

Yunpeng Cao

List of Publications by Year in descending order

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69
papers

1,733
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304602

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#	ARTICLE	IF	CITATIONS
1	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.	1.7	143
2	MYB Transcription Factors as Regulators of Secondary Metabolism in Plants. <i>Biology</i> , 2020, 9, 61.	1.3	123
3	Comparative Genomic Analysis of the GRF Genes in Chinese Pear (<i>Pyrus bretschneideri</i> Rehd), Poplar (<i>Populus</i>), Grape (<i>Vitis vinifera</i>), Arabidopsis and Rice (<i>Oryza sativa</i>). <i>Frontiers in Plant Science</i> , 2016, 7, 1750.	1.7	97
4	Structural, Evolutionary, and Functional Analysis of the Class III Peroxidase Gene Family in Chinese Pear (<i>Pyrus bretschneideri</i>). <i>Frontiers in Plant Science</i> , 2016, 7, 1874.	1.7	83
5	Genome-Wide Analysis Suggests the Relaxed Purifying Selection Affect the Evolution of WOX Genes in <i>Pyrus bretschneideri</i> , <i>Prunus persica</i> , <i>Prunus mume</i> , and <i>Fragaria vesca</i> . <i>Frontiers in Genetics</i> , 2017, 8, 78.	1.1	68
6	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.	0.8	65
7	B-BOX genes: genome-wide identification, evolution and their contribution to pollen growth in pear (<i>Pyrus bretschneideri</i> Rehd.). <i>BMC Plant Biology</i> , 2017, 17, 156.	1.6	56
8	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, 89.	1.0	51
9	The Sucrose Synthase Gene Family in Chinese Pear (<i>Pyrus bretschneideri</i> Rehd.): Structure, Expression, and Evolution. <i>Molecules</i> , 2018, 23, 1144.	1.7	47
10	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.	1.7	41
11	The role of <i>VvMYBA2r</i> and <i>VvMYBA2w</i> alleles of the <i>MYBA2</i> 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.	4.1	39
12	Expansion and evolutionary patterns of GDSL-type esterases/lipases in Rosaceae genomes. <i>Functional and Integrative Genomics</i> , 2018, 18, 673-684.	1.4	37
13	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, 520.	1.8	37
14	The Cytochrome P450 Monooxygenase Inventory of Grapevine (<i>Vitis vinifera</i> L.): Genome-Wide Identification, Evolutionary Characterization and Expression Analysis. <i>Frontiers in Genetics</i> , 2020, 11, 44.	1.1	35
15	Genome-Wide Analysis Characterization and Evolution of SBP Genes in <i>Fragaria vesca</i> , <i>Pyrus bretschneideri</i> , <i>Prunus persica</i> and <i>Prunus mume</i> . <i>Frontiers in Genetics</i> , 2018, 9, 64.	1.1	33
16	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, 880.	1.7	32
17	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.	1.6	31
18	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.	1.1	30

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19	Integrative analysis reveals evolutionary patterns and potential functions of SWEET transporters in Euphorbiaceae. <i>International Journal of Biological Macromolecules</i> , 2019, 139, 1-11.	3.6	29
20	Integrative Analysis of the Core Fruit Lignification Toolbox in Pear Reveals Targets for Fruit Quality Bioengineering. <i>Biomolecules</i> , 2019, 9, 504.	1.8	28
21	In Silico Genome-Wide Analysis of the Pear (<i>Pyrus bretschneideri</i>) KNOX Family and the Functional Characterization of PbKNOX1, an Arabidopsis BREVIPEDICELLUS Orthologue Gene, Involved in Cell Wall and Lignin Biosynthesis. <i>Frontiers in Genetics</i> , 2019, 10, 632.	1.1	28
22	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.	1.6	28
23	Genome-Wide Identification, Characterization, and Transcript Analysis of the TCP Transcription Factors in <i>Vitis vinifera</i> . <i>Frontiers in Genetics</i> , 2019, 10, 1276.	1.1	27
24	Genome-wide dissection of the chalcone synthase gene family in <i>Oryza sativa</i> . <i>Molecular Breeding</i> , 2017, 37, 1.	1.0	26
25	Comparative and Expression Analysis of Ubiquitin Conjugating Domain-Containing Genes in Two <i>Pyrus</i> Species. <i>Cells</i> , 2018, 7, 77.	1.8	24
26	Zinc Finger-Homeodomain Transcriptional Factors (ZHDs) in Upland Cotton (<i>Gossypium hirsutum</i>): Genome-Wide Identification and Expression Analysis in Fiber Development. <i>Frontiers in Genetics</i> , 2018, 9, 357.	1.1	23
27	Expansion and Molecular Characterization of AP2/ERF Gene Family in Wheat (<i>Triticum aestivum</i> L.). <i>Frontiers in Genetics</i> , 2021, 12, 632155.	1.1	23
28	Haplotype-resolved genome assembly of <i>Bletilla striata</i> (Thunb.) Reichb.f. to elucidate medicinal value. <i>Plant Journal</i> , 2022, 111, 1340-1353.	2.8	22
29	Systematic analysis and comparison of the PHD-Finger gene family in Chinese pear (<i>Pyrus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 519-531.	1.4	21
30	Evolutionary and functional analysis of the plant-specific NADPH oxidase gene family in <i>Brassica rapa</i> L.. <i>Royal Society Open Science</i> , 2019, 6, 181727.	1.1	21
31	Gene structure, evolution and expression analysis of the P-ATPase gene family in Chinese pear (<i>Pyrus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	1.1	21
32	Comprehensive Comparative Analysis of the GATA Transcription Factors in Four Rosaceae Species and Phytohormonal Response in Chinese Pear (<i>Pyrus bretschneideri</i>) Fruit. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12492.	1.8	21
33	Effects of Different Pollens on Primary Metabolism and Lignin Biosynthesis in Pear. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2273.	1.8	20
34	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.	1.6	20
35	iTRAQ-Based Identification of Proteins Related to Lignin Synthesis in the Pear Pollinated with Pollen from Different Varieties. <i>Molecules</i> , 2018, 23, 548.	1.7	18
36	Genomic Comparison of the P-ATPase Gene Family in Four Cotton Species and Their Expression Patterns in <i>Gossypium hirsutum</i> . <i>Molecules</i> , 2018, 23, 1092.	1.7	18

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37	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</i>). <i>Trends in Plant Science</i> , 2017, 12, 107-114.	1.0	17
38	Comparative genomic analysis of the PKS genes in five species and expression analysis in upland cotton. <i>PeerJ</i> , 2017, 5, e3974.	0.9	17
39	Genome Wide Identification, Evolutionary, and Expression Analysis of VQ Genes from Two <i>Pyrus</i> Species. <i>Genes</i> , 2018, 9, 224.	1.0	16
40	A Chinese White Pear (<i>Pyrus bretschneideri</i>) BZR Gene PbBZR1 Act as a Transcriptional Repressor of Lignin Biosynthetic Genes in Fruits. <i>Frontiers in Plant Science</i> , 2020, 11, 1087.	1.7	16
41	Genome-wide analysis suggests high level of microsynteny and purifying selection affect the evolution of EIN3/EIL family in Rosaceae. <i>PeerJ</i> , 2017, 5, e3400.	0.9	16
42	Evolution and functional divergence of MADS-box genes in <i>Pyrus</i> . <i>Scientific Reports</i> , 2019, 9, 1266.	1.6	15
43	The Effect of Different Pollination on the Expression of Dangshan Su Pear MicroRNA. <i>BioMed Research International</i> , 2017, 2017, 1-18.	0.9	13
44	Controllable synthesis and stabilization of <i>Tamarix</i> aphylla-mediated copper oxide nanoparticles for the management of Fusarium wilt on musk melon. <i>3 Biotech</i> , 2022, 12, .	1.1	13
45	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.	1.4	12
46	The red flower wintersweet genome provides insights into the evolution of magnoliids and the molecular mechanism for tepal color development. <i>Plant Journal</i> , 2021, 108, 1662-1678.	2.8	12
47	Evolutionary Rate Heterogeneity and Functional Divergence of Orthologous Genes in <i>Pyrus</i> . <i>Biomolecules</i> , 2019, 9, 490.	1.8	10
48	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.	3.6	10
49	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.	1.1	9
50	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.	3.6	9
51	Cold induced genes (CIGs) regulate flower development and dormancy in <i>Prunus avium</i> L.. <i>Plant Science</i> , 2021, 313, 111061.	1.7	8
52	Comparative genomic analysis of the IDD genes in five Rosaceae species and expression analysis in Chinese white pear (<i>Pyrus bretschneideri</i>). <i>PeerJ</i> , 2019, 7, e6628.	0.9	8
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.	1.4	7
54	AHLs' life 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.	3.6	7

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55	A new insight into the evolution and functional divergence of <i>FRK</i> genes in <i>Pyrus bretschneideri</i> . Royal Society Open Science, 2018, 5, 171463.	1.1	6
56	Comparative Analysis and Expression Patterns of the PLP _{deC} Genes in <i>Dendrobium officinale</i> . International Journal of Molecular Sciences, 2020, 21, 54.	1.8	6
57	Removal of the main inflorescence to induce reflowering of loquat. Horticultural Plant Journal, 2022, 8, 35-43.	2.3	6
58	Molecular characterization and overexpression of <i>mnp6</i> and <i>vp3</i> from <i>Pleurotus ostreatus</i> revealed their involvement in biodegradation of cotton stalk lignin. Biology Open, 2019, 8, .	0.6	5
59	Evolutionary and Integrative Analysis of Gibberellin-Dioxygenase Gene Family and Their Expression Profile in Three Rosaceae Genomes (<i>F. vesca</i> , <i>P. mume</i> , and <i>P. avium</i>) Under Phytohormone Stress. Frontiers in Plant Science, 0, 13, .	1.7	5
60	Identification and Comprehensive Genome-Wide Analysis of Glutathione S-Transferase Gene Family in Sweet Cherry (<i>Prunus avium</i>) and Their Expression Profiling Reveals a Likely Role in Anthocyanin Accumulation. Frontiers in Plant Science, 0, 13, .	1.7	5
61	RIGD: A Database for Intronless Genes in the Rosaceae. Frontiers in Genetics, 2020, 11, 868.	1.1	4
62	Integrative Analysis of the DICER-like (DCL) Genes From Peach (<i>Prunus persica</i>): A Critical Role in Response to Drought Stress. Frontiers in Ecology and Evolution, 0, 10, .	1.1	4
63	Method for fast staining and obtaining high-magnification and high-resolution cell images of <i>Nicotiana benthamiana</i> . Physiology and Molecular Biology of Plants, 2021, 27, 181-188.	1.4	3
64	Potential of Genome Editing to Capture Diversity From Australian Wild Rice Relatives. Frontiers in Genome Editing, 2022, 4, 875243.	2.7	3
65	Network Pharmacology and Inflammatory Microenvironment Strategy Approach to Finding the Potential Target of <i>Siraitia grosvenorii</i> (Luo Han Guo) for Glioblastoma. Frontiers in Genetics, 2021, 12, 799799.	1.1	2
66	Analysis of the Î²-Glucosidase Family Reveals Genes Involved in the Lignification of Stone Cells in Chinese White Pear (<i>Pyrus bretschneideri</i> Rehd.). Frontiers in Plant Science, 2022, 13, .	1.7	2
67	Application of miRNA in fruit quality improvement. , 2020, , 469-491.		1
68	Regulatory Sequences of Pear. Compendium of Plant Genomes, 2019, , 153-177.	0.3	0
69	Deciphering Evolutionary Dynamics of WRKY I Genes in Rosaceae Species. Frontiers in Ecology and Evolution, 2021, 9, .	1.1	0