

Jin Zhang

List of Publications by Year in descending order

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88
papers

2,748
citations

201385

27
h-index

214527

47
g-index

93
all docs

93
docs citations

93
times ranked

3239
citing authors

#	ARTICLE	IF	CITATIONS
1	Regulation of Lignin Biosynthesis and Its Role in Growth-Defense Tradeoffs. <i>Frontiers in Plant Science</i> , 2018, 9, 1427.	1.7	231
2	Genome-wide association studies and expression-based quantitative trait loci analyses reveal roles of HCT2 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
3	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
4	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
5	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
6	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
7	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
8	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
9	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
10	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
11	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
12	Drought tolerance through overexpression of monoubiquitin in transgenic tobacco. <i>Journal of Plant Physiology</i> , 2008, 165, 1745-1755.	1.6	69
13	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
14	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
15	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
16	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
17	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
18	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

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19	Transcriptional Regulation of Drought Response in Arabidopsis and Woody Plants. <i>Frontiers in Plant Science</i> , 2020, 11, 572137.	1.7	43
20	Mediation of plant-mycorrhizal interaction by a lectin receptor-like kinase. <i>Nature Plants</i> , 2019, 5, 676-680.	4.7	42
21	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
22	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
23	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
24	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
25	Transcriptional and Post-transcriptional Regulation of Lignin Biosynthesis Pathway Genes in <i>Populus</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 652.	1.7	34
26	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
27	Genome-Wide Identification, Classification, and Expression Analysis of the Hsf Gene Family in Carnation (<i>Dianthus caryophyllus</i>). <i>International Journal of Molecular Sciences</i> , 2019, 20, 5233.	1.8	31
28	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
29	Defining the genetic components of callus formation: A GWAS approach. <i>PLoS ONE</i> , 2018, 13, e0202519.	1.1	27
30	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
31	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
32	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
33	An Efficient Agrobacterium-Mediated Transformation Method for Hybrid Poplar 84K (<i>Populus alba</i> × <i>P. trichocarpa</i>). <i>Plant Cell Reports</i> , 2014, 33, 147-154.	1.8	25
34	Overexpression of an Agave Phosphoenolpyruvate Carboxylase Improves Plant Growth and Stress Tolerance. <i>Cells</i> , 2021, 10, 582.	1.8	24
35	A New Perspective on Ecological Prediction Reveals Limits to Climate Adaptation in a Temperate Tree Species. <i>Current Biology</i> , 2020, 30, 1447-1453.e4.	1.8	23
36	Overexpression of monoubiquitin improves photosynthesis in transgenic tobacco plants following high temperature stress. <i>Plant Science</i> , 2014, 226, 92-100.	1.7	22

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37	Agronomic performance of <i>Populus deltoides</i> trees engineered for biofuel production. <i>Biotechnology for Biofuels</i> , 2017, 10, 253.	6.2	22
38	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
39	PtWOX11 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
40	Genome resequencing reveals demographic history and genetic architecture of seed salinity tolerance in <i>Populus euphratica</i> . <i>Journal of Experimental Botany</i> , 2020, 71, 4308-4320.	2.4	21
41	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
42	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
43	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
44	Advances and perspectives in discovery and functional analysis of small secreted proteins in plants. <i>Horticulture Research</i> , 2021, 8, 130.	2.9	20
45	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
46	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
47	Transporters and ascorbate-glutathione metabolism for differential cadmium accumulation and tolerance in two contrasting willow genotypes. <i>Tree Physiology</i> , 2020, 40, 1126-1142.	1.4	18
48	An Empirical Assessment of Transgene Flow from a Bt Transgenic Poplar Plantation. <i>PLoS ONE</i> , 2017, 12, e0170201.	1.1	18
49	Overexpression of a Prefoldin \hat{I}^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
50	Arabidopsis C-terminal binding protein ANGUSTIFOLIA modulates transcriptional co-regulation of MYB46 and WRKY33. <i>New Phytologist</i> , 2020, 228, 1627-1639.	3.5	17
51	Integrated regulatory network reveals the early salt tolerance mechanism of <i>Populus euphratica</i> . <i>Scientific Reports</i> , 2017, 7, 6769.	1.6	16
52	Evolutionary Divergence of Duplicated Hsf Genes in <i>Populus</i> . <i>Cells</i> , 2019, 8, 438.	1.8	16
53	Plant Biosystems Design Research Roadmap 1.0. <i>Biodesign Research</i> , 2020, 2020, .	0.8	16
54	Manipulation of monoubiquitin improves salt tolerance in transgenic tobacco. <i>Plant Biology</i> , 2012, 14, 315-324.	1.8	15

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55	Lignin biosynthesis and accumulation in response to abiotic stresses in woody plants. <i>Forestry Research</i> , 2022, 2, 0-0.	0.5	15
56	Proteomic analysis and candidate allergenic proteins in <i>Populus deltoides</i> CL. mature pollen. <i>Frontiers in Plant Science</i> , 2015, 6, 548.	1.7	14
57	Insights of Molecular Mechanism of Xylem Development in Five Black Poplar Cultivars. <i>Frontiers in Plant Science</i> , 2020, 11, 620.	1.7	14
58	Transcriptome Sequencing and Identification of Cold Tolerance Genes in Hardy <i>Corylus</i> Species (C.). <i>Frontiers in Plant Science</i> , 2020, 11, 1410.	1.1	14
59	AtBET5 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
60	A Single Amino Acid Change in <i>Nramp6</i> from <i>Sedum alfredii</i> Hance Affects Cadmium Accumulation. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3169.	1.8	12
61	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
62	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
63	Genome-wide transcriptomic analysis of a desert willow, <i>Salix psammophila</i> , reveals the function of hub genes <i>SpMDP1</i> and <i>SpWRKY33</i> in drought tolerance. <i>BMC Plant Biology</i> , 2019, 19, 356.	1.6	11
64	The <i>Salix psammophila</i> <i>SpRLCK1</i> involved in drought and salt tolerance. <i>Plant Physiology and Biochemistry</i> , 2019, 144, 222-233.	2.8	11
65	Light-responsive expression atlas reveals the effects of light quality and intensity in <i>Kalanchoe fedtschenkoi</i> , a plant with crassulacean acid metabolism. <i>GigaScience</i> , 2020, 9, .	3.3	11
66	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
67	Opportunities and barriers for biofuel and bioenergy production from poplar. <i>GCB Bioenergy</i> , 2021, 13, 905-913.	2.5	10
68	Transcriptional Regulation and Signaling of Developmental Programmed Cell Death in Plants. <i>Frontiers in Plant Science</i> , 2021, 12, 702928.	1.7	10
69	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
70	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
71	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
72	The <i>WUSCHELa</i> (<i>PtoWUSa</i>) is Involved in Developmental Plasticity of Adventitious Root in Poplar. <i>Genes</i> , 2020, 11, 176.	1.0	9

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73	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
74	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
75	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
76	Transcriptome and structure analysis in root of <i>Casuarina equisetifolia</i> under NaCl treatment. <i>PeerJ</i> , 2021, 9, e12133.	0.9	6
77	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
78	Identification of functional single nucleotide polymorphism of <i>Populus trichocarpa</i> PtrEPSPâ€”F and determination of its transcriptional effect. <i>Plant Direct</i> , 2020, 4, e00178.	0.8	4
79	Protocol for Projecting Allele Frequency Change under Future Climate Change at Adaptive-Associated Loci. <i>STAR Protocols</i> , 2020, 1, 100061.	0.5	4
80	Genetic architecture of leaf morphological and physiological traits in a <i>Populus deltoides</i> “Danhong” – <i>P. simonii</i> “Tongliao1” pedigree revealed by quantitative trait locus analysis. <i>Tree Genetics and Genomes</i> , 2020, 16, 1.	0.6	4
81	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
82	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
83	Genetic identification of 91 poplar cultivars based on SSR markers. <i>Nordic Journal of Botany</i> , 2020, 38, .	0.2	2
84	Diversity and conservation of plant small secreted proteins associated with arbuscular mycorrhizal symbiosis. <i>Horticulture Research</i> , 2022, 9, .	2.9	1
85	<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
86	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
87	Editorial: Biofuels and Bioenergy. <i>Frontiers in Plant Science</i> , 2020, 11, 621380.	1.7	0
88	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