

# Haichao Hu

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2679040/publications.pdf>

Version: 2024-02-01

8  
papers

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1684188  
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#	ARTICLE	IF	CITATIONS
1	Integrated LC-MS/MS and Transcriptome Sequencing Analysis Reveals the Mechanism of Color Formation During Prickly Ash Fruit Ripening. <i>Frontiers in Nutrition</i> , 2022, 9, 847823.	3.7	2
2	Genome-Wide Identification of the NAC Gene Family in <i>Zanthoxylum bungeanum</i> and Their Transcriptional Responses to Drought Stress. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4769.	4.1	8
3	Pollination promotes ABA synthesis but not sexual reproduction in the apomictic species <i>Zanthoxylum bungeanum</i> Maxim.. <i>Tree Physiology</i> , 2021, 41, 1497-1509.	3.1	1
4	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
5	Transcriptome and Metabolome Dynamics Explain Aroma Differences between Green and Red Prickly Ash Fruit. <i>Foods</i> , 2021, 10, 391.	4.3	28
6	Small RNA sequencing provides candidate miRNA-target pairs for revealing the mechanism of apomixis in <i>Zanthoxylum bungeanum</i> . <i>BMC Plant Biology</i> , 2021, 21, 178.	3.6	5
7	Integrated Analysis of Metabolome and Transcriptome Data for Uncovering Flavonoid Components of <i>Zanthoxylum bungeanum</i> Maxim. Leaves Under Drought Stress. <i>Frontiers in Nutrition</i> , 2021, 8, 801244.	3.7	14
8	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