

# Dong Zhang

## List of Publications by Year in descending order

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123  
papers

3,031  
citations

159525

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docs citations

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times ranked

2279  
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#	ARTICLE	IF	CITATIONS
1	Genetic diversity and similarity of pear ( <i>Pyrus L.</i> ) cultivars native to East Asia revealed by SSR (simple) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	0.8	921
2	Transcription Profiles Reveal Sugar and Hormone Signaling Pathways Mediating Flower Induction in Apple ( <i>Malus domestica</i> Borkh.). <i>Plant and Cell Physiology</i> , 2015, 56, 2052-2068.	1.5	118
3	Effect of exogenous GA 3 and its inhibitor paclobutrazol on floral formation, endogenous hormones, and flowering-associated genes in 'Fuji' apple ( <i>Malus domestica</i> Borkh.). <i>Plant Physiology and Biochemistry</i> , 2016, 107, 178-186.	2.8	92
4	Effects of high temperatures on UV-B/visible irradiation induced postharvest anthocyanin accumulation in 'Yunhongli No. 1' ( <i>Pyrus pyrifolia</i> Nakai) pears. <i>Scientia Horticulturae</i> , 2012, 134, 53-59.	1.7	82
5	Response of miR156-SPL Module during the Red Peel Coloration of Bagging-Treated Chinese Sand Pear ( <i>Pyrus pyrifolia</i> Nakai). <i>Frontiers in Physiology</i> , 2017, 8, 550.	1.3	71
6	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.	4.1	69
7	Transcriptome analysis of bagging-treated red Chinese sand pear peels reveals light-responsive pathway functions in anthocyanin accumulation. <i>Scientific Reports</i> , 2017, 7, 63.	1.6	67
8	Comprehensive analysis of GASA family members in the <i>Malus domestica</i> genome: identification, characterization, and their expressions in response to apple flower induction. <i>BMC Genomics</i> , 2017, 18, 827.	1.2	64
9	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.	1.2	60
10	The red sport of 'Zaosu' pear and its red-striped pigmentation pattern are associated with demethylation of the PyMYB10 promoter. <i>Phytochemistry</i> , 2014, 107, 16-23.	1.4	60
11	Identification and Expression Analysis of Polygalacturonase Family Members during Peach Fruit Softening. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1933.	1.8	60
12	An assessment of genetic variability and relationships within Asian pears based on AFLP (amplified) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.7	59
13	Isolation of anthocyanin biosynthetic genes in red Chinese sand pear ( <i>Pyrus pyrifolia</i> Nakai) and their expression as affected by organ/tissue, cultivar, bagging and fruit side. <i>Scientia Horticulturae</i> , 2012, 136, 29-37.	1.7	54
14	Inhibition of adventitious root development in apple rootstocks by cytokinin is based on its suppression of adventitious root primordia formation. <i>Physiologia Plantarum</i> , 2019, 166, 663-676.	2.6	54
15	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.	1.2	52
16	Characteristics and regulatory pathway of the PrupeSEP1 SEPALLATA gene during ripening and softening in peach fruits. <i>Plant Science</i> , 2017, 257, 63-73.	1.7	49
17	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.	1.8	48
18	Sequencing of a Wild Apple ( <i>Malus baccata</i> ) Genome Unravels the Differences Between Cultivated and Wild Apple Species Regarding Disease Resistance and Cold Tolerance. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2051-2060.	0.8	47

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19	Identification and expression analysis of the IPT and CKX gene families during axillary bud outgrowth in apple ( <i>Malus domestica</i> Borkh.). <i>Gene</i> , 2018, 651, 106-117.	1.0	46
20	Identification, Classification, and Expression Analysis of GRAS Gene Family in <i>Malus domestica</i> . <i>Frontiers in Physiology</i> , 2017, 8, 253.	1.3	45
21	Effect of exogenous 6-benzylaminopurine (6-BA) on branch type, floral induction and initiation, and related gene expression in "Fuji" apple ( <i>Malus domestica</i> Borkh.). <i>Plant Growth Regulation</i> , 2016, 79, 65-70.	1.8	43
22	Isolation and Expression Analysis of Anthocyanin Biosynthesis Genes from the Red Chinese Sand Pear, <i>Pyrus pyrifolia</i> Nakai cv. Mantianhong, in Response to Methyl Jasmonate Treatment and UV-B/VIS Conditions. <i>Plant Molecular Biology Reporter</i> , 2014, 32, 428-437.	1.0	42
23	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.	1.8	41
24	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.	2.8	40
25	Postharvest pigmentation in red Chinese sand pears ( <i>Pyrus pyrifolia</i> Nakai) in response to optimum light and temperature. <i>Postharvest Biology and Technology</i> , 2014, 91, 64-71.	2.9	39
26	Role of Cytokinin, Strigolactone, and Auxin Export on Outgrowth of Axillary Buds in Apple. <i>Frontiers in Plant Science</i> , 2019, 10, 616.	1.7	38
27	Robustness improvement of NIR-based determination of soluble solids in apple fruit by local calibration. <i>Postharvest Biology and Technology</i> , 2018, 139, 82-90.	2.9	36
28	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.	2.8	36
29	Analysis of different pigmentation patterns in "Mantianhong" ( <i>Pyrus pyrifolia</i> Nakai) and "Cascade" ( <i>Pyrus communis</i> L.) under bagging treatment and postharvest UV-B/visible irradiation conditions. <i>Scientia Horticulturae</i> , 2013, 151, 75-82.	1.7	35
30	Identification of TPS family members in apple ( <i>Malus x domestica</i> Borkh.) and the effect of sucrose sprays on TPS expression and floral induction. <i>Plant Physiology and Biochemistry</i> , 2017, 120, 10-23.	2.8	34
31	Melatonin promotes adventitious root formation in apple by promoting the function of MdWOX11. <i>BMC Plant Biology</i> , 2020, 20, 536.	1.6	34
32	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.	1.7	33
33	Effect of exogenous Brassinolide (BR) application on the morphology, hormone status, and gene expression of developing lateral roots in <i>Malus hupehensis</i> . <i>Plant Growth Regulation</i> , 2017, 82, 391-401.	1.8	33
34	Genome Identification of B-BOX Gene Family Members in Seven Rosacea Species and Their Expression Analysis in Response to Flower Induction in <i>Malus domestica</i> . <i>Molecules</i> , 2018, 23, 1763.	1.7	32
35	Expression analysis of key auxin synthesis, transport, and metabolism genes in different young dwarfing apple trees. <i>Acta Physiologiae Plantarum</i> , 2016, 38, 1.	1.0	31
36	Proteome Analyses Using iTRAQ Labeling Reveal Critical Mechanisms in Alternate Bearing in <i>Malus prunifolia</i> . <i>Journal of Proteome Research</i> , 2016, 15, 3602-3616.	1.8	30

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37	Phylogenetic analysis of IDD gene family and characterization of its expression in response to flower induction in <i>Malus</i> . <i>Molecular Genetics and Genomics</i> , 2017, 292, 755-771.	1.0	29
38	Chronic cement dust load induce novel damages in foliage and buds of <i>Malus domestica</i> . <i>Scientific Reports</i> , 2020, 10, 12186.	1.6	29
39	Genome-wide identification, characterization and expression analysis of long non-coding RNAs in different tissues of apple. <i>Gene</i> , 2018, 666, 44-57.	1.0	28
40	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.	1.5	27
41	Genome-wide identification, evolution, and expression analysis of GATA transcription factors in apple ( <i>Malus domestica</i> Borkh.). <i>Gene</i> , 2017, 627, 460-472.	1.0	26
42	Complete Chloroplast Genomes from <i>Sanguisorba</i> : Identity and Variation Among Four Species. <i>Molecules</i> , 2018, 23, 2137.	1.7	25
43	Correlation of production constraints with the yield gap of apple cropping systems in Luochuan County, China. <i>Journal of Integrative Agriculture</i> , 2019, 18, 1714-1725.	1.7	25
44	Transcriptomic analysis reveals the regulatory module of apple ( <i>Malus domestica</i> ) floral transition in response to 6-BA. <i>BMC Plant Biology</i> , 2019, 19, 93.	1.6	25
45	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.	1.2	25
46	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.	1.7	24
47	Genome-Wide Identification of the MdKNOX Gene Family and Characterization of Its Transcriptional Regulation in <i>Malus domestica</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 128.	1.7	24
48	Molecular role of cytokinin in bud activation and outgrowth in apple branching based on transcriptomic analysis. <i>Plant Molecular Biology</i> , 2018, 98, 261-274.	2.0	23
49	Identification and characterization of NRT gene family reveals their critical response to nitrate regulation during adventitious root formation and development in apple rootstock. <i>Scientia Horticulturae</i> , 2021, 275, 109642.	1.7	23
50	miRNA and Degradome Sequencing Reveal miRNA and Their Target Genes That May Mediate Shoot Growth in Spur Type Mutant <i>Yanfu 6</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 441.	1.7	22
51	Mediation of Flower Induction by Gibberellin and its Inhibitor Paclobutrazol: mRNA and miRNA Integration Comprises Complex Regulatory Cross-Talk in Apple. <i>Plant and Cell Physiology</i> , 2018, 59, 2288-2307.	1.5	21
52	Identification and characterization of histone modification gene family reveal their critical responses to flower induction in apple. <i>BMC Plant Biology</i> , 2018, 18, 173.	1.6	21
53	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.	1.8	21
54	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.	2.0	21

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55	A transcriptome analysis of two apple ( <i>Malus domestica</i> ) cultivars with different flowering abilities reveals a gene network module associated with floral transitions. <i>Scientia Horticulturae</i> , 2018, 239, 269-281.	1.7	20
56	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.	2.8	20
57	Effect of fruit maturity on UV-B-induced post-harvest anthocyanin accumulation in red Chinese sand pear. <i>Acta Physiologiae Plantarum</i> , 2013, 35, 2857-2866.	1.0	19
58	Identification and expression analysis of cytokinin response-regulator genes during floral induction in apple ( <i>Malus domestica</i> Borkh). <i>Plant Growth Regulation</i> , 2017, 83, 455-464.	1.8	19
59	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.	1.6	19
60	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.	0.6	19
61	Effect of exogenous indole-3-butanoic acid (IBA) application on the morphology, hormone status, and gene expression of developing lateral roots in <i>Malus hupehensis</i> . <i>Scientia Horticulturae</i> , 2018, 232, 112-120.	1.7	18
62	Genome-wide identification and expression analysis of GRF genes regulating apple tree architecture. <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	0.6	18
63	Mdm-miR160 Participates in Auxin-Induced Adventitious Root formation of apple rootstock. <i>Scientia Horticulturae</i> , 2020, 270, 109442.	1.7	17
64	Genome-wide identification and expression analysis of brassinosteroid biosynthesis and metabolism genes regulating apple tree shoot and lateral root growth. <i>Journal of Plant Physiology</i> , 2018, 231, 68-85.	1.6	16
65	MdKNOX15, a class I knotted-like transcription factor of apple, controls flowering and plant height by regulating GA levels through promoting the MdGA2ox7 transcription. <i>Environmental and Experimental Botany</i> , 2021, 185, 104411.	2.0	16
66	Transcriptome analysis reveals the inhibitory nature of high nitrate during adventitious roots formation in the apple rootstock. <i>Physiologia Plantarum</i> , 2021, 173, 867-882.	2.6	16
67	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.	2.8	15
68	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.	1.0	15
69	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.	1.7	15
70	The TAZ domain-containing proteins play important role in the heavy metals stress biology in plants. <i>Environmental Research</i> , 2021, 197, 111030.	3.7	15
71	Influence of heat stress on leaf ultrastructure, photosynthetic performance, and ascorbate peroxidase gene expression of two pear cultivars ( <i>Pyrus pyrifolia</i> ). <i>Journal of Zhejiang University: Science B</i> , 2013, 14, 1070-1083.	1.3	14
72	Dynamic Cytosine DNA Methylation Patterns Associated with mRNA and siRNA Expression Profiles in Alternate Bearing Apple Trees. <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 5250-5264.	2.4	14

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73	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.	1.6	14
74	Genome-wide identification and expression profiling of the YUCCA gene family in <i>Malus domestica</i> . <i>Scientific Reports</i> , 2020, 10, 10866.	1.6	14
75	Mdm-MIR393b-mediated adventitious root formation by targeted regulation of MdTIR1A expression and weakened sensitivity to auxin in apple rootstock. <i>Plant Science</i> , 2021, 308, 110909.	1.7	14
76	The downregulation of PpPG21 and PpPG22 influences peach fruit texture and softening. <i>Planta</i> , 2021, 254, 22.	1.6	14
77	High nitrate inhibited adventitious roots formation in apple rootstock by altering hormonal contents and miRNAs expression profiles. <i>Scientia Horticulturae</i> , 2021, 286, 110230.	1.7	14
78	Characterization of the complete chloroplast genome of the Chinese crabapple <i>Malus prunifolia</i> (Rosales: Rosaceae: Maloideae). <i>Conservation Genetics Resources</i> , 2016, 8, 227-229.	0.4	13
79	Revealing critical mechanisms of BR-mediated apple nursery tree growth using iTRAQ-based proteomic analysis. <i>Journal of Proteomics</i> , 2018, 173, 139-154.	1.2	13
80	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.	1.2	13
81	Shoot tip cryotherapy for plant pathogen eradication. <i>Plant Pathology</i> , 2022, 71, 1241-1254.	1.2	12
82	Genome-wide identification and expression profiling analysis of brassinolide signal transduction genes regulating apple tree architecture. <i>Acta Physiologiae Plantarum</i> , 2017, 39, 1.	1.0	11
83	Mining and expression analysis of candidate genes involved in regulating the chilling requirement fulfillment of <i>Paeonia lactiflora</i> ‘Hang Baishao’™. <i>BMC Plant Biology</i> , 2017, 17, 262.	1.6	11
84	Cement dust induce stress and attenuates photosynthesis in <i>Arachis hypogaea</i> . <i>Environmental Science and Pollution Research</i> , 2019, 26, 19490-19501.	2.7	11
85	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.	1.0	11
86	Evaluating the Comprehensive Performance of Herbaceous Peonies at low latitudes by the Integration of Long-running Quantitative Observation and Multi-Criteria Decision Making Approach. <i>Scientific Reports</i> , 2019, 9, 15079.	1.6	10
87	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.	2.4	10
88	Nitrate application affects root morphology by altering hormonal status and gene expression patterns in B9 apple rootstock nursery plants. <i>Fruit Research</i> , 2021, 1, 1-11.	0.9	10
89	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.	2.4	9
90	Identification of apple TFL1-interacting proteins uncovers an expanded flowering network. <i>Plant Cell Reports</i> , 2021, 40, 2325-2340.	2.8	9

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91	Effect of exogenous abscisic acid (ABA) on the morphology, phytohormones, and related gene expression of developing lateral roots in ‘Qingzhen 1’™ apple plants. <i>Plant Cell, Tissue and Organ Culture</i> , 0, , 1.	1.2	9
92	Early Sucrose Degradation and the Dominant Sucrose Cleavage Pattern Influence <i>Lycoris sprengeri</i> Bulblet Regeneration In Vitro. <i>International Journal of Molecular Sciences</i> , 2021, 22, 11890.	1.8	9
93	Insights into Factors Controlling Adventitious Root Formation in Apples. <i>Horticulturae</i> , 2022, 8, 276.	1.2	9
94	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.	1.7	9
95	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.	1.7	8
96	Transcriptome Analysis Reveals Multiple Genes and Complex Hormonal-Mediated Interactions with PEG during Adventitious Root Formation in Apple. <i>International Journal of Molecular Sciences</i> , 2022, 23, 976.	1.8	8
97	Efficient somatic embryogenesis and bulblet regeneration of the endangered bulbous flower <i>Griffinia liboniana</i> . <i>Plant Cell, Tissue and Organ Culture</i> , 2018, 135, 523-533.	1.2	7
98	Annual growth cycle observation, hybridization and forcing culture for improving the ornamental application of <i>Paeonia lactiflora</i> Pall. in the low-latitude regions. <i>PLoS ONE</i> , 2019, 14, e0218164.	1.1	7
99	Modeling canopy photosynthesis and light interception partitioning among shoots in bi-axis and single-axis apple trees ( <i>Malus domestica</i> Borkh.). <i>Trees - Structure and Function</i> , 2021, 35, 845-861.	0.9	7
100	Nitrate Application Induces Adventitious Root Growth by Regulating Gene Expression Patterns in Apple Rootstocks. <i>Journal of Plant Growth Regulation</i> , 2022, 41, 3467-3478.	2.8	7
101	A Comparative Study between Evergreen and Deciduous Daylily Species Reveals the Potential Contributions of Winter Shoot Growth and Leaf Freezing Tolerance to Foliar Habits. <i>Journal of Plant Growth Regulation</i> , 2020, 39, 1030-1045.	2.8	6
102	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.	1.0	6
103	MADS-box transcription factors determine the duration of temporary winter dormancy in closely related evergreen and deciduous <i>Iris</i> spp.. <i>Journal of Experimental Botany</i> , 2022, 73, 1429-1449.	2.4	6
104	Cyclanilide Induces Lateral Bud Outgrowth by Modulating Cytokinin Biosynthesis and Signalling Pathways in Apple Identified via Transcriptome Analysis. <i>International Journal of Molecular Sciences</i> , 2022, 23, 581.	1.8	6
105	Characterization of the complete chloroplast genome of the wild Himalayan pear <i>Pyrus pashia</i> (Rosales: Rosaceae: Maloideae). <i>Conservation Genetics Resources</i> , 2017, 9, 569-571.	0.4	5
106	Comparative genomics and phylogenetic perspectives of six fertile <i>Lycoris</i> species endemic to East Asia based on plastome characterization. <i>Nordic Journal of Botany</i> , 2022, 2022, .	0.2	5
107	Transcriptome analysis reveals the regulatory mechanism by which <i>MdWOX11</i> suppresses adventitious shoot formation in apple. <i>Horticulture Research</i> , 2022, 9, .	2.9	5
108	MdGRF11, a growth-regulating factor, participates in the regulation of flowering time and interacts with MdTFL1/MdFT1 in apple. <i>Plant Science</i> , 2022, 321, 111339.	1.7	5



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109	MdNup62 interactions with MdHSFs involved in flowering and heat-stress tolerance in apple. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	5
110	Genome-wide Identification and Expression Analysis of Half-size ABCG Genes in <i>Malus domestica</i> . <i>Horticultural Plant Journal</i> , 2018, 4, 45-54.	2.3	4
111	Effects of exogenous methyl-jasmonate on the morphology, hormone status, and gene expression of developing lateral roots in <i>Malus hupehensis</i> . <i>Scientia Horticulturae</i> , 2021, 289, 110419.	1.7	4
112	Effect of darkness treatment on the morphology, hormone status and gene expression of developing adventitious root in apple rootstock. <i>Plant Cell, Tissue and Organ Culture</i> , 2022, 148, 331-346.	1.2	4
113	PrupeFUL4 regulates ripening and softening of peach fruits through ethylene biosynthesis. <i>Acta Physiologiae Plantarum</i> , 2022, 44, 1.	1.0	4
114	Transcriptome analysis reveals that cytokinins inhibit adventitious root formation through the MdRR12-MdCRF8 module in apple rootstock. <i>Plant Science</i> , 2022, 318, 111220.	1.7	4
115	Different miRNAs and hormones are involved in PEG-induced inhibition of adventitious root formation in apple. <i>Scientia Horticulturae</i> , 2022, 303, 111206.	1.7	4
116	Hybrid Origin of <i>Lycoris shaanxiensis</i> Revealed by Karyotype Survey. <i>Cytologia</i> , 2018, 83, 133-136.	0.2	3
117	A new Amaryllidaceae genus, <i>Shoubiaonia</i> , from Yunnan Province, China. <i>Nordic Journal of Botany</i> , 2021, 39, .	0.2	3
118	PpSAUR43, an Auxin-Responsive Gene, Is Involved in the Post-Ripening and Softening of Peaches. <i>Horticulturae</i> , 2022, 8, 379.	1.2	3
119	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.	2.0	3
120	The nutrient, hormone, and antioxidant status of scion affects the rootstock activity in apple. <i>Scientia Horticulturae</i> , 2022, 302, 111157.	1.7	3
121	A Reduced Starch Level in Plants at Early Stages of Infection by Viruses Can Be Considered a Broad-Range Indicator of Virus Presence. <i>Viruses</i> , 2022, 14, 1176.	1.5	2
122	GENETIC DIVERSITY OF RED SKINNED CHINESE SAND PEAR CULTIVARS REVEALED BY AFLP MARKERS. <i>Acta Horticulturae</i> , 2011, , 679-684.	0.1	1
123	Photosynthetic capacity in 'Fuji' apple trees influenced by interstocks at leaf and canopy scale. <i>Acta Horticulturae</i> , 2019, , 77-84.	0.1	1