

# Caiping Zhao

## List of Publications by Year in descending order

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47  
papers

1,078  
citations

394421

19  
h-index

454955

30  
g-index

52  
all docs

52  
docs citations

52  
times ranked

953  
citing authors

#	ARTICLE	IF	CITATIONS
1	Shoot bending promotes flower bud formation by miRNA-mediated regulation in apple ( <i>Malus domestica</i> Borkh.). <i>Plant Biotechnology Journal</i> , 2016, 14, 749-770.	8.3	69
2	Genome-wide identification of vegetative phase transition-associated microRNAs and target predictions using degradome sequencing in <i>Malus hupehensis</i> . <i>BMC Genomics</i> , 2014, 15, 1125.	2.8	60
3	Identification and Expression Analysis of Polygalacturonase Family Members during Peach Fruit Softening. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1933.	4.1	60
4	Transcriptome analysis reveals the effects of sugar metabolism and auxin and cytokinin signaling pathways on root growth and development of grafted apple. <i>BMC Genomics</i> , 2016, 17, 150.	2.8	52
5	Characteristics and regulatory pathway of the PrupeSEP1 SEPALLATA gene during ripening and softening in peach fruits. <i>Plant Science</i> , 2017, 257, 63-73.	3.6	49
6	Transcriptome Analysis Reveals Multiple Hormones, Wounding and Sugar Signaling Pathways Mediate Adventitious Root Formation in Apple Rootstock. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2201.	4.1	48
7	Down-Regulation of PpBGAL10 and PpBGAL16 Delays Fruit Softening in Peach by Reducing Polygalacturonase and Pectin Methylesterase Activity. <i>Frontiers in Plant Science</i> , 2018, 9, 1015.	3.6	46
8	iTRAQ-Based Proteomic Analysis Reveals Potential Regulation Networks of IBA-Induced Adventitious Root Formation in Apple. <i>International Journal of Molecular Sciences</i> , 2018, 19, 667.	4.1	41
9	Genome-wide analysis of carotenoid cleavage oxygenase genes and their responses to various phytohormones and abiotic stresses in apple ( <i>Malus domestica</i> ). <i>Plant Physiology and Biochemistry</i> , 2018, 123, 81-93.	5.8	40
10	miRNAs associated with auxin signaling, stress response, and cellular activities mediate adventitious root formation in apple rootstocks. <i>Plant Physiology and Biochemistry</i> , 2019, 139, 66-81.	5.8	36
11	Genome-Wide Sequence Variation Identification and Floral-Associated Trait Comparisons Based on the Re-sequencing of the "Nagafu No. 2" and "Qinguan" Varieties of Apple ( <i>Malus domestica</i> Borkh.). <i>Frontiers in Plant Science</i> , 2016, 7, 908.	3.6	33
12	Expression analysis of key auxin synthesis, transport, and metabolism genes in different young dwarfing apple trees. <i>Acta Physiologiae Plantarum</i> , 2016, 38, 1.	2.1	31
13	Proteome Analyses Using iTRAQ Labeling Reveal Critical Mechanisms in Alternate Bearing <i>Malus prunifolia</i> . <i>Journal of Proteome Research</i> , 2016, 15, 3602-3616.	3.7	30
14	Regulation of the expression of lipoxygenase genes in <i>Prunus persica</i> fruit ripening. <i>Acta Physiologiae Plantarum</i> , 2011, 33, 1345-1352.	2.1	29
15	Comparative RNA-Sequencing and DNA Methylation Analyses of Apple ( <i>Malus domestica</i> Borkh.) Buds with Diverse Flowering Capabilities Reveal Novel Insights into the Regulatory Mechanisms of Flower Bud Formation. <i>Plant and Cell Physiology</i> , 2019, 60, 1702-1721.	3.1	27
16	Genome-wide identification of the 14 <sup>3-3</sup> gene family and its participation in floral transition by interacting with TFL1/FT in apple. <i>BMC Genomics</i> , 2021, 22, 41.	2.8	25
17	Spermidine application affects the adventitious root formation and root morphology of apple rootstock by altering the hormonal profile and regulating the gene expression pattern. <i>Scientia Horticulturae</i> , 2020, 266, 109310.	3.6	24
18	The role of $\beta$ -hexosaminidase in peach ( <i>Prunus persica</i> ) fruit softening. <i>Scientia Horticulturae</i> , 2014, 169, 226-233.	3.6	22

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19	Genome-wide identification, characterization and expression analysis of novel long non-coding RNAs that mediate IBA-induced adventitious root formation in apple rootstocks. <i>Plant Growth Regulation</i> , 2019, 87, 287-302.	3.4	21
20	Transcription profiles reveal the regulatory mechanisms of spur bud changes and flower induction in response to shoot bending in apple ( <i>Malus domestica</i> Borkh.). <i>Plant Molecular Biology</i> , 2019, 99, 45-66.	3.9	21
21	Transcriptome analysis reveals the promotive effect of potassium by hormones and sugar signaling pathways during adventitious roots formation in the apple rootstock. <i>Plant Physiology and Biochemistry</i> , 2021, 165, 123-136.	5.8	20
22	Comparative RNA-sequencing-based transcriptome profiling of buds from profusely flowering ‘Qinguan’™ and weakly flowering ‘Nagafu no. 2’™ apple varieties reveals novel insights into the regulatory mechanisms underlying floral induction. <i>BMC Plant Biology</i> , 2018, 18, 370.	3.6	19
23	Zinc Finger-Homeodomain Genes: Evolution, Functional Differentiation, and Expression Profiling Under Flowering-Related Treatments and Abiotic Stresses in Plants. <i>Evolutionary Bioinformatics</i> , 2019, 15, 117693431986793.	1.2	19
24	Mdm-miR160 Participates in Auxin-Induced Adventitious Root formation of apple rootstock. <i>Scientia Horticulturae</i> , 2020, 270, 109442.	3.6	17
25	Expression of genes in the potential regulatory pathways controlling alternate bearing in ‘Fuji’™ ( <i>Malus domestica</i> Borkh.) apple trees during flower induction. <i>Plant Physiology and Biochemistry</i> , 2018, 132, 579-589.	5.8	15
26	Exogenous application of GA3 inactively regulates axillary bud outgrowth by influencing of branching-inhibitors and bud-regulating hormones in apple ( <i>Malus domestica</i> Borkh.). <i>Molecular Genetics and Genomics</i> , 2018, 293, 1547-1563.	2.1	15
27	MdKNOX19, a class II knotted-like transcription factor of apple, plays roles in ABA signalling/sensitivity by targeting ABI5 during organ development. <i>Plant Science</i> , 2021, 302, 110701.	3.6	15
28	Construction of a high-density SNP-based genetic map and identification of fruit-related QTLs and candidate genes in peach [ <i>Prunus persica</i> (L.) Batsch]. <i>BMC Plant Biology</i> , 2020, 20, 438.	3.6	14
29	Genome-wide identification and expression profiling of the YUCCA gene family in <i>Malus domestica</i> . <i>Scientific Reports</i> , 2020, 10, 10866.	3.3	14
30	The downregulation of PpPG21 and PpPG22 influences peach fruit texture and softening. <i>Planta</i> , 2021, 254, 22.	3.2	14
31	High nitrate inhibited adventitious roots formation in apple rootstock by altering hormonal contents and miRNAs expression profiles. <i>Scientia Horticulturae</i> , 2021, 286, 110230.	3.6	14
32	Revealing critical mechanisms of BR-mediated apple nursery tree growth using iTRAQ-based proteomic analysis. <i>Journal of Proteomics</i> , 2018, 173, 139-154.	2.4	13
33	Genome-wide identification of SERK genes in apple and analyses of their role in stress responses and growth. <i>BMC Genomics</i> , 2018, 19, 962.	2.8	13
34	Identification and Characterization of miRNAs in Self-Rooted and Grafted <i>Malus</i> Reveals Critical Networks Associated with Flowering. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2384.	4.1	13
35	Genome-wide identification and expression profiling analysis of brassinolide signal transduction genes regulating apple tree architecture. <i>Acta Physiologiae Plantarum</i> , 2017, 39, 1.	2.1	11
36	Selection and Validation of Reliable Reference Genes for Gene Expression Studies in Different Genotypes and TRV-Infected Fruits of Peach ( <i>Prunus persica</i> L. Batsch) during Ripening. <i>Genes</i> , 2022, 13, 160.	2.4	11

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37	Molecular mechanism of MdWUS2-MdTCP12 interaction in mediating cytokinin signaling to control axillary bud outgrowth. <i>Journal of Experimental Botany</i> , 2021, 72, 4822-4838.	4.8	10
38	Transcriptome Analysis Reveals New Insights into MdBAK1-Mediated Plant Growth in <i>Malus domestica</i> . <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 9757-9771.	5.2	9
39	Identification of apple TFL1-interacting proteins uncovers an expanded flowering network. <i>Plant Cell Reports</i> , 2021, 40, 2325-2340.	5.6	9
40	PpePL1 and PpePL15 Are the Core Members of the Pectate Lyase Gene Family Involved in Peach Fruit Ripening and Softening. <i>Frontiers in Plant Science</i> , 2022, 13, 844055.	3.6	9
41	Influence of endogenous and exogenous RNases on the variation of pollen cytosolic-free Ca <sup>2+</sup> in <i>Pyrus serotina</i> Rehd. <i>Acta Physiologiae Plantarum</i> , 2008, 30, 233-241.	2.1	8
42	15NITROGEN STUDY ON ABSORPTION, DISTRIBUTION AND UTILIZATION OF NITROGEN APPLIED IN EARLY SUMMER IN RED FUJI APPLE. <i>Journal of Plant Nutrition</i> , 2012, 35, 1557-1571.	1.9	8
43	Identification of Peach NAP Transcription Factor Genes and Characterization of their Expression in Vegetative and Reproductive Organs during Development and Senescence. <i>Frontiers in Plant Science</i> , 2016, 7, 147.	3.6	8
44	Identification of CDF family members in apple and their expression in response to sucrose during floral induction. <i>Journal of Plant Interactions</i> , 2020, 15, 241-256.	2.1	6
45	PrupeFUL4 regulates ripening and softening of peach fruits through ethylene biosynthesis. <i>Acta Physiologiae Plantarum</i> , 2022, 44, 1.	2.1	4
46	PpSAUR43, an Auxin-Responsive Gene, Is Involved in the Post-Ripening and Softening of Peaches. <i>Horticulturae</i> , 2022, 8, 379.	2.8	3
47	The East Asian wild apples, <i>Malus baccata</i> (L.) Borkh and <i>Malus hupehensis</i> (Pamp.) Rehder., are additional contributors to the genomes of cultivated European and Chinese varieties. <i>Molecular Ecology</i> , 2023, 32, 5125-5139.	3.9	3