

# Shaojun Dai

## List of Publications by Year in descending order

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Version: 2024-02-01

65  
papers

3,961  
citations

147801

31  
h-index

128289

60  
g-index

72  
all docs

72  
docs citations

72  
times ranked

4389  
citing authors

#	ARTICLE	IF	CITATIONS
1	Plant immunity suppression via PHR1â€RALFâ€FERONIA shapes the root microbiome to alleviate phosphate starvation. <i>EMBO Journal</i> , 2022, 41, e109102.	7.8	58
2	Arabidopsis CAP1 mediates ammonium-regulated root hair growth by influencing vesicle trafficking and the cytoskeletal arrangement in root hair cells. <i>Journal of Genetics and Genomics</i> , 2022, 49, 986-989.	3.9	4
3	Pto Interaction Proteins: Critical Regulators in Plant Development and Stress Response. <i>Frontiers in Plant Science</i> , 2022, 13, 774229.	3.6	6
4	The ubiquitinâ€proteasome system regulates meiotic chromosome organization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2106902119.	7.1	11
5	Multilayered synergistic regulation of phytoalexin biosynthesis by ethylene, jasmonate, and MAPK signaling pathways in Arabidopsis. <i>Plant Cell</i> , 2022, 34, 3066-3087.	6.6	30
6	Genome-wide identification and expression analysis reveals spinach brassinosteroid-signaling kinase (BSK) gene family functions in temperature stress response. <i>BMC Genomics</i> , 2022, 23, .	2.8	5
7	Selection and Validation of Reference Genes for RT-qPCR Analysis in Spinacia oleracea under Abiotic Stress. <i>BioMed Research International</i> , 2021, 2021, 1-12.	1.9	6
8	Exploring the diversity of plant proteome. <i>Journal of Integrative Plant Biology</i> , 2021, 63, 1197-1210.	8.5	12
9	Genome-wide identification of PTI1 family in Setaria italica and salinity-responsive functional analysis of SiPTI1â€5. <i>BMC Plant Biology</i> , 2021, 21, 319.	3.6	8
10	MPK3/6â€induced degradation of ARR1/10/12 promotes salt tolerance in Arabidopsis. <i>EMBO Reports</i> , 2021, 22, e52457.	4.5	37
11	Establishment of an efficient Agrobacterium-mediated genetic transformation system in halophyte Puccinellia tenuiflora. <i>Molecular Breeding</i> , 2021, 41, 1.	2.1	6
12	Phosphoproteomic Profiling Reveals Early Salt-Responsive Mechanisms in Two Foxtail Millet Cultivars. <i>Frontiers in Plant Science</i> , 2021, 12, 712257.	3.6	8
13	Differential Quantitative Requirements for NPR1 Between Basal Immunity and Systemic Acquired Resistance in Arabidopsis thaliana. <i>Frontiers in Plant Science</i> , 2020, 11, 570422.	3.6	13
14	How Plant Hormones Mediate Salt Stress Responses. <i>Trends in Plant Science</i> , 2020, 25, 1117-1130.	8.8	426
15	Na2CO3-responsive Photosynthetic and ROS Scavenging Mechanisms in Chloroplasts of Alkaligrass Revealed by Phosphoproteomics. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 271-288.	6.9	10
16	Integrative analyses of transcriptomics and metabolomics upon seed germination of foxtail millet in response to salinity. <i>Scientific Reports</i> , 2020, 10, 13660.	3.3	45
17	Differential Phosphorylation of the Transcription Factor WRKY33 by the Protein Kinases CPK5/CPK6 and MPK3/MPK6 Cooperatively Regulates Camalexin Biosynthesis in Arabidopsis. <i>Plant Cell</i> , 2020, 32, 2621-2638.	6.6	110
18	AtHB7/12 Regulate Root Growth in Response to Aluminum Stress. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4080.	4.1	19

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19	A high-quality genome sequence of alkaligrass provides insights into halophyte stress tolerance. <i>Science China Life Sciences</i> , 2020, 63, 1269-1282.	4.9	19
20	Plant Chloroplast Stress Response: Insights from Thiol Redox Proteomics. <i>Antioxidants and Redox Signaling</i> , 2020, 33, 35-57.	5.4	29
21	Myc-Miz-1 signaling promotes self-renewal of leukemia stem cells by repressing Cebp $\beta$ and Cebp $\gamma$ . <i>Blood</i> , 2020, 135, 1133-1145.	1.4	8
22	Heat-Responsive Proteomics of a Heat-Sensitive Spinach Variety. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3872.	4.1	23
23	SpinachBase: a central portal for spinach genomics. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	3.0	30
24	Physiological and comparative proteomic analyses of saline-alkali NaHCO <sub>3</sub> -responses in leaves of halophyte <i>Puccinellia tenuiflora</i> . <i>Plant and Soil</i> , 2019, 437, 137-158.	3.7	41
25	NaCl-responsive ROS scavenging and energy supply in alkaligrass callus revealed from proteomic analysis. <i>BMC Genomics</i> , 2019, 20, 990.	2.8	19
26	Nitrate Accumulation and Expression Patterns of Genes Involved in Nitrate Transport and Assimilation in Spinach. <i>Molecules</i> , 2018, 23, 2231.	3.8	16
27	A Membrane-Bound NAC-Like Transcription Factor OsNLT5 Represses the Flowering in <i>Oryza sativa</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 555.	3.6	77
28	Proteomics and Phosphoproteomics of Heat Stress-Responsive Mechanisms in Spinach. <i>Frontiers in Plant Science</i> , 2018, 9, 800.	3.6	79
29	The DNA Methylome and Association of Differentially Methylated Regions with Differential Gene Expression during Heat Stress in <i>Brassica rapa</i> . <i>International Journal of Molecular Sciences</i> , 2018, 19, 1414.	4.1	80
30	Proteomic discovery of H <sub>2</sub> O <sub>2</sub> response in roots and functional characterization of PutGLP gene from alkaligrass. <i>Planta</i> , 2018, 248, 1079-1099.	3.2	18
31	Draft genome of spinach and transcriptome diversity of 120 <i>Spinacia</i> accessions. <i>Nature Communications</i> , 2017, 8, 15275.	12.8	156
32	Bicarbonate Induced Redox Proteome Changes in <i>Arabidopsis</i> Suspension Cells. <i>Frontiers in Plant Science</i> , 2017, 8, 58.	3.6	36
33	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
34	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.	4.1	20
35	Heat-Responsive Photosynthetic and Signaling Pathways in Plants: Insight from Proteomics. <i>International Journal of Molecular Sciences</i> , 2017, 18, 2191.	4.1	51
36	Salinity Response in Chloroplasts: Insights from Gene Characterization. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1011.	4.1	94

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37	Proteomic Analysis Reveals the Leaf Color Regulation Mechanism in Chimera Hosta "Gold Standard" Leaves. <i>International Journal of Molecular Sciences</i> , 2016, 17, 346.	4.1	9
38	Drought-Responsive Mechanisms in Plant Leaves Revealed by Proteomics. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1706.	4.1	198
39	De novo and comparative transcriptome analysis of cultivated and wild spinach. <i>Scientific Reports</i> , 2016, 5, 17706.	3.3	41
40	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
41	Na <sub>2</sub> CO <sub>3</sub> -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
42	Cytological and proteomic analyses of horsetail ( <i>Equisetum arvense</i> L.) spore germination. <i>Frontiers in Plant Science</i> , 2015, 6, 441.	3.6	11
43	Comparative proteomic analysis of <i>Populus trichocarpa</i> early stem from primary to secondary growth. <i>Journal of Proteomics</i> , 2015, 126, 94-108.	2.4	22
44	Fern spore germination in response to environmental factors. <i>Frontiers in Biology</i> , 2015, 10, 358-376.	0.7	27
45	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
46	Understanding Information Processes at the Proteomics Level. , 2014, , 57-72.		2
47	Protein Kinase LTRPK1 Influences Cold Adaptation and Microtubule Stability in Rice. <i>Journal of Plant Growth Regulation</i> , 2013, 32, 483-490.	5.1	30
48	Proteomics-based investigation of salt-responsive mechanisms in plant roots. <i>Journal of Proteomics</i> , 2013, 82, 230-253.	2.4	150
49	Proteomic insights into seed germination in response to environmental factors. <i>Proteomics</i> , 2013, 13, 1850-1870.	2.2	63
50	Comparative Proteomics of Peanut Gynophore Development under Dark and Mechanical Stimulation. <i>Journal of Proteome Research</i> , 2013, 12, 5502-5511.	3.7	16
51	Comparative Proteomic Analysis of <i>Puccinellia tenuiflora</i> Leaves under Na <sub>2</sub> CO <sub>3</sub> Stress. <i>International Journal of Molecular Sciences</i> , 2013, 14, 1740-1762.	4.1	53
52	Integrated Proteomics and Metabolomics of <i>Arabidopsis</i> Acclimation to Gene-Dosage Dependent Perturbation of Isopropylmalate Dehydrogenases. <i>PLoS ONE</i> , 2013, 8, e57118.	2.5	24
53	Single-cell-type Proteomics: Toward a Holistic Understanding of Plant Function. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1622-1630.	3.8	44
54	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

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55	Mechanisms of Plant Salt Response: Insights from Proteomics. <i>Journal of Proteome Research</i> , 2012, 11, 49-67.	3.7	340
56	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
57	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
58	Proteomics characteristics of rice leaves in response to environmental factors. <i>Frontiers in Biology</i> , 2010, 5, 246-254.	0.7	24
59	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
60	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
61	Desiccation Tolerance Mechanism in Resurrection Fern-Ally <i>Selaginella tamariscina</i> Revealed by Physiological and Proteomic Analysis. <i>Journal of Proteome Research</i> , 2010, 9, 6561-6577.	3.7	116
62	Functional Differentiation of Brassica napus Guard Cells and Mesophyll Cells Revealed by Comparative Proteomics. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 752-766.	3.8	106
63	Proteomics Identification of Differentially Expressed Proteins Associated with Pollen Germination and Tube Growth Reveals Characteristics of Germinated <i>Oryza sativa</i> Pollen. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 207-230.	3.8	133
64	Proteomics of Pollen Development and Germination. <i>Journal of Proteome Research</i> , 2007, 6, 4556-4563.	3.7	36
65	Proteomic analyses of <i>Oryza sativa</i> mature pollen reveal novel proteins associated with pollen germination and tube growth. <i>Proteomics</i> , 2006, 6, 2504-2529.	2.2	165