Jun Niu

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Transcriptome analysis of distinct Lindera glauca tissues revealed the differences in the unigenes related to terpenoid biosynthesis. Gene, 2015, 559, 22-30.	2.2	49
2	Populus euphratica WRKY1 binds the promoter of H+-ATPase gene to enhance gene expression and salt tolerance. Journal of Experimental Botany, 2020, 71, 1527-1539.	4.8	47
3	Selection of Reference Genes for Gene Expression Studies in Siberian Apricot (Prunus sibirica L.) Germplasm Using Quantitative Real-Time PCR. PLoS ONE, 2014, 9, e103900.	2.5	46
4	Hydrogen Sulfide Mediates K+ and Na+ Homeostasis in the Roots of Salt-Resistant and Salt-Sensitive Poplar Species Subjected to NaCl Stress. Frontiers in Plant Science, 2018, 9, 1366.	3.6	41
5	Disruption of metabolic function and redox homeostasis as antibacterial mechanism of Lindera glauca fruit essential oil against Shigella flexneri. Food Control, 2021, 130, 108282.	5.5	41
6	Amelioration of nitrate uptake under salt stress by ectomycorrhiza with and without a Hartig net. New Phytologist, 2019, 222, 1951-1964.	7.3	38
7	Integrated transcriptome sequencing and dynamic analysis reveal carbon source partitioning between terpenoid and oil accumulation in developing Lindera glauca fruits. Scientific Reports, 2015, 5, 15017.	3.3	36
8	Populus euphratica J3 mediates root K+/Na+ homeostasis by activating plasma membrane H+-ATPase in transgenic Arabidopsis under NaCl salinity. Plant Cell, Tissue and Organ Culture, 2017, 131, 75-88.	2.3	35
9	De novo transcriptome analysis of the Siberian apricot (Prunus sibirica L.) and search for potential SSR markers by 454 pyrosequencing. Gene, 2014, 544, 220-227.	2.2	30
10	Physiological and transcriptomic analysis revealed the involvement of crucial factors in heat stress response of Rhododendron hainanense. Gene, 2018, 660, 109-119.	2.2	30
11	Transcriptomic analysis revealed the mechanism of oil dynamic accumulation during developing Siberian apricot (Prunus sibirica L.) seed kernels for the development of woody biodiesel. Biotechnology for Biofuels, 2015, 8, 29.	6.2	28
12	Integrated analysis of 454 and Illumina transcriptomic sequencing characterizes carbon flux and energy source for fatty acid synthesis in developing Lindera glauca fruits for woody biodiesel. Biotechnology for Biofuels, 2017, 10, 134.	6.2	27
13	Transcriptomics and Metabolomics Reveal Purine and Phenylpropanoid Metabolism Response to Drought Stress in Dendrobium sinense, an Endemic Orchid Species in Hainan Island. Frontiers in Genetics, 2021, 12, 692702.	2.3	25
14	Fruit characteristics, soluble sugar compositions and transcriptome analysis during the development of Citrus maxima "seedlessâ€; and identification of SUS and INV genes involved in sucrose degradation. Gene, 2019, 689, 131-140.	2.2	24
15	Integrated mRNA and miRNA transcriptome reveal a cross-talk between developing response and hormone signaling for the seed kernels of Siberian apricot. Scientific Reports, 2016, 6, 35675.	3.3	23
16	Cross-talk between freezing response and signaling for regulatory transcriptions of MIR475b and its targets by miR475b promoter in Populus suaveolens. Scientific Reports, 2016, 6, 20648.	3.3	19
17	WRINKLED1 transcription factor orchestrates the regulation of carbon partitioning for C18:1 (oleic) Tj ETQq1 1	0.784314	∙rgBT /Overl⊃
18	Identification of AUXIN RESPONSE FACTOR gene family from Prunus sibirica and its expression analysis	3.6	16

during mesocarp and kernel development. BMC Plant Biology, 2018, 18, 21.

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19	Comparative study on antioxidative system in normal and vitrified shoots of Populus suaveolens in tissue culture. Forestry Studies in China, 2004, 6, 1-8.	0.4	15
20	Populus euphratica remorin 6.5 activates plasma membrane H+-ATPases to mediate salt tolerance. Tree Physiology, 2020, 40, 731-745.	3.1	15
21	Effects of exogenous abscisic acid on oil content, fatty acid composition, biodiesel properties and lipid components in developing Siberian apricot (Prunus sibirica) seeds. Plant Physiology and Biochemistry, 2020, 154, 260-267.	5.8	13
22	Cloning, characterization, and expression analysis of acyl–acyl carrier protein (ACP)-thioesterase B from seeds of Chinese Spicehush (Lindera communis). Gene, 2014, 542, 16-22.	2.2	12
23	Populus euphratica JRL Mediates ABA Response, Ionic and ROS Homeostasis in Arabidopsis under Salt Stress. International Journal of Molecular Sciences, 2019, 20, 815.	4.1	11
24	Volatile Constituents from the Fruits of <i>Lindera glauca</i> (Sieb. et Zucc.) with Different Maturities. Journal of Essential Oil-bearing Plants: JEOP, 2016, 19, 926-935.	1.9	10
25	Comprehensive evaluation of fuel properties and complex regulation of intracellular transporters for high oil production in developing seeds of Prunus sibirica for woody biodiesel. Biotechnology for Biofuels, 2019, 12, 6.	6.2	10
26	Transcriptome analysis of genes involved in starch biosynthesis in developing Chinese chestnut (Castanea mollissima Blume) seed kernels. Scientific Reports, 2021, 11, 3570.	3.3	10
27	Integrated metabolome and transcriptome revealed the flavonoid biosynthetic pathway in developing <i>Vernonia amygdalina</i> leaves. PeerJ, 2021, 9, e11239.	2.0	10
28	Genome-wide characterization of the NUCLEAR FACTOR-Y (NF-Y) family in Citrus grandis identified CgNF-YB9 involved in the fructose and glucose accumulation. Genes and Genomics, 2019, 41, 1341-1355.	1.4	8
29	Metabolite analysis in Nymphaea †Bird' petals reveal the roles of flavonoids in color formation, stress amelioration, and bee orientation. Plant Science, 2021, 312, 111025.	3.6	7
30	Characterization of the Key Bibenzyl Synthase in Dendrobium sinense. International Journal of Molecular Sciences, 2022, 23, 6780.	4.1	6
31	One rapid and efficient method for isolation of total RNA from shoots regenerated in vitro of populus suaveolens. Forestry Studies in China, 2004, 6, 18-21.	0.4	5
32	Identification of CpTI gene integration for 2-year-old transgenic poplars at DNA level. Forestry Studies in China, 2004, 6, 15-19.	0.4	5
33	Using lipidomics to reveal details of lipid accumulation in developing Siberian apricot (<i>Prunus) Tj ETQq1 1 0.</i>	784314 rg	BT /Overlock
34	Transcriptome Analysis Reveals the Senescence Process Controlling the Flower Opening and Closure Rhythm in the Waterlilies (Nymphaea L.). Frontiers in Plant Science, 2021, 12, 701633.	3.6	5
35	Characterization and role of glucose-6-phosphate dehydrogenase of Populus suaveolens in induction of freezing resistance. Forestry Studies in China, 2004, 6, 1-7.	0.4	4
36	The complete plastid genome of Chinese cinnamon, <i>Cinnamomum aromaticum </i> Nees (Lauraceae). Mitochondrial DNA Part B: Resources, 2019, 4, 3831-3833.	0.4	4

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37	Natural and Synthetic Hydrophilic Polymers Enhance Salt and Drought Tolerance of Metasequoia glyptostroboides Hu and W.C.Cheng Seedlings. Forests, 2018, 9, 643.	2.1	3
38	Analysis of promoter activity of PtDrlO2 gene in white poplars. Journal of Plant Biochemistry and Biotechnology, 2012, 21, 88-97.	1.7	2
39	Transient expression and enzymatic assay identified uridine-diphosphate glucosyltransferases related to flavonoid glycosylation in Vernonia amygdalina leaves. Industrial Crops and Products, 2021, 172, 114005.	5.2	2
40	Expression profiling of NBS-encoding genes in a triploid white poplar. Journal of Plant Biochemistry and Biotechnology, 2015, 24, 283-291.	1.7	1
41	DNA extraction from Eriocaulon plants and construction of RAPD system. Forestry Studies in China, 2004, 6, 22-26.	0.4	0