

# Yulin Liu

## List of Publications by Year in descending order

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16  
papers

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citations

1040056

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940533

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16  
docs citations

16  
times ranked

275  
citing authors

#	ARTICLE	IF	CITATIONS
1	Dynamics of soil microbial C:N:P stoichiometry and its driving mechanisms following natural vegetation restoration after farmland abandonment. <i>Science of the Total Environment</i> , 2019, 693, 133613.	8.0	79
2	De novo transcriptome assembly of <i>Zanthoxylum bungeanum</i> using Illumina sequencing for evolutionary analysis and simple sequence repeat marker development. <i>Scientific Reports</i> , 2017, 7, 16754.	3.3	38
3	miRNAs and their target genes regulate the antioxidant system of <i>Zanthoxylum bungeanum</i> under drought stress. <i>Plant Physiology and Biochemistry</i> , 2020, 150, 196-203.	5.8	23
4	The steps from sexual reproduction to apomixis. <i>Planta</i> , 2019, 249, 1715-1730.	3.2	22
5	Patterns of Drought Response of 38 WRKY Transcription Factors of <i>Zanthoxylum bungeanum</i> Maxim.. <i>International Journal of Molecular Sciences</i> , 2019, 20, 68.	4.1	22
6	<i>Zanthoxylum</i> -specific whole genome duplication and recent activity of transposable elements in the highly repetitive paleotetraploid <i>Z. bungeanum</i> genome. <i>Horticulture Research</i> , 2021, 8, 205.	6.3	19
7	Effects of location, climate, soil conditions and plant species on levels of potentially toxic elements in Chinese Prickly Ash pericarps from the main cultivation regions in China. <i>Chemosphere</i> , 2020, 244, 125501.	8.2	16
8	Identification of Key Genes in the Synthesis Pathway of Volatile Terpenoids in Fruit of <i>Zanthoxylum bungeanum</i> Maxim. <i>Forests</i> , 2019, 10, 328.	2.1	15
9	Single-Molecule Long-Read Sequencing of <i>Zanthoxylum bungeanum</i> Maxim. Transcriptome: Identification of Aroma-Related Genes. <i>Forests</i> , 2018, 9, 765.	2.1	14
10	ZbAGL11, a class D MADS-box transcription factor of <i>Zanthoxylum bungeanum</i> , is involved in sporophytic apomixis. <i>Horticulture Research</i> , 2021, 8, 23.	6.3	14
11	Transcriptomic Analysis of a Potential Bioenergy Tree, <i>Pistacia chinensis</i> Bunge, and Identification of Candidate Genes Involved in the Biosynthesis of Oil. <i>Bioenergy Research</i> , 2016, 9, 740-749.	3.9	10
12	Genome survey of <i>Zanthoxylum bungeanum</i> and development of genomic-SSR markers in congeneric species. <i>Bioscience Reports</i> , 2020, 40, .	2.4	8
13	RNA sequencing and functional analyses reveal regulation of novel drought-responsive, long-non-coding RNA in <i>Zanthoxylum bungeanum</i> Maxim. <i>Plant Growth Regulation</i> , 2020, 90, 425-440.	3.4	7
14	Volatile Oil Profile of Prickly Ash ( <i>Zanthoxylum</i> ) Pericarps from Different Locations in China. <i>Foods</i> , 2021, 10, 2386.	4.3	7
15	De novo assembly of the seed transcriptome and search for potential EST-SSR markers for an endangered, economically important tree species: <i>Elaeagnus mollis</i> Diels. <i>Journal of Forestry Research</i> , 2020, 31, 759-767.	3.6	5
16	Comprehensive profiling of phytochemical compounds, antioxidant activities, anti-HepG2 cell proliferation, and cholinesterase inhibitory potential of <i>Elaeagnus mollis</i> leaf extracts. <i>PLoS ONE</i> , 2020, 15, e0239497.	2.5	2