

Wei Wang

List of Publications by Year in descending order

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92
papers

3,930
citations

136950

32
h-index

133252

59
g-index

98
all docs

98
docs citations

98
times ranked

5150
citing authors

#	ARTICLE	IF	CITATIONS
1	A universal and rapid protocol for protein extraction from recalcitrant plant tissues for proteomic analysis. <i>Electrophoresis</i> , 2006, 27, 2782-2786.	2.4	482
2	Protein extraction for two-dimensional electrophoresis from olive leaf, a plant tissue containing high levels of interfering compounds. <i>Electrophoresis</i> , 2003, 24, 2369-2375.	2.4	366
3	Polyamines function in stress tolerance: from synthesis to regulation. <i>Frontiers in Plant Science</i> , 2015, 6, 827.	3.6	322
4	Universal sample preparation method integrating trichloroacetic acid/acetone precipitation with phenol extraction for crop proteomic analysis. <i>Nature Protocols</i> , 2014, 9, 362-374.	12.0	173
5	Optimizing protein extraction from plant tissues for enhanced proteomics analysis. <i>Journal of Separation Science</i> , 2008, 31, 2032-2039.	2.5	139
6	Heat shock protein 70 regulates the abscisic acid-induced antioxidant response of maize to combined drought and heat stress. <i>Plant Growth Regulation</i> , 2010, 60, 225-235.	3.4	117
7	Phosphoproteomic analysis of the response of maize leaves to drought, heat and their combination stress. <i>Frontiers in Plant Science</i> , 2015, 6, 298.	3.6	117
8	The Difference of Physiological and Proteomic Changes in Maize Leaves Adaptation to Drought, Heat, and Combined Both Stresses. <i>Frontiers in Plant Science</i> , 2016, 7, 1471.	3.6	104
9	A mutation in <i>THERMOSENSITIVE MALE STERILE 1</i> , encoding a heat shock protein with DnaJ and PDI domains, leads to thermosensitive gametophytic male sterility in Arabidopsis. <i>Plant Journal</i> , 2009, 57, 870-882.	5.7	102
10	Protein extraction from plant tissues for 2DE and its application in proteomic analysis. <i>Proteomics</i> , 2014, 14, 645-658.	2.2	84
11	Omics of Maize Stress Response for Sustainable Food Production: Opportunities and Challenges. <i>OMICS A Journal of Integrative Biology</i> , 2014, 18, 714-732.	2.0	82
12	Expansins are involved in cell growth mediated by abscisic acid and indole-3-acetic acid under drought stress in wheat. <i>Plant Cell Reports</i> , 2012, 31, 671-685.	5.6	79
13	Characterization of Small Heat Shock Proteins Associated with Maize Tolerance to Combined Drought and Heat Stress. <i>Journal of Plant Growth Regulation</i> , 2010, 29, 455-464.	5.1	73
14	Advances in crop proteomics: PTMs of proteins under abiotic stress. <i>Proteomics</i> , 2016, 16, 847-865.	2.2	67
15	Modified TCA/acetone precipitation of plant proteins for proteomic analysis. <i>PLoS ONE</i> , 2018, 13, e0202238.	2.5	66
16	Quantitative iTRAQ-based proteomic analysis of phosphoproteins and ABA-regulated phosphoproteins in maize leaves under osmotic stress. <i>Scientific Reports</i> , 2015, 5, 15626.	3.3	57
17	Protein sHSP26 improves chloroplast performance under heat stress by interacting with specific chloroplast proteins in maize (<i>Zea mays</i>). <i>Journal of Proteomics</i> , 2015, 115, 81-92.	2.4	57
18	Genetic Modification for Improving Seed Vigor Is Transitioning from Model Plants to Crop Plants. <i>Frontiers in Plant Science</i> , 2017, 8, 8.	3.6	56

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19	Making better maize plants for sustainable grain production in a changing climate. <i>Frontiers in Plant Science</i> , 2015, 6, 835.	3.6	52
20	Abscisic Acid Refines the Synthesis of Chloroplast Proteins in Maize (<i>Zea mays</i>) in Response to Drought and Light. <i>PLoS ONE</i> , 2012, 7, e49500.	2.5	52
21	Improving soil protein extraction for metaproteome analysis and glomalin-related soil protein detection. <i>Proteomics</i> , 2009, 9, 4970-4973.	2.2	51
22	Proteomic analysis of seed viability in maize. <i>Acta Physiologiae Plantarum</i> , 2011, 33, 181-191.	2.1	49
23	Quantitative Proteomic Analyses Identify ABA-Related Proteins and Signal Pathways in Maize Leaves under Drought Conditions. <i>Frontiers in Plant Science</i> , 2016, 7, 1827.	3.6	43
24	Cross-talks between Ca ²⁺ /CaM and H ₂ O ₂ in abscisic acid-induced antioxidant defense in leaves of maize plants exposed to water stress. <i>Plant Growth Regulation</i> , 2008, 55, 183-198.	3.4	41
25	A new adenylyl cyclase, putative disease-resistance RPP13-like protein 3, participates in abscisic acid-mediated resistance to heat stress in maize. <i>Journal of Experimental Botany</i> , 2021, 72, 283-301.	4.8	41
26	Proteomic analysis of crop plants under abiotic stress conditions: where to focus our research?. <i>Frontiers in Plant Science</i> , 2015, 6, 418.	3.6	39
27	Biochemical Characterization and Cellular Localization of 11 Type Storage Proteins in Olive (<i>Olea</i>) Tj ETQq1 1 0.784314 rgBT ₃₈ /Overlo	5.2	38
28	Post-translational modifications of β -tubulin in <i>Zea mays</i> L. are highly tissue specific. <i>Planta</i> , 2004, 218, 460-465.	3.2	37
29	Removal of lipid contaminants by organic solvents from oilseed protein extract prior to electrophoresis. <i>Analytical Biochemistry</i> , 2004, 329, 139-141.	2.4	37
30	Differential expression of proteins in maize roots in response to abscisic acid and drought. <i>Acta Physiologiae Plantarum</i> , 2011, 33, 2437-2446.	2.1	35
31	Identification of proteins regulated by ABA in response to combined drought and heat stress in maize roots. <i>Acta Physiologiae Plantarum</i> , 2013, 35, 501-513.	2.1	35
32	Papain-like and legumain-like proteases in rice: genome-wide identification, comprehensive gene feature characterization and expression analysis. <i>BMC Plant Biology</i> , 2018, 18, 87.	3.6	34
33	Root protein profile changes induced by Al exposure in two rice cultivars differing in Al tolerance. <i>Journal of Proteomics</i> , 2013, 78, 281-293.	2.4	33
34	Identification of drought tolerant mechanisms in a drought-tolerant maize mutant based on physiological, biochemical and transcriptomic analyses. <i>BMC Plant Biology</i> , 2020, 20, 315.	3.6	32
35	Enhancing Omics Research of Crop Responses to Drought under Field Conditions. <i>Frontiers in Plant Science</i> , 2017, 8, 174.	3.6	31
36	Proteomic analysis reveals differential accumulation of small heat shock proteins and late embryogenesis abundant proteins between ABA-deficient mutant vp5 seeds and wild-type Vp5 seeds in maize. <i>Frontiers in Plant Science</i> , 2014, 5, 801.	3.6	30

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37	ZmCIPK8, a CBL-interacting protein kinase, regulates maize response to drought stress. <i>Plant Cell, Tissue and Organ Culture</i> , 2016, 124, 459-469.	2.3	30
38	Protein Subcellular Location: The Gap Between Prediction and Experimentation. <i>Plant Molecular Biology Reporter</i> , 2016, 34, 52-61.	1.8	30
39	Protein Extraction Methods Shape Much of the Extracted Proteomes. <i>Frontiers in Plant Science</i> , 2018, 9, 802.	3.6	30
40	QTLs for constitutive aerenchyma from <i>Zea nicaraguensis</i> improve tolerance of maize to root-zone oxygen deficiency. <i>Journal of Experimental Botany</i> , 2019, 70, 6475-6487.	4.8	29
41	Organ-specific genetic interactions between paralogues of the <i>PXY</i> and <i>ER</i> receptor kinases enforce radial patterning in <i>Arabidopsis</i> vascular tissue. <i>Development (Cambridge)</i> , 2019, 146, .	2.5	23
42	Evaluation of Three Protein-Extraction Methods for Proteome Analysis of Maize Leaf Midrib, a Compound Tissue Rich in Sclerenchyma Cells. <i>Frontiers in Plant Science</i> , 2016, 7, 856.	3.6	21
43	Characterization of olive seed storage proteins. <i>Acta Physiologiae Plantarum</i> , 2007, 29, 439-444.	2.1	20
44	Proteomic identification of differentially expressed proteins in mature and germinated maize pollen. <i>Acta Physiologiae Plantarum</i> , 2011, 33, 1467-1474.	2.1	19
45	Increasing Confidence of Proteomics Data Regarding the Identification of Stress-Responsive Proteins in Crop Plants. <i>Frontiers in Plant Science</i> , 2016, 7, 702.	3.6	19
46	Physiological and transcriptional response to heat stress in heat-resistant and heat-sensitive maize (<i>Zea mays</i> L.) inbred lines at seedling stage. <i>Protoplasma</i> , 2020, 257, 1615-1637.	2.1	19
47	Chloroform-Assisted Phenol Extraction Improving Proteome Profiling of Maize Embryos through Selective Depletion of High-Abundance Storage Proteins. <i>PLoS ONE</i> , 2014, 9, e112724.	2.5	18
48	Maize mesocotyl: Role in response to stress and deep sowing tolerance. <i>Plant Breeding</i> , 2020, 139, 466-473.	1.9	18
49	Male-sterile mutation alters <i>Zea mays</i> <i>EXPANSIN1</i> (<i>EXPANSIN1</i>) accumulation in a maize mutant. <i>Sexual Plant Reproduction</i> , 2004, 17, 41-47.	2.2	17
50	Evaluation and improvement of spectrophotometric assays of TTC reduction: maize (<i>Zea mays</i>) embryo as an example. <i>Acta Physiologiae Plantarum</i> , 2010, 32, 815-819.	2.1	17
51	Diversity and function of maize pollen coat proteins: from biochemistry to proteomics. <i>Frontiers in Plant Science</i> , 2015, 06, 199.	3.6	17
52	Quaternary ammonium iminofullerenes improve root growth of oxidative-stress maize through ASA-GSH cycle modulating redox homeostasis of roots and ROS-mediated root-hair elongation. <i>Journal of Nanobiotechnology</i> , 2022, 20, 15.	9.1	17
53	Proteomic analysis of β -1,3-glucanase in grape berry tissues. <i>Acta Physiologiae Plantarum</i> , 2009, 31, 597-604.	2.1	16
54	Proteome Profiling of Maize Pollen Coats Reveals Novel Protein Components. <i>Plant Molecular Biology Reporter</i> , 2015, 33, 975-986.	1.8	16

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55	Exploiting the potential of 2DE in proteomics analyses. <i>Expert Review of Proteomics</i> , 2016, 13, 901-903.	3.0	16
56	Proteomic Identification of Differentially Expressed Proteins between Male and Female Plants in <i>Pistacia chinensis</i> . <i>PLoS ONE</i> , 2013, 8, e64276.	2.5	16
57	Characterization of five CIPK genes expressions in maize under water stress. <i>Acta Physiologiae Plantarum</i> , 2013, 35, 1555-1564.	2.1	15
58	The GATA Gene Family in Chickpea: Structure Analysis and Transcriptional Responses to Abscisic Acid and Dehydration Treatments Revealed Potential Genes Involved in Drought Adaptation. <i>Journal of Plant Growth Regulation</i> , 2020, 39, 1647-1660.	5.1	15
59	Localization of group-1 allergen Zea m 1 in the coat and wall of maize pollen. <i>Acta Histochemica</i> , 2006, 108, 395-400.	1.8	13
60	Improving gel-based proteome analysis of soluble protein extracts by heat prefractionation. <i>Proteomics</i> , 2012, 12, 938-943.	2.2	13
61	Sequential Extraction Results in Improved Proteome Profiling of Medicinal Plant <i>Pinellia ternata</i> Tubers, Which Contain Large Amounts of High-Abundance Proteins. <i>PLoS ONE</i> , 2012, 7, e50497.	2.5	13
62	Rapid desalting and protein recovery with phenol after ammonium sulfate fractionation. <i>Electrophoresis</i> , 2007, 28, 2358-2360.	2.4	12
63	Accumulation Profiles of Embryonic Salt-Soluble Proteins in Maize Hybrids and Parental Lines Indicate Matroclinous Inheritance: A Proteomic Analysis. <i>Frontiers in Plant Science</i> , 2017, 8, 1824.	3.6	12
64	Proteomic Analysis of Starch Biosynthesis in Maize Seeds. <i>Starch/Staerke</i> , 2019, 71, 1800294.	2.1	11
65	Differences in properties and proteomes of the midribs contribute to the size of the leaf angle in two near-isogenic maize lines. <i>Journal of Proteomics</i> , 2015, 128, 113-122.	2.4	10
66	Subcellular locations of potential cell wall proteins in plants: predictors, databases and cross-referencing. <i>Briefings in Bioinformatics</i> , 2018, 19, 1130-1140.	6.5	10
67	Proteomic identification of lipid-bodies-associated proteins in maize seeds. <i>Acta Physiologiae Plantarum</i> , 2019, 41, 1.	2.1	9
68	Function of Small Peptides During Male-Female Crosstalk in Plants. <i>Frontiers in Plant Science</i> , 2021, 12, 671196.	3.6	9
69	2-DE-based proteomic analysis of protein changes associated with etiolated mesocotyl growth in <i>Zea mays</i> . <i>BMC Genomics</i> , 2019, 20, 758.	2.8	8
70	Jasmonic acid-induced hydrogen sulfide activates MEK1/2 in regulating the redox state of ascorbate in <i>Arabidopsis thaliana</i> leaves. <i>Plant Signaling and Behavior</i> , 2019, 14, 1629265.	2.4	8
71	Quaternary ammonium iminofullerenes promote root growth and osmotic-stress tolerance in maize via ROS neutralization and improved energy status. <i>Plant Physiology and Biochemistry</i> , 2021, 164, 122-131.	5.8	7
72	Proteomic Characterization of Differential Abundant Proteins Accumulated between Lower and Upper Epidermises of Fleishy Scales in Onion (<i>Allium cepa</i> L.) Bulbs. <i>PLoS ONE</i> , 2016, 11, e0168959.	2.5	7

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73	Functional assignment to maize group 1 LEA protein EMB564 within the cell nucleus using computational analysis. <i>Bioinformatics</i> , 2013, 9, 276-280.	0.5	7
74	Reduction and Alkylation of Proteins in 2D Gel Electrophoresis: Before or after Isoelectric Focusing?. <i>Frontiers in Chemistry</i> , 2017, 5, 59.	3.6	6
75	On the Promising Role of Enzyme Activity Assay in Interpreting Comparative Proteomic Data in Plants. <i>Proteomics</i> , 2018, 18, e1800234.	2.2	6
76	A rapid and universal method for isolating starch granules in plant tissues. <i>Plant, Cell and Environment</i> , 2019, 42, 3355-3371.	5.7	6
77	Digging for Stress-Responsive Cell Wall Proteins for Developing Stress-Resistant Maize. <i>Frontiers in Plant Science</i> , 2020, 11, 576385.	3.6	6
78	Characterization of eight CBL genes expressions in maize early seeding development. <i>Acta Physiologiae Plantarum</i> , 2014, 36, 3307-3314.	2.1	5
79	Proteomics: a promising tool for research on sex-related differences in dioecious plants. <i>Frontiers in Plant Science</i> , 2015, 6, 954.	3.6	5
80	Comparative proteomic analysis of leaves between photoperiod-sensitive and photoperiod-insensitive maize inbred seedlings under long day treatments. <i>Acta Physiologiae Plantarum</i> , 2015, 37, 1.	2.1	5
81	Editorial: Protein Quality Controlling Systems in Plant Responses to Environmental Stresses. <i>Frontiers in Plant Science</i> , 2018, 9, 908.	3.6	5
82	Current Initiatives in Proteomics of the Olive Tree. , 2010, , 25-32.		4
83	The Response of Chloroplast Proteome to Abiotic Stress. , 2016, , 237-249.		4
84	Comparison of protein extraction methods for 2DE-based proteomic analysis of duckweed <i>Spirodela polyrhiza</i> , a small aquatic model plant. <i>Aquatic Botany</i> , 2020, 163, 103216.	1.6	4
85	Protein Analysis of Pollen Tubes after the Treatments of Membrane Trafficking Inhibitors Gains Insights on Molecular Mechanism Underlying Pollen Tube Polar Growth. <i>Protein Journal</i> , 2021, 40, 205-222.	1.6	3
86	Proteomics in Sex Determination of Dioecious Plants. , 2016, , 363-380.		2
87	Genome-Wide Identification and Comparison of Cysteine Proteases in the Pollen Coat and Other Tissues in Maize. <i>Frontiers in Plant Science</i> , 2021, 12, 709534.	3.6	2
88	Proteomics Driven Research of Abiotic Stress Responses in Crop Plants. , 2016, , 351-362.		1
89	Commentary: Leucine-rich Repeat Receptor-Like Gene Screen Reveals that <i>Nicotiana glauca</i> RXEG1 Regulates Glycoside Hydrolase 12 MAMP Detection. <i>Frontiers in Genetics</i> , 2019, 10, 162.	2.3	1
90	Differential abundance proteins associated with rapid growth of etiolated coleoptiles in maize. <i>Plant Direct</i> , 2021, 5, e00332.	1.9	1

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91	Proteomic Analysis of Generative and Vegetative Nuclei Reveals Molecular Characteristics of Pollen Cell Differentiation in Lily. <i>Frontiers in Plant Science</i> , 2021, 12, 641517.	3.6	1
92	Commentary: Rapid Phosphoproteomic Effects of Abscisic Acid (ABA) on Wild-Type and ABA Receptor-Deficient <i>A. thaliana</i> Mutants. <i>Frontiers in Plant Science</i> , 2016, 7, 1062.	3.6	0