

# Libo Xing

## List of Publications by Year in descending order

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Version: 2024-02-01

53  
papers

1,193  
citations

361413

20  
h-index

434195

31  
g-index

54  
all docs

54  
docs citations

54  
times ranked

898  
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	Effect of ambient temperature on the model stability of handheld devices for predicting the apple soluble solids content. <i>European Journal of Agronomy</i> , 2022, 133, 126430.	4.1	3
3	Selection and Validation of Reliable Reference Genes for Gene Expression Studies in Different Genotypes and TRV-Infected Fruits of Peach ( <i>Prunus persica</i> L. Batsch) during Ripening. <i>Genes</i> , 2022, 13, 160.	2.4	11
4	Transcriptome Analysis Reveals Multiple Genes and Complex Hormonal-Mediated Interactions with PEG during Adventitious Root Formation in Apple. <i>International Journal of Molecular Sciences</i> , 2022, 23, 976.	4.1	8
5	PpePL1 and PpePL15 Are the Core Members of the Pectate Lyase Gene Family Involved in Peach Fruit Ripening and Softening. <i>Frontiers in Plant Science</i> , 2022, 13, 844055.	3.6	9
6	The nutrient, hormone, and antioxidant status of scion affects the rootstock activity in apple. <i>Scientia Horticulturae</i> , 2022, 302, 111157.	3.6	3
7	MdNup62 interactions with MdHSFs involved in flowering and heat-stress tolerance in apple. <i>BMC Plant Biology</i> , 2022, 22, .	3.6	5
8	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
9	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
10	Quality monitoring method for apples of different maturity under long-term cold storage. <i>Infrared Physics and Technology</i> , 2021, 112, 103580.	2.9	14
11	Integrative transcriptomic and metabolomic analyses provide insight into the long-term submergence response mechanisms of young <i>Salix variegata</i> stems. <i>Planta</i> , 2021, 253, 88.	3.2	3
12	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
13	Molecular mechanism of MdWUS2-MdTCP12 interaction in mediating cytokinin signaling to control axillary bud outgrowth. <i>Journal of Experimental Botany</i> , 2021, 72, 4822-4838.	4.8	10
14	Transcriptome analysis reveals the inhibitory nature of high nitrate during adventitious roots formation in the apple rootstock. <i>Physiologia Plantarum</i> , 2021, 173, 867-882.	5.2	16
15	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
16	Identification of apple TFL1-interacting proteins uncovers an expanded flowering network. <i>Plant Cell Reports</i> , 2021, 40, 2325-2340.	5.6	9
17	ITRAQ-based proteomic analysis of apple buds provides new insights into regulatory mechanisms of flowering in response to shoot bending. <i>Scientia Horticulturae</i> , 2021, 290, 110526.	3.6	1
18	Modification of the effect of maturity variation on nondestructive detection of apple quality based on the compensation model. <i>Spectrochimica Acta - Part A: Molecular and Biomolecular Spectroscopy</i> , 2021, 267, 120598.	3.9	5

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19	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
20	Genomic identification and expression analysis of nuclear pore proteins in <i>Malus domestica</i> . <i>Scientific Reports</i> , 2020, 10, 17426.	3.3	10
21	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
22	Determination of bagged “Fuji” apple maturity by visible and near-infrared spectroscopy combined with a machine learning algorithm. <i>Infrared Physics and Technology</i> , 2020, 111, 103529.	2.9	29
23	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
24	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
25	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
26	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
27	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
28	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
29	Effects of Chronic Dust Load On Leaf Pigments of the Landscape Plant <i>Murraya Paniculata</i> . <i>Gesunde Pflanzen</i> , 2019, 71, 249-258.	3.0	10
30	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
31	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
32	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
33	Cement dust induce stress and attenuates photosynthesis in <i>Arachis hypogaea</i> . <i>Environmental Science and Pollution Research</i> , 2019, 26, 19490-19501.	5.3	11
34	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
35	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
36	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

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37	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
38	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
39	Genome-wide Identification, Classification, Molecular Evolution and Expression Analysis of Malate Dehydrogenases in Apple. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3312.	4.1	15
40	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
41	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
42	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
43	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
44	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
45	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
46	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
47	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
48	Proteome Analyses Using iTRAQ Labeling Reveal Critical Mechanisms in Alternate Bearing <i>Malus prunifolia</i> . <i>Journal of Proteome Research</i> , 2016, 15, 3602-3616.	3.7	30
49	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
50	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
51	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
52	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
53	MdNup54 Interactions With MdHSP70 Involved in Flowering in Apple. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	1