

Na An

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6154622/publications.pdf>

Version: 2024-02-01

35
papers

850
citations

516710

16
h-index

526287

27
g-index

41
all docs

41
docs citations

41
times ranked

746
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	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
3	Genome-wide identification of the 14 β -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
4	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
5	The TAZ domain-containing proteins play important role in the heavy metals stress biology in plants. <i>Environmental Research</i> , 2021, 197, 111030.	7.5	15
6	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
7	Identification of apple TFL1-interacting proteins uncovers an expanded flowering network. <i>Plant Cell Reports</i> , 2021, 40, 2325-2340.	5.6	9
8	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
9	Genomic identification and expression analysis of nuclear pore proteins in <i>Malus domestica</i> . <i>Scientific Reports</i> , 2020, 10, 17426.	3.3	10
10	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
11	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
12	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
13	Transcriptome Analysis Reveals New Insights into <i>MdBAK1</i> -Mediated Plant Growth in <i>Malus domestica</i> . <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 9757-9771.	5.2	9
14	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
15	Comparative RNA-Sequencing and DNA Methylation Analyses of Apple (<i>Malus domestica</i>) 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	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
17	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
18	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

#	ARTICLE	IF	CITATIONS
19	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
20	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
21	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
22	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
23	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
24	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
25	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
26	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
27	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
28	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
29	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
30	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
31	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
32	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
33	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.	3.1	118
34	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
35	Transcript profiling of papaya (<i>Carica papaya</i> L.) with CTS-N fertiliser after inoculation with PRSV. <i>Journal of Horticultural Science and Biotechnology</i> , 0, , 1-10.	1.9	0