

# Wei-Hong Sun

## List of Publications by Year in descending order

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23  
papers

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citations

933447

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times ranked

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#	ARTICLE	IF	CITATIONS
1	The <i>Melastoma dodecandrum</i> genome and the evolution of Myrtales. <i>Journal of Genetics and Genomics</i> , 2022, 49, 120-131.	3.9	14
2	The camphor tree genome enhances the understanding of magnoliid evolution. <i>Journal of Genetics and Genomics</i> , 2022, 49, 249-253.	3.9	7
3	High-Throughput Sequencing Analysis of the Composition and Diversity of the Bacterial Community in <i>Cinnamomum camphora</i> Soil. <i>Microorganisms</i> , 2022, 10, 72.	3.6	6
4	Genomes of leafy and leafless <i>Platanthera</i> orchids illuminate the evolution of mycoheterotrophy. <i>Nature Plants</i> , 2022, 8, 373-388.	9.3	36
5	Comparative analysis of <i>Phytophthora</i> genomes reveals oomycete pathogenesis in crops. <i>Heliyon</i> , 2021, 7, e06317.	3.2	3
6	Wolfberry genomes and the evolution of <i>Lycium</i> (Solanaceae). <i>Communications Biology</i> , 2021, 4, 671.	4.4	40
7	Genetic diversity and population structure of <i>Euscaphis japonica</i> , a monotypic species. <i>PeerJ</i> , 2021, 9, e12024.	2.0	2
8	OrchidBase 4.0: a database for orchid genomics and molecular biology. <i>BMC Plant Biology</i> , 2021, 21, 371.	3.6	10
9	The genome of <i>Cymbidium sinense</i> revealed the evolution of orchid traits. <i>Plant Biotechnology Journal</i> , 2021, 19, 2501-2516.	8.3	46
10	Chromosome-scale assembly of the <i>Dendrobium chrysotoxum</i> genome enhances the understanding of orchid evolution. <i>Horticulture Research</i> , 2021, 8, 183.	6.3	41
11	The <i>Euscaphis japonica</i> genome and the evolution of malvids. <i>Plant Journal</i> , 2021, 108, 1382-1399.	5.7	6
12	Frequent germplasm exchanges drive the high genetic diversity of Chinese-cultivated common apricot germplasm. <i>Horticulture Research</i> , 2021, 8, 215.	6.3	16
13	The <i>Cymbidium</i> genome reveals the evolution of unique morphological traits. <i>Horticulture Research</i> , 2021, 8, 255.	6.3	33
14	The complete chloroplast genome sequence of <i>Tapiscia sinensis</i> (Staphyleaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2658-2660.	0.4	1
15	The complete chloroplast genome sequence of <i>Turpinia montana</i> (Staphyleaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3354-3356.	0.4	0
16	The <i>Phoebe</i> genome sheds light on the evolution of magnoliids. <i>Horticulture Research</i> , 2020, 7, 146.	6.3	41
17	Chromosome-scale assembly of the <i>Kandelia obovata</i> genome. <i>Horticulture Research</i> , 2020, 7, 75.	6.3	38
18	Comprehensive transcriptome analysis of reference genes for fruit development of <i>Euscaphis konishii</i> . <i>PeerJ</i> , 2020, 8, e8474.	2.0	4

#	ARTICLE	IF	CITATIONS
19	Multivariate analysis reveals phenotypic diversity of <i>Euscaphis japonica</i> population. PLoS ONE, 2019, 14, e0219046.	2.5	13
20	The complete chloroplast genome sequence of <i>Euscaphis japonica</i> (Staphyleaceae). Mitochondrial DNA Part B: Resources, 2019, 4, 3484-3485.	0.4	6
21	Comparative transcriptome among <i>Euscaphis konishii</i> Hayata tissues and analysis of genes involved in flavonoid biosynthesis and accumulation. BMC Genomics, 2019, 20, 24.	2.8	29
22	Sequencing of <i>Euscaphis konishii</i> Endocarp Transcriptome Points to Molecular Mechanisms of Endocarp Coloration. International Journal of Molecular Sciences, 2018, 19, 3209.	4.1	5
23	Selection and evaluation of reference genes for qRT-PCR analysis in <i>Euscaphis konishii</i> Hayata based on transcriptome data. Plant Methods, 2018, 14, 42.	4.3	42