

Deqiang Zhang

List of Publications by Year in descending order

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112
papers

3,087
citations

182225

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223390

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117
all docs

117
docs citations

117
times ranked

3507
citing authors

#	ARTICLE	IF	CITATIONS
1	Dynamic physiological and transcriptome changes reveal a potential relationship between the circadian clock and salt stress response in <i>Ulmus pumila</i> . <i>Molecular Genetics and Genomics</i> , 2022, 297, 303-317.	1.0	5
2	Transposable Elements: Distribution, Polymorphism, and Climate Adaptation in <i>Populus</i> . <i>Frontiers in Plant Science</i> , 2022, 13, 814718.	1.7	3
3	Transcriptome and miRNAome analysis reveals components regulating tissue differentiation of bamboo shoots. <i>Plant Physiology</i> , 2022, 188, 2182-2198.	2.3	16
4	The Genetic Basis of Phosphorus Utilization Efficiency in Plants Provide New Insight into Woody Perennial Plants Improvement. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2353.	1.8	10
5	LncRNA PMATâ€PtoMYB46 module represses PtoMATE and PtoARF2 promoting Pb ²⁺ uptake and plant growth in poplar. <i>Journal of Hazardous Materials</i> , 2022, 433, 128769.	6.5	12
6	Singleâ€cell RNA sequencing profiles of stemâ€differentiating xylem in poplar. <i>Plant Biotechnology Journal</i> , 2022, 20, 417-419.	4.1	32
7	Miniature inverted repeat transposable elements <i>cis</i> -regulate circular RNA expression and promote ethylene biosynthesis, reducing heat tolerance in <i>Populus tomentosa</i> . <i>Journal of Experimental Botany</i> , 2021, 72, 1978-1994.	2.4	9
8	Transcriptome analysis and association mapping reveal the genetic regulatory network response to cadmium stress in <i>Populus tomentosa</i> . <i>Journal of Experimental Botany</i> , 2021, 72, 576-591.	2.4	21
9	Genetic Architecture Underlying the Metabolites of Chlorogenic Acid Biosynthesis in <i>Populus tomentosa</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 2386.	1.8	7
10	Synonymous mutation in <i>Growth Regulating Factor 15</i> of miR396a target sites enhances photosynthetic efficiency and heat tolerance in poplar. <i>Journal of Experimental Botany</i> , 2021, 72, 4502-4519.	2.4	18
11	Genome-wide association studies reveal the coordinated regulatory networks underlying photosynthesis and wood formation in <i>Populus</i> . <i>Journal of Experimental Botany</i> , 2021, 72, 5372-5389.	2.4	12
12	Gene Coexpression Network Analysis Indicates that Hub Genes Related to Photosynthesis and Starch Synthesis Modulate Salt Stress Tolerance in <i>Ulmus pumila</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 4410.	1.8	10
13	Genetic architecture of the metabolic pathway of salicylic acid biosynthesis in <i>Populus</i> . <i>Tree Physiology</i> , 2021, 41, 2198-2215.	1.4	13
14	Genetic Effects and Expression Patterns of the Nitrate Transporter (NRT) Gene Family in <i>Populus tomentosa</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 661635.	1.7	16
15	Integration of genome wide association studies and coâ€expression networks reveal roles of <i>PtoWRKY42</i> â€ <i>PtoUGT76C1</i> in <i>trans</i> -zeatin metabolism and cytokinin sensitivity in poplar. <i>New Phytologist</i> , 2021, 231, 1462-1477.	3.5	13
16	Association Study and Mendelian Randomization Analysis Reveal Effects of the Genetic Interaction Between PtoMIR403b and PtoGT31B-1 on Wood Formation in <i>Populus tomentosa</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 704941.	1.7	2
17	Genetic Architecture and Genome-Wide Adaptive Signatures Underlying Stem Lenticel Traits in <i>Populus tomentosa</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 9249.	1.8	3
18	Multi-omics analysis provides insights into genetic architecture of flavonoid metabolites in <i>Populus</i> . <i>Industrial Crops and Products</i> , 2021, 168, 113612.	2.5	7

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19	Pyramiding superior haplotypes and epistatic alleles to accelerate wood quality and yield improvement in poplar breeding. <i>Industrial Crops and Products</i> , 2021, 171, 113891.	2.5	7
20	Drought Stress Triggers Shifts in the Root Microbial Community and Alters Functional Categories in the Microbial Gene Pool. <i>Frontiers in Microbiology</i> , 2021, 12, 744897.	1.5	26
21	Genetic dissection of the gene coexpression network underlying photosynthesis in <i>Populus</i> . <i>Plant Biotechnology Journal</i> , 2020, 18, 1015-1026.	4.1	21
22	Linkage disequilibrium dissection of the epigenetic quantitative trait loci (epiQTLs) underlying growth and wood properties in <i>Populus</i> . <i>New Phytologist</i> , 2020, 225, 1218-1233.	3.5	25
23	High-Temperature-Responsive Poplar lncRNAs Modulate Target Gene Expression via RNA Interference and Act as RNA Scaffolds to Enhance Heat Tolerance. <i>International Journal of Molecular Sciences</i> , 2020, 21, 6808.	1.8	16
24	Genome Cytosine Methylation May Affect Growth and Wood Property Traits in Populations of <i>Populus tomentosa</i> . <i>Forests</i> , 2020, 11, 828.	0.9	1
25	Genetic interactions among Pto-miR319 family members and their targets influence growth and wood properties in <i>Populus tomentosa</i> . <i>Molecular Genetics and Genomics</i> , 2020, 295, 855-870.	1.0	2
26	Key Genes and Genetic Interactions of Plant-Pathogen Functional Modules in Poplar Infected by <i>Marssonina brunnea</i> . <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 1080-1090.	1.4	11
27	Evolution and Functional Divergence of the Fructokinase Gene Family in <i>Populus</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 484.	1.7	6
28	Identification of a transcriptional regulatory module that reduces leaf temperature in poplar under heat stress. <i>Tree Physiology</i> , 2020, 40, 1108-1125.	1.4	5
29	Changes in DNA Methylation in Response to 6-Benzylaminopurine Affect Allele-Specific Gene Expression in <i>Populus tomentosa</i> . <i>International Journal of Molecular Sciences</i> , 2020, 21, 2117.	1.8	3
30	Machine learning models for net photosynthetic rate prediction using poplar leaf phenotype data. <i>PLoS ONE</i> , 2020, 15, e0228645.	1.1	14
31	A Higher Order Prediction Model of <i>Populus simonii</i> 's Net Photosynthetic Rate Based on Improved Gradient Boosting Method. <i>Communications in Computer and Information Science</i> , 2020, , 373-385.	0.4	0
32	Osmotic stress-responsive promoter upstream transcripts (PROMPTS) act as carriers of MYB transcription factors to induce the expression of target genes in <i>Populus simonii</i> . <i>Plant Biotechnology Journal</i> , 2019, 17, 164-177.	4.1	29
33	Genetic architecture underlying the lignin biosynthesis pathway involves noncoding RNA and transcription factors for growth and wood properties in <i>Populus</i> . <i>Plant Biotechnology Journal</i> , 2019, 17, 302-315.	4.1	54
34	Time-specific and pleiotropic quantitative trait loci coordinately modulate stem growth in <i>Populus</i> . <i>Plant Biotechnology Journal</i> , 2019, 17, 608-624.	4.1	34
35	Indole-3-acetic acid has long-term effects on long non-coding RNA gene methylation and growth in <i>Populus tomentosa</i> . <i>Molecular Genetics and Genomics</i> , 2019, 294, 1511-1525.	1.0	9
36	Origination and Function of Plant Pseudogenes. <i>Plant Signaling and Behavior</i> , 2019, 14, 1625698.	1.2	8

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37	Transcription factors involved in the regulatory networks governing the Calvinâ€“Bensonâ€“Bascham cycle. <i>Tree Physiology</i> , 2019, 39, 1159-1172.	1.4	3
38	Evolutionary Origins of Pseudogenes and Their Association with Regulatory Sequences in Plants. <i>Plant Cell</i> , 2019, 31, 563-578.	3.1	47
39	Transcriptional regulation of chilling stress responsive long noncoding RNAs in <i>Populus simonii</i> . <i>Trees - Structure and Function</i> , 2019, 33, 733-749.	0.9	3
40	Conserved noncoding sequences conserve biological networks and influence genome evolution. <i>Heredity</i> , 2018, 120, 437-451.	1.2	13
41	Genome-Wide Association Studies to Improve Wood Properties: Challenges and Prospects. <i>Frontiers in Plant Science</i> , 2018, 9, 1912.	1.7	34
42	Association Genetics in <i>Populus</i> Reveal the Allelic Interactions of Pto-MIR167a and Its Targets in Wood Formation. <i>Frontiers in Plant Science</i> , 2018, 9, 744.	1.7	14
43	Genetic variation in transcription factors and photosynthesis light-reaction genes regulates photosynthetic traits. <i>Tree Physiology</i> , 2018, 38, 1871-1885.	1.4	6
44	Genetic variants in microRNA biogenesis genes as novel indicators for secondary growth in <i>Populus</i> . <i>New Phytologist</i> , 2018, 219, 1263-1282.	3.5	8
45	Adaptive evolution and functional innovation of <i>Populus</i> -specific recently evolved microRNAs. <i>New Phytologist</i> , 2017, 213, 206-219.	3.5	36
46	Identification and allelic dissection uncover roles of lncRNAs in secondary growth of <i>Populus tomentosa</i> . <i>DNA Research</i> , 2017, 24, 473-486.	1.5	37
47	The Role of Long Noncoding RNAs in Plant Stress Tolerance. <i>Methods in Molecular Biology</i> , 2017, 1631, 41-68.	0.4	15
48	Allelic variation in PtoPsbW associated with photosynthesis, growth, and wood properties in <i>Populus tomentosa</i> . <i>Molecular Genetics and Genomics</i> , 2017, 292, 77-91.	1.0	10
49	The Interactions between the Long Non-coding RNA NERDL and Its Target Gene Affect Wood Formation in <i>Populus tomentosa</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 1035.	1.7	12
50	Allelic Interactions among Pto-MIR475b and Its Four Target Genes Potentially Affect Growth and Wood Properties in <i>Populus</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 1055.	1.7	9
51	Dissection of Insertionâ€“Deletion Variants within Differentially Expressed Genes Involved in Wood Formation in <i>Populus</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 2199.	1.7	17
52	The Role of DNA Methylation in Xylogenesis in Different Tissues of Poplar. <i>Frontiers in Plant Science</i> , 2016, 7, 1003.	1.7	20
53	Association Studies in <i>Populus tomentosa</i> Reveal the Genetic Interactions of Pto-MIR156c and Its Targets in Wood Formation. <i>Frontiers in Plant Science</i> , 2016, 7, 1159.	1.7	12
54	Genetic variations and miRNAâ€“target interactions contribute to natural phenotypic variations in <i>Populus</i> . <i>New Phytologist</i> , 2016, 212, 150-160.	3.5	17

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55	Genetic architecture of growth traits in <i>Populus</i> revealed by integrated quantitative trait locus (QTL) analysis and association studies. <i>New Phytologist</i> , 2016, 209, 1067-1082.	3.5	73
56	Association genetics and transcriptome analysis reveal a gibberellin-responsive pathway involved in regulating photosynthesis. <i>Journal of Experimental Botany</i> , 2016, 67, 3325-3338.	2.4	30
57	Dissection of additive, dominant, epistatic roles of allelic variation within heat shock factor genes in Chinese indigenous poplar (<i>Populus simonii</i>). <i>Tree Genetics and Genomes</i> , 2016, 12, 1.	0.6	2
58	Poplar CBF1 functions specifically in an integrated cold regulatory network. <i>Tree Physiology</i> , 2016, 37, 98-115.	1.4	9
59	Single nucleotide polymorphisms in two GID1 orthologs associate with growth and wood property traits in <i>Populus tomentosa</i> . <i>Tree Genetics and Genomes</i> , 2016, 12, 1.	0.6	1
60	Association studies reveal the effect of genetic variation in lncRNA UGTRL and its putative target PtoUGT88A1 on wood formation in <i>Populus tomentosa</i> . <i>Tree Genetics and Genomes</i> , 2016, 12, 1.	0.6	8
61	Association genetics in <i>Populus</i> reveals the interactions between Pto-miR160a and its target Pto-ARF16. <i>Molecular Genetics and Genomics</i> , 2016, 291, 1069-1082.	1.0	22
62	Variation in genomic methylation in natural populations of <i>Populus simonii</i> is associated with leaf shape and photosynthetic traits. <i>Journal of Experimental Botany</i> , 2016, 67, 723-737.	2.4	34
63	Population genomic analysis of gibberellin-responsive long non-coding RNAs in <i>Populus</i> . <i>Journal of Experimental Botany</i> , 2016, 67, 2467-2482.	2.4	98
64	Stable methylation of a non-coding RNA gene regulates gene expression in response to abiotic stress in <i>Populus simonii</i> . <i>Journal of Experimental Botany</i> , 2016, 67, 1477-1492.	2.4	57
65	The genetic regulatory network centered on Pto-Wuschela and its targets involved in wood formation revealed by association studies. <i>Scientific Reports</i> , 2015, 5, 16507.	1.6	2
66	Methylation of miRNA genes in the response to temperature stress in <i>Populus simonii</i> . <i>Frontiers in Plant Science</i> , 2015, 6, 921.	1.7	67
67	Association genetics and expression patterns of a CBF4 homolog in <i>Populus</i> under abiotic stress. <i>Molecular Genetics and Genomics</i> , 2015, 290, 913-928.	1.0	7
68	Methylation of microRNA genes regulates gene expression in bisexual flower development in andromonoecious poplar. <i>Journal of Experimental Botany</i> , 2015, 66, 1891-1905.	2.4	55
69	Identification of additive, dominant, and epistatic variation conferred by key genes in cellulose biosynthesis pathway in <i>Populus tomentosa</i> . <i>DNA Research</i> , 2015, 22, 53-67.	1.5	46
70	Exploring the Secrets of Long Noncoding RNAs. <i>International Journal of Molecular Sciences</i> , 2015, 16, 5467-5496.	1.8	125
71	Association genetics in <i>Populus</i> reveals the interactions between Pt-miR397a and its target genes. <i>Scientific Reports</i> , 2015, 5, 11672.	1.6	8
72	Transcript abundance patterns of <i>Populus</i> C-repeat binding factor2 orthologs and genetic association of PsCBF2 allelic variation with physiological and biochemical traits in response to abiotic stress. <i>Planta</i> , 2015, 242, 295-312.	1.6	4

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73	Populus endo- β -1,4-glucanases gene family: genomic organization, phylogenetic analysis, expression profiles and association mapping. <i>Planta</i> , 2015, 241, 1417-1434.	1.6	16
74	Association mapping in <i>Populus</i> reveals the interaction between Pto-miR530a and its target Pto-KNAT1. <i>Planta</i> , 2015, 242, 77-95.	1.6	9
75	Transcript profiling of <i>Populus tomentosa</i> genes in normal, tension, and opposite wood by RNA-seq. <i>BMC Genomics</i> , 2015, 16, 164.	1.2	58
76	Genome-wide identification of novel long non-coding RNAs in <i>Populus tomentosa</i> tension wood, opposite wood and normal wood xylem by RNA-seq. <i>Planta</i> , 2015, 241, 125-143.	1.6	109
77	Association of Allelic Variation in PtoXET16A with Growth and Wood Properties in <i>Populus tomentosa</i> . <i>International Journal of Molecular Sciences</i> , 2014, 15, 16949-16974.	1.8	16
78	Single nucleotide polymorphisms in a cellulose synthase gene (PtoCesA3) are associated with growth and wood properties in <i>Populus tomentosa</i> . <i>Planta</i> , 2014, 240, 1269-1286.	1.6	4
79	Biochemical, physiological and gene expression analysis reveals sex-specific differences in <i>Populus tomentosa</i> floral development. <i>Physiologia Plantarum</i> , 2014, 150, 18-31.	2.6	14
80	Effects of high temperature on photosynthesis and related gene expression in poplar. <i>BMC Plant Biology</i> , 2014, 14, 111.	1.6	188
81	Single-nucleotide polymorphisms in PtoCesA7 and their association with growth and wood properties in <i>Populus tomentosa</i> . <i>Molecular Genetics and Genomics</i> , 2014, 289, 439-455.	1.0	23
82	Identification of Genes Differentially Expressed in Shoot Apical Meristems and in Mature Xylem of <i>Populus tomentosa</i> . <i>Plant Molecular Biology Reporter</i> , 2014, 32, 452-464.	1.0	7
83	Single-nucleotide polymorphisms in the 5' UTR of UDP-glucose dehydrogenase (PtUGDH) associate with wood properties in <i>Populus tomentosa</i> . <i>Tree Genetics and Genomes</i> , 2014, 10, 339-354.	0.6	11
84	Variation in growth, leaf, and wood property traits of Chinese white poplar (<i>Populus tomentosa</i>), a major industrial tree species in Northern China. <i>Canadian Journal of Forest Research</i> , 2014, 44, 326-339.	0.8	70
85	Comparison of the physiological effects and transcriptome responses of <i>Populus simonii</i> under different abiotic stresses. <i>Plant Molecular Biology</i> , 2014, 86, 139-156.	2.0	41
86	Identification and characterization of nuclear genes involved in photosynthesis in <i>Populus</i> . <i>BMC Plant Biology</i> , 2014, 14, 81.	1.6	20
87	Allelic variation within the S-adenosyl-L-homocysteine hydrolase gene family is associated with wood properties in Chinese white poplar (<i>Populus tomentosa</i>). <i>BMC Genetics</i> , 2014, 15, S4.	2.7	8
88	Association mapping for morphological and physiological traits in <i>Populus simonii</i> . <i>BMC Genetics</i> , 2014, 15, S3.	2.7	11
89	Sexual dimorphic floral development in dioecious plants revealed by transcriptome, phytohormone, and DNA methylation analysis in <i>Populus tomentosa</i> . <i>Plant Molecular Biology</i> , 2013, 83, 559-576.	2.0	66
90	Transcriptome profiling reveals differential transcript abundance in response to chilling stress in <i>Populus simonii</i> . <i>Plant Cell Reports</i> , 2013, 32, 1407-1425.	2.8	38

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91	The SUPERMAN gene family in Populus: nucleotide diversity and gene expression in a dioecious plant. <i>Plant Cell Reports</i> , 2013, 32, 1277-1288.	2.8	4
92	The low fertility of Chinese white poplar: dynamic changes in anatomical structure, endogenous hormone concentrations, and key gene expression in the reproduction of a naturally occurring hybrid. <i>Plant Cell Reports</i> , 2013, 32, 401-414.	2.8	9
93	Genome-Wide Analysis of Gene Expression in Response to Drought Stress in <i>Populus simonii</i> . <i>Plant Molecular Biology Reporter</i> , 2013, 31, 946-962.	1.0	46
94	Development and Application of Microsatellites in Candidate Genes Related to Wood Properties in the Chinese White Poplar (<i>Populus tomentosa</i> Carr.). <i>DNA Research</i> , 2013, 20, 31-44.	1.5	29
95	Polymorphic simple sequence repeat (<scp>SSR</scp>) loci within cellulose synthase (<scp><i>PtoCesA</i></scp>) genes are associated with growth and wood properties in <i>P</i><scp>opulus tomentosa</i>. <i>New Phytologist</i> , 2013, 197, 763-776.	3.5	47
96	Genetic Diversity and Population Structure in Chinese Indigenous Poplar (<i>Populus simonii</i>) Populations Using Microsatellite Markers. <i>Plant Molecular Biology Reporter</i> , 2013, 31, 620-632.	1.0	42
97	Allelic Variation in a Cellulose Synthase Gene (<i>PtoCesA4</i>) Associated with Growth and Wood Properties in <i>Populus tomentosa</i>. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 2069-2084.	0.8	28
98	The UDP-Glucuronate Decarboxylase Gene Family in Populus: Structure, Expression, and Association Genetics. <i>PLoS ONE</i> , 2013, 8, e60880.	1.1	24
99	Sexual Dimorphism Floral MicroRNA Profiling and Target Gene Expression in Andromonoecious Poplar (<i>Populus tomentosa</i>). <i>PLoS ONE</i> , 2013, 8, e62681.	1.1	31
100	Variation in Genomic Methylation in Natural Populations of Chinese White Poplar. <i>PLoS ONE</i> , 2013, 8, e63977.	1.1	20
101	Photosynthetic response to genome methylation affects the growth of Chinese white poplar. <i>Tree Genetics and Genomes</i> , 2012, 8, 1407-1421.	0.6	25
102	Genetic Diversity and Population Structure of Chinese White Poplar (<i>Populus tomentosa</i>) Revealed by SSR Markers. <i>Journal of Heredity</i> , 2012, 103, 853-862.	1.0	129
103	Transcriptional profiling by cDNA-AFLP analysis showed differential transcript abundance in response to water stress in <i>Populus hopeiensis</i> . <i>BMC Genomics</i> , 2012, 13, 286.	1.2	29
104	Sex-specific DNA methylation and gene expression in andromonoecious poplar. <i>Plant Cell Reports</i> , 2012, 31, 1393-1405.	2.8	38
105	Allelic Variation in PtGA20Ox Associates with Growth and Wood Properties in <i>Populus</i> spp. <i>PLoS ONE</i> , 2012, 7, e53116.	1.1	22
106	The sucrose synthase gene family in Populus: structure, expression, and evolution. <i>Tree Genetics and Genomes</i> , 2011, 7, 443-456.	0.6	77
107	Preparation and properties of solution-processed zinc tin oxide films from a new organic precursor. <i>Science China Chemistry</i> , 2011, 54, 651-655.	4.2	3
108	The actin multigene family in Populus: organization, expression and phylogenetic analysis. <i>Molecular Genetics and Genomics</i> , 2010, 284, 105-119.	1.0	56

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109	Expression and nucleotide diversity of the poplar COBL gene. <i>Tree Genetics and Genomes</i> , 2010, 6, 331-344.	0.6	20
110	Salt-induced expression of genes related to Na ⁺ /K ⁺ and ROS homeostasis in leaves of salt-resistant and salt-sensitive poplar species. <i>Plant Molecular Biology</i> , 2010, 73, 251-269.	2.0	129
111	Identification of a <i>Cis</i> -Acting Regulatory Polymorphism in a Eucalypt <i>COBRA</i> -Like Gene Affecting Cellulose Content. <i>Genetics</i> , 2009, 183, 1153-1164.	1.2	89
112	QTL analysis of growth and wood chemical content traits in an interspecific backcross family of white poplar (<i>Populus tomentosa</i> × <i>P. bolleana</i>) × <i>P. tomentosa</i> . <i>Canadian Journal of Forest Research</i> , 2006, 36, 2015-2023.	0.8	36