

Hancheng Zhao

List of Publications by Year in descending order

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#	ARTICLE	IF	CITATIONS
1	Genome Identification and Expression Profiles in Response to Nitrogen Treatment Analysis of the Class I CCoAMT Gene Family in Populus. <i>Biochemical Genetics</i> , 2022, 60, 656-675.	1.7	6
2	Effects of different nitrogen forms and concentrations on seedling growth traits and physiological characteristics of <i>Populus simonii</i> P. nigra. <i>Journal of Forestry Research</i> , 2022, 33, 1593-1606.	3.6	4
3	Identification and expression analysis of the PtGATL genes under different nitrogen and carbon dioxide treatments in <i>Populus trichocarpa</i> . <i>3 Biotech</i> , 2022, 12, 67.	2.2	0
4	Identification and Characterization of the APX Gene Family and Its Expression Pattern under Phytohormone Treatment and Abiotic Stress in <i>Populus trichocarpa</i> . <i>Genes</i> , 2021, 12, 334.	2.4	19
5	Genome-wide analysis of UGDH genes in <i>Populus trichocarpa</i> and responsiveness to nitrogen treatment. <i>3 Biotech</i> , 2021, 11, 149.	2.2	5
6	Bioinformatics analysis of PAE family in <i>Populus trichocarpa</i> and responsiveness to carbon and nitrogen treatment. <i>3 Biotech</i> , 2021, 11, 370.	2.2	2
7	Genome-wide identification of FRK genes in <i>Populus trichocarpa</i> and their expression under different nitrogen treatments. <i>Physiology and Molecular Biology of Plants</i> , 2021, 27, 1919-1931.	3.1	2
8	Analysis of the energy source at the early stage of poplar seed germination: verification of Perl TM s pathway. <i>3 Biotech</i> , 2020, 10, 418.	2.2	2
9	Genome-wide analysis of the RGP gene family in <i>Populus trichocarpa</i> and their expression under nitrogen treatment. <i>Gene Expression Patterns</i> , 2020, 38, 119142.	0.8	4
10	Functional characterization and expression patterns of PnATX genes under different abiotic stress treatments in <i>Populus</i> . <i>Tree Physiology</i> , 2020, 40, 520-537.	3.1	2
11	Genome-wide identification of BXL genes in <i>Populus trichocarpa</i> and their expression under different nitrogen treatments. <i>3 Biotech</i> , 2020, 10, 57.	2.2	5
12	Non-Targeted Metabolomics Reveals Patterns of Metabolic Changes during Poplar Seed Germination. <i>Forests</i> , 2019, 10, 659.	2.1	5
13	Comprehensive dissection of transcript and metabolite shifts during seed germination and post-germination stages in poplar. <i>BMC Plant Biology</i> , 2019, 19, 279.	3.6	16
14	The transcriptional events and their relationship to physiological changes during poplar seed germination and post-germination. <i>BMC Genomics</i> , 2019, 20, 801.	2.8	2
15	Functional Research on Three Presumed Asparagine Synthetase Family Members in Poplar. <i>Genes</i> , 2019, 10, 326.	2.4	18
16	Identification and expression analyses of the alanine aminotransferase (AlaAT) gene family in poplar seedlings. <i>Scientific Reports</i> , 2017, 7, 45933.	3.3	20
17	Genome-wide identification and expression profile analysis of <i>CCH</i> gene family in <i>Populus</i> . <i>PeerJ</i> , 2017, 5, e3962.	2.0	11
18	Cytological and Proteomic Analyses of <i>Osmunda cinnamomea</i> Germinating Spores Reveal Characteristics of Fern Spore Germination and Rhizoid Tip Growth*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2510-2534.	3.8	51

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19	Sequence and expression analysis of the AMT gene family in poplar. <i>Frontiers in Plant Science</i> , 2015, 6, 337.	3.6	43
20	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