

Qing-long Dong

List of Publications by Year in descending order

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Version: 2024-02-01

29
papers

966
citations

516710

16
h-index

454955

30
g-index

30
all docs

30
docs citations

30
times ranked

999
citing authors

#	ARTICLE	IF	CITATIONS
1	Overexpression of <i>MdVQ37</i> reduces drought tolerance by altering leaf anatomy and SA homeostasis in transgenic apple. <i>Tree Physiology</i> , 2022, 42, 160-174.	3.1	15
2	Genome-Wide Identification, Expression, and Interaction Analysis of BEL-Like Homeodomain Gene Family in Peach. <i>Biochemical Genetics</i> , 2022, 60, 2037-2051.	1.7	2
3	Overexpression of <i>MdVQ37</i> reduces salt stress tolerance in <i>Malus domestica</i> . <i>Scientia Horticulturae</i> , 2022, 300, 111077.	3.6	6
4	Genome-wide analysis of the apple CaCA superfamily reveals that MdCAX proteins are involved in the abiotic stress response as calcium transporters. <i>BMC Plant Biology</i> , 2021, 21, 81.	3.6	23
5	<i>MdVQ37</i> overexpression reduces basal thermotolerance in transgenic apple by affecting transcription factor activity and salicylic acid homeostasis. <i>Horticulture Research</i> , 2021, 8, 220.	6.3	20
6	<i>MdWRKY30</i> , a group IIa WRKY gene from apple, confers tolerance to salinity and osmotic stresses in transgenic apple callus and <i>Arabidopsis</i> seedlings. <i>Plant Science</i> , 2020, 299, 110611.	3.6	42
7	Genome-wide analysis of the light-harvesting chlorophyll a/b-binding gene family in apple (<i>Malus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf osmotic stress. <i>Plant Physiology and Biochemistry</i> , 2020, 154, 517-529.	5.8	33
8	Cloning, sequencing, and expression analysis of 32 NAC transcription factors (<i>MdNAC</i>) in apple. <i>PeerJ</i> , 2020, 8, e8249.	2.0	8
9	Isolation, sequencing, and expression analysis of 30 AP2/ERF transcription factors in apple. <i>PeerJ</i> , 2020, 8, e8391.	2.0	5
10	Full-length transcriptome and targeted metabolome analyses provide insights into defense mechanisms of <i>Malus sieversii</i> against <i>Agrilus mali</i> . <i>PeerJ</i> , 2020, 8, e8992.	2.0	9
11	High-efficient utilization and uptake of N contribute to higher NUE of 'Qinguan' apple under drought and N-deficient conditions compared with 'Honeycrisp'. <i>Tree Physiology</i> , 2019, 39, 1880-1895.	3.1	24
12	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.	1.6	16
13	Genome-wide identification, expression, and interaction analysis for ovate family proteins in peach. <i>Molecular Biology Reports</i> , 2019, 46, 3755-3764.	2.3	10
14	Overexpression of <i>MdIAA9</i> confers high tolerance to osmotic stress in transgenic tobacco. <i>PeerJ</i> , 2019, 7, e7935.	2.0	11
15	Isolation and expression analysis of eight MADS-box genes in peach (<i>Prunus persica</i> var. <i>nectarina</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf	1.7	5
16	Identification and expression analysis of 11 MADS-box genes in peach (<i>Prunus persica</i> var. <i>nectarina</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.9	5
17	Comprehensive genomic analysis of the TYROSINE AMINOTRANSFERASE (TAT) genes in apple (<i>Malus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf stresses in plants. <i>Plant Physiology and Biochemistry</i> , 2018, 133, 81-91.	5.8	16
18	Genome-wide analyses of genes encoding FK506-binding proteins reveal their involvement in abiotic stress responses in apple. <i>BMC Genomics</i> , 2018, 19, 707.	2.8	16

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19	Genome-Wide Identification and Analysis of Apple NITRATE TRANSPORTER 1/PEPTIDE TRANSPORTER Family (NPF) Genes Reveals MdNPF6.5 Confers High Capacity for Nitrogen Uptake under Low-Nitrogen Conditions. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2761.	4.1	34
20	Mapping QTLs for water-use efficiency reveals the potential candidate genes involved in regulating the trait in apple under drought stress. <i>BMC Plant Biology</i> , 2018, 18, 136.	3.6	42
21	Structural and functional analyses of genes encoding VQ proteins in apple. <i>Plant Science</i> , 2018, 272, 208-219.	3.6	46
22	Genome-Wide Analysis and Cloning of the Apple Stress-Associated Protein Gene Family Reveals MdSAP15, Which Confers Tolerance to Drought and Osmotic Stresses in Transgenic Arabidopsis. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2478.	4.1	40
23	Genome Wide Identification and Characterization of Apple bHLH Transcription Factors and Expression Analysis in Response to Drought and Salt Stress. <i>Frontiers in Plant Science</i> , 2017, 8, 480.	3.6	148
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.	8.3	100
25	Polycomb-group protein SIMS11 represses the expression of fruit-ripening genes to prolong shelf life in tomato. <i>Scientific Reports</i> , 2016, 6, 31806.	3.3	25
26	Genome-wide identification and analysis of the MADS-box gene family in apple. <i>Gene</i> , 2015, 555, 277-290.	2.2	95
27	MdVHA-A encodes an apple subunit A of vacuolar H ⁺ -ATPase and enhances drought tolerance in transgenic tobacco seedlings. <i>Journal of Plant Physiology</i> , 2013, 170, 601-609.	3.5	30
28	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.	5.6	71
29	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.	3.5	59