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List of Publications by Year in descending order

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35
papers

850
citations

516710

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526287

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times ranked

746
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 1 | 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 |
| 2 | 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 |
| 3 | 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 |
| 4 | 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 |
| 5 | 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 |
| 6 | 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 |
| 7 | 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 |
| 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 | 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 |
| 10 | 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 |
| 11 | Genome-wide identification of the 14 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 |
| 12 | 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 |
| 13 | 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 |
| 14 | 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 |
| 15 | 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 |
| 16 | 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 |
| 17 | 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 |
| 18 | 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 |

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|----|---|-----|-----------|
| 19 | 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 |
| 20 | 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 |
| 21 | 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 |
| 22 | 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 |
| 23 | 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 |
| 24 | 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 |
| 25 | 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 |
| 26 | 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 |
| 27 | 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 |
| 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 | Genomic identification and expression analysis of nuclear pore proteins in <i>Malus domestica</i> . <i>Scientific Reports</i> , 2020, 10, 17426. | 3.3 | 10 |
| 30 | 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 |
| 31 | Identification of apple TFL1-interacting proteins uncovers an expanded flowering network. <i>Plant Cell Reports</i> , 2021, 40, 2325-2340. | 5.6 | 9 |
| 32 | 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 |
| 33 | 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 |
| 34 | 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 |
| 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 |