

# Juhua Liu

## List of Publications by Year in descending order

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Version: 2024-02-01

39  
papers

1,427  
citations

361413

20  
h-index

330143

37  
g-index

41  
all docs

41  
docs citations

41  
times ranked

1468  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-Wide Analysis of the Banana WRKY Transcription Factor Gene Family Closely Related to Fruit Ripening and Stress. <i>Plants</i> , 2022, 11, 662.	3.5	14
2	Identification and expression of the BAHD family during development, ripening, and stress response in banana. <i>Molecular Biology Reports</i> , 2021, 48, 1127-1138.	2.3	9
3	Genome-Wide Identification and Transcript Analysis of TCP Gene Family in Banana ( <i>Musa acuminata</i> L.). <i>Biochemical Genetics</i> , 2021, , 1.	1.7	10
4	Transient virus-induced gene silencing of MaBAM9b efficiently suppressed starch degradation during postharvest banana fruit ripening. <i>Plant Biotechnology Reports</i> , 2021, 15, 527-536.	1.5	3
5	Transcription factor MaMADS36 plays a central role in regulating banana fruit ripening. <i>Journal of Experimental Botany</i> , 2021, 72, 7078-7091.	4.8	21
6	Overexpression of a Banana Aquaporin Gene MaPIP1;1 Enhances Tolerance to Multiple Abiotic Stresses in Transgenic Banana and Analysis of Its Interacting Transcription Factors. <i>Frontiers in Plant Science</i> , 2021, 12, 699230.	3.6	10
7	Elucidating the mechanism of MaGWD1-mediated starch degradation cooperatively regulated by MaMADS36 and MaMADS55 in banana. <i>Postharvest Biology and Technology</i> , 2021, 179, 111587.	6.0	13
8	Identification, Expression, and Interaction Network Analyses of the CDPK Gene Family Reveal Their Involvement in the Development, Ripening, and Abiotic Stress Response in Banana. <i>Biochemical Genetics</i> , 2020, 58, 40-62.	1.7	18
9	An aquaporin gene MaPIP2-7 is involved in tolerance to drought, cold and salt stresses in transgenic banana ( <i>Musa acuminata</i> L.). <i>Plant Physiology and Biochemistry</i> , 2020, 147, 66-76.	5.8	54
10	Characteristics of banana B genome MADS-box family demonstrate their roles in fruit development, ripening, and stress. <i>Scientific Reports</i> , 2020, 10, 20840.	3.3	2
11	Genomic and Transcriptional Analysis of Banana Ovate Family Proteins Reveals Their Relationship with Fruit Development and Ripening. <i>Biochemical Genetics</i> , 2020, 58, 412-429.	1.7	8
12	Molecular identification of the key starch branching enzyme-encoding gene SBE2.3 and its interacting transcription factors in banana fruits. <i>Horticulture Research</i> , 2020, 7, 101.	6.3	18
13	A novel aquaporin gene MaSIP2-1 confers tolerance to drought and cold stresses in transgenic banana. <i>Molecular Breeding</i> , 2020, 40, 1.	2.1	9
14	<i>Musa balbisiana</i> genome reveals subgenome evolution and functional divergence. <i>Nature Plants</i> , 2019, 5, 810-821.	9.3	132
15	<i>MuMADS1</i> and <i>MaOFP1</i> regulate fruit quality in a tomato <i>ovate</i> mutant. <i>Plant Biotechnology Journal</i> , 2018, 16, 989-1001.	8.3	33
16	Overexpression of a Novel ROP Gene from the Banana (MaROP5g) Confers Increased Salt Stress Tolerance. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3108.	4.1	22
17	Identification of a novel promoter from banana aquaporin family gene ( MaTIP1;2 ) which responses to drought and salt-stress in transgenic <i>Arabidopsis thaliana</i> . <i>Plant Physiology and Biochemistry</i> , 2018, 128, 163-169.	5.8	24
18	Comparative physiological and transcriptomic analyses provide integrated insight into osmotic, cold, and salt stress tolerance mechanisms in banana. <i>Scientific Reports</i> , 2017, 7, 43007.	3.3	65

#	ARTICLE	IF	CITATIONS
19	Genome-wide analyses of SWEET family proteins reveal involvement in fruit development and abiotic/biotic stress responses in banana. <i>Scientific Reports</i> , 2017, 7, 3536.	3.3	80
20	Elucidating the Mechanisms of the Tomato <i>ovate</i> Mutation in Regulating Fruit Quality Using Proteomics Analysis. <i>Journal of Agricultural and Food Chemistry</i> , 2017, 65, 10048-10057.	5.2	10
21	Genome-wide analysis of banana MADS-box family closely related to fruit development and ripening. <i>Scientific Reports</i> , 2017, 7, 3467.	3.3	36
22	Efficient regeneration and genetic transformation platform applicable to five <i>Musa</i> varieties. <i>Electronic Journal of Biotechnology</i> , 2017, 25, 33-38.	2.2	18
23	The core regulatory network of the abscisic acid pathway in banana: genome-wide identification and expression analyses during development, ripening, and abiotic stress. <i>BMC Plant Biology</i> , 2017, 17, 145.	3.6	51
24	Soluble Starch Synthase III-1 in Amylopectin Metabolism of Banana Fruit: Characterization, Expression, Enzyme Activity, and Functional Analyses. <i>Frontiers in Plant Science</i> , 2017, 8, 454.	3.6	19
25	The AGPase Family Proteins in Banana: Genome-Wide Identification, Phylogeny, and Expression Analyses Reveal Their Involvement in the Development, Ripening, and Abiotic/Biotic Stress Responses. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1581.	4.1	34
26	A Novel Role for Banana MaASR in the Regulation of Flowering Time in Transgenic Arabidopsis. <i>PLoS ONE</i> , 2016, 11, e0160690.	2.5	4
27	Genome-wide analyses of the bZIP family reveal their involvement in the development, ripening and abiotic stress response in banana. <i>Scientific Reports</i> , 2016, 6, 30203.	3.3	65
28	Genome-wide identification and expression analysis of the $\beta$ -amylase genes strongly associated with fruit development, ripening, and abiotic stress response in two banana cultivars. <i>Frontiers of Agricultural Science and Engineering</i> , 2016, 3, 346.	1.4	18
29	Role for the banana <i>AGAMOUS</i> -like gene <i>MaMADS7</i> in regulation of fruit ripening and quality. <i>Physiologia Plantarum</i> , 2015, 155, 217-231.	5.2	35
30	Genome-Wide Identification and Expression Analyses of Aquaporin Gene Family during Development and Abiotic Stress in Banana. <i>International Journal of Molecular Sciences</i> , 2015, 16, 19728-19751.	4.1	69
31	Banana Ovate Family Protein MaOFP1 and MADS-Box Protein MuMADS1 Antagonistically Regulated Banana Fruit Ripening. <i>PLoS ONE</i> , 2015, 10, e0123870.	2.5	24
32	The auxin response factor gene family in banana: genome-wide identification and expression analyses during development, ripening, and abiotic stress. <i>Frontiers in Plant Science</i> , 2015, 6, 742.	3.6	131
33	The MaASR gene as a crucial component in multiple drought stress response pathways in Arabidopsis. <i>Functional and Integrative Genomics</i> , 2015, 15, 247-260.	3.5	24
34	A banana aquaporin gene, MaPIP1;1, is involved in tolerance to drought and salt stresses. <i>BMC Plant Biology</i> , 2014, 14, 59.	3.6	175
35	Molecular cloning and expression analysis of the MaASR1 gene in banana and functional characterization under salt stress. <i>Electronic Journal of Biotechnology</i> , 2014, 17, 287-295.	2.2	10
36	Isolation of an abscisic acid senescence and ripening inducible gene from litchi and functional characterization under water stress. <i>Planta</i> , 2013, 237, 1025-1036.	3.2	19

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37	De Novo characterization of the banana root transcriptome and analysis of gene expression under <i>Fusarium oxysporum</i> f. sp. <i>Cubense</i> tropical race 4 infection. <i>BMC Genomics</i> , 2012, 13, 650.	2.8	74
38	Regeneration and production of transgenic <i>Lilium longiflorum</i> via <i>Agrobacterium tumefaciens</i> . <i>In Vitro Cellular and Developmental Biology - Plant</i> , 2011, 47, 348-356.	2.1	16
39	Involvement of a banana MADS-box transcription factor gene in ethylene-induced fruit ripening. <i>Plant Cell Reports</i> , 2009, 28, 103-111.	5.6	50