

Jin Zhang

List of Publications by Year in descending order

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88
papers

2,748
citations

201385

27
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214527

47
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93
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93
docs citations

93
times ranked

3239
citing authors

#	ARTICLE	IF	CITATIONS
1	Diversity and conservation of plant small secreted proteins associated with arbuscular mycorrhizal symbiosis. <i>Horticulture Research</i> , 2022, 9, .	2.9	1
2	An Efficient Agrobacterium-Mediated Transformation Method for Hybrid Poplar 84K (<i>Populus alba</i> × <i>P. trichocarpa</i>). <i>Overlock</i> 10	1.8	25
3	Opportunities and Challenges of Predictive Approaches for the Non-coding RNA in Plants. <i>Frontiers in Plant Science</i> , 2022, 13, 890663.	1.7	4
4	The PagKNAT2/6b-PagBOP1/2a Regulatory Module Controls Leaf Morphogenesis in <i>Populus</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 5581.	1.8	0
5	Lignin biosynthesis and accumulation in response to abiotic stresses in woody plants. <i>Forestry Research</i> , 2022, 2, 0-0.	0.5	15
6	Expression and localization of SWEETs in <i>Populus</i> and the effect of SWEET7 overexpression in secondary growth. <i>Tree Physiology</i> , 2021, 41, 882-899.	1.4	20
7	Genome-wide identification, evolution and expression analysis of the aspartic protease gene family during rapid growth of moso bamboo (<i>Phyllostachys edulis</i>) shoots. <i>BMC Genomics</i> , 2021, 22, 45.	1.2	9
8	Overexpression of an Agave Phosphoenolpyruvate Carboxylase Improves Plant Growth and Stress Tolerance. <i>Cells</i> , 2021, 10, 582.	1.8	24
9	Opportunities and barriers for biofuel and bioenergy production from poplar. <i>GCB Bioenergy</i> , 2021, 13, 905-913.	2.5	10
10	Advances and perspectives in discovery and functional analysis of small secreted proteins in plants. <i>Horticulture Research</i> , 2021, 8, 130.	2.9	20
11	Transcriptional Regulation and Signaling of Developmental Programmed Cell Death in Plants. <i>Frontiers in Plant Science</i> , 2021, 12, 702928.	1.7	10
12	Recent Advances in the Roles of HSFs and HSPs in Heat Stress Response in Woody Plants. <i>Frontiers in Plant Science</i> , 2021, 12, 704905.	1.7	29
13	Transcriptome and structure analysis in root of <i>Casuarina equisetifolia</i> under NaCl treatment. <i>PeerJ</i> , 2021, 9, e12133.	0.9	6
14	The Ancient Salicoid Genome Duplication Event: A Platform for Reconstruction of De Novo Gene Evolution in <i>Populus trichocarpa</i> . <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	9
15	Overexpression of a Prefoldin β^2 subunit gene reduces biomass recalcitrance in the bioenergy crop <i>Populus</i> . <i>Plant Biotechnology Journal</i> , 2020, 18, 859-871.	4.1	17
16	Identification of functional single nucleotide polymorphism of <i>Populus trichocarpa</i> PtrEPSPâ€³ and determination of its transcriptional effect. <i>Plant Direct</i> , 2020, 4, e00178.	0.8	4
17	Agronomic performance of 27 <i>Populus</i> clones evaluated after two 3-year coppice rotations in Henan, China. <i>GCB Bioenergy</i> , 2020, 12, 168-181.	2.5	18
18	An essential role for Arabidopsis Trs33 in cell growth and organization in plant apical meristems. <i>Plant Cell Reports</i> , 2020, 39, 381-391.	2.8	0

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19	Protocol for Projecting Allele Frequency Change under Future Climate Change at Adaptive-Associated Loci. STAR Protocols, 2020, 1, 100061.	0.5	4
20	Editorial: Biofuels and Bioenergy. Frontiers in Plant Science, 2020, 11, 621380.	1.7	0
21	Arabidopsis C-terminal binding protein ANGUSTIFOLIA modulates transcriptional coregulation of MYB46 and WRKY33. New Phytologist, 2020, 228, 1627-1639.	3.5	17
22	Transcriptional and Post-transcriptional Regulation of Lignin Biosynthesis Pathway Genes in Populus. Frontiers in Plant Science, 2020, 11, 652.	1.7	34
23	Insights of Molecular Mechanism of Xylem Development in Five Black Poplar Cultivars. Frontiers in Plant Science, 2020, 11, 620.	1.7	14
24	A Single Amino Acid Change in Nramp6 from Sedum Alfredii Hance Affects Cadmium Accumulation. International Journal of Molecular Sciences, 2020, 21, 3169.	1.8	12
25	Genetic architecture of leaf morphological and physiological traits in a Populus deltoides ‘Danhong’ – P. simonii ‘Tongliao1’ pedigree revealed by quantitative trait locus analysis. Tree Genetics and Genomes, 2020, 16, 1.	0.6	4
26	Genetic identification of 91 poplar cultivars based on SSR markers. Nordic Journal of Botany, 2020, 38, .	0.2	2
27	Transporters and ascorbate-glutathione metabolism for differential cadmium accumulation and tolerance in two contrasting willow genotypes. Tree Physiology, 2020, 40, 1126-1142.	1.4	18
28	Light-responsive expression atlas reveals the effects of light quality and intensity in Kalanchoe fedtschenkoi, a plant with crassulacean acid metabolism. GigaScience, 2020, 9, .	3.3	11
29	Genome resequencing reveals demographic history and genetic architecture of seed salinity tolerance in Populus euphratica. Journal of Experimental Botany, 2020, 71, 4308-4320.	2.4	21
30	A New Perspective on Ecological Prediction Reveals Limits to Climate Adaptation in a Temperate Tree Species. Current Biology, 2020, 30, 1447-1453.e4.	1.8	23
31	Transcriptional Regulation of Drought Response in Arabidopsis and Woody Plants. Frontiers in Plant Science, 2020, 11, 572137.	1.7	43
32	The WUSCHELa (PtoWUSa) is Involved in Developmental Plasticity of Adventitious Root in Poplar. Genes, 2020, 11, 176.	1.0	9
33	Plant Biosystems Design Research Roadmap 1.0. Biodesign Research, 2020, 2020, .	0.8	16
34	Genome-wide transcriptomic analysis of a desert willow, Salix psammophila, reveals the function of hub genes SpMDP1 and SpWRKY33 in drought tolerance. BMC Plant Biology, 2019, 19, 356.	1.6	11
35	Mediation of plant-mycorrhizal interaction by a lectin receptor-like kinase. Nature Plants, 2019, 5, 676-680.	4.7	42
36	Genome-Wide Identification, Classification, and Expression Analysis of the Hsf Gene Family in Carnation (Dianthus caryophyllus). International Journal of Molecular Sciences, 2019, 20, 5233.	1.8	31

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37	The <i>Salix psammophila</i> SpRLCK1 involved in drought and salt tolerance. <i>Plant Physiology and Biochemistry</i> , 2019, 144, 222-233.	2.8	11
38	Overexpression of a serine hydroxymethyltransferase increases biomass production and reduces recalcitrance in the bioenergy crop <i>Populus</i> . <i>Sustainable Energy and Fuels</i> , 2019, 3, 195-207.	2.5	27
39	Evolutionary Divergence of Duplicated Hsf Genes in <i>Populus</i> . <i>Cells</i> , 2019, 8, 438.	1.8	16
40	De novo Characterization of the <i>Platycladus orientalis</i> Transcriptome and Analysis of Photosynthesis-Related Genes during Aging. <i>Forests</i> , 2019, 10, 393.	0.9	4
41	Molecular response of poplar to single and combined ozone and drought. <i>Science of the Total Environment</i> , 2019, 655, 1364-1375.	3.9	19
42	Proteome-Level Analysis of Metabolism- and Stress-Related Proteins during Seed Dormancy and Germination in <i>Gnetum parvifolium</i> . <i>Journal of Agricultural and Food Chemistry</i> , 2018, 66, 3019-3029.	2.4	8
43	The WUSCHEL-related homeobox 5a (<i>PtoWOX5a</i>) is involved in adventitious root development in poplar. <i>Tree Physiology</i> , 2018, 38, 139-153.	1.4	48
44	Recent Advances in the Transcriptional Regulation of Secondary Cell Wall Biosynthesis in the Woody Plants. <i>Frontiers in Plant Science</i> , 2018, 9, 1535.	1.7	110
45	Genome-wide characterization of protein phosphatase 2C genes in <i>Populus euphratica</i> and their expression profiling under multiple abiotic stresses. <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	0.6	7
46	Genome-Wide Characterization of the sHsp Gene Family in <i>Salix suchowensis</i> Reveals Its Functions under Different Abiotic Stresses. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3246.	1.8	20
47	<i>PtWOX11</i> acts as master regulator conducting the expression of key transcription factors to induce de novo shoot organogenesis in poplar. <i>Plant Molecular Biology</i> , 2018, 98, 389-406.	2.0	21
48	Association mapping, transcriptomics, and transient expression identify candidate genes mediating plant-pathogen interactions in a tree. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 11573-11578.	3.3	61
49	Defining the genetic components of callus formation: A GWAS approach. <i>PLoS ONE</i> , 2018, 13, e0202519.	1.1	27
50	Regulation of Lignin Biosynthesis and Its Role in Growth-Defense Tradeoffs. <i>Frontiers in Plant Science</i> , 2018, 9, 1427.	1.7	231
51	<i>AtBET5</i> is essential for exine pattern formation and apical meristem organization in <i>Arabidopsis</i> . <i>Plant Science</i> , 2018, 274, 231-241.	1.7	12
52	A Variable Polyglutamine Repeat Affects Subcellular Localization and Regulatory Activity of a <i>Populus</i> <i>ANGUSTIFOLIA</i> Protein. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2631-2641.	0.8	9
53	Whole-genome re-sequencing reveals molecular mechanisms of biomass changes in 11-year-old Bt transgenic poplar. <i>Trees - Structure and Function</i> , 2018, 32, 1609-1620.	0.9	2
54	Proteomic Analysis and Identification of Possible Allergenic Proteins in Mature Pollen of <i>Populus tomentosa</i> . <i>International Journal of Molecular Sciences</i> , 2018, 19, 250.	1.8	11

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55	<sc>Genome-wide association studies</sc> and expression-based quantitative trait loci analyses reveal roles of <sc>HCT</sc>2 in caffeoylquinic acid biosynthesis and its regulation by defense-responsive transcription factors in <i>Populus</i> . <i>New Phytologist</i> , 2018, 220, 502-516.	3.5	112
56	Characterization of the <i>Populus</i> Rab family genes and the function of PtRabE1b in salt tolerance. <i>BMC Plant Biology</i> , 2018, 18, 124.	1.6	27
57	A 5-Enolpyruvylshikimate 3-Phosphate Synthase Functions as a Transcriptional Repressor in <i>Populus</i> . <i>Plant Cell</i> , 2018, 30, 1645-1660.	3.1	56
58	Integrated regulatory network reveals the early salt tolerance mechanism of <i>Populus euphratica</i> . <i>Scientific Reports</i> , 2017, 7, 6769.	1.6	16
59	<i>Platycladus orientalis</i> PoKub3 is involved in abiotic stress responses in transgenic arabidopsis. <i>Journal of Plant Biology</i> , 2017, 60, 322-334.	0.9	0
60	Transcriptome differences between 20- and 3,000-year-old <i>Platycladus orientalis</i> reveal that ROS are involved in senescence regulation. <i>Electronic Journal of Biotechnology</i> , 2017, 29, 68-77.	1.2	8
61	Construction of a high-density linkage map and mapping of sex determination and growth-related loci in the mandarin fish (<i>Siniperca chuatsi</i>). <i>BMC Genomics</i> , 2017, 18, 446.	1.2	82
62	Expression and integrated network analyses revealed functional divergence of NHX-type Na ⁺ /H ⁺ exchanger genes in poplar. <i>Scientific Reports</i> , 2017, 7, 2607.	1.6	50
63	Agronomic performance of <i>Populus deltoides</i> trees engineered for biofuel production. <i>Biotechnology for Biofuels</i> , 2017, 10, 253.	6.2	22
64	An Empirical Assessment of Transgene Flow from a Bt Transgenic Poplar Plantation. <i>PLoS ONE</i> , 2017, 12, e0170201.	1.1	18
65	Comparative Proteomic Analysis of Mature Pollen in Triploid and Diploid <i>Populus deltoides</i> . <i>International Journal of Molecular Sciences</i> , 2016, 17, 1475.	1.8	10
66	Selection of Reliable Reference Genes for Gene Expression Analysis under Abiotic Stresses in the Desert Biomass Willow, <i>Salix psammophila</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 1505.	1.7	36
67	De novo transcriptome assembly, development of EST-SSR markers and population genetic analyses for the desert biomass willow, <i>Salix psammophila</i> . <i>Scientific Reports</i> , 2016, 6, 39591.	1.6	36
68	The <i>Populus trichocarpa</i> PtHSP17.8 involved in heat and salt stress tolerances. <i>Plant Cell Reports</i> , 2016, 35, 1587-1599.	2.8	37
69	Genome-wide survey and expression analysis of the stress-associated protein gene family in desert poplar, <i>Populus euphratica</i> . <i>Tree Genetics and Genomes</i> , 2016, 12, 1.	0.6	21
70	Molecular evolution and expression divergence of the <i>Populus euphratica</i> Hsf genes provide insight into the stress acclimation of desert poplar. <i>Scientific Reports</i> , 2016, 6, 30050.	1.6	31
71	Genome-Wide Identification, Classification, and Expression Analysis of 14-3-3 Gene Family in <i>Populus</i> . <i>PLoS ONE</i> , 2015, 10, e0123225.	1.1	52
72	Expression and Functional Analysis of WRKY Transcription Factors in Chinese Wild Hazel, <i>Corylus heterophylla</i> Fisch. <i>PLoS ONE</i> , 2015, 10, e0135315.	1.1	11

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73	Proteomic analysis and candidate allergenic proteins in <i>Populus deltoides</i> CL. "KENT" mature pollen. <i>Frontiers in Plant Science</i> , 2015, 6, 548.	1.7	14
74	A <i>Populus</i> TIR1 gene family survey reveals differential expression patterns and responses to 1-naphthaleneacetic acid and stress treatments. <i>Frontiers in Plant Science</i> , 2015, 6, 719.	1.7	26
75	The heat shock factor gene family in <i>Salix suchowensis</i> : a genome-wide survey and expression profiling during development and abiotic stresses. <i>Frontiers in Plant Science</i> , 2015, 6, 748.	1.7	40
76	Hsf and Hsp gene families in <i>Populus</i> : genome-wide identification, organization and correlated expression during development and in stress responses. <i>BMC Genomics</i> , 2015, 16, 181.	1.2	90
77	Aldehyde Dehydrogenase Gene Superfamily in <i>Populus</i> : Organization and Expression Divergence between Paralogous Gene Pairs. <i>PLoS ONE</i> , 2015, 10, e0124669.	1.1	21
78	A survey of <i>Populus</i> PIN-FORMED family genes reveals their diversified expression patterns. <i>Journal of Experimental Botany</i> , 2014, 65, 2437-2448.	2.4	46
79	WUSCHEL-related Homeobox genes in <i>Populus tomentosa</i> : diversified expression patterns and a functional similarity in adventitious root formation. <i>BMC Genomics</i> , 2014, 15, 296.	1.2	103
80	Overexpression of monoubiquitin improves photosynthesis in transgenic tobacco plants following high temperature stress. <i>Plant Science</i> , 2014, 226, 92-100.	1.7	22
81	Transcriptome Sequencing and Identification of Cold Tolerance Genes in Hardy <i>Corylus</i> Species (C.) Tj ETQq1 1 0.784314 rgBT ₁₄ /Overl	1.1	14
82	Genome-wide analysis of the <i>Populus</i> Hsp90 gene family reveals differential expression patterns, localization, and heat stress responses. <i>BMC Genomics</i> , 2013, 14, 532.	1.2	109
83	Enhanced stability of thylakoid membrane proteins and antioxidant competence contribute to drought stress resistance in the <i>tasg1</i> wheat stay-green mutant. <i>Journal of Experimental Botany</i> , 2013, 64, 1509-1520.	2.4	101
84	Manipulation of monoubiquitin improves salt tolerance in transgenic tobacco. <i>Plant Biology</i> , 2012, 14, 315-324.	1.8	15
85	Drought tolerance through over-expression of the expansin gene TaEXPB23 in transgenic tobacco. <i>Journal of Plant Physiology</i> , 2011, 168, 960-966.	1.6	85
86	Improvement of heat and drought photosynthetic tolerance in wheat by overaccumulation of glycinebetaine. <i>Plant Biotechnology Reports</i> , 2010, 4, 213-222.	0.9	84
87	Overaccumulation of glycine betaine enhances tolerance of the photosynthetic apparatus to drought and heat stress in wheat. <i>Photosynthetica</i> , 2010, 48, 30-41.	0.9	105
88	Drought tolerance through overexpression of monoubiquitin in transgenic tobacco. <i>Journal of Plant Physiology</i> , 2008, 165, 1745-1755.	1.6	69