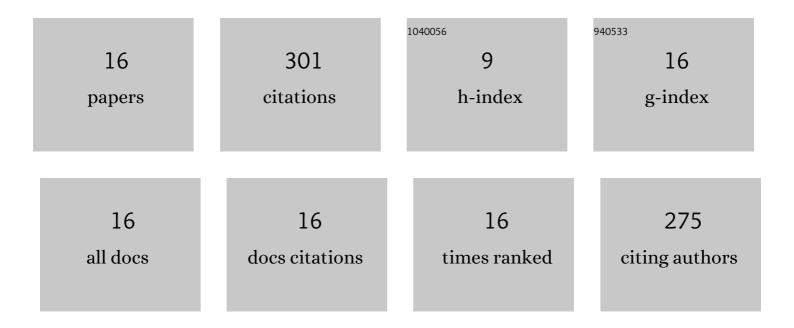
## Yulin Liu

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7764531/publications.pdf Version: 2024-02-01



Υπιτικί Γιπ

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