

Mingyu Han

List of Publications by Year in descending order

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88
papers

2,129
citations

201674

27
h-index

315739

38
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96
all docs

96
docs citations

96
times ranked

1736
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	The nutrient, hormone, and antioxidant status of scion affects the rootstock activity in apple. <i>Scientia Horticulturae</i> , 2022, 302, 111157.	3.6	3
3	MdNup62 interactions with MdHSFs involved in flowering and heat-stress tolerance in apple. <i>BMC Plant Biology</i> , 2022, 22, .	3.6	5
4	Identification of MdMED family, key role of MdMED81, and salicylic acid at the right time of year triggers MdMED81 to induce flowering in <i>Malus domestica</i> . <i>Scientia Horticulturae</i> , 2022, 304, 111341.	3.6	3
5	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
6	Genome-wide identification of the 14 α -3-3 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
7	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.	1.9	7
8	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.	4.2	16
9	Molecular mechanism of MdWUS2 α -MdTCP12 interaction in mediating cytokinin signaling to control axillary bud outgrowth. <i>Journal of Experimental Botany</i> , 2021, 72, 4822-4838.	4.8	10
10	Regulation of Flowering Time by Improving Leaf Health Markers and Expansion by Salicylic Acid Treatment: A New Approach to Induce Flowering in <i>Malus domestica</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 655974.	3.6	6
11	The downregulation of PpPG21 and PpPG22 influences peach fruit texture and softening. <i>Planta</i> , 2021, 254, 22.	3.2	14
12	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.	3.6	4
13	Melatonin promotes adventitious root formation in apple by promoting the function of MdWOX11. <i>BMC Plant Biology</i> , 2020, 20, 536.	3.6	34
14	Chronic cement dust load induce novel damages in foliage and buds of <i>Malus domestica</i> . <i>Scientific Reports</i> , 2020, 10, 12186.	3.3	29
15	Genomic identification and expression analysis of nuclear pore proteins in <i>Malus domestica</i> . <i>Scientific Reports</i> , 2020, 10, 17426.	3.3	10
16	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
17	Epigenomic Regulatory Mechanism in Vegetative Phase Transition of <i>Malus hupehensis</i> . <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 4812-4829.	5.2	10
18	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.	3.6	24

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19	Exogenous 6-aminocaproic acid application affects root morphology by altering hormone status and gene expression of developing lateral roots in <i>Malus hupehensis</i> . <i>Plant Biology</i> , 2020, 22, 1150-1159.	3.8	15
20	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
21	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
22	Transcriptomic and Metabolic Analyses Provide New Insights into the Apple Fruit Quality Decline during Long-Term Cold Storage. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 4699-4716.	5.2	32
23	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.	5.2	54
24	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
25	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
26	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.	1.8	47
27	Role of Cytokinin, Strigolactone, and Auxin Export on Outgrowth of Axillary Buds in Apple. <i>Frontiers in Plant Science</i> , 2019, 10, 616.	3.6	38
28	Effects of Brassinosteroid Associated with Auxin and Gibberellin on Apple Tree Growth and Gene Expression Patterns. <i>Horticultural Plant Journal</i> , 2019, 5, 93-108.	5.0	23
29	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.	5.2	14
30	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.	3.6	25
31	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
32	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
33	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
34	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.	2.2	46
35	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
36	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.	5.0	4

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37	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
38	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
39	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
40	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.	3.9	23
41	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
42	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.	3.5	16
43	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
44	Genome-wide identification and expression analysis of GRF genes regulating apple tree architecture. <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	1.6	18
45	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
46	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
47	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.	3.6	20
48	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
49	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.	3.8	32
50	Genome-wide identification, characterization and expression analysis of long non-coding RNAs in different tissues of apple. <i>Gene</i> , 2018, 666, 44-57.	2.2	28
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.	3.1	21
52	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
53	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.	3.6	21
54	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.	3.4	33

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55	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
56	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.	2.1	29
57	Effect of root pruning and nitrogen fertilization on growth of young 'Fuji' apple (<i>Malus domestica</i>) Tj ETQq1 1.0.784314 rgBT / 1.9.784314	1.9	3
58	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.	5.8	34
59	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.	3.4	19
60	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
61	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.	2.2	26
62	Branch bending affected floral bud development and nutrient accumulation in shoot terminals of 'Fuji' and 'Gala' apples. <i>Acta Physiologiae Plantarum</i> , 2017, 39, 1.	2.1	11
63	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.	2.8	64
64	Identification, Classification, and Expression Analysis of GRAS Gene Family in <i>Malus domestica</i> . <i>Frontiers in Physiology</i> , 2017, 8, 253.	2.8	45
65	miRNA and Degradome Sequencing Reveal miRNA and Their Target Genes That May Mediate Shoot Growth in Spur Type Mutant 'Yanfu 6'. <i>Frontiers in Plant Science</i> , 2017, 8, 441.	3.6	22
66	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
67	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
68	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
69	Identification and Phylogenetic Analysis of the POLYGALACTURONASE Gene Family in Apple. <i>Horticultural Plant Journal</i> , 2016, 2, 241-252.	5.0	28
70	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
71	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
72	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

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73	Genomewide analysis of ABCBs with a focus on ABCB1 and ABCB19 in <i>Malus domestica</i> . <i>Journal of Genetics</i> , 2016, 95, 141-149.	0.7	10
74	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.	0.8	13
75	The impact of long-term water stress on tree architecture and production is related to changes in transitions between vegetative and reproductive growth in the "Granny Smith" apple cultivar. <i>Tree Physiology</i> , 2016, 36, 1369-1381.	3.1	11
76	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.	3.7	30
77	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.	5.8	92
78	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.	3.4	43
79	Effect of bending on the dynamic changes of endogenous hormones in shoot terminals of "Fuji" and "Gala" apple trees. <i>Acta Physiologiae Plantarum</i> , 2015, 37, 1.	2.1	16
80	Optimizing planting density for production of high-quality apple nursery stock in China. <i>New Zealand Journal of Crop and Horticultural Science</i> , 2015, 43, 7-17.	1.3	5
81	Root growth, yield and fruit quality of 'Red Fuji' apple trees in relation to planting depth of dwarfing interstock on the Loess Plateau. <i>European Journal of Horticultural Science</i> , 2015, 80, 109-116.	0.7	15
82	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
83	The role of β -hexosaminidase in peach (<i>Prunus persica</i>) fruit softening. <i>Scientia Horticulturae</i> , 2014, 169, 226-233.	3.6	22
84	15N-NITROGEN 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
85	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
86	Exogenous Salicylic Acid Alleviates Growth Inhibition and Oxidative Stress Induced by Hypoxia Stress in <i>Malus robusta</i> Rehd. <i>Journal of Plant Growth Regulation</i> , 2009, 28, 358-366.	5.1	31
87	Characteristics of canopy and light transmittance in three types of apple orchards in Weibei areas of Shaanxi Province, China. <i>Frontiers of Agriculture in China</i> , 2008, 2, 93-96.	0.2	4
88	MdNup54 Interactions With MdHSP70 Involved in Flowering in Apple. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	1