

Yunpeng Cao

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

60
papers

701
citations

15
h-index

23
g-index

69
ext. papers

1,302
ext. citations

4.8
avg, IF

4.28
L-index

#	Paper	IF	Citations
60	MYB transcription factor family in sweet cherry (<i>Prunus avium</i> L.): genome-wide investigation, evolution, structure, characterization and expression patterns.. <i>BMC Plant Biology</i> , 2022 , 22, 2	5.3	4
59	AHLsSlife in plants: Especially their potential roles in responding to Fusarium wilt and repressing the seed oil accumulation.. <i>International Journal of Biological Macromolecules</i> , 2022 , 208, 509-519	7.9	1
58	The Multifaceted Roles of MYC2 in Plants: Toward Transcriptional Reprogramming and Stress Tolerance by Jasmonate Signaling.. <i>Frontiers in Plant Science</i> , 2022 , 13, 868874	6.2	1
57	Potential of Genome Editing to Capture Diversity From Australian Wild Rice Relatives.. <i>Frontiers in Genome Editing</i> , 2022 , 4, 875243	2.5	0
56	Expansion and Molecular Characterization of AP2/ERF Gene Family in Wheat (L.). <i>Frontiers in Genetics</i> , 2021 , 12, 632155	4.5	5
55	Removal of the Main Inflorescence to Induce Reflowering of Loquat. <i>Horticultural Plant Journal</i> , 2021 , 8, 35-35	4.3	1
54	Deciphering the roles of leucine-rich repeat receptor-like protein kinases (LRR-RLKs) in response to Fusarium wilt in the <i>Vernicia fordii</i> (Tung tree). <i>Phytochemistry</i> , 2021 , 185, 112686	4	3
53	Functional analysis of four Class III peroxidases from Chinese pear fruit: a critical role in lignin polymerization. <i>Physiology and Molecular Biology of Plants</i> , 2021 , 27, 515-522	2.8	1
52	The role of VvMYBA2r and VvMYBA2w alleles of the MYBA2 locus in the regulation of anthocyanin biosynthesis for molecular breeding of grape (<i>Vitis</i> spp.) skin coloration. <i>Plant Biotechnology Journal</i> , 2021 , 19, 1216-1239	11.6	15
51	Genome-wide investigation and comparative analysis of MATE gene family in Rosaceae species and their regulatory role in abiotic stress responses in Chinese pear (<i>Pyrus bretschneideri</i>). <i>Physiologia Plantarum</i> , 2021 , 173, 1163-1178	4.6	3
50	Genome-wide identification and characterization of bZIP transcription factors and their expression profile under abiotic stresses in Chinese pear (<i>Pyrus bretschneideri</i>). <i>BMC Plant Biology</i> , 2021 , 21, 413	5.3	2
49	Cold induced genes (CIGs) regulate flower development and dormancy in <i>Prunus avium</i> L. <i>Plant Science</i> , 2021 , 313, 111061	5.3	1
48	Method for fast staining and obtaining high-magnification and high-resolution cell images of. <i>Physiology and Molecular Biology of Plants</i> , 2021 , 27, 181-188	2.8	0
47	Network Pharmacology and Inflammatory Microenvironment Strategy Approach to Finding the Potential Target of (Luo Han Guo) for Glioblastoma.. <i>Frontiers in Genetics</i> , 2021 , 12, 799799	4.5	0
46	MYB Transcription Factors as Regulators of Secondary Metabolism in Plants. <i>Biology</i> , 2020 , 9,	4.9	31
45	The Cytochrome P450 Monooxygenase Inventory of Grapevine (L.): Genome-Wide Identification, Evolutionary Characterization and Expression Analysis. <i>Frontiers in Genetics</i> , 2020 , 11, 44	4.5	9
44	Integrative analysis of the RNA interference toolbox in two Salicaceae willow species, and their roles in stress response in poplar (<i>Populus trichocarpa</i> Torr. & Gray). <i>International Journal of Biological Macromolecules</i> , 2020 , 162, 1127-1139	7.9	5

43	A Chinese White Pear () Gene Act as a Transcriptional Repressor of Lignin Biosynthetic Genes in Fruits. <i>Frontiers in Plant Science</i> , 2020 , 11, 1087	6.2	2
42	Hidden in plain sight: Systematic investigation of Leucine-rich repeat containing genes unveil the their regulatory network in response to Fusarium wilt in tung tree. <i>International Journal of Biological Macromolecules</i> , 2020 , 163, 1759-1767	7.9	4
41	RIGD: A Database for Intronless Genes in the Rosaceae. <i>Frontiers in Genetics</i> , 2020 , 11, 868	4.5	1
40	Gene structure, evolution and expression analysis of the P-ATPase gene family in Chinese pear (<i>Pyrus bretschneideri</i>). <i>Computational Biology and Chemistry</i> , 2020 , 88, 107346	3.6	10
39	Application of miRNA in fruit quality improvement 2020 , 469-491		0
38	Integrative Analysis of the Core Fruit Lignification Toolbox in Pear Reveals Targets for Fruit Quality Bioengineering. <i>Biomolecules</i> , 2019 , 9,	5.9	8
37	Genome-Wide Analysis of the Pear () Family and the Functional Characterization of , an Orthologue Gene, Involved in Cell Wall and Lignin Biosynthesis. <i>Frontiers in Genetics</i> , 2019 , 10, 632	4.5	14
36	In Silico Genome-Wide Analysis of Respiratory Burst Oxidase Homolog (RBOH) Family Genes in Five Fruit-Producing Trees, and Potential Functional Analysis on Lignification of Stone Cells in Chinese White Pear. <i>Cells</i> , 2019 , 8,	7.9	19
35	Comparative analysis of B-BOX genes and their expression pattern analysis under various treatments in <i>Dendrobium officinale</i> . <i>BMC Plant Biology</i> , 2019 , 19, 245	5.3	19
34	Evolutionary and functional analysis of the plant-specific NADPH oxidase gene family in <i>L. Royal Society Open Science</i> , 2019 , 6, 181727	3.3	11
33	Metacaspase gene family in Rosaceae genomes: Comparative genomic analysis and their expression during pear pollen tube and fruit development. <i>PLoS ONE</i> , 2019 , 14, e0211635	3.7	5
32	Evolution and functional divergence of MADS-box genes in <i>Pyrus</i> . <i>Scientific Reports</i> , 2019 , 9, 1266	4.9	4
31	Integrative analysis reveals evolutionary patterns and potential functions of SWEET transporters in Euphorbiaceae. <i>International Journal of Biological Macromolecules</i> , 2019 , 139, 1-11	7.9	16
30	Regulatory Sequences of Pear. <i>Compendium of Plant Genomes</i> , 2019 , 153-177	0.8	
29	Evolutionary Rate Heterogeneity and Functional Divergence of Orthologous Genes in. <i>Biomolecules</i> , 2019 , 9,	5.9	3
28	Comparative genomic analysis of the IDD genes in five Rosaceae species and expression analysis in Chinese white pear (). <i>PeerJ</i> , 2019 , 7, e6628	3.1	3
27	Comparative Analysis and Expression Patterns of the Genes in. <i>International Journal of Molecular Sciences</i> , 2019 , 21,	6.3	1
26	Comprehensive genome-wide analysis of the pear (<i>Pyrus bretschneideri</i>) laccase gene (PbLAC) family and functional identification of PbLAC1 involved in lignin biosynthesis. <i>PLoS ONE</i> , 2019 , 14, e0210892	3.7	12

25	Genome-Wide Identification, Characterization, and Transcript Analysis of the TCP Transcription Factors in. <i>Frontiers in Genetics</i> , 2019 , 10, 1276	4.5	9
24	Molecular characterization and overexpression of and from revealed their involvement in biodegradation of cotton stalk lignin. <i>Biology Open</i> , 2019 , 8,	2.2	2
23	Systematic analysis and comparison of the PHD-Finger gene family in Chinese pear (<i>Pyrus bretschneideri</i>) and its role in fruit development. <i>Functional and Integrative Genomics</i> , 2018 , 18, 519-531	3.8	14
22	Effects of Different Pollens on Primary Metabolism and Lignin Biosynthesis in Pear. <i>International Journal of Molecular Sciences</i> , 2018 , 19,	6.3	13
21	Genome-Wide Analysis Characterization and Evolution of Genes in , , and. <i>Frontiers in Genetics</i> , 2018 , 9, 64	4.5	18
20	Genome Wide Identification, Evolutionary, and Expression Analysis of VQ Genes from Two <i>Pyrus</i> Species. <i>Genes</i> , 2018 , 9,	4.2	12
19	Systematic Analysis of the <i>Pleurotus ostreatus</i> Laccase Gene (PoLac) Family and Functional Characterization of PoLac2 Involved in the Degradation of Cotton-Straw Lignin. <i>Molecules</i> , 2018 , 23,	4.8	14
18	The Sucrose Synthase Gene Family in Chinese Pear (<i>Rehd.</i>): Structure, Expression, and Evolution. <i>Molecules</i> , 2018 , 23,	4.8	21
17	Comparative and Expression Analysis of Ubiquitin Conjugating Domain-Containing Genes in Two Species. <i>Cells</i> , 2018 , 7,	7.9	11
16	Expansion and evolutionary patterns of GDSL-type esterases/lipases in Rosaceae genomes. <i>Functional and Integrative Genomics</i> , 2018 , 18, 673-684	3.8	17
15	A new insight into the evolution and functional divergence of genes in. <i>Royal Society Open Science</i> , 2018 , 5, 171463	3.3	2
14	Zinc Finger-Homeodomain Transcriptional Factors (ZHDs) in Upland Cotton (<i>G.</i>): Genome-Wide Identification and Expression Analysis in Fiber Development. <i>Frontiers in Genetics</i> , 2018 , 9, 357	4.5	13
13	iTRAQ-Based Identification of Proteins Related to Lignin Synthesis in the Pear Pollinated with Pollen from Different Varieties. <i>Molecules</i> , 2018 , 23,	4.8	12
12	Genomic Comparison of the P-ATPase Gene Family in Four Cotton Species and Their Expression Patterns in. <i>Molecules</i> , 2018 , 23,	4.8	8
11	Genome-wide dissection of the chalcone synthase gene family in <i>Oryza sativa</i> . <i>Molecular Breeding</i> , 2017 , 37, 1	3.4	10
10	B-BOX genes: genome-wide identification, evolution and their contribution to pollen growth in pear (<i>Pyrus bretschneideri</i> <i>Rehd.</i>). <i>BMC Plant Biology</i> , 2017 , 17, 156	5.3	29
9	Impact of integrated application of biochar and nitrogen fertilizers on maize growth and nitrogen recovery in alkaline calcareous soil. <i>Soil Science and Plant Nutrition</i> , 2017 , 63, 488-498	1.6	41
8	Genome-Wide Analysis Suggests the Relaxed Purifying Selection Affect the Evolution of Genes in , , and. <i>Frontiers in Genetics</i> , 2017 , 8, 78	4.5	22

7	The Effect of Different Pollination on the Expression of Dangshan Su Pear MicroRNA. <i>BioMed Research International</i> , 2017 , 2017, 2794040	3	10
6	Genome-wide analysis suggests high level of microsynteny and purifying selection affect the evolution of family in Rosaceae. <i>PeerJ</i> , 2017 , 5, e3400	3.1	8
5	Comparative genomic analysis of the PKS genes in five species and expression analysis in upland cotton. <i>PeerJ</i> , 2017 , 5, e3974	3.1	8
4	Systematic Analysis of the 4-Coumarate:Coenzyme A Ligase (4CL) Related Genes and Expression Profiling during Fruit Development in the Chinese Pear. <i>Genes</i> , 2016 , 7,	4.2	27
3	MYB Transcription Factors in Chinese Pear (<i>Pyrus bretschneideri</i> Rehd.): Genome-Wide Identification, Classification, and Expression Profiling during Fruit Development. <i>Frontiers in Plant Science</i> , 2016 , 7, 577	6.2	75
2	Comparative Genomic Analysis of the Genes in Chinese Pear (), Poplar (), Grape (), and Rice (). <i>Frontiers in Plant Science</i> , 2016 , 7, 1750	6.2	43
1	Structural, Evolutionary, and Functional Analysis of the Class III Peroxidase Gene Family in Chinese Pear (). <i>Frontiers in Plant Science</i> , 2016 , 7, 1874	6.2	44