

Guifeng Liu

List of Publications by Year in descending order

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53
papers

1,070
citations

430874

18
h-index

454955

30
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54
all docs

54
docs citations

54
times ranked

1210
citing authors

#	ARTICLE	IF	CITATIONS
1	A WRKY gene from <i>Tamarix hispida</i> , ThWRKY4, mediates abiotic stress responses by modulating reactive oxygen species and expression of stress-responsive genes. <i>Plant Molecular Biology</i> , 2013, 82, 303-320.	3.9	82
2	Loss of GLK1 transcription factor function reveals new insights in chlorophyll biosynthesis and chloroplast development. <i>Journal of Experimental Botany</i> , 2019, 70, 3125-3138.	4.8	75
3	The salt-responsive transcriptome of <i>Populus simonii</i> — <i>Populus nigra</i> via DGE. <i>Gene</i> , 2012, 504, 203-212.	2.2	62
4	Overexpression of an AP2/ERF family gene, BpERF13, in birch enhances cold tolerance through upregulating CBF genes and mitigating reactive oxygen species. <i>Plant Science</i> , 2020, 292, 110375.	3.6	62
5	<i>Populus simonii</i> — <i>Populus nigra</i> WRKY70 is involved in salt stress and leaf blight disease responses. <i>Tree Physiology</i> , 2017, 37, 827-844.	3.1	54
6	Cloning of Ten Peroxidase (POD) Genes from <i>Tamarix hispida</i> and Characterization of their Responses to Abiotic Stress. <i>Plant Molecular Biology Reporter</i> , 2010, 28, 77-89.	1.8	51
7	The Conserved Endoribonuclease YbeY Is Required for Chloroplast Ribosomal RNA Processing in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2015, 168, 205-221.	4.8	49
8	Analysis of Gene Expression Profile of <i>Limonium bicolor</i> under NaHCO ₃ Stress Using cDNA Microarray. <i>Plant Molecular Biology Reporter</i> , 2008, 26, 241-254.	1.8	46
9	Overexpression of a Vacuolar H ⁺ -ATPase c Subunit Gene Mediates Physiological Changes Leading to Enhanced Salt Tolerance in Transgenic Tobacco. <i>Plant Molecular Biology Reporter</i> , 2011, 29, 424-430.	1.8	38
10	The rooting of poplar cuttings: a review. <i>New Forests</i> , 2014, 45, 21-34.	1.7	31
11	BpAP1 directly regulates BpDEF to promote male inflorescence formation in <i>Betula platyphylla</i> — <i>B. pendula</i> . <i>Tree Physiology</i> , 2019, 39, 1046-1060.	3.1	29
12	Variance and stability analyses of growth characters in half-sib <i>Betula platyphylla</i> families at three different sites in China. <i>Euphytica</i> , 2016, 208, 173-186.	1.2	28
13	Negative feedback loop between BpAP1 and BpPI/BpDEF heterodimer in <i>Betula platyphylla</i> — <i>B. pendula</i> . <i>Plant Science</i> , 2019, 289, 110280.	3.6	28
14	Functional characterization of CCR in birch (<i>Betula platyphylla</i> — <i>Betula tatarica</i>) overlock 10 283-296.	5.2	27
15	BpGH3.5, an early auxin-response gene, regulates root elongation in <i>Betula platyphylla</i> — <i>Betula pendula</i> . <i>Plant Cell, Tissue and Organ Culture</i> , 2015, 120, 239-250.	2.3	26
16	Comparative Analysis of Growth and Photosynthetic Characteristics of (<i>Populus simonii</i> — <i>P. nigra</i>)—(<i>P. nigra</i> — <i>P. simonii</i>) Hybrid Clones of Different Ploidies. <i>PLoS ONE</i> , 2015, 10, e0119259.	2.5	23
17	Analysis of genetic effects on a complete diallel cross test of <i>Betula platyphylla</i> . <i>Euphytica</i> , 2014, 200, 221-229.	1.2	22
18	Phylogenetic and stress-responsive expression analysis of 20 WRKY genes in <i>Populus simonii</i> — <i>Populus nigra</i> . <i>Gene</i> , 2015, 565, 130-139.	2.2	22

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19	Comprehensive characterization of T-DNA integration induced chromosomal rearrangement in a birch T-DNA mutant. <i>BMC Genomics</i> , 2019, 20, 311.	2.8	22
20	A novel synthetic-genetic-array-based yeast one-hybrid system for high discovery rate and short processing time. <i>Genome Research</i> , 2019, 29, 1343-1351.	5.5	20
21	Genetic Linkage Maps of <i>Betula platyphylla</i> Suk Based on ISSR and AFLP Markers. <i>Plant Molecular Biology Reporter</i> , 2010, 28, 169-175.	1.8	19
22	Influence of Nitrogen, Phosphorus, and Potassium Fertilization on Flowering and Expression of Flowering-Associated Genes in White Birch (<i>Betula platyphylla</i> Suk.). <i>Plant Molecular Biology Reporter</i> , 2011, 29, 794-801.	1.8	18
23	Variation and genetic stability analyses of transgenic TaLEA poplar clones from four different sites in China. <i>Euphytica</i> , 2015, 206, 331-342.	1.2	17
24	Genome-wide transcriptome profiling reveals the mechanism of the effects of uniconazole on root development in <i>Glycine Max</i> . <i>Journal of Plant Biology</i> , 2017, 60, 387-403.	2.1	16
25	Characterization and Identification of a woody lesion mimic mutant lmd, showing defence response and resistance to <i>Alternaria alternate</i> in birch. <i>Scientific Reports</i> , 2017, 7, 11308.	3.3	15
26	Study on the physiological indices of <i>Pinus sibirica</i> and <i>Pinus koraiensis</i> seedlings under cold stress. <i>Journal of Forestry Research</i> , 2019, 30, 1255-1265.	3.6	15
27	Physiological and Transcriptome Analysis of a Yellow-Green Leaf Mutant in Birch (<i>Betula platyphylla</i> Å–) Tj ETQq1 1,0,784314 rgBT /O 2.1 148	2.1	14
28	Functional Study of BpPP2C1 Revealed Its Role in Salt Stress in <i>Betula platyphylla</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 617635.	3.6	14
29	Time-Course Analysis of Levels of Indole-3-Acetic Acid and Expression of Auxin-Responsive GH3 Genes in <i>Betula platyphylla</i> . <i>Plant Molecular Biology Reporter</i> , 2011, 29, 898-905.	1.8	13
30	BpMADS12 gene role in lignin biosynthesis of <i>Betula platyphylla</i> Suk by transcriptome analysis. <i>Journal of Forestry Research</i> , 2016, 27, 1111-1120.	3.6	13
31	Building an mRNA transcriptome from the shoots of <i>Betula platyphylla</i> by using Solexa technology. <i>Tree Genetics and Genomes</i> , 2012, 8, 1031-1040.	1.6	10
32	Overexpression of BpCUC2 Influences Leaf Shape and Internode Development in <i>Betula pendula</i> . <i>International Journal of Molecular Sciences</i> , 2019, 20, 4722.	4.1	10
33	Genetic variation and selection of introduced provenances of Siberian Pine (<i>Pinus sibirica</i>) in frigid regions of the Greater Xing'an Range, Northeast China. <i>Journal of Forestry Research</i> , 2014, 25, 549-556.	3.6	9
34	Analysis of three types of triterpenoids in tetraploid white birches (<i>Betula platyphylla</i> Suk.) and selection of plus trees. <i>Journal of Forestry Research</i> , 2015, 26, 623-633.	3.6	9
35	Analysis of the promoter features of BpCUC2 in <i>Betula platyphylla</i> and <i>Betula pendula</i> . <i>Plant Cell, Tissue and Organ Culture</i> , 2018, 132, 191-199.	2.3	9
36	A R2R3-MYB Transcription Factor Gene, BpMYB123, Regulates BpLEA14 to Improve Drought Tolerance in <i>Betula platyphylla</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 791390.	3.6	8

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37	Expression of BpPIN is associated with IAA levels and the formation of lobed leaves in <i>Betula pendula</i> "Dalecartica". <i>Journal of Forestry Research</i> , 2020, 31, 87-97.	3.6	7
38	Somatic embryogenesis and plant regeneration in <i>Betula platyphylla</i> . <i>Journal of Forestry Research</i> , 2021, 32, 937-944.	3.6	7
39	BpMADS12 mediates endogenous hormone signaling: effect on plant development <i>Betula platyphylla</i> . <i>Plant Cell, Tissue and Organ Culture</i> , 2016, 124, 169-180.	2.3	6
40	Evaluation of <i>Betula platyphylla</i> Families Based on Growth and Wood Property Traits. <i>Forest Science</i> , 0, , .	1.0	6
41	Characterization and T-DNA insertion sites identification of a multiple-branches mutant br in <i>Betula platyphylla</i> "Betula pendula". <i>BMC Plant Biology</i> , 2019, 19, 491.	3.6	5
42	Transcriptome sequencing to reveal the genetic regulation of leaf margin variation at early stage in birch. <i>Tree Genetics and Genomes</i> , 2019, 15, 1.	1.6	5
43	Expression of BpIAA10 from <i>Betula platyphylla</i> (birch) is differentially regulated by different hormones and light intensities. <i>Plant Cell, Tissue and Organ Culture</i> , 2018, 132, 371-381.	2.3	4
44	Expression profiling of the BpIAA gene family and the determination of IAA levels in <i>Betula platyphylla</i> tetraploids. <i>Journal of Forestry Research</i> , 2019, 30, 855-867.	3.6	4
45	Transcriptome analysis provides new insights into leaf shape variation in birch. <i>Trees - Structure and Function</i> , 2019, 33, 1265-1281.	1.9	4
46	Global Analysis of the WOX Transcription Factor Gene Family in <i>Populus</i> "xiaohei". T. S. Hwang et Liang Reveals Their Stress Responsive Patterns. <i>Forests</i> , 2022, 13, 122.	2.1	4
47	Progeny test of tetraploid <i>Betula platyphylla</i> and preliminary selection of hybrid parents. <i>Journal of Forestry Research</i> , 2016, 27, 665-674.	3.6	3
48	Transcriptome Analysis of a Multiple-Branches Mutant Terminal Buds in <i>Betula platyphylla</i> "B. pendula". <i>Forests</i> , 2019, 10, 374.	2.1	3
49	Investigation of temporal variations in endogenous gibberellin A3 and A4 in the leaves of birch (<i>Betula</i>) Tj ETQq1 1 0,784314 ₂ gBT /Ov	1.9	2
50	Inhibition of BpEIN3 causes plaques in leaves of <i>Betula platyphylla</i> "B. pendula". <i>Trees - Structure and Function</i> , 2020, 34, 483-495.	1.9	2
51	Selection and optimum fertilization of <i>Betula platyphylla</i> hybrid clones for growth. <i>Trees - Structure and Function</i> , 2021, 35, 469-478.	1.9	1
52	Selection of elite lines of BpGH3.5-transgenic <i>Betula platyphylla</i> using growth adaptability analysis. <i>Journal of Forestry Research</i> , 0, , 1.	3.6	1
53	Effect of mouse calcineurin on induction and growth of rice callus transformed by the calcineurin gene. <i>Plant Cell, Tissue and Organ Culture</i> , 2006, 86, 1-6.	2.3	0