

# Heng-fu Yin

## List of Publications by Year in descending order

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71  
papers

2,175  
citations

279798

23  
h-index

243625

44  
g-index

75  
all docs

75  
docs citations

75  
times ranked

2421  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Flavonoid Biosynthesis Network in Plants. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12824.	4.1	248
2	A roadmap for research on crassulacean acid metabolism (<scp>CAM</scp>) to enhance sustainable food and bioenergy production in a hotter, drier world. <i>New Phytologist</i> , 2015, 207, 491-504.	7.3	211
3	The <i>Kalanchoë</i> genome provides insights into convergent evolution and building blocks of crassulacean acid metabolism. <i>Nature Communications</i> , 2017, 8, 1899.	12.8	159
4	Transcript, protein and metabolite temporal dynamics in the CAM plant <i>Agave</i> . <i>Nature Plants</i> , 2016, 2, 16178.	9.3	158
5	EUI1, Encoding a Putative Cytochrome P450 Monooxygenase, Regulates Internode Elongation by Modulating Gibberellin Responses in Rice. <i>Plant and Cell Physiology</i> , 2006, 47, 181-191.	3.1	151
6	Integration of small <scp>RNA</scp>s, degradome and transcriptome sequencing in hyperaccumulator <i>Sedum alfredii</i> uncovers a complex regulatory network and provides insights into cadmium phytoremediation. <i>Plant Biotechnology Journal</i> , 2016, 14, 1470-1483.	8.3	96
7	NECK LEAF 1, a GATA type transcription factor, modulates organogenesis by regulating the expression of multiple regulatory genes during reproductive development in rice. <i>Cell Research</i> , 2009, 19, 598-611.	12.0	74
8	Genome-wide transcriptome profiling provides insights into floral bud development of summer-flowering <i>Camellia azalea</i> . <i>Scientific Reports</i> , 2015, 5, 9729.	3.3	72
9	The genome of oil- <i>Camellia</i> and population genomics analysis provide insights into seed oil domestication. <i>Genome Biology</i> , 2022, 23, 14.	8.8	68
10	Diel rewiring and positive selection of ancient plant proteins enabled evolution of CAM photosynthesis in <i>Agave</i> . <i>BMC Genomics</i> , 2018, 19, 588.	2.8	64
11	Mitigating climate change through managing constructed-microbial communities in agriculture. <i>Agriculture, Ecosystems and Environment</i> , 2016, 216, 304-308.	5.3	56
12	Seed Transcriptomics Analysis in <i>Camellia oleifera</i> Uncovers Genes Associated with Oil Content and Fatty Acid Composition. <i>International Journal of Molecular Sciences</i> , 2018, 19, 118.	4.1	56
13	Functional analyses of a flavonol synthase-like gene from <i>Camellia nitidissima</i> reveal its roles in flavonoid metabolism during floral pigmentation. <i>Journal of Biosciences</i> , 2013, 38, 593-604.	1.1	49
14	Systems and synthetic biology approaches to alter plant cell walls and reduce biomass recalcitrance. <i>Plant Biotechnology Journal</i> , 2014, 12, 1207-1216.	8.3	46
15	Distinct double flower varieties in <i>Camellia japonica</i> exhibit both expansion and contraction of C-class gene expression. <i>BMC Plant Biology</i> , 2014, 14, 288.	3.6	40
16	Development of <i>Agave</i> as a dedicated biomass source: production of biofuels from whole plants. <i>Biotechnology for Biofuels</i> , 2015, 8, 79.	6.2	38
17	<i>Populus trichocarpa</i> encodes small, effector-like secreted proteins that are highly induced during mutualistic symbiosis. <i>Scientific Reports</i> , 2017, 7, 382.	3.3	36
18	Two terpene synthases in resistant <scp><i>Pinus massoniana</i></scp> contribute to defence against <i>Bursaphelenchus xylophilus</i>. <i>Plant, Cell and Environment</i> , 2021, 44, 257-274.	5.7	36

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19	SUI-family genes encode phosphatidylserine synthases and regulate stem development in rice. <i>Planta</i> , 2013, 237, 15-27.	3.2	33
20	Phylogenetic tree-informed microRNAome analysis uncovers conserved and lineage-specific miRNAs in <i>Camellia</i> during floral organ development. <i>Journal of Experimental Botany</i> , 2016, 67, 2641-2653.	4.8	33
21	The APETALA1 and FRUITFUL homologs in <i>Camellia japonica</i> and their roles in double flower domestication. <i>Molecular Breeding</i> , 2014, 33, 821-834.	2.1	31
22	<i>PHOSPHATIDYLSERINE SYNTHASE1</i> is Required for Inflorescence Meristem and Organ Development in <i>Arabidopsis</i> . <i>Journal of Integrative Plant Biology</i> , 2013, 55, 682-695.	8.5	26
23	Overexpression of the Gibberellin 2-Oxidase Gene from <i>Camellia lipoensis</i> Induces Dwarfism and Smaller Flowers in <i>Nicotiana tabacum</i> . <i>Plant Molecular Biology Reporter</i> , 2016, 34, 182-191.	1.8	26
24	Functional Genomics of Drought Tolerance in Bioenergy Crops. <i>Critical Reviews in Plant Sciences</i> , 2014, 33, 205-224.	5.7	25
25	Overexpression of geranyl diphosphate synthase small subunit 1 (LcGPPS.SSU1) enhances the monoterpene content and biomass. <i>Industrial Crops and Products</i> , 2020, 143, 111926.	5.2	22
26	Global gene expression defines faded whorl specification of double flower domestication in <i>Camellia</i> . <i>Scientific Reports</i> , 2017, 7, 3197.	3.3	21
27	Comparative Transcriptomics Atlases Reveals Different Gene Expression Pattern Related to Fusarium Wilt Disease Resistance and Susceptibility in Two <i>Vernicia</i> Species. <i>Frontiers in Plant Science</i> , 2016, 7, 1974.	3.6	18
28	Overexpression of CaAPX Induces Orchestrated Reactive Oxygen Scavenging and Enhances Cold and Heat Tolerances in Tobacco. <i>BioMed Research International</i> , 2017, 2017, 1-15.	1.9	17
29	Identification of <i>Populus</i> Small RNAs Responsive to Mutualistic Interactions With Mycorrhizal Fungi, <i>Laccaria bicolor</i> and <i>Rhizophagus irregularis</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 515.	3.5	17
30	Genetic diversity in the endangered <i>Camellia nitidissima</i> assessed using transcriptome-based SSR markers. <i>Trees - Structure and Function</i> , 2020, 34, 543-552.	1.9	16
31	Plant Biosystems Design Research Roadmap 1.0. <i>Biodesign Research</i> , 2020, 2020, .	1.9	16
32	Comparative genomics analysis reveals gene family expansion and changes of expression patterns associated with natural adaptations of flowering time and secondary metabolism in yellow <i>Camellia</i> . <i>Functional and Integrative Genomics</i> , 2018, 18, 659-671.	3.5	14
33	Composition analysis of floral scent within genus <i>Camellia</i> uncovers substantial interspecific variations. <i>Scientia Horticulturae</i> , 2019, 250, 207-213.	3.6	13
34	Identification of alternatively spliced gene isoforms and novel noncoding RNAs by single-molecule long-read sequencing in <i>Camellia</i> . <i>RNA Biology</i> , 2020, 17, 966-976.	3.1	13
35	Overexpression of phosphoenolpyruvate carboxylase from <i>Jatropha curcas</i> increases fatty acid accumulation in <i>Nicotiana tabacum</i> . <i>Acta Physiologiae Plantarum</i> , 2013, 35, 2269-2279.	2.1	12
36	A Model of Hormonal Regulation of Stamen Abortion during Pre-Meiosis of <i>Litsea cubeba</i> . <i>Genes</i> , 2020, 11, 48.	2.4	12

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37	Unraveling the Roles of Regulatory Genes during Domestication of Cultivated Camellia: Evidence and Insights from Comparative and Evolutionary Genomics. <i>Genes</i> , 2018, 9, 488.	2.4	11
38	Functional Diversification of the Dihydroflavonol 4-Reductase from <i>Camellia nitidissima</i> Chi. in the Control of Polyphenol Biosynthesis. <i>Genes</i> , 2020, 11, 1341.	2.4	9
39	Alternative Polyadenylation in response to temperature stress contributes to gene regulation in <i>Populus trichocarpa</i> . <i>BMC Genomics</i> , 2021, 22, 53.	2.8	9
40	Flavonoid 3- $\beta$ -hydroxylase of <i>Camellia nitidissima</i> Chi. promotes the synthesis of polyphenols better than flavonoids. <i>Molecular Biology Reports</i> , 2021, 48, 3903-3912.	2.3	9
41	Association Genetics Identifies Single Nucleotide Polymorphisms Related to Kernel Oil Content and Quality in <i>Camellia oleifera</i> . <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 2547-2562.	5.2	8
42	Integrated Physiological and Transcriptomic Analyses Reveal a Regulatory Network of Anthocyanin Metabolism Contributing to the Ornamental Value in a Novel Hybrid Cultivar of <i>Camellia japonica</i> . <i>Plants</i> , 2020, 9, 1724.	3.5	8
43	Overexpression of geranyl diphosphate synthase ( <i>PmGPPS1</i> ) boosts monoterpene and diterpene production involved in the response to pine wood nematode invasion. <i>Tree Physiology</i> , 2022, 42, 411-424.	3.1	8
44	Evolutionary analyses of non-family genes in plants. <i>Plant Journal</i> , 2013, 73, 788-797.	5.7	7
45	Genome-Wide Identification and Characterization of the <i>LRR-RLK</i> Gene Family in Two <i>Vernicia</i> Species. <i>International Journal of Genomics</i> , 2015, 2015, 1-17.	1.6	7
46	CcBLH6, a bell-like homeodomain-containing transcription factor, regulates the fruit lignification pattern. <i>Planta</i> , 2021, 253, 90.	3.2	7
47	Transcriptomic and Chemical Analyses Reveal the Hub Regulators of Flower Color Variation from <i>Camellia japonica</i> Bud Sport. <i>Horticulturae</i> , 2022, 8, 129.	2.8	7
48	Identification and characterization of NF-YB family genes in tung tree. <i>Molecular Genetics and Genomics</i> , 2015, 290, 2187-2198.	2.1	6
49	Characterization of the complete chloroplast genome of <i>Camellia brevistyla</i> , an oil-rich and evergreen shrub. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 386-387.	0.4	6
50	Overexpression and silent expression of <i>CrGA20ox1</i> from <i>Camellia reticulata</i> 'Hentiangao' and its effect on morphological alterations in transgenic tobacco plants. <i>Plant Breeding</i> , 2018, 137, 903-911.	1.9	5
51	Characterization and phylogenetic significance of the complete chloroplast genome of <i>Camellia Kissii</i> , an economic crop for producing oil. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 362-363.	0.4	5
52	Transcriptome and Degradome Profiling Reveals a Role of miR530 in the Circadian Regulation of Gene Expression in <i>Kalanchoe pinnatifida</i> . <i>Cells</i> , 2021, 10, 1526.	4.1	5
53	Comparative Transcriptome and Pigment Analyses Reveal Changes in Gene Expression Associated with Flavonol Metabolism in Yellow Camellia. <i>Forests</i> , 2022, 13, 1094.	2.1	5
54	CjPLE, a PLENA-like gene, is a potential regulator of fruit development via activating the FRUITFUL homolog in <i>Camellia</i> . <i>Journal of Experimental Botany</i> , 2019, 70, 3153-3164.	4.8	4

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55	IsoSplitter: identification and characterization of alternative splicing sites without a reference genome. <i>Rna</i> , 2021, 27, 868-875.	3.5	4
56	Multi-Approach Analysis Reveals Pathways of Cold Tolerance Divergence in <i>Camellia japonica</i> . <i>Frontiers in Plant Science</i> , 2022, 13, 811791.	3.6	4
57	Characterization of the complete chloroplast genome of <i>Camellia yuhsienensis</i> Hu, a resilient shrub with strong floral fragrance. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2998-2999.	0.4	3
58	Comparative Transcriptome Analysis of Flower Senescence of <i>Camellia lutchuensis</i> . <i>Current Genomics</i> , 2022, 23, 66-76.	1.6	3
59	GESearch: An Interactive GUI Tool for Identifying Gene Expression Signature. <i>BioMed Research International</i> , 2015, 2015, 1-8.	1.9	2
60	The complete chloroplast genome of <i>Camellia vietnamensis</i> , an economic shrub producing edible seed oil. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3736-3737.	0.4	2
61	Ectopic Expression of <i>Litsea cubeba</i> LcMADS20 Modifies Silique Architecture. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 4139-4147.	1.8	2
62	GEsture: an online hand-drawing tool for gene expression pattern search. <i>PeerJ</i> , 2018, 6, e4927.	2.0	2
63	D6 protein kinase in root xylem benefiting resistance to <i>Fusarium</i> reveals infection and defense mechanisms in tung trees. <i>Horticulture Research</i> , 2021, 8, 240.	6.3	2
64	The complete chloroplast genome of <i>Camellia grijsii</i> , an ornamental shrub with floral aroma. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 748-749.	0.4	1
65	The complete chloroplast genome of <i>Camellia fluviatilis</i> (Theaceae), a wild oil-Camellia species. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 3511-3512.	0.4	1
66	The complete chloroplast genome of <i>Camellia grijsii</i> "zhenzhucha"™, a variant cultivar with floral aroma. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2546-2547.	0.4	0
67	Characterization and phylogenetic analysis of the complete chloroplast genome of <i>Camellia chrysanthoides</i> (Theaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 3103-3104.	0.4	0
68	Molecular Cloning and Expression Analysis of C Function Gene <i>CjPLE</i> in Double Flower Varieties of <i>Camellia japonica</i> . <i>Molecular Plant Breeding</i> , 0, , .	0.0	0
69	Molecular Cloning and Expression Analysis of C Function Gene <i>CjPLE</i> in Double Flower Varieties of <i>Camellia japonica</i> . <i>Molecular Plant Breeding</i> , 0, , .	0.0	0
70	FRONT COVER IMAGE. <i>Plant, Cell and Environment</i> , 2021, 44, i.	5.7	0
71	Transcriptomic Analysis Reveals Key Candidate Genes Related to Seed Abortion in Chinese Jujube ( <i>Ziziphus jujuba</i> Mill.). <i>Current Genomics</i> , 2021, 22, .	1.6	0