

Deqiang Zhang

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

109
papers

2,044
citations

26
h-index

41
g-index

117
ext. papers

2,713
ext. citations

5.2
avg, IF

5.05
L-index

#	Paper	IF	Citations
109	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	3.1	1
108	Transposable Elements: Distribution, Polymorphism, and Climate Adaptation in .. <i>Frontiers in Plant Science</i> , 2022 , 13, 814718	6.2	0
107	LncRNA PMAT-PtoMYB46 module represses PtoMATE and PtoARF2 promoting Pb uptake and plant growth in poplar.. <i>Journal of Hazardous Materials</i> , 2022 , 433, 128769	12.8	2
106	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	5.7	3
105	Synonymous mutation in Growth Regulating Factor 15 of miR396a target sites enhances photosynthetic efficiency and heat tolerance in poplar. <i>Journal of Experimental Botany</i> , 2021 , 72, 4502-4519	7.19	7
104	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	7	2
103	Gene Coexpression Network Analysis Indicates that Hub Genes Related to Photosynthesis and Starch Synthesis Modulate Salt Stress Tolerance in. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	3
102	Genetic architecture of the metabolic pathway of salicylic acid biosynthesis in <i>Populus</i> . <i>Tree Physiology</i> , 2021 , 41, 2198-2215	4.2	1
101	Genetic Effects and Expression Patterns of the Nitrate Transporter (NRT) Gene Family in. <i>Frontiers in Plant Science</i> , 2021 , 12, 661635	6.2	4
100	Integration of genome wide association studies and co-expression networks reveal roles of PtoWRKY 42-PtoUGT76C1-1 in trans-zeatin metabolism and cytokinin sensitivity in poplar. <i>New Phytologist</i> , 2021 , 231, 1462-1477	9.8	4
99	Miniature inverted repeat transposable elements cis-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	7	1
98	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	7	6
97	Genetic Architecture Underlying the Metabolites of Chlorogenic Acid Biosynthesis in. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	3
96	Association Study and Mendelian Randomization Analysis Reveal Effects of the Genetic Interaction Between and on Wood Formation in. <i>Frontiers in Plant Science</i> , 2021 , 12, 704941	6.2	
95	Multi-omics analysis provides insights into genetic architecture of flavonoid metabolites in <i>Populus</i> . <i>Industrial Crops and Products</i> , 2021 , 168, 113612	5.9	1
94	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	5.9	1
93	Single-cell RNA sequencing profiles of stem-differentiating xylem in poplar. <i>Plant Biotechnology Journal</i> , 2021 ,	11.6	2

92	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	3.1	2
91	Key Genes and Genetic Interactions of Plant-Pathogen Functional Modules in Poplar Infected by. <i>Molecular Plant-Microbe Interactions</i> , 2020 , 33, 1080-1090	3.6	4
90	Evolution and Functional Divergence of the Gene Family in. <i>Frontiers in Plant Science</i> , 2020 , 11, 484	6.2	2
89	Identification of a transcriptional regulatory module that reduces leaf temperature in poplar under heat stress. <i>Tree Physiology</i> , 2020 , 40, 1108-1125	4.2	1
88	Changes in DNA Methylation in Response to 6-Benzylaminopurine Affect Allele-Specific Gene Expression in. <i>International Journal of Molecular Sciences</i> , 2020 , 21,	6.3	1
87	Machine learning models for net photosynthetic rate prediction using poplar leaf phenotype data. <i>PLoS ONE</i> , 2020 , 15, e0228645	3.7	6
86	A Higher Order Prediction Model of <i>Populus Simonii</i> Net Photosynthetic Rate Based on Improved Gradient Boosting Method. <i>Communications in Computer and Information Science</i> , 2020 , 373-385	0.3	
85	Linkage-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	9.8	8
84	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,	6.3	5
83	Genome Cytosine Methylation May Affect Growth and Wood Property Traits in Populations of <i>Populus tomentosa</i> . <i>Forests</i> , 2020 , 11, 828	2.8	0
82	Genetic dissection of the gene coexpression network underlying photosynthesis in <i>Populus</i> . <i>Plant Biotechnology Journal</i> , 2020 , 18, 1015-1026	11.6	8
81	Origination and Function of Plant Pseudogenes. <i>Plant Signaling and Behavior</i> , 2019 , 14, 1625698	2.5	4
80	Transcription factors involved in the regulatory networks governing the Calvin-Benson-Bassham cycle. <i>Tree Physiology</i> , 2019 , 39, 1159-1172	4.2	1
79	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	11.6	12
78	Genetic architecture underlying the lignin biosynthesis pathway involves noncoding RNAs and transcription factors for growth and wood properties in <i>Populus</i> . <i>Plant Biotechnology Journal</i> , 2019 , 17, 302-315	11.6	28
77	Time-specific and pleiotropic quantitative trait loci coordinately modulate stem growth in <i>Populus</i> . <i>Plant Biotechnology Journal</i> , 2019 , 17, 608-624	11.6	15
76	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	3.1	6
75	Evolutionary Origins of Pseudogenes and Their Association with Regulatory Sequences in Plants. <i>Plant Cell</i> , 2019 , 31, 563-578	11.6	19

74	Transcriptional regulation of chilling stress responsive long noncoding RNAs in <i>Populus simonii</i> . <i>Trees - Structure and Function</i> , 2019 , 33, 733-749	2.6	
73	Conserved noncoding sequences conserve biological networks and influence genome evolution. <i>Heredity</i> , 2018 , 120, 437-451	3.6	8
72	Association Genetics in Reveal the Allelic Interactions of and Its Targets in Wood Formation. <i>Frontiers in Plant Science</i> , 2018 , 9, 744	6.2	8
71	Genetic variation in transcription factors and photosynthesis light-reaction genes regulates photosynthetic traits. <i>Tree Physiology</i> , 2018 , 38, 1871-1885	4.2	3
70	Genetic variants in microRNA biogenesis genes as novel indicators for secondary growth in <i>Populus</i> . <i>New Phytologist</i> , 2018 , 219, 1263-1282	9.8	6
69	Genome-Wide Association Studies to Improve Wood Properties: Challenges and Prospects. <i>Frontiers in Plant Science</i> , 2018 , 9, 1912	6.2	18
68	Adaptive evolution and functional innovation of <i>Populus</i> -specific recently evolved microRNAs. <i>New Phytologist</i> , 2017 , 213, 206-219	9.8	20
67	Identification and allelic dissection uncover roles of lncRNAs in secondary growth of <i>Populus tomentosa</i> . <i>DNA Research</i> , 2017 , 24, 473-486	4.5	24
66	Poplar CBF1 functions specifically in an integrated cold regulatory network. <i>Tree Physiology</i> , 2017 , 37, 98-115	4.2	9
65	Dissection of Insertion-Deletion Variants within Differentially Expressed Genes Involved in Wood Formation in. <i>Frontiers in Plant Science</i> , 2017 , 8, 2199	6.2	9
64	The Role of Long Noncoding RNAs in Plant Stress Tolerance. <i>Methods in Molecular Biology</i> , 2017 , 1631, 41-68	1.4	9
63	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	3.1	9
62	The Interactions between the Long Non-coding RNA NERDL and Its Target Gene Affect Wood Formation in. <i>Frontiers in Plant Science</i> , 2017 , 8, 1035	6.2	9
61	Allelic Interactions among and Its Four Target Genes Potentially Affect Growth and Wood Properties in. <i>Frontiers in Plant Science</i> , 2017 , 8, 1055	6.2	9
60	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	2.1	0
59	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	2.1	5
58	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, 1069-82	3.1	10
57	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, 723-37	7	22

56	Population genomic analysis of gibberellin-responsive long non-coding RNAs in Populus. <i>Journal of Experimental Botany</i> , 2016 , 67, 2467-82	7	58
55	Stable methylation of a non-coding RNA gene regulates gene expression in response to abiotic stress in Populus simonii. <i>Journal of Experimental Botany</i> , 2016 , 67, 1477-92	7	43
54	The Role of DNA Methylation in Xylogenesis in Different Tissues of Poplar. <i>Frontiers in Plant Science</i> , 2016 , 7, 1003	6.2	13
53	Association Studies in Populus tomentosa Reveal the Genetic Interactions of Pto-MIR156c and Its Targets in Wood Formation. <i>Frontiers in Plant Science</i> , 2016 , 7, 1159	6.2	9
52	Genetic variations and miRNA-target interactions contribute to natural phenotypic variations in Populus. <i>New Phytologist</i> , 2016 , 212, 150-60	9.8	12
51	Genetic architecture of growth traits in Populus revealed by integrated quantitative trait locus (QTL) analysis and association studies. <i>New Phytologist</i> , 2016 , 209, 1067-82	9.8	50
50	Association genetics and transcriptome analysis reveal a gibberellin-responsive pathway involved in regulating photosynthesis. <i>Journal of Experimental Botany</i> , 2016 , 67, 3325-38	7	19
49	Dissection of additive, dominant, epistatic roles of allelic variation within heat shock factor genes in Chinese indigenous poplar (Populus simonii). <i>Tree Genetics and Genomes</i> , 2016 , 12, 1	2.1	1
48	Identification of additive, dominant, and epistatic variation conferred by key genes in cellulose biosynthesis pathway in Populus tomentosa. <i>DNA Research</i> , 2015 , 22, 53-67	4.5	29
47	Exploring the secrets of long noncoding RNAs. <i>International Journal of Molecular Sciences</i> , 2015 , 16, 5467-96	9.6	86
46	Association genetics in Populus reveals the interactions between Pt-miR397a and its target genes. <i>Scientific Reports</i> , 2015 , 5, 11672	4.9	7
45	Transcript abundance patterns of Populus 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	4.7	4
44	Populus endo- β -1,4-glucanases gene family: genomic organization, phylogenetic analysis, expression profiles and association mapping. <i>Planta</i> , 2015 , 241, 1417-34	4.7	10
43	Association mapping in Populus reveals the interaction between Pto-miR530a and its target Pto-KNAT1. <i>Planta</i> , 2015 , 242, 77-95	4.7	7
42	Transcript profiling of Populus tomentosa genes in normal, tension, and opposite wood by RNA-seq. <i>BMC Genomics</i> , 2015 , 16, 164	4.5	38
41	Genome-wide identification of novel long non-coding RNAs in Populus tomentosa tension wood, opposite wood and normal wood xylem by RNA-seq. <i>Planta</i> , 2015 , 241, 125-43	4.7	70
40	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	4.9	1
39	Methylation of miRNA genes in the response to temperature stress in Populus simonii. <i>Frontiers in Plant Science</i> , 2015 , 6, 921	6.2	43

38	Association genetics and expression patterns of a CBF4 homolog in <i>Populus</i> under abiotic stress. <i>Molecular Genetics and Genomics</i> , 2015 , 290, 913-28	3.1	6
37	Methylation of microRNA genes regulates gene expression in bisexual flower development in andromonoecious poplar. <i>Journal of Experimental Botany</i> , 2015 , 66, 1891-905	7	33
36	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, 439-55	3.1	13
35	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	1.7	7
34	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	2.1	10
33	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	1.9	49
32	Comparison of the physiological effects and transcriptome responses of <i>Populus simonii</i> under different abiotic stresses. <i>Plant Molecular Biology</i> , 2014 , 86, 139-56	4.6	32
31	Identification and characterization of nuclear genes involved in photosynthesis in <i>Populus</i> . <i>BMC Plant Biology</i> , 2014 , 14, 81	5.3	17
30	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 Suppl 1, S4	2.6	7
29	Association mapping for morphological and physiological traits in <i>Populus simonii</i> . <i>BMC Genetics</i> , 2014 , 15 Suppl 1, S3	2.6	10
28	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, 16949-74	6.3	7
27	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, 1269-86	4.7	4
26	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	4.6	12
25	Effects of high temperature on photosynthesis and related gene expression in poplar. <i>BMC Plant Biology</i> , 2014 , 14, 111	5.3	135
24	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, 559-76	4.6	50
23	Transcriptome profiling reveals differential transcript abundance in response to chilling stress in <i>Populus simonii</i> . <i>Plant Cell Reports</i> , 2013 , 32, 1407-25	5.1	35
22	The SUPERMAN gene family in <i>Populus</i> : nucleotide diversity and gene expression in a dioecious plant. <i>Plant Cell Reports</i> , 2013 , 32, 1277-88	5.1	2
21	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, 401-14	5.1	3

20	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	1.7	37
19	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	4.5	25
18	Polymorphic simple sequence repeat (SSR) loci within cellulose synthase (PtoCesA) genes are associated with growth and wood properties in <i>Populus tomentosa</i> . <i>New Phytologist</i> , 2013 , 197, 763-776	9.8	41
17	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	1.7	34
16	Allelic variation in a cellulose synthase gene (PtoCesA4) associated with growth and wood properties in <i>Populus tomentosa</i> . <i>G3: Genes, Genomes, Genetics</i> , 2013 , 3, 2069-84	3.2	21
15	The UDP-glucuronate decarboxylase gene family in <i>Populus</i> : structure, expression, and association genetics. <i>PLoS ONE</i> , 2013 , 8, e60880	3.7	21
14	Sexual dimorphism floral microRNA profiling and target gene expression in andromonoecious poplar (<i>Populus tomentosa</i>). <i>PLoS ONE</i> , 2013 , 8, e62681	3.7	28
13	Variation in genomic methylation in natural populations of chinese white poplar. <i>PLoS ONE</i> , 2013 , 8, e63977	3.7	17
12	Photosynthetic response to genome methylation affects the growth of Chinese white poplar. <i>Tree Genetics and Genomes</i> , 2012 , 8, 1407-1421	2.1	23
11	Genetic diversity and population structure of Chinese White poplar (<i>Populus tomentosa</i>) revealed by SSR markers. <i>Journal of Heredity</i> , 2012 , 103, 853-62	2.4	90
10	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	4.5	25
9	Sex-specific DNA methylation and gene expression in andromonoecious poplar. <i>Plant Cell Reports</i> , 2012 , 31, 1393-405	5.1	32
8	Allelic variation in PtGA20Ox associates with growth and wood properties in <i>Populus</i> spp. <i>PLoS ONE</i> , 2012 , 7, e53116	3.7	20
7	The sucrose synthase gene family in <i>Populus</i> : structure, expression, and evolution. <i>Tree Genetics and Genomes</i> , 2011 , 7, 443-456	2.1	66
6	Preparation and properties of solution-processed zinc tin oxide films from a new organic precursor. <i>Science China Chemistry</i> , 2011 , 54, 651-655	7.9	3
5	The actin multigene family in <i>Populus</i> : organization, expression and phylogenetic analysis. <i>Molecular Genetics and Genomics</i> , 2010 , 284, 105-19	3.1	48
4	Expression and nucleotide diversity of the poplar COBL gene. <i>Tree Genetics and Genomes</i> , 2010 , 6, 331-344	3.4	19
3	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, 251-69	4.6	115

2	Identification of a Cis-acting regulatory polymorphism in a Eucalypt COBRA-like gene affecting cellulose content. <i>Genetics</i> , 2009 , 183, 1153-64	4	70
1	QTL analysis of growth and wood chemical content traits in an interspecific backcross family of white poplar (<i>Populus tomentosa</i> [P. bolleana] P. tomentosa). <i>Canadian Journal of Forest Research</i> , 2006 , 36, 2015-2023	1.9	32