

Yu-Jin Hao

List of Publications by Year in descending order

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171
papers

9,840
citations

31949

53
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45285

90
g-index

174
all docs

174
docs citations

174
times ranked

5640
citing authors

#	ARTICLE	IF	CITATIONS
1	A R2R3 Type MYB Transcription Factor Is Involved in the Cold Regulation of CBF Genes and in Acquired Freezing Tolerance. <i>Journal of Biological Chemistry</i> , 2006, 281, 37636-37645.	1.6	776
2	The bHLH transcription factor MdbHLH3 promotes anthocyanin accumulation and fruit colouration in response to low temperature in apples. <i>Plant, Cell and Environment</i> , 2012, 35, 1884-1897.	2.8	525
3	MdCOP1 Ubiquitin E3 Ligases Interact with MdMYB1 to Regulate Light-Induced Anthocyanin Biosynthesis and Red Fruit Coloration in Apple. <i>Plant Physiology</i> , 2012, 160, 1011-1022.	2.3	381
4	MdMYB9 and MdMYB11 are Involved in the Regulation of the JA-Induced Biosynthesis of Anthocyanin and Proanthocyanidin in Apples. <i>Plant and Cell Physiology</i> , 2015, 56, 650-662.	1.5	264
5	The bZIP transcription factor MdHY5 regulates anthocyanin accumulation and nitrate assimilation in apple. <i>Horticulture Research</i> , 2017, 4, 17023.	2.9	216
6	MdMYB1 Regulates Anthocyanin and Malate Accumulation by Directly Facilitating Their Transport into Vacuoles in Apples. <i>Plant Physiology</i> , 2016, 170, 1315-1330.	2.3	203
7	The apple WD40 protein MdTTG1 interacts with bHLH but not MYB proteins to regulate anthocyanin accumulation. <i>Journal of Plant Physiology</i> , 2012, 169, 710-717.	1.6	198
8	An apple MYB transcription factor regulates cold tolerance and anthocyanin accumulation and undergoes MIEL1-mediated degradation. <i>Plant Biotechnology Journal</i> , 2020, 18, 337-353.	4.1	198
9	EIN3-LIKE1, MYB1, and ETHYLENE RESPONSE FACTOR3 Act in a Regulatory Loop That Synergistically Modulates Ethylene Biosynthesis and Anthocyanin Accumulation. <i>Plant Physiology</i> , 2018, 178, 808-823.	2.3	191
10	Apple bZIP transcription factor MdbZIP44 regulates abscisic acid-promoted anthocyanin accumulation. <i>Plant, Cell and Environment</i> , 2018, 41, 2678-2692.	2.8	189
11	The ERF transcription factor MdERF38 promotes drought stress-induced anthocyanin biosynthesis in apple. <i>Plant Journal</i> , 2020, 101, 573-589.	2.8	181
12	R2R3-MYB transcription factor MdMYB23 is involved in the cold tolerance and proanthocyanidin accumulation in apple. <i>Plant Journal</i> , 2018, 96, 562-577.	2.8	178
13	Genome Wide Analysis of the Apple MYB Transcription Factor Family Allows the Identification of MdMYB121 Gene Confering Abiotic Stress Tolerance in Plants. <i>PLoS ONE</i> , 2013, 8, e69955.	1.1	174
14	The cold-induced basic helix-loop-helix transcription factor gene MdCibHLH1 encodes an ICE-like protein in apple. <i>BMC Plant Biology</i> , 2012, 12, 22.	1.6	162
15	Transcription Factor AREB2 Is Involved in Soluble Sugar Accumulation by Activating Sugar Transporter and Amylase Genes. <i>Plant Physiology</i> , 2017, 174, 2348-2362.	2.3	153
16	Glucose Sensor MdHXX1 Phosphorylates and Stabilizes MdbHLH3 to Promote Anthocyanin Biosynthesis in Apple. <i>PLoS Genetics</i> , 2016, 12, e1006273.	1.5	127
17	Isolation and characterization of an apple cytosolic malate dehydrogenase gene reveal its function in malate synthesis. <i>Journal of Plant Physiology</i> , 2011, 168, 474-480.	1.6	121
18	MdWRKY40 promotes wounding-induced anthocyanin biosynthesis in association with MdMYB1 and undergoes MdBT2-mediated degradation. <i>New Phytologist</i> , 2019, 224, 380-395.	3.5	121

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19	Overexpression of <i>MdSOS2L1</i> , a <i>CIPK</i> protein kinase, increases the antioxidant metabolites to enhance salt tolerance in apple and tomato. <i>Physiologia Plantarum</i> , 2016, 156, 201-214.	2.6	111
20	The R2R3 MYB transcription factor <i>MdMYB30</i> modulates plant resistance against pathogens by regulating cuticular wax biosynthesis. <i>BMC Plant Biology</i> , 2019, 19, 362.	1.6	105
21	The Nitrate-Responsive Protein <i>MdbT2</i> Regulates Anthocyanin Biosynthesis by Interacting with the <i>MdMYB1</i> Transcription Factor. <i>Plant Physiology</i> , 2018, 178, 890-906.	2.3	102
22	<i>MdBBX22</i> regulates UV-induced anthocyanin biosynthesis through regulating the function of <i>MdHY5</i> and is targeted by <i>MdBt2</i> for 26S proteasome-mediated degradation. <i>Plant Biotechnology Journal</i> , 2019, 17, 2231-2233.	4.1	102
23	<i>MdSnRK1.1</i> interacts with <i>MdJAZ18</i> to regulate sucrose-induced anthocyanin and proanthocyanidin accumulation in apple. <i>Journal of Experimental Botany</i> , 2017, 68, 2977-2990.	2.4	101
24	The enhancement of tolerance to salt and cold stresses by modifying the redox state and salicylic acid content via the cytosolic malate dehydrogenase gene in transgenic apple plants. <i>Plant Biotechnology Journal</i> , 2016, 14, 1986-1997.	4.1	100
25	Overexpression of <i>MdbHLH104</i> gene enhances the tolerance to iron deficiency in apple. <i>Plant Biotechnology Journal</i> , 2016, 14, 1633-1645.	4.1	100
26	The molecular cloning and functional characterization of <i>MdMYC2</i> , a bHLH transcription factor in apple. <i>Plant Physiology and Biochemistry</i> , 2016, 108, 24-31.	2.8	99
27	Overexpression of a <i>R2R3 MYB</i> gene <i>MdSIMYB1</i> increases tolerance to multiple stresses in transgenic tobacco and apples. <i>Physiologia Plantarum</i> , 2014, 150, 76-87.	2.6	98
28	The <i>R2R3 MYB</i> transcription factor <i>MdMYB73</i> is involved in malate accumulation and vacuolar acidification in apple. <i>Plant Journal</i> , 2017, 91, 443-454.	2.8	96
29	An apple NAC transcription factor negatively regulates cold tolerance via CBF-dependent pathway. <i>Journal of Plant Physiology</i> , 2018, 221, 74-80.	1.6	93
30	Ubiquitination-Related <i>MdBt</i> Scaffold Proteins Target a bHLH Transcription Factor for Iron Homeostasis. <i>Plant Physiology</i> , 2016, 172, 1973-1988.	2.3	92
31	Molecular cloning and functional characterization of a novel apple <i>MdCIPK6L</i> gene reveals its involvement in multiple abiotic stress tolerance in transgenic plants. <i>Plant Molecular Biology</i> , 2012, 79, 123-135.	2.0	89
32	The regulatory module <i>MdPUB29-MdbHLH3</i> connects ethylene biosynthesis with fruit quality in apple. <i>New Phytologist</i> , 2019, 221, 1966-1982.	3.5	88
33	Apple Box protein <i>BBX37</i> regulates jasmonic acid mediated cold tolerance through the <i>JAZa-BBX37-CE1a-CBF</i> pathway and undergoes MIEL1-mediated ubiquitination and degradation. <i>New Phytologist</i> , 2021, 229, 2707-2729.	3.5	88
34	Genome-wide analysis and identification of stress-responsive genes of the NAM-ATAF1,2-CUC2 transcription factor family in apple. <i>Plant Physiology and Biochemistry</i> , 2013, 71, 11-21.	2.8	81
35	An apple NAC transcription factor enhances salt stress tolerance by modulating the ethylene response. <i>Physiologia Plantarum</i> , 2018, 164, 279-289.	2.6	80
36	Apple AP2/EREBP transcription factor <i>MdSHINE2</i> confers drought resistance by regulating wax biosynthesis. <i>Planta</i> , 2019, 249, 1627-1643.	1.6	80

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37	An apple sucrose transporter MdSUT2.2 is a phosphorylation target for protein kinase MdCIPK22 in response to drought. <i>Plant Biotechnology Journal</i> , 2019, 17, 625-637.	4.1	77
38	Expression of arginine decarboxylase and ornithine decarboxylase genes in apple cells and stressed shoots. <i>Journal of Experimental Botany</i> , 2005, 56, 1105-1115.	2.4	76
39	MdbHLH93, an apple activator regulating leaf senescence, is regulated by ABA and MdBT2 in antagonistic ways. <i>New Phytologist</i> , 2019, 222, 735-751.	3.5	76
40	The small ubiquitin-like modifier E3 ligase MdSIZ1 promotes anthocyanin accumulation by sumoylating MdMYB1 under low temperature conditions in apple. <i>Plant, Cell and Environment</i> , 2017, 40, 2068-2080.	2.8	75
41	Tobacco Transcription Factor NtbHLH123 Confers Tolerance to Cold Stress by Regulating the NtCBF Pathway and Reactive Oxygen Species Homeostasis. <i>Frontiers in Plant Science</i> , 2018, 9, 381.	1.7	75
42	Molecular cloning and functional characterization of MdSOS2 reveals its involvement in salt tolerance in apple callus and Arabidopsis. <i>Plant Cell Reports</i> , 2012, 31, 713-722.	2.8	71
43	The SUMO E3 Ligase MdSIZ1 Targets MdbHLH104 to Regulate Plasma Membrane H ⁺ -ATPase Activity and Iron Homeostasis. <i>Plant Physiology</i> , 2019, 179, 88-106.	2.3	71
44	An Apple B-Box Protein MdBBX37 Modulates Anthocyanin Biosynthesis and Hypocotyl Elongation Synergistically with MdMYBs and MdHY5. <i>Plant and Cell Physiology</i> , 2020, 61, 130-143.	1.5	70
45	A CIPK protein kinase targets sucrose transporter MdSUT2.2 at Ser ²⁵⁴ for phosphorylation to enhance salt tolerance. <i>Plant, Cell and Environment</i> , 2019, 42, 918-930.	2.8	68
46	ABI5 regulates ABA-induced anthocyanin biosynthesis by modulating the MYB1-bHLH3 complex in apple. <i>Journal of Experimental Botany</i> , 2021, 72, 1460-1472.	2.4	68
47	How do anthocyanins paint our horticultural products?. <i>Scientia Horticulturae</i> , 2019, 249, 257-262.	1.7	66
48	Molecular cloning of three malic acid related genes MdPEPC, MdVHA-A, MdCYME and their expression analysis in apple fruits. <i>Scientia Horticulturae</i> , 2009, 122, 404-408.	1.7	65
49	An apple CIPK protein kinase targets a novel residue of AREB transcription factor for ABA-dependent phosphorylation. <i>Plant, Cell and Environment</i> , 2017, 40, 2207-2219.	2.8	64
50	Dynamic regulation of anthocyanin biosynthesis at different light intensities by the BT2-TCP46-MYB1 module in apple. <i>Journal of Experimental Botany</i> , 2020, 71, 3094-3109.	2.4	64
51	MdVHP1 encodes an apple vacuolar H ⁺ -PPase and enhances stress tolerance in transgenic apple callus and tomato. <i>Journal of Plant Physiology</i> , 2011, 168, 2124-2133.	1.6	59
52	The Glucose Sensor MdHXK1 Phosphorylates a Tonoplast Na ⁺ /H ⁺ Exchanger to Improve Salt Tolerance. <i>Plant Physiology</i> , 2018, 176, 2977-2990.	2.3	59
53	MdHY5 positively regulates cold tolerance via CBF-dependent and CBF-independent pathways in apple. <i>Journal of Plant Physiology</i> , 2017, 218, 275-281.	1.6	56
54	A novel gene, screened by cDNA-AFLP approach, contributes to lowering the acidity of fruit in apple. <i>Plant Physiology and Biochemistry</i> , 2007, 45, 139-145.	2.8	52

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55	The apple bHLH transcription factor MdbHLH3 functions in determining the fruit carbohydrates and malate. <i>Plant Biotechnology Journal</i> , 2021, 19, 285-299.	4.1	52
56	A Neighboring Aromatic-Aromatic Amino Acid Combination Governs Activity Divergence between Tomato Phytoene Synthases. <i>Plant Physiology</i> , 2019, 180, 1988-2003.	2.3	50
57	MdbHLH130, an Apple bHLH Transcription Factor, Confers Water Stress Resistance by Regulating Stomatal Closure and ROS Homeostasis in Transgenic Tobacco. <i>Frontiers in Plant Science</i> , 2020, 11, 543696.	1.7	50
58	The AP2 transcription factor <i>NtERF172</i> confers drought resistance by modifying <i>NtCAT</i> . <i>Plant Biotechnology Journal</i> , 2020, 18, 2444-2455.	4.1	50
59	Jasmonate induces biosynthesis of anthocyanin and proanthocyanidin in apple by mediating the JAZ1-TRB1-MYB9 complex. <i>Plant Journal</i> , 2021, 106, 1414-1430.	2.8	49
60	A Genome-Wide Analysis of the LBD (LATERAL ORGAN BOUNDARIES Domain) Gene Family in <i>Malus domestica</i> with a Functional Characterization of MdLBD11. <i>PLoS ONE</i> , 2013, 8, e57044.	1.1	49
61	MdGRF11, an apple 14-3-3 protein, acts as a positive regulator of drought and salt tolerance. <i>Plant Science</i> , 2019, 288, 110219.	1.7	47
62	Apple RING E3 ligase MdMIEL1 inhibits anthocyanin accumulation by ubiquitinating and degrading MdMYB1 protein. <i>Plant and Cell Physiology</i> , 2017, 58, 1953-1962.	1.5	46
63	Chrysanthemum MADS-box transcription factor CmANR1 modulates lateral root development via homo-/heterodimerization to influence auxin accumulation in <i>Arabidopsis</i> . <i>Plant Science</i> , 2018, 266, 27-36.	1.7	45
64	Tobacco transcription factor bHLH123 improves salt tolerance by activating NADPH oxidase <i>NtRbohE</i> expression. <i>Plant Physiology</i> , 2021, 186, 1706-1720.	2.3	43
65	The MdWRKY31 transcription factor binds to the MdRAV1 promoter to mediate ABA sensitivity. <i>Horticulture Research</i> , 2019, 6, 66.	2.9	42
66	Apple F-Box Protein MdMAX2 Regulates Plant Photomorphogenesis and Stress Response. <i>Frontiers in Plant Science</i> , 2016, 7, 1685.	1.7	41
67	Genome-wide identification and characterization of apple long-chain Acyl-CoA synthetases and expression analysis under different stresses. <i>Plant Physiology and Biochemistry</i> , 2018, 132, 320-332.	2.8	41
68	The apple U-box E3 ubiquitin ligase MdPUB29 contributes to activate plant immune response to the fungal pathogen <i>Botryosphaeria dothidea</i> . <i>Planta</i> , 2019, 249, 1177-1188.	1.6	41
69	MdWRKY15 improves resistance of apple to <i>Botryosphaeria dothidea</i> via the salicylic acid-mediated pathway by directly binding the <i>MdICS1</i> promoter. <i>Journal of Integrative Plant Biology</i> , 2020, 62, 527-543.	4.1	40
70	Apple ethylene response factor MdERF11 confers resistance to fungal pathogen <i>Botryosphaeria dothidea</i> . <i>Plant Science</i> , 2020, 291, 110351.	1.7	40
71	Ectopic expression of the apple Md-miRNA156h gene regulates flower and fruit development in <i>Arabidopsis</i> . <i>Plant Cell, Tissue and Organ Culture</i> , 2013, 112, 343-351.	1.2	39
72	The basic helix-loop-helix transcription factor MdbHLH3 modulates leaf senescence in apple via the regulation of dehydratase-enolase-phosphatase complex 1. <i>Horticulture Research</i> , 2020, 7, 50.	2.9	39

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73	Molecular cloning and functional analysis of a UV-B photoreceptor gene, MdLVR8 (UV Resistance) Tj ETQq1 1 0.784314 rgBT ₁ /Overlook	1.7	37
74	MdCER2 conferred to wax accumulation and increased drought tolerance in plants. <i>Plant Physiology and Biochemistry</i> , 2020, 149, 277-285.	2.8	37
75	Molecular cloning and functional characterization of the apple sucrose transporter gene MdSUT2. <i>Plant Physiology and Biochemistry</i> , 2016, 109, 442-451.	2.8	36
76	Cloning and elucidation of the functional role of apple MdLBD13 in anthocyanin biosynthesis and nitrate assimilation. <i>Plant Cell, Tissue and Organ Culture</i> , 2017, 130, 47-59.	1.2	36
77	MdSWEET17, a sugar transporter in apple, enhances drought tolerance in tomato. <i>Journal of Integrative Agriculture</i> , 2019, 18, 2041-2051.	1.7	35
78	BTB protein MdBT2 inhibits anthocyanin and proanthocyanidin biosynthesis by triggering MdMYB9 degradation in apple. <i>Tree Physiology</i> , 2018, 38, 1578-1587.	1.4	34
79	An apple long-chain acyl-CoA synthetase 2 gene enhances plant resistance to abiotic stress by regulating the accumulation of cuticular wax. <i>Tree Physiology</i> , 2020, 40, 1450-1465.	1.4	34
80	BTB-TAZ Domain Protein MdBT2 Modulates Malate Accumulation and Vacuolar Acidification in Response to Nitrate. <i>Plant Physiology</i> , 2020, 183, 750-764.	2.3	33
81	Functional characterization of the apple MhGAI1 gene through ectopic expression and grafting experiments in tomatoes. <i>Journal of Plant Physiology</i> , 2012, 169, 303-310.	1.6	32
82	Genome wide analysis and functional identification of MdKCS genes in apple. <i>Plant Physiology and Biochemistry</i> , 2020, 151, 299-312.	2.8	32
83	MdABI5 works with its interaction partners to regulate abscisic acid-mediated leaf senescence in apple. <i>Plant Journal</i> , 2021, 105, 1566-1581.	2.8	32
84	Apple MdMYC2 reduces aluminum stress tolerance by directly regulating MdERF3 gene. <i>Plant and Soil</i> , 2017, 418, 255-266.	1.8	31
85	Auxin regulates anthocyanin biosynthesis through the auxin repressor protein MdIAA26. <i>Biochemical and Biophysical Research Communications</i> , 2020, 533, 717-722.	1.0	31
86	Functional identification of MdSIZ1 as a SUMO E3 ligase in apple. <i>Journal of Plant Physiology</i> , 2016, 198, 69-80.	1.6	30
87	Apple MdERF4 negatively regulates salt tolerance by inhibiting MdERF3 transcription. <i>Plant Science</i> , 2018, 276, 181-188.	1.7	30
88	Advances in Biosynthesis, Regulation, and Function of Apple Cuticular Wax. <i>Frontiers in Plant Science</i> , 2020, 11, 1165.	1.7	30
89	Apple <sc>BT2</sc> protein negatively regulates jasmonic acid-triggered leaf senescence by modulating the stability of <sc>MYC2</sc> and <sc>JAZ2</sc>. <i>Plant, Cell and Environment</i> , 2021, 44, 216-233.	2.8	30
90	Isolation and functional identification of an apple MdCER1 gene. <i>Plant Cell, Tissue and Organ Culture</i> , 2019, 136, 1-13.	1.2	29

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91	BTB/TAZ protein MdbT2 integrates multiple hormonal and environmental signals to regulate anthocyanin biosynthesis in apple. <i>Journal of Integrative Plant Biology</i> , 2020, 62, 1643-1646.	4.1	29
92	R2R3-MYB Transcription Factor MdMYB73 Confers Increased Resistance to the Fungal Pathogen <i>Botryosphaeria dothidea</i> in Apples via the Salicylic Acid Pathway. <i>Journal of Agricultural and Food Chemistry</i> , 2021, 69, 447-458.	2.4	29
93	Conserved vacuolar H ⁺ -ATPase subunit B1 improves salt stress tolerance in apple calli and tomato plants. <i>Scientia Horticulturae</i> , 2015, 197, 107-116.	1.7	27
94	Functional identification of MdPIF1 as a Phytochrome Interacting Factor in Apple. <i>Plant Physiology and Biochemistry</i> , 2017, 119, 178-188.	2.8	27
95	Apple RING finger E3 ubiquitin ligase MdMIEL1 negatively regulates salt and oxidative stresses tolerance. <i>Journal of Plant Biology</i> , 2017, 60, 137-145.	0.9	26
96	An Apple Protein Kinase MdSnRK1.1 Interacts with MdCAIP1 to Regulate ABA Sensitivity. <i>Plant and Cell Physiology</i> , 2017, 58, 1631-1641.	1.5	26
97	The apple C2H2-type zinc finger transcription factor MdZAT10 positively regulates JA-induced leaf senescence by interacting with MdbT2. <i>Horticulture Research</i> , 2021, 8, 159.	2.9	26
98	MdWRKY46-Enhanced Apple Resistance to <i>Botryosphaeria dothidea</i> by Activating the Expression of MdPBS3.1 in the Salicylic Acid Signaling Pathway. <i>Molecular Plant-Microbe Interactions</i> , 2019, 32, 1391-1401.	1.4	25
99	BTB-BACK-TAZ domain protein MdbT2-mediated MdMYB73 ubiquitination negatively regulates malate accumulation and vacuolar acidification in apple. <i>Horticulture Research</i> , 2020, 7, 151.	2.9	25
100	The apple 14-3-3 protein MdGRF11 interacts with the BTB protein MdbT2 to regulate nitrate deficiency-induced anthocyanin accumulation. <i>Horticulture Research</i> , 2021, 8, 22.	2.9	25
101	BTB-BACK Domain E3 Ligase MdPOB1 Suppresses Plant Pathogen Defense against <i>Botryosphaeria dothidea</i> by Ubiquitinating and Degrading MdPUB29 Protein in Apple. <i>Plant and Cell Physiology</i> , 2019, 60, 2129-2140.	1.5	24
102	MdDREB2A in apple is involved in the regulation of multiple abiotic stress responses. <i>Horticultural Plant Journal</i> , 2021, 7, 197-208.	2.3	24
103	MdCIB1, an apple bHLH transcription factor, plays a positive regulator in response to drought stress. <i>Environmental and Experimental Botany</i> , 2021, 188, 104523.	2.0	24
104	MdMYB58 Modulates Fe Homeostasis by Directly Binding to the MdMATE43 Promoter in Plants. <i>Plant and Cell Physiology</i> , 2018, 59, 2476-2489.	1.5	23
105	The regulatory module MdbT2-MdMYB88/MdMYB124-MdNRTs regulates nitrogen usage in apple. <i>Plant Physiology</i> , 2021, 185, 1924-1942.	2.3	23
106	dsRNA-binding protein MdDRB1 associated with miRNA biogenesis modifies adventitious rooting and tree architecture in apple. <i>Plant Biotechnology Journal</i> , 2014, 12, 183-192.	4.1	22
107	Cloning and functional identification of a strigolactone receptor gene MdD14 in apple. <i>Plant Cell, Tissue and Organ Culture</i> , 2020, 140, 197-208.	1.2	22
108	An apple long-chain acyl-CoA synthetase, MdLACS4, induces early flowering and enhances abiotic stress resistance in Arabidopsis. <i>Plant Science</i> , 2020, 297, 110529.	1.7	22

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109	Low nitrate alleviates iron deficiency by regulating iron homeostasis in apple. <i>Plant, Cell and Environment</i> , 2021, 44, 1869-1884.	2.8	22
110	Genome-Wide Identification of Apple Ubiquitin SINA E3 Ligase and Functional Characterization of MdSINA2. <i>Frontiers in Plant Science</i> , 2020, 11, 1109.	1.7	21
111	Ectopic expression of an apple cytochrome P450 gene MdCYPM1 negatively regulates plant photomorphogenesis and stress response in Arabidopsis. <i>Biochemical and Biophysical Research Communications</i> , 2017, 483, 1-9.	1.0	19
112	MdHIR4 transcription and translation levels associated with disease in apple are regulated by MdWRKY31. <i>Plant Molecular Biology</i> , 2019, 101, 149-162.	2.0	19
113	Apple MdSAT1 encodes a bHLHm1 transcription factor involved in salinity and drought responses. <i>Planta</i> , 2021, 253, 46.	1.6	19
114	MdSOS2L1 phosphorylates MdVHA-B1 to modulate malate accumulation in response to salinity in apple. <i>Plant Cell Reports</i> , 2016, 35, 705-718.	2.8	18
115	The Growth-Promoting Mechanism of <i>Brevibacillus laterosporus</i> AMCC100017 on Apple Rootstock <i>Malus robusta</i> . <i>Horticultural Plant Journal</i> , 2022, 8, 22-34.	2.3	18
116	Ectopic expression of the apple Md-miR172e gene alters flowering time and floral organ identity in Arabidopsis. <i>Plant Cell, Tissue and Organ Culture</i> , 2015, 123, 535-546.	1.2	17
117	The Characterization, Authentication, and Gene Expression Pattern of the MdCER Family in <i>Malus domestica</i> . <i>Horticultural Plant Journal</i> , 2019, 5, 1-9.	2.3	17
118	Identification of Phytochrome-Interacting Factor Family Members and Functional Analysis of MdPIF4 in <i>Malus domestica</i> . <i>International Journal of Molecular Sciences</i> , 2020, 21, 7350.	1.8	17
119	NIN-like protein 7 promotes nitrate-mediated lateral root development by activating transcription of TRYPTOPHAN AMINOTRANSFERASE RELATED 2. <i>Plant Science</i> , 2021, 303, 110771.	1.7	17
120	The apple palmitoyltransferase MdPAT16 influences sugar content and salt tolerance via an MdCBL1-MdCIPK13-MdSUT2.2 pathway. <i>Plant Journal</i> , 2021, 106, 689-705.	2.8	17
121	Ectopic overexpression of Arabidopsis AtmiR393a gene changes auxin sensitivity and enhances salt resistance in tobacco. <i>Acta Physiologiae Plantarum</i> , 2010, 32, 997-1003.	1.0	16
122	Genome-wide identification, expression profiling, and protein-protein interaction properties of ovate family proteins in apple. <i>Tree Genetics and Genomes</i> , 2019, 15, 1.	0.6	16
123	A basic/helix-loop-helix transcription factor controls leaf shape by regulating auxin signaling in apple. <i>New Phytologist</i> , 2020, 228, 1897-1913.	3.5	16
124	Apple SUMO E3 ligase MdsIZ1 facilitates SUMOylation of MdARF8 to regulate lateral root formation. <i>New Phytologist</i> , 2021, 229, 2206-2222.	3.5	16
125	The MdABI5 transcription factor interacts with the MdNRT1.5/MdNPF7.3 promoter to fine-tune nitrate transport from roots to shoots in apple. <i>Horticulture Research</i> , 2021, 8, 236.	2.9	16
126	Functional characterization of MdMYB73 reveals its involvement in cold stress response in apple calli and Arabidopsis. <i>Journal of Integrative Agriculture</i> , 2017, 16, 2215-2221.	1.7	15

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127	The ectopic expression of apple MYB1 and bHLH3 differentially activates anthocyanin biosynthesis in tobacco. <i>Plant Cell, Tissue and Organ Culture</i> , 2017, 131, 183-194.	1.2	15
128	Apple SUMO E3 ligase MdsIZ1 is involved in the response to phosphate deficiency. <i>Journal of Plant Physiology</i> , 2019, 232, 216-225.	1.6	15
129	Functional identification of apple MdMYB2 gene in phosphate-starvation response. <i>Journal of Plant Physiology</i> , 2020, 244, 153089.	1.6	15
130	An apple AP2/EREBP-type transcription factor, MdWRI4, enhances plant resistance to abiotic stress by increasing cuticular wax load. <i>Environmental and Experimental Botany</i> , 2020, 180, 104206.	2.0	15
131	Genome-wide analysis of auxin response factor (ARF) genes and functional identification of MdARF2 reveals the involvement in the regulation of anthocyanin accumulation in apple. <i>New Zealand Journal of Crop and Horticultural Science</i> , 2021, 49, 78-91.	0.7	15
132	Identification and functional characterization of MdPIF3 in response to cold and drought stress in <i>Malus domestica</i> . <i>Plant Cell, Tissue and Organ Culture</i> , 2021, 144, 435-447.	1.2	15
133	Phosphorylation of a malate transporter promotes malate excretion and reduces cadmium uptake in apple. <i>Journal of Experimental Botany</i> , 2020, 71, 3437-3449.	2.4	14
134	Identification of the SRO gene family in apples (<i>Malus domestica</i>) with a functional characterization of MdRCD1. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	13
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