 2011, 10, 2064-2078.	3.7	59

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55	Advances in Understanding the Physiological and Molecular Responses of Sugar Beet to Salt Stress. <i>Frontiers in Plant Science</i> , 2019, 10, 1431.	3.6	59
56	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.	5.7	58
57	Metabolomics of Early Stage Plant Cell-Microbe Interaction Using Stable Isotope Labeling. <i>Frontiers in Plant Science</i> , 2018, 9, 760.	3.6	58
58	Proteomics of Arabidopsis redox proteins in response to methyl jasmonate. <i>Journal of Proteomics</i> , 2009, 73, 30-40.	2.4	57
59	Sugar beet M14 glyoxalase I gene can enhance plant tolerance to abiotic stresses. <i>Journal of Plant Research</i> , 2013, 126, 415-425.	2.4	56
60	Chemodiversity of the Glucosinolate-Myrosinase System at the Single Cell Type Resolution. <i>Frontiers in Plant Science</i> , 2019, 10, 618.	3.6	56
61	Glucosinolate Biosynthesis and the Glucosinolate-Myrosinase System in Plant Defense. <i>Agronomy</i> , 2020, 10, 1786.	3.0	56
62	The Arabidopsis MIK2 receptor elicits immunity by sensing a conserved signature from phyto cytokines and microbes. <i>Nature Communications</i> , 2021, 12, 5494.	12.8	54
63	Comparative Proteomic Analysis of <i>Puccinellia tenuiflora</i> Leaves under Na ₂ CO ₃ Stress. <i>International Journal of Molecular Sciences</i> , 2013, 14, 1740-1762.	4.1	53
64	Plant Vacuolar ATP-binding Cassette Transporters That Translocate Folates and Antifolates in Vitro and Contribute to Antifolate Tolerance in Vivo. <i>Journal of Biological Chemistry</i> , 2009, 284, 8449-8460.	3.4	52
65	cysTMTRAQ-An Integrative Method for Unbiased Thiol-based Redox Proteomics. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 237-242.	3.8	52
66	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.	3.8	51
67	Nitrogen starvation-induced accumulation of triacylglycerol in the green algae: evidence for a role for ROC40, a transcription factor involved in circadian rhythm. <i>Plant Journal</i> , 2016, 85, 743-757.	5.7	49
68	Comparative proteomics and metabolomics of JAZ7-mediated drought tolerance in Arabidopsis. <i>Journal of Proteomics</i> , 2019, 196, 81-91.	2.4	49
69	Functional Expression and Characterization of the Myrosinase MYR1 from <i>Brassica napus</i> in <i>Saccharomyces cerevisiae</i> . <i>Protein Expression and Purification</i> , 1999, 17, 414-420.	1.3	47
70	Proteomics and Metabolomics of Arabidopsis Responses to Perturbation of Glucosinolate Biosynthesis. <i>Molecular Plant</i> , 2012, 5, 1138-1150.	8.3	47
71	Directions for research and training in plant omics: Big Questions and Big Data. <i>Plant Direct</i> , 2019, 3, e00133.	1.9	47
72	Proteomic Analysis of Salt Tolerance in Sugar Beet Monosomic Addition Line M14. <i>Journal of Proteome Research</i> , 2013, 12, 4931-4950.	3.7	46

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73	New nodes and edges in the glucosinolate molecular network revealed by proteomics and metabolomics of <i>Arabidopsis myb28/29</i> and <i>cyp79B2/B3</i> glucosinolate mutants. <i>Journal of Proteomics</i> , 2016, 138, 1-19.	2.4	45
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.	3.3	45
75	Functional specification of <i>Arabidopsis</i> isopropylmalate isomerases in glucosinolate and leucine biosynthesis. <i>Plant and Cell Physiology</i> , 2010, 51, 1480-1487.	3.1	44
76	Single-cell-type Proteomics: Toward a Holistic Understanding of Plant Function. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1622-1630.	3.8	44
77	Methyl Jasmonate Responsive Proteins in <i>Brassica napus</i> Guard Cells Revealed by iTRAQ-Based Quantitative Proteomics. <i>Journal of Proteome Research</i> , 2012, 11, 3728-3742.	3.7	43
78	Characterization of Glucosinolate Uptake by Leaf Protoplasts of <i>Brassica napus</i> . <i>Journal of Biological Chemistry</i> , 2000, 275, 22955-22960.	3.4	42
79	PARylation of the forkhead-associated domain protein DAWDLE regulates plant immunity. <i>EMBO Reports</i> , 2016, 17, 1799-1813.	4.5	42
80	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.	3.6	41
81	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.	3.7	41
82	Quantitative proteomics of tomato defense against <i>Pseudomonas syringae</i> infection. <i>Proteomics</i> , 2013, 13, 1934-1946.	2.2	40
83	Functional characterization of <i>Arabidopsis thaliana</i> isopropylmalate dehydrogenases reveals their important roles in gametophyte development. <i>New Phytologist</i> , 2011, 189, 160-175.	7.3	39
84	Structural and Functional Evolution of Isopropylmalate Dehydrogenases in the Leucine and Glucosinolate Pathways of <i>Arabidopsis thaliana</i> . <i>Journal of Biological Chemistry</i> , 2011, 286, 28794-28801.	3.4	39
85	Archaeal JAB1/MPN/MOV34 metalloenzyme (HvJAMM1) cleaves ubiquitin-like small archaeal modifier proteins (SAMPs) from protein-conjugates. <i>Molecular Microbiology</i> , 2012, 86, 971-987.	2.5	39
86	Polyploidy and the proteome. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2016, 1864, 896-907.	2.3	39
87	Characterization of glucosinolate myrosinase system in developing salt cress <i>Thellungiella halophila</i> . <i>Physiologia Plantarum</i> , 2009, 136, 1-9.	5.2	38
88	Comparative Interactomics: Analysis of <i>Arabidopsis</i> 14-3-3 Complexes Reveals Highly Conserved 14-3-3 Interactions between Humans and Plants. <i>Journal of Proteome Research</i> , 2009, 8, 1913-1924.	3.7	38
89	Metabolomic Responses of Guard Cells and Mesophyll Cells to Bicarbonate. <i>PLoS ONE</i> , 2015, 10, e0144206.	2.5	38
90	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 <i>Lilium davidii</i> . <i>Journal of Integrative Plant Biology</i> , 2010, 52, 1043-1058.	8.5	37

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91	Gene-Expression Novelty in Allopolyploid Cotton: A Proteomic Perspective. <i>Genetics</i> , 2015, 200, 91-104.	2.9	37
92	Protein Phosphorylation and Redox Modification in Stomatal Guard Cells. <i>Frontiers in Physiology</i> , 2016, 7, 26.	2.8	37
93	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.	2.4	37
94	Identification of thioredoxin targets in guard cell enriched epidermal peels using cystTMT proteomics. <i>Journal of Proteomics</i> , 2016, 133, 48-53.	2.4	37
95	A Phosphorylation Switch on Lon Protease Regulates Bacterial Type III Secretion System in Host. <i>MBio</i> , 2018, 9, .	4.1	37
96	Proteomics of Pollen Development and Germination. <i>Journal of Proteome Research</i> , 2007, 6, 4556-4563.	3.7	36
97	Bicarbonate Induced Redox Proteome Changes in Arabidopsis Suspension Cells. <i>Frontiers in Plant Science</i> , 2017, 8, 58.	3.6	36
98	Overexpression of a S-Adenosylmethionine Decarboxylase from Sugar Beet M14 Increased Arabidopsis Salt Tolerance. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1990.	4.1	36
99	The γ -Subunit of the SnRK1 Complex Is Phosphorylated by the Plant Cell Death Suppressor Adi3. <i>Plant Physiology</i> , 2012, 159, 1277-1290.	4.8	35
100	Protein-protein interactions in plant mitogen-activated protein kinase cascades. <i>Journal of Experimental Botany</i> , 2016, 67, 607-618.	4.8	35
101	MPK4 Phosphorylation Dynamics and Interacting Proteins in Plant Immunity. <i>Journal of Proteome Research</i> , 2019, 18, 826-840.	3.7	35
102	Analysis of the vacuolar luminal proteome of <i>Saccharomyces cerevisiae</i> . <i>FEBS Journal</i> , 2007, 274, 4287-4305.	4.7	33
103	Cloning of a cystatin gene from sugar beet M14 that can enhance plant salt tolerance. <i>Plant Science</i> , 2012, 191-192, 93-99.	3.6	33
104	Advances in understanding CO2 responsive plant metabolomes in the era of climate change. <i>Metabolomics</i> , 2015, 11, 1478-1491.	3.0	33
105	Phosphoproteomics technologies and applications in plant biology research. <i>Frontiers in Plant Science</i> , 2015, 6, 430.	3.6	32
106	UBASH3A Regulates the Synthesis and Dynamics of TCR-CD3 Complexes. <i>Journal of Immunology</i> , 2019, 203, 2827-2836.	0.8	32
107	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.	4.1	31
108	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.	3.6	31

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109	Vision, challenges and opportunities for a Plant Cell Atlas. <i>ELife</i> , 2021, 10, .	6.0	31
110	Effect of salt treatment on the glucosinolate-myrosinase system in <i>Thellungiella salsuginea</i> . <i>Plant and Soil</i> , 2012, 355, 363-374.	3.7	30
111	Redox proteomics of tomato in response to <i>Pseudomonas syringae</i> infection. <i>Horticulture Research</i> , 2015, 2, 15043.	6.3	30
112	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.	0.9	30
113	Molecular Reprogramming of <i>Arabidopsis</i> in Response to Perturbation of Jasmonate Signaling. <i>Journal of Proteome Research</i> , 2014, 13, 5751-5766.	3.7	29
114	Plant Chloroplast Stress Response: Insights from Thiol Redox Proteomics. <i>Antioxidants and Redox Signaling</i> , 2020, 33, 35-57.	5.4	29
115	Comparative Investigations of the Glucosinolate-Myrosinase System in <i>Arabidopsis</i> Suspension Cells and Hypocotyls. <i>Plant and Cell Physiology</i> , 2008, 49, 324-333.	3.1	28
116	Ubiquitin-Like Proteasome System Represents a Eukaryotic-Like Pathway for Targeted Proteolysis in Archaea. <i>MBio</i> , 2016, 7, .	4.1	28
117	Chilling-responsive mechanisms in halophyte <i>Puccinellia tenuiflora</i> seedlings revealed from proteomics analysis. <i>Journal of Proteomics</i> , 2016, 143, 365-381.	2.4	28
118	Metabolomics and Proteomics of <i>Brassica napus</i> Guard Cells in Response to Low CO ₂ . <i>Frontiers in Molecular Biosciences</i> , 2017, 4, 51.	3.5	28
119	S-Nitroso-Proteome Revealed in Stomatal Guard Cell Response to Flg22. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1688.	4.1	28
120	Treatment with the Proteasome Inhibitor MG132 during the End of Oocyte Maturation Improves Oocyte Competence for Development after Fertilization in Cattle. <i>PLoS ONE</i> , 2012, 7, e48613.	2.5	27
121	Fern spore germination in response to environmental factors. <i>Frontiers in Biology</i> , 2015, 10, 358-376.	0.7	27
122	Functional Characterization of a Sugar Beet <i>BvbHLH93</i> Transcription Factor in Salt Stress Tolerance. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3669.	4.1	27
123	Adaptive Engineering of Phytochelatin-based Heavy Metal Tolerance. <i>Journal of Biological Chemistry</i> , 2015, 290, 17321-17330.	3.4	26
124	Regulation of BZR1 in fruit ripening revealed by iTRAQ proteomics analysis. <i>Scientific Reports</i> , 2016, 6, 33635.	3.3	26
125	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.	3.6	26
126	Bioinformatic analysis of molecular network of glucosinolate biosynthesis. <i>Computational Biology and Chemistry</i> , 2011, 35, 10-18.	2.3	25

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127	Proteomics profiling of fiber development and domestication in upland cotton (<i>Gossypium hirsutum</i>) Tj ETQq1 1 0.784314 rgBT /Ove	3.2	25
128	Salt stress response of membrane proteome of sugar beet monosomic addition line M14. <i>Journal of Proteomics</i> , 2015, 127, 18-33.	2.4	25
129	CUB domain-containing protein 1 and the epidermal growth factor receptor cooperate to induce cell detachment. <i>Breast Cancer Research</i> , 2016, 18, 80.	5.0	25
130	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.	5.7	25
131	Proteomics characteristics of rice leaves in response to environmental factors. <i>Frontiers in Biology</i> , 2010, 5, 246-254.	0.7	24
132	Integrated Proteomics and Metabolomics of Arabidopsis Acclimation to Gene-Dosage Dependent Perturbation of Isopropylmalate Dehydrogenases. <i>PLoS ONE</i> , 2013, 8, e57118.	2.5	24
133	Plant immune responses - from guard cells and local responses to systemic defense against bacterial pathogens. <i>Plant Signaling and Behavior</i> , 2019, 14, e1588667.	2.4	24
134	Oxidation and phosphorylation of MAP kinase 4 cause protein aggregation. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015, 1854, 156-165.	2.3	23
135	Differential metabolomic responses of PAMP-triggered immunity and effector-triggered immunity in Arabidopsis suspension cells. <i>Metabolomics</i> , 2016, 12, 1.	3.0	23
136	The stomata frontline of plant interaction with the environment-perspectives from hormone regulation. <i>Frontiers in Biology</i> , 2012, 7, 96-112.	0.7	22
137	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.	3.9	22
138	Three-in-One Simultaneous Extraction of Proteins, Metabolites and Lipids for Multi-Omics. <i>Frontiers in Genetics</i> , 2021, 12, 635971.	2.3	22
139	Dihydroxyacid dehydratase is important for gametophyte development and disruption causes increased susceptibility to salinity stress in Arabidopsis. <i>Journal of Experimental Botany</i> , 2015, 66, 879-888.	4.8	21
140	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.	3.7	21
141	A Robust Methodology for Assessing Differential Homeolog Contributions to the Transcriptomes of Allopolyploids. <i>Genetics</i> , 2018, 210, 883-894.	2.9	21
142	Multiplex quantitative SILAC for analysis of archaeal proteomes: a case study of oxidative stress responses. <i>Environmental Microbiology</i> , 2018, 20, 385-401.	3.8	21
143	Advances in Plant Metabolomics and Its Applications in Stress and Single-Cell Biology. <i>International Journal of Molecular Sciences</i> , 2022, 23, 6985.	4.1	21
144	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.	3.9	20

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145	Hydrogen Peroxide Response in Leaves of Poplar (<i>Populus simonii</i> Å— <i>Populus nigra</i>) Revealed from Physiological and Proteomic Analyses. <i>International Journal of Molecular Sciences</i> , 2017, 18, 2085.	4.1	20
146	Proteomic Insight into the Response of Arabidopsis Chloroplasts to Darkness. <i>PLoS ONE</i> , 2016, 11, e0154235.	2.5	20
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