

Pingfang Yang

List of Publications by Year in descending order

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100
papers

3,999
citations

117625

34
h-index

133252

59
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104
all docs

104
docs citations

104
times ranked

4504
citing authors

#	ARTICLE	IF	CITATIONS
1	A stress-associated protein OsSAP8 modulates gibberellic acid biosynthesis by reducing the promotive effect of transcription factor OsbZIP58 on <i>OsK2</i> . <i>Journal of Experimental Botany</i> , 2022, 73, 2420-2433.	4.8	6
2	Genome-wide Identification and Expression Analysis of CaM/CML Gene Family in Sacred Lotus (<i>Nelumbo</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 3	1.8	5
3	Editorial: Proteomics of Post-translational Modifications in Plants. <i>Frontiers in Plant Science</i> , 2022, 13, .	3.6	1
4	Studies on Lotus Genomics and the Contribution to Its Breeding. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7270.	4.1	3
5	A bHLH gene NnTT8 of <i>Nelumbo nucifera</i> regulates anthocyanin biosynthesis. <i>Plant Physiology and Biochemistry</i> , 2021, 158, 518-523.	5.8	31
6	The lotus NnFTIP1 and NnFT1 regulate flowering time in Arabidopsis. <i>Plant Science</i> , 2021, 302, 110677.	3.6	7
7	A CONSTANS-LIKE gene of <i>Nelumbo nucifera</i> could promote potato tuberization. <i>Planta</i> , 2021, 253, 65.	3.2	11
8	Metabolomics Analyses of Cotyledon and Plumule Showing the Potential Domestic Selection in Lotus Breeding. <i>Molecules</i> , 2021, 26, 913.	3.8	4
9	Advances on Post-translational Modifications Involved in Seed Germination. <i>Frontiers in Plant Science</i> , 2021, 12, 642979.	3.6	20
10	Biased allelic expression in tissues of F1 hybrids between tropical and temperate lotus (<i>Nelumbo</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 3	3.9	9
11	Genome-wide analysis of AP2/ERF superfamily in lotus (<i>Nelumbo nucifera</i>) and the association between NnADAP and rhizome morphology. <i>BMC Genomics</i> , 2021, 22, 171.	2.8	13
12	Genetic dissection of rhizome yield-related traits in <i>Nelumbo nucifera</i> through genetic linkage map construction and QTL mapping. <i>Plant Physiology and Biochemistry</i> , 2021, 160, 155-165.	5.8	10
13	Protein Phosphorylation Response to Abiotic Stress in Plants. <i>Methods in Molecular Biology</i> , 2021, 2358, 17-43.	0.9	19
14	Metabolomic Analysis on the Petal of "Chen Xi" Rose with Light-Induced Color Changes. <i>Plants</i> , 2021, 10, 2065.	3.5	2
15	Comparative transcriptomic analysis provides insight into carpel petaloidy in lotus (<i>Nelumbo</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 3	2.8	1
16	Improving the Genome Annotation of <i>Rhizoctonia solani</i> Using Proteogenomics. <i>Current Genomics</i> , 2021, 22, 373-383.	1.6	1
17	Quantitative ubiquitylomics approach for characterizing the dynamic change and extensive modulation of ubiquitylation in rice seed germination. <i>Plant Journal</i> , 2020, 101, 1430-1447.	5.7	21
18	Mutations on ent-kaurene oxidase 1 encoding gene attenuate its enzyme activity of catalyzing the reaction from ent-kaurene to ent-kaurenoic acid and lead to delayed germination in rice. <i>PLoS Genetics</i> , 2020, 16, e1008562.	3.5	24

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19	Integrated Omics Analyses Identify Key Pathways Involved in Petiole Rigidity Formation in Sacred Lotus. International Journal of Molecular Sciences, 2020, 21, 5087.	4.1	6
20	Advances on Plant Ubiquitylomeâ€”From Mechanism to Application. International Journal of Molecular Sciences, 2020, 21, 7909.	4.1	9
21	Genome-wide identification of MADS-box gene family in sacred lotus (<i>Nelumbo nucifera</i>) identifies a SEPALLATA homolog gene involved in floral development. BMC Plant Biology, 2020, 20, 497.	3.6	23
22	In-Depth Investigation of Low-Abundance Proteins in Matured and Filling Stages Seeds of <i>Glycine max</i> Employing a Combination of Protamine Sulfate Precipitation and TMT-Based Quantitative Proteomic Analysis. Cells, 2020, 9, 1517.	4.1	19
23	Mechanism of GA-mediated leaf sheath growth in rice: a proteomic approach. Plant Growth Regulation, 2020, 91, 23-36.	3.4	3
24	Proteomic analysis reveals that calcium channel blockers affect radicle protrusion during rice seed germination. Plant Growth Regulation, 2020, 90, 393-407.	3.4	9
25	The Latest Studies on Lotus (<i>Nelumbo nucifera</i>)-an Emerging Horticultural Model Plant. International Journal of Molecular Sciences, 2019, 20, 3680.	4.1	64
26	Proteomic analysis showing the signaling pathways involved in the rhizome enlargement process in <i>Nelumbo nucifera</i> . BMC Genomics, 2019, 20, 766.	2.8	18
27	The Rice Alpha-Amylase, Conserved Regulator of Seed Maturation and Germination. International Journal of Molecular Sciences, 2019, 20, 450.	4.1	96
28	Genome-Wide DNA Methylation Profiling in the Lotus (<i>Nelumbo nucifera</i>) Flower Showing its Contribution to the Stamen Petaloid. Plants, 2019, 8, 135.	3.5	18
29	The complexity of alternative splicing and landscape of tissue-specific expression in lotus (<i>Nelumbo</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 142 Td (2019, 26, 301-311.	3.4	28
30	Proteomics Study in Rice Responses and Tolerance to Salt Stress. , 2019, , 781-789.		3
31	TMT-based quantitative proteomics analysis reveals the response of tea plant (<i>Camellia sinensis</i>) to fluoride. Journal of Proteomics, 2018, 176, 71-81.	2.4	45
32	Label-free proteomic analysis to characterize ginger from China and Ghana. Food Chemistry, 2018, 249, 1-7.	8.2	28
33	Transcriptomic profiling of tall fescue in response to heat stress and improved thermotolerance by melatonin and 24-epibrassinolide. BMC Genomics, 2018, 19, 224.	2.8	78
34	Whole genome re-sequencing reveals evolutionary patterns of sacred lotus (<i>Nelumbo</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 142 Td (2018, 19, 1-12.	8.5	37
35	Systematic transcriptomic analysis provides insights into lotus (<i>Nelumbo nucifera</i>) seed development. Plant Growth Regulation, 2018, 86, 339-350.	3.4	21
36	Transcriptomic analysis identifies the key genes involved in stamen petaloid in lotus (<i>Nelumbo</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 142 Td (2018, 86, 339-350.	2.8	24

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37	Evolutionarily conserved function of the sacred lotus (<i>Nelumbo nucifera</i> Gaertn.) CER2-LIKE family in very-long-chain fatty acid elongation. <i>Planta</i> , 2018, 248, 715-727.	3.2	10
38	Low genetic diversity and functional constraint of miRNA genes participating pollen-pistil interaction in rice. <i>Plant Molecular Biology</i> , 2017, 95, 89-98.	3.9	4
39	Carbonylated protein changes between active germinated embryos and quiescent embryos give insights into rice seed germination regulation. <i>Plant Growth Regulation</i> , 2017, 83, 335-350.	3.4	7
40	Proteomics analysis identified a DRT protein involved in arsenic resistance in <i>Populus</i> . <i>Plant Cell Reports</i> , 2017, 36, 1855-1869.	5.6	5
41	The evolution of plant microRNAs: insights from a basal eudicot sacred lotus. <i>Plant Journal</i> , 2017, 89, 442-457.	5.7	45
42	Chromosome Nomenclature and Cytological Characterization of Sacred Lotus. <i>Cytogenetic and Genome Research</i> , 2017, 153, 223-231.	1.1	12
43	iTRAQ-Based Quantitative Proteomics Analysis on Rice Anther Responding to High Temperature. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1811.	4.1	36
44	iTRAQ-based Comparative Proteomic Analyses of Two Grapevine Cultivars in Response to Cold Stress. <i>Current Proteomics</i> , 2017, 14, 42-52.	0.3	7
45	Metabolomic and Proteomic Profiles Reveal the Dynamics of Primary Metabolism during Seed Development of Lotus (<i>Nelumbo nucifera</i>). <i>Frontiers in Plant Science</i> , 2016, 7, 750.	3.6	43
46	Differential Molecular Responses of Rapeseed Cotyledons to Light and Dark Reveal Metabolic Adaptations toward Autotrophy Establishment. <i>Frontiers in Plant Science</i> , 2016, 7, 988.	3.6	7
47	Ancient microRNA families that regulate transcription factors are preferentially preserved during plant radiation. <i>Plant Signaling and Behavior</i> , 2016, 11, e1261233.	2.4	3
48	A proteomic analysis of salt stress response in seedlings of two African rice cultivars. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2016, 1864, 1570-1578.	2.3	31
49	Analysis of dynamic protein carbonylation in rice embryo during germination through AP-SWATH. <i>Proteomics</i> , 2016, 16, 989-1000.	2.2	29
50	Genome-Wide Analysis of the R2R3 MYB Subfamily Genes in Lotus (<i>Nelumbo nucifera</i>). <i>Plant Molecular Biology Reporter</i> , 2016, 34, 1016-1026.	1.8	16
51	Global Proteome Analyses of Lysine Acetylation and Succinylation Reveal the Widespread Involvement of both Modification in Metabolism in the Embryo of Germinating Rice Seed. <i>Journal of Proteome Research</i> , 2016, 15, 879-890.	3.7	119
52	Identification of phosphorus deficiency responsive proteins in a high phosphorus acquisition soybean (<i>Glycine max</i>) cultivar through proteomic analysis. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2016, 1864, 427-434.	2.3	17
53	Exploration of rice pistil responses during early post-pollination through a combined proteomic and transcriptomic analysis. <i>Journal of Proteomics</i> , 2016, 131, 214-226.	2.4	21
54	Two Dimensional Gel Electrophoresis-Based Plant Phosphoproteomics. <i>Methods in Molecular Biology</i> , 2016, 1355, 213-223.	0.9	7

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55	Induction and quantitative proteomic analysis of cell dedifferentiation during callus formation of lotus (<i>Nelumbo nucifera</i> Gaertn.spp. baijianlian). <i>Journal of Proteomics</i> , 2016, 131, 61-70.	2.4	25
56	Transcriptomic Analysis of the Regulation of Rhizome Formation in Temperate and Tropical Lotus (<i>Nelumbo nucifera</i>). <i>Scientific Reports</i> , 2015, 5, 13059.	3.3	101
57	LOTUS-DB: an integrative and interactive database for <i>Nelumbo nucifera</i> study. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav023.	3.0	18
58	Analysis of Flavonoids in Lotus (<i>Nelumbo nucifera</i>) Leaves and Their Antioxidant Activity Using Macroporous Resin Chromatography Coupled with LC-MS/MS and Antioxidant Biochemical Assays. <i>Molecules</i> , 2015, 20, 10553-10565.	3.8	100
59	RNA-Seq Uncovers SNPs and Alternative Splicing Events in Asian Lotus (<i>Nelumbo nucifera</i>). <i>PLoS ONE</i> , 2015, 10, e0125702.	2.5	24
60	Genome-Wide Dissection of the MicroRNA Expression Profile in Rice Embryo during Early Stages of Seed Germination. <i>PLoS ONE</i> , 2015, 10, e0145424.	2.5	28
61	Proteomics of Important Food Crops in the Asia Oceania Region: Current Status and Future Perspectives. <i>Journal of Proteome Research</i> , 2015, 14, 2723-2744.	3.7	16
62	Proteomic Analysis of Phosphoproteins in the Rice Nucleus During the Early Stage of Seed Germination. <i>Journal of Proteome Research</i> , 2015, 14, 2884-2896.	3.7	23
63	Proteomic and Epigenetic Analyses of Lotus (<i>Nelumbo nucifera</i>) Petals Between Red and White cultivars. <i>Plant and Cell Physiology</i> , 2015, 56, 1546-1555.	3.1	48
64	Studies on the molecular mechanisms of seed germination. <i>Proteomics</i> , 2015, 15, 1671-1679.	2.2	154
65	Physiological and proteomic analyses on artificially aged <i>Brassica napus</i> seed. <i>Frontiers in Plant Science</i> , 2015, 6, 112.	3.6	50
66	Phosphoproteomics in Cereals. <i>Methods in Molecular Biology</i> , 2015, 1306, 47-57.	0.9	1
67	Morphological and Proteomic Analysis Reveal the Role of Pistil under Pollination in <i>Liriodendron chinense</i> (Hemsl.) Sarg. <i>PLoS ONE</i> , 2014, 9, e99970.	2.5	13
68	Proteomics Advances in the Understanding of Pollen-Pistil Interactions. <i>Proteomes</i> , 2014, 2, 468-484.	3.5	5
69	The Mitochondrion-Located Protein OsB12D1 Enhances Flooding Tolerance during Seed Germination and Early Seedling Growth in Rice. <i>International Journal of Molecular Sciences</i> , 2014, 15, 13461-13481.	4.1	17
70	Analysis of phosphoproteome in rice pistil. <i>Proteomics</i> , 2014, 14, 2319-2334.	2.2	43
71	Quantitative Proteomics Reveals the Role of Protein Phosphorylation in Rice Embryos during Early Stages of Germination. <i>Journal of Proteome Research</i> , 2014, 13, 1766-1782.	3.7	63
72	Gel-Based Comparative Phosphoproteomic Analysis on Rice Embryo During Germination. <i>Plant and Cell Physiology</i> , 2014, 55, 1376-1394.	3.1	35

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73	In-Depth Proteomic Analysis of Rice Embryo Reveals its Important Roles in Seed Germination. <i>Plant and Cell Physiology</i> , 2014, 55, 1826-1847.	3.1	69
74	The Cysteine ² /Histidine ² -Type Transcription Factor <i>ZINC FINGER OF ARABIDOPSIS THALIANA6</i> Modulates Biotic and Abiotic Stress Responses by Activating Salicylic Acid-Related Genes and <i>C-REPEAT-BINDING FACTOR</i> Genes in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2014, 165, 1367-1379.	4.8	152
75	Comparative Proteomic Analysis of Rice Shoots Exposed to High Arsenate. <i>Journal of Integrative Plant Biology</i> , 2013, 55, 965-978.	8.5	19
76	Label-Free Quantitative Proteomic Analysis of Abscisic Acid Effect in Early-Stage Soybean under Flooding. <i>Journal of Proteome Research</i> , 2013, 12, 4769-4784.	3.7	120
77	<i>ORFH79</i> impairs mitochondrial function via interaction with a subunit of electron transport chain complex <i>III</i> in <i>Honglian</i> cytoplasmic male sterile rice. <i>New Phytologist</i> , 2013, 198, 408-418.	7.3	107
78	Exploring the response of rice (<i>Oryza sativa</i>) leaf to gibberellins: a proteomic strategy. <i>Rice</i> , 2013, 6, 17.	4.0	15
79	Comparative analysis of the dynamic proteomic profiles in berry skin between red and white grapes (<i>Vitis vinifera</i> L.) during fruit coloration. <i>Scientia Horticulturae</i> , 2013, 164, 238-248.	3.6	8
80	Systematic qualitative and quantitative assessment of anthocyanins, flavones and flavonols in the petals of 108 lotus (<i>Nelumbo nucifera</i>) cultivars. <i>Food Chemistry</i> , 2013, 139, 307-312.	8.2	86
81	Proteomics and Applications to Food Science in Rice. , 2013, , 379-397.		0
82	Manipulation of arginase expression modulates abiotic stress tolerance in <i>Arabidopsis</i> : effect on arginine metabolism and ROS accumulation. <i>Journal of Experimental Botany</i> , 2013, 64, 1367-1379.	4.8	181
83	Application of proteomics for improving crop protection/artificial regulation. <i>Frontiers in Plant Science</i> , 2013, 4, 522.	3.6	24
84	Gene, protein, and network of male sterility in rice. <i>Frontiers in Plant Science</i> , 2013, 4, 92.	3.6	39
85	Proteomics of rice seed germination. <i>Frontiers in Plant Science</i> , 2013, 4, 246.	3.6	108
86	Proteome Analysis of Peroxisomes from Etiolated <i>Arabidopsis</i> Seedlings Identifies a Peroxisomal Protease Involved in β -Oxidation and Development. <i>Plant Physiology</i> , 2013, 163, 1518-1538.	4.8	69
87	Analysis of Proteome Profile in Germinating Soybean Seed, and Its Comparison with Rice Showing the Styles of Reserves Mobilization in Different Crops. <i>PLoS ONE</i> , 2013, 8, e56947.	2.5	67
88	Transcriptomic and Physiological Variations of Three <i>Arabidopsis</i> Ecotypes in Response to Salt Stress. <i>PLoS ONE</i> , 2013, 8, e69036.	2.5	45
89	Comparative proteomic analyses reveal the changes of metabolic features in soybean (<i>Glycine max</i>) pistils upon pollination. <i>Sexual Plant Reproduction</i> , 2012, 25, 281-291.	2.2	27
90	Proteomic studies of the abiotic stresses response in model moss <i>Physcomitrella patens</i> . <i>Frontiers in Plant Science</i> , 2012, 3, 258.	3.6	24

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91	Identification of Conserved and Novel microRNAs from <i>Liriodendron chinense</i> Floral Tissues. <i>PLoS ONE</i> , 2012, 7, e44696.	2.5	15
92	Gene Expression Profile Changes in Germinating Rice. <i>Journal of Integrative Plant Biology</i> , 2011, 53, 835-844.	8.5	31
93	Constructing the metabolic and regulatory pathways in germinating rice seeds through proteomic approach. <i>Proteomics</i> , 2011, 11, 2693-2713.	2.2	134
94	Proteomic analysis of rice seedlings infected by <i>Sinorhizobium meliloti</i> 1021. <i>Proteomics</i> , 2010, 10, 1861-1874.	2.2	110
95	In-Depth Proteome Analysis of Arabidopsis Leaf Peroxisomes Combined with in Vivo Subcellular Targeting Verification Indicates Novel Metabolic and Regulatory Functions of Peroxisomes. <i>Plant Physiology</i> , 2009, 150, 125-143.	4.8	240
96	Proteomic analysis of the cold stress response in the moss, <i>Physcomitrella patens</i> . <i>Proteomics</i> , 2009, 9, 4529-4538.	2.2	68
97	Proteomic analysis of de-etiolated rice seedlings upon exposure to light. <i>Proteomics</i> , 2007, 7, 2459-2468.	2.2	40
98	Proteomic analysis of rice (<i>Oryza sativa</i>) seeds during germination. <i>Proteomics</i> , 2007, 7, 3358-3368.	2.2	263
99	Proteome analysis of rice uppermost internodes at the milky stage. <i>Proteomics</i> , 2006, 6, 3330-3338.	2.2	32
100	Comparative Analysis of the Endosperm Proteins Separated by 2-D Electrophoresis for Two Cultivars of Hybrid Rice (<i>Oryza sativa</i> L.). <i>Journal of Integrative Plant Biology</i> , 2006, 48, 1028-1033.	8.5	6