## **Chuanping Yang**

List of Publications by Year in descending order

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71 papers

1,785 citations

218677
26
h-index

302126 39 g-index

72 all docs

72 docs citations

times ranked

72

2160 citing authors

#	Article	IF	CITATIONS
1	Functional roles of the birch BpRAV1 transcription factor in salt and osmotic stress response. Plant Science, 2022, 315, 111131.	3.6	10
2	PtrHAT22, as a higher hierarchy regulator, coordinately regulates secondary cell wall component biosynthesis in Populus trichocarpa. Plant Science, 2022, 316, 111170.	3.6	7
3	Effects of different nitrogen forms and concentrations on seedling growth traits and physiological characteristics of Populus simonii × P. nigra. Journal of Forestry Research, 2022, 33, 1593-1606.	3.6	4
4	Genetic variation and superior provenances selection for wood properties of Larix olgensis at four trials. Journal of Forestry Research, 2022, 33, 1867-1879.	3.6	5
5	Identification and expression analysis of the PtGATL genes under different nitrogen and carbon dioxide treatments in Populus trichocarpa. 3 Biotech, 2022, 12, 67.	2.2	O
6	Qu-2, a robust poplar suspension cell line for molecular biology. Journal of Forestry Research, 2021, 32, 733-740.	3.6	4
7	Identification and Characterization of the APX Gene Family and Its Expression Pattern under Phytohormone Treatment and Abiotic Stress in Populus trichocarpa. Genes, 2021, 12, 334.	2.4	19
8	Genome sequence and evolution of <i>Betula platyphylla </i> Ii>. Horticulture Research, 2021, 8, 37.	6.3	53
9	Genetic stability of Larix olgensis provenances planted in different sites in northeast China. Forest Ecology and Management, 2021, 485, 118988.	3.2	11
10	Bioinformatics analysis of PAE family in Populus trichocarpa and responsiveness to carbon and nitrogen treatment. 3 Biotech, 2021, 11, 370.	2.2	2
11	Functional Characterisation of the Poplar Atypical Aspartic Protease Gene PtAP66 in Wood Secondary Cell Wall Deposition. Forests, 2021, 12, 1002.	2.1	3
12	Chloroplast (Cp) Transcriptome of P. davidiana Dode×P. bolleana Lauch provides insight into the Cp drought response and Populus Cp phylogeny. BMC Evolutionary Biology, 2020, 20, 51.	3.2	5
13	Progeny performance and selection of superior trees within families in Larix olgensis. Euphytica, 2020, 216, 1.	1.2	11
14	Functional characterization and expression patterns of PnATX genes under different abiotic stress treatments in Populus. Tree Physiology, 2020, 40, 520-537.	3.1	2
15	Expression analysis of the BpARF genes in Betula platyphylla under drought stress. Plant Physiology and Biochemistry, 2020, 148, 273-281.	5.8	13
16	Genome Survey Sequencing of Betula platyphylla. Forests, 2019, 10, 826.	2.1	10
17	Genome-wide characterization of aspartic protease (AP) gene family in Populus trichocarpa and identification of the potential PtAPs involved in wood formation. BMC Plant Biology, 2019, 19, 276.	3.6	23
18	BpNAC012 Positively Regulates Abiotic Stress Responses and Secondary Wall Biosynthesis. Plant Physiology, 2019, 179, 700-717.	4.8	68

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19	Optimization of Poplar mRNA purification for trancriptome library construction. Acta Biochimica Et Biophysica Sinica, 2018, 50, 224-226.	2.0	1
20	Complete chloroplast genome sequence of Betula platyphylla: gene organization, RNA editing, and comparative and phylogenetic analyses. BMC Genomics, 2018, 19, 950.	2.8	33
21	The Effect of Poplar PsnGS1.2 Overexpression on Growth, Secondary Cell Wall, and Fiber Characteristics in Tobacco. Frontiers in Plant Science, 2018, 9, 9.	3.6	33
22	Identification of novel <i>cis</i> â€elements bound by BplMYB46 involved in abiotic stress responses and secondary wall deposition. Journal of Integrative Plant Biology, 2018, 60, 1000-1014.	8.5	18
23	Two novel eukaryotic translation initiation factor 5A genes from Populus simoniiÂ×ÂP. nigra confer tolerance to abiotic stresses in Saccharomyces cerevisiae. Journal of Forestry Research, 2017, 28, 453-463.	3.6	1
24	Identification, phylogeny, and transcript profiling of aquaporin genes in response to abiotic stress in Tamarix hispida. Tree Genetics and Genomes, 2017, 13, 1.	1.6	7
25	Expression of the <scp>MYB</scp> transcription factor gene <i>Bpl<scp>MYB</scp>46</i> affects abiotic stress tolerance and secondary cell wall deposition in <i>Betula platyphylla</i> Plant Biotechnology Journal, 2017, 15, 107-121.	8.3	154
26	Genome-wide identification and expression profile analysis of <i>CCH</i> gene family in <i>Populus</i> . PeerJ, 2017, 5, e3962.	2.0	11
27	Overexpression of ThGSTZ1 from Tamarix hispida improves tolerance to exogenous ABA and methyl viologen. Trees - Structure and Function, 2016, 30, 1935-1944.	1.9	10
28	Comprehensive analysis of trihelix genes and their expression under biotic and abiotic stresses in Populus trichocarpa. Scientific Reports, 2016, 6, 36274.	3.3	44
29	Gene expression profiles in different stem internodes reveal the genetic regulation of primary and secondary stem development in Betula platyphylla. Tree Genetics and Genomes, 2016, 12, 1.	1.6	3
30	Clonal variations in nutritional components of Pinus koreansis seeds collected from seed orchards in Northeastern China. Journal of Forestry Research, 2016, 27, 295-311.	3.6	6
31	Identification of genes regulated by histone acetylation during root development in Populus trichocarpa. BMC Genomics, 2016, 17, 96.	2.8	28
32	Characterization of early transcriptional responses to cadmium in the root and leaf of Cd-resistant Salix matsudana Koidz. BMC Genomics, 2015, 16, 705.	2.8	52
33	Exogenous GA3 Application Enhances Xylem Development and Induces the Expression of Secondary Wall Biosynthesis Related Genes in Betula platyphylla. International Journal of Molecular Sciences, 2015, 16, 22960-22975.	4.1	34
34	Comparative Analysis of Growth and Photosynthetic Characteristics of (Populus simonii × P. nigra) × (P. nigra × P. simonii) Hybrid Clones of Different Ploidides. PLoS ONE, 2015, 10, e0119259.	2.5	23
35	Comparative proteomic analysis of Populus trichocarpa early stem from primary to secondary growth. Journal of Proteomics, 2015, 126, 94-108.	2.4	22
36	Designing Microarray and RNA-Seq Experiments for Greater Systems Biology Discovery in Modern Plant Genomics. Molecular Plant, 2015, 8, 196-206.	8.3	24

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37	Overexpression of the Tamarix hispida ThMT3 gene increases copper tolerance and adventitious root induction in Salix matsudana Koidz Plant Cell, Tissue and Organ Culture, 2015, 121, 469-479.	2.3	35
38	Cytological and Proteomic Analyses of Osmunda cinnamomea Germinating Spores Reveal Characteristics of Fern Spore Germination and Rhizoid Tip Growth*. Molecular and Cellular Proteomics, 2015, 14, 2510-2534.	3.8	51
39	Sequence and expression analysis of the AMT gene family in poplar. Frontiers in Plant Science, 2015, 6, 337.	3.6	43
40	The Conserved Endoribonuclease YbeY Is Required for Chloroplast Ribosomal RNA Processing in Arabidopsis. Plant Physiology, 2015, 168, 205-221.	4.8	49
41	Analysis of three types of triterpenoids in tetraploid white birches (Betula platyphylla Suk.) and selection of plus trees. Journal of Forestry Research, 2015, 26, 623-633.	3.6	9
42	Identification of genes associated with male sterility in a mutant of white birch (Betula platyphylla) Tj ETQq0 0 C	) rgBT/Ove	erlogk 10 Tf 50
43	Comprehensive Transcriptome Analysis of Developing Xylem Responding to Artificial Bending and Gravitational Stimuli in Betula platyphylla. PLoS ONE, 2014, 9, e87566.	2.5	20
44	Shotgun Bisulfite Sequencing of the Betula platyphylla Genome Reveals the Tree's DNA Methylation Patterning. International Journal of Molecular Sciences, 2014, 15, 22874-22886.	4.1	15
45	Overexpression of a GST gene (ThGSTZ1) from Tamarix hispida improves drought and salinity tolerance by enhancing the ability to scavenge reactive oxygen species. Plant Cell, Tissue and Organ Culture, 2014, 117, 99-112.	2.3	108
46	The rooting of poplar cuttings: a review. New Forests, 2014, 45, 21-34.	1.7	31
47	A letter to readers and authors of Journal of Forestry Research. Journal of Forestry Research, 2014, 25, 1-2.	3.6	4
48	Designing Microarray and RNA-seq Experiments for Greater Systems Biology Discovery in Modern Plant Genomics. Molecular Plant, 2014, , .	8.3	2
49	Agrobacterium tumefaciens-mediated genetic transformation of Salix matsudana Koidz. using mature seeds. Tree Physiology, 2013, 33, 628-639.	3.1	27
50	Four Novel Cellulose Synthase (CESA) Genes from Birch (Betula platyphylla Suk.) Involved in Primary and Secondary Cell Wall Biosynthesis. International Journal of Molecular Sciences, 2012, 13, 12195-12212.	4.1	17
51	Building an mRNA transcriptome from the shoots of Betula platyphylla by using Solexa technology. Tree Genetics and Genomes, 2012, 8, 1031-1040.	1.6	10
52	Investigation of temporal variations in endogenous gibberellin A3 and A4 in the leaves of birch (Betula) Tj ETQq0	) 0 0 rgBT	/Overlock 10
53	Overexpression of a heat shock protein (ThHSP18.3) from Tamarix hispida confers stress tolerance to yeast. Molecular Biology Reports, 2012, 39, 4889-4897.	2.3	41
54	Cloning and Functional Characterization of a Novel Glutathione S-Transferase Gene from Limonium bicolor. Plant Molecular Biology Reporter, 2011, 29, 77-87.	1.8	30

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55	Time-Course Analysis of Levels of Indole-3-Acetic Acid and Expression of Auxin-Responsive GH3 Genes in Betula platyphylla. Plant Molecular Biology Reporter, 2011, 29, 898-905.	1.8	13
56	Tamarix hispida metallothionein-like ThMT3, a reactive oxygen species scavenger, increases tolerance against Cd2+, Zn2+, Cu2+, and NaCl in transgenic yeast. Molecular Biology Reports, 2011, 38, 1567-1574.	2.3	45
57	Functional characterization of a plasma membrane Na+/H+ antiporter from alkali grass (Puccinellia) Tj ETQq1 I	1 0.784314 2.3	rgBT <sub>33</sub> /Overlo
58	Cloning of Ten Peroxidase (POD) Genes from Tamarix Hispida and Characterization of their Responses to Abiotic Stress. Plant Molecular Biology Reporter, 2010, 28, 77-89.	1.8	51
59	Genetic Linkage Maps of Betula platyphylla Suk Based on ISSR and AFLP Markers. Plant Molecular Biology Reporter, 2010, 28, 169-175.	1.8	19
60	Isolation and Characterization of Expressed Sequence Tags (ESTs) from Cambium Tissue of Birch (Betula platyphylla Suk). Plant Molecular Biology Reporter, 2010, 28, 438-449.	1.8	24
61	A novel bZIP gene from Tamarix hispida mediates physiological responses to salt stress in tobacco plants. Journal of Plant Physiology, 2010, 167, 222-230.	3.5	140
62	Cloning and expression analysis of 14 lipid transfer protein genes from Tamarix hispida responding to different abiotic stresses. Tree Physiology, 2009, 29, 1607-1619.	3.1	32
63	Investigation of anti-salt stress on tetraploid Robinia pseudoacacia. Frontiers of Forestry in China: Selected Publications From Chinese Universities, 2009, 4, 227-235.	0.2	4
64	Effect of Hormones on Tumor Formation in Tobacco Hybrids. Journal of Plant Biochemistry and Biotechnology, 2009, 18, 169-173.	1.7	2
65	Expression profiling of salinity-alkali stress responses by large-scale expressed sequence tag analysis in Tamarix hispid. Plant Molecular Biology, 2008, 66, 245-258.	3.9	51
66	Generation and analysis of expressed sequence tags from a NaHCO3-treated Limonium bicolor cDNA library. Plant Physiology and Biochemistry, 2008, 46, 977-986.	5.8	25
67	Identification of expressed sequence tags in an alkali grass (Puccinellia tenuiflora) cDNA library. Journal of Plant Physiology, 2007, 164, 78-89.	3.5	45
68	Molecular characterization and fermentative hydrogen production of a wild anaerobe in clostridium genus. Frontiers of Energy and Power Engineering in China, 2007, 1, 403-407.	0.4	0
69	Cloning and sequence analysis of gene encoding plasma aquaporin of Tamarix albiflonum. Frontiers of Forestry in China: Selected Publications From Chinese Universities, 2007, 2, 217-221.	0.2	1
70	Development of a cDNA microarray to identify gene expression of Puccinellia tenuiflora under saline–alkali stress. Plant Physiology and Biochemistry, 2007, 45, 567-576.	5.8	49
71	Effect of mouse calcineurin on induction and growth of rice callus transformed by the calcineurin gene. Plant Cell, Tissue and Organ Culture, 2006, 86, 1-6.	2.3	0