

# Yong-Hua Qin

## List of Publications by Year in descending order

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46  
papers

1,423  
citations

430874

18  
h-index

345221

36  
g-index

49  
all docs

49  
docs citations

49  
times ranked

1229  
citing authors

#	ARTICLE	IF	CITATIONS
1	Advance of the negative regulation of anthocyanin biosynthesis by MYB transcription factors. <i>Plant Physiology and Biochemistry</i> , 2019, 136, 178-187.	5.8	166
2	LcMYB1 Is a Key Determinant of Differential Anthocyanin Accumulation among Genotypes, Tissues, Developmental Phases and ABA and Light Stimuli in <i>Litchi chinensis</i> . <i>PLoS ONE</i> , 2014, 9, e86293.	2.5	114
3	LcGST4 is an anthocyanin-related glutathione S-transferase gene in <i>Litchi chinensis</i> Sonn.. <i>Plant Cell Reports</i> , 2016, 35, 831-843.	5.6	106
4	Two LcbHLH Transcription Factors Interacting with LcMYB1 in Regulating Late Structural Genes of Anthocyanin Biosynthesis in <i>Nicotiana</i> and <i>Litchi chinensis</i> During Anthocyanin Accumulation. <i>Frontiers in Plant Science</i> , 2016, 7, 166.	3.6	79
5	Metabolomic characterization of pitaya fruit from three red-skinned cultivars with different pulp colors. <i>Plant Physiology and Biochemistry</i> , 2018, 126, 117-125.	5.8	75
6	Transcriptomic analysis of <i>Litchi chinensis</i> pericarp during maturation with a focus on chlorophyll degradation and flavonoid biosynthesis. <i>BMC Genomics</i> , 2015, 16, 225.	2.8	74
7	Patterns of enzyme activities and gene expressions in sucrose metabolism in relation to sugar accumulation and composition in the aril of <i>Litchi chinensis</i> Sonn.. <i>Journal of Plant Physiology</i> , 2013, 170, 731-740.	3.5	72
8	Identification of MicroRNAs and Their Target Genes Related to the Accumulation of Anthocyanins in <i>Litchi chinensis</i> by High-Throughput Sequencing and Degradome Analysis. <i>Frontiers in Plant Science</i> , 2016, 7, 2059.	3.6	69
9	The WRKY transcription factor HpWRKY44 regulates CytP450-like1 expression in red pitaya fruit ( <i>Hylocereus polyrhizus</i> ). <i>Horticulture Research</i> , 2017, 4, 17039.	6.3	62
10	Identification of reliable reference genes for quantitative real-time PCR normalization in pitaya. <i>Plant Methods</i> , 2019, 15, 70.	4.3	48
11	A chromosome-scale genome sequence of pitaya ( <i>Hylocereus undatus</i> ) provides novel insights into the genome evolution and regulation of betalain biosynthesis. <i>Horticulture Research</i> , 2021, 8, 164.	6.3	44
12	Three LcABFs are Involved in the Regulation of Chlorophyll Degradation and Anthocyanin Biosynthesis During Fruit Ripening in <i>Litchi chinensis</i> . <i>Plant and Cell Physiology</i> , 2019, 60, 448-461.	3.1	42
13	Pitaya HpWRKY3 Is Associated with Fruit Sugar Accumulation by Transcriptionally Modulating Sucrose Metabolic Genes HpINV2 and HpSuSy1. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1890.	4.1	39
14	Genome-wide identification and expression analysis of SWEET gene family in <i>Litchi chinensis</i> reveal the involvement of LcSWEET2a/3b in early seed development. <i>BMC Plant Biology</i> , 2019, 19, 499.	3.6	34
15	Genome-Wide Characterization of R2R3-MYB Transcription Factors in Pitaya Reveals a R2R3-MYB Repressor HuMYB1 Involved in Fruit Ripening through Regulation of Betalain Biosynthesis by Repressing Betalain Biosynthesis-Related Genes. <i>Cells</i> , 2021, 10, 1949.	4.1	26
16	A Novel WRKY Transcription Factor HmoWRKY40 Associated with Betalain Biosynthesis in Pitaya ( <i>Hylocereus monacanthus</i> ) through Regulating HmoCYP76AD1. <i>International Journal of Molecular Sciences</i> , 2021, 22, 2171.	4.1	23
17	Transcriptome profiling of <i>Litchi chinensis</i> pericarp in response to exogenous cytokinins and abscisic acid. <i>Plant Growth Regulation</i> , 2018, 84, 437-450.	3.4	22
18	Transcriptomics-based identification and characterization of glucosyltransferases involved in betalain biosynthesis in <i>Hylocereus megalanthus</i> . <i>Plant Physiology and Biochemistry</i> , 2020, 152, 112-124.	5.8	21

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19	Agrobacterium rhizogenes-mediated hairy root transformation as an efficient system for gene function analysis in <i>Litchi chinensis</i> . <i>Plant Methods</i> , 2021, 17, 103.	4.3	21
20	Comparative transcriptome analyses of a late-maturing mandarin mutant and its original cultivar reveals gene expression profiling associated with citrus fruit maturation. <i>PeerJ</i> , 2017, 5, e3343.	2.0	19
21	Integrated sRNAome and RNA-Seq analysis reveals miRNA effects on betalain biosynthesis in pitaya. <i>BMC Plant Biology</i> , 2020, 20, 437.	3.6	18
22	Identification of differentially expressed genes in pistils from self-incompatible <i>Citrus reticulata</i> by suppression subtractive hybridization. <i>Molecular Biology Reports</i> , 2013, 40, 159-169.	2.3	17
23	Identification and expression profile analysis of the sucrose phosphate synthase gene family in <i>Litchi chinensis</i> Sonn.. <i>PeerJ</i> , 2018, 6, e4379.	2.0	16
24	Pitaya Genome and Multiomics Database (PGMD): A Comprehensive and Integrative Resource of <i>Selenicereus undatus</i> . <i>Genes</i> , 2022, 13, 745.	2.4	16
25	Proteomic Analysis of <i>Hylocereus polyrhizus</i> Reveals Metabolic Pathway Changes. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1606.	4.1	14
26	Maintenance of Postharvest Quality and Reactive Oxygen Species Homeostasis of Pitaya Fruit by Essential Oil p-Anisaldehyde Treatment. <i>Foods</i> , 2021, 10, 2434.	4.3	14
27	A protocol for rapid in vitro propagation of genetically diverse pitaya. <i>Plant Cell, Tissue and Organ Culture</i> , 2015, 120, 741-745.	2.3	13
28	Transcriptomics-based identification and characterization of genes related to sugar metabolism in 'Hongshuijing' pitaya. <i>Horticultural Plant Journal</i> , 2022, 8, 450-460.	5.0	13
29	Comparative transcript profiling of gene expression between self-incompatible and self-compatible mandarins by suppression subtractive hybridization and cDNA microarray. <i>Molecular Breeding</i> , 2015, 35, 1.	2.1	12
30	Comparative transcriptional survey between self-incompatibility and self-compatibility in <i>Citrus reticulata</i> Blanco. <i>Gene</i> , 2017, 609, 52-61.	2.2	12
31	Differential gene expression between the vigorous and dwarf litchi cultivars based on RNA-Seq transcriptome analysis. <i>PLoS ONE</i> , 2018, 13, e0208771.	2.5	12
32	Identifying Differentially Expressed Genes in Pollen from Self-Incompatible 'Wuzishatangju' and Self-Compatible 'Shatangju' Mandarins. <i>International Journal of Molecular Sciences</i> , 2013, 14, 8538-8555.	4.1	11
33	R3-MYB transcription factor LcMYBx from <i>Litchi chinensis</i> negatively regulates anthocyanin biosynthesis by ectopic expression in tobacco. <i>Gene</i> , 2022, 812, 146105.	2.2	11
34	CrWSKP1, an SKP1-like Gene, Is Involved in the Self-Incompatibility Reaction of 'Wuzishatangju' (Citrus Tj ET0000000000/Overlo	4.1	10
35	Genome-Wide Identification of Aquaporin Gene Family in Pitaya Reveals an HuNIP6;1 Involved in Flowering Process. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7689.	4.1	10
36	LcCOP1 and LcHY5 control the suppression and induction of anthocyanin accumulation in bagging and debagging litchi fruit pericarp. <i>Scientia Horticulturae</i> , 2021, 287, 110281.	3.6	10

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37	HuNAC20 and HuNAC25, Two Novel NAC Genes from Pitaya, Confer Cold Tolerance in Transgenic Arabidopsis. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2189.	4.1	10
38	Molecular characterization and expression analysis of ubiquitin-activating enzyme E1 gene in <i>Citrus reticulata</i> . <i>Gene</i> , 2013, 513, 249-259.	2.2	8
39	A Genome-Wide Identification Study Reveals That HmoCYP76AD1, HmoDODA±1 and HmocDOPA5GT Involved in Betalain Biosynthesis in <i>Hylocereus</i> . <i>Genes</i> , 2021, 12, 1858.	2.4	7
40	Sugar Transport, Metabolism and Signaling in Fruit Development of <i>Litchi chinensis</i> Sonn: A Review. <i>International Journal of Molecular Sciences</i> , 2021, 22, 11231.	4.1	6
41	SKP1-like protein, CrSKP1-e, interacts with pollen-specific F-box proteins and assembles into SCF-type E3 complex in "Wuzishatangju"™ ( <i>Citrus reticulata</i> Blanco) pollen. <i>PeerJ</i> , 2020, 8, e10578.	2.0	6
42	Metabolic Profiling of Sugars and Organic Acids, and Expression Analyses of Metabolism-Associated Genes in Two Yellow-Peel Pitaya Species. <i>Plants</i> , 2022, 11, 694.	3.5	6
43	Identification of an up-accumulated polyamine oxidase 2 in pollen of self-incompatible "Wuzishatangju"™ mandarin using comparative proteomic analysis. <i>Scientia Horticulturae</i> , 2020, 266, 109279.	3.6	5
44	Breeding of "Hongguan No. 1"™ and "Shuangse No. 1"™ Pitayas with Superior Quality. <i>Hortscience: A Publication of the American Society for Horticultural Science</i> , 2018, 53, 404-409.	1.0	3
45	Construction of a High-Density Genetic Map for Pitaya Using the Whole Genome Resequencing Approach. <i>Horticulturae</i> , 2021, 7, 534.	2.8	3
46	Metabolic Profiling of Organic Acids Reveals the Involvement of HuiPMS2 in Citramalic Acid Synthesis in Pitaya. <i>Horticulturae</i> , 2022, 8, 167.	2.8	3