

Jun Wu

List of Publications by Year in descending order

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96
papers

4,568
citations

117453

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110170

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97
all docs

97
docs citations

97
times ranked

3789
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide comparison of the GRAS protein family in eight Rosaceae species and <i>GRAS</i> gene expression analysis in Chinese white pear (<i>Pyrus bretschneideri</i> Rehder). <i>New Zealand Journal of Crop and Horticultural Science</i> , 2022, 50, 303-325.	0.7	5
2	Genome-wide genetic diversity and IBD analysis reveals historic dissemination routes of pear in China. <i>Tree Genetics and Genomes</i> , 2022, 18, 1.	0.6	3
3	Pear genetics: Recent advances, new prospects, and a roadmap for the future. <i>Horticulture Research</i> , 2022, 9, .	2.9	12
4	Alternative splicing analysis provides insight into the domestication and improvement of pear (<i>Pyrus</i>) Tj ETQq0 0 0 19 BT /Overlock 10 TF	1.7	3
5	Metabolomics Combined with Proteomics Provide a Novel Interpretation of the Changes in Flavonoid Glycosides during White Tea Processing. <i>Foods</i> , 2022, 11, 1226.	1.9	17
6	Taxonomic Uncertainty and Its Conservation Implications in Management, a Case from <i>Pyrus hopeiensis</i> (Rosaceae). <i>Diversity</i> , 2022, 14, 417.	0.7	4
7	The Variation of Stone Cell Content in 236 Germplasms of Sand Pear (<i>Pyrus pyrifolia</i>) and Identification of Related Candidate Genes. <i>Horticultural Plant Journal</i> , 2021, 7, 108-116.	2.3	25
8	Genome-wide association studies provide insights into the genetic determination of fruit traits of pear. <i>Nature Communications</i> , 2021, 12, 1144.	5.8	44
9	An accumulation of genetic variation and selection across the disease-related genes during apple domestication. <i>Tree Genetics and Genomes</i> , 2021, 17, 1.	0.6	10
10	Dynamic Diversity of NLR Genes in Triticum and Mining of Promising NLR Alleles for Disease Resistance. <i>Current Issues in Molecular Biology</i> , 2021, 43, 965-977.	1.0	0
11	The PyPIF5-PymiR156a-PySPL9-PyMYB114/MYB10 module regulates light-induced anthocyanin biosynthesis in red pear. <i>Molecular Horticulture</i> , 2021, 1, .	2.3	16
12	A systems genetics approach reveals PbrNSC as a regulator of lignin and cellulose biosynthesis in stone cells of pear fruit. <i>Genome Biology</i> , 2021, 22, 313.	3.8	32
13	Genome-wide comparative analysis of the BAHD superfamily in seven Rosaceae species and expression analysis in pear (<i>Pyrus bretschneideri</i>). <i>BMC Plant Biology</i> , 2020, 20, 14.	1.6	22
14	Contrasting genetic variation and positive selection followed the divergence of NBS-encoding genes in Asian and European pears. <i>BMC Genomics</i> , 2020, 21, 809.	1.2	7
15	Mining and evolution analysis of lateral organ boundaries domain (LBD) genes in Chinese white pear (<i>Pyrus bretschneideri</i>). <i>BMC Genomics</i> , 2020, 21, 644.	1.2	18
16	Pearprocess: A new phenotypic tool for stone cell trait evaluation in pear fruit. <i>Journal of Integrative Agriculture</i> , 2020, 19, 1625-1634.	1.7	10
17	Genome-wide identification and comparative analysis of the ADH gene family in Chinese white pear (<i>Pyrus bretschneideri</i>) and other Rosaceae species. <i>Genomics</i> , 2020, 112, 3484-3496.	1.3	20
18	Overexpression of sugar transporter gene PbSWEET4 of pear causes sugar reduce and early senescence in leaves. <i>Gene</i> , 2020, 743, 144582.	1.0	27

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19	PyWRKY26 and PylHLH3 cotargeted the PyMYB114 promoter to regulate anthocyanin biosynthesis and transport in red-skinned pears. <i>Horticulture Research</i> , 2020, 7, 37.	2.9	95
20	CRISPR-Cas12b enables efficient plant genome engineering. <i>Nature Plants</i> , 2020, 6, 202-208.	4.7	116
21	Identification of key genes related to seedlessness by genome-wide detection of structural variation and transcriptome analysis in "Shijiwuhe" pear. <i>Gene</i> , 2020, 738, 144480.	1.0	2
22	Comparison of multiple algorithms to reliably detect structural variants in pears. <i>BMC Genomics</i> , 2020, 21, 61.	1.2	15
23	Homozygosity Mapping Reveals Population History and Trait Architecture in Self-Incompatible Pear (<i>Pyrus</i> spp.). <i>Frontiers in Plant Science</i> , 2020, 11, 590846.	1.7	7
24	Genome-wide survey and expression analysis of the SLAC/SLAH gene family in pear (<i>Pyrus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 542 Td	1.3	10
25	<i>PbrmiR397a</i> regulates lignification during stone cell development in pear fruit. <i>Plant Biotechnology Journal</i> , 2019, 17, 103-117.	4.1	114
26	The β -amylase <i>PbrBAM3</i> from pear (<i>Pyrus betulaefolia</i>) regulates soluble sugar accumulation and ROS homeostasis in response to cold stress. <i>Plant Science</i> , 2019, 287, 110184.	1.7	52
27	Transcriptomic and Gas Chromatography-Mass Spectrometry Metabolomic Profiling Analysis of the Epidermis Provides Insights into Cuticular Wax Regulation in Developing "Yuluxiang" Pear Fruit. <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 8319-8331.	2.4	15
28	Marker-trait associations and genomic predictions of interspecific pear (<i>Pyrus</i>) fruit characteristics. <i>Scientific Reports</i> , 2019, 9, 9072.	1.6	38
29	The Genome of Pear. <i>Compendium of Plant Genomes</i> , 2019, , 133-143.	0.3	1
30	Single-pollen-cell sequencing for gamete-based phased diploid genome assembly in plants. <i>Genome Research</i> , 2019, 29, 1889-1899.	2.4	28
31	The bracteatus pineapple genome and domestication of clonally propagated crops. <i>Nature Genetics</i> , 2019, 51, 1549-1558.	9.4	60
32	Development of an integrated 200K SNP genotyping array and application for genetic mapping, genome assembly improvement and genome wide association studies in pear (<i>Pyrus</i>). <i>Plant Biotechnology Journal</i> , 2019, 17, 1582-1594.	4.1	46
33	<i>PbrMYB169</i> positively regulates lignification of stone cells in pear fruit. <i>Journal of Experimental Botany</i> , 2019, 70, 1801-1814.	2.4	73
34	Genome-wide identification, expression and functional analysis of the phosphofructokinase gene family in Chinese white pear (<i>Pyrus bretschneideri</i>). <i>Gene</i> , 2019, 702, 133-142.	1.0	15
35	Fine-mapping and validation of the genomic region underpinning pear red skin colour. <i>Horticulture Research</i> , 2019, 6, 29.	2.9	31
36	Comparative Transcriptomic Analysis Provides Insight into the Domestication and Improvement of Pear (<i>P. pyrifolia</i>) Fruit. <i>Plant Physiology</i> , 2019, 180, 435-452.	2.3	33

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37	The involvement of PybZIPa in light-induced anthocyanin accumulation via the activation of PyUGFT through binding to tandem G-boxes in its promoter. <i>Horticulture Research</i> , 2019, 6, 134.	2.9	61
38	The mining and evolutionary investigation of AP2/ERF genes in pear (<i>Pyrus</i>). <i>BMC Plant Biology</i> , 2018, 18, 46.	1.6	41
39	Characterisation of the whole-genome wide hexokinase gene family unravels the functional divergence in pear (<i>Pyrus bretschneideri</i> Rehd.). <i>Journal of Horticultural Science and Biotechnology</i> , 2018, 93, 244-254.	0.9	6
40	Dynamic transcriptome analysis of root nitrate starvation and re-supply provides insights into nitrogen metabolism in pear (<i>Pyrus bretschneideri</i>). <i>Plant Science</i> , 2018, 277, 322-333.	1.7	15
41	Different Modes of Gene Duplication Show Divergent Evolutionary Patterns and Contribute Differently to the Expansion of Gene Families Involved in Important Fruit Traits in Pear (<i>Pyrus</i>) Tj ETQq1 1 0.784314 rgBT /Overdock 10	0.9	38
42	Diversification and independent domestication of Asian and European pears. <i>Genome Biology</i> , 2018, 19, 77.	3.8	149
43	The southwestern origin and eastward dispersal of pear (<i>Pyrus pyrifolia</i>) in East Asia revealed by comprehensive genetic structure analysis with SSR markers. <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	0.6	12
44	Genetic variation and population structure of ‘Zangli’ pear landraces in Tibet revealed by SSR markers. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	7
45	Integrated high-density consensus genetic map of <i>Pyrus</i> and anchoring of the ‘Bartlett’™ v1.0 (<i>Pyrus communis</i>) genome. <i>DNA Research</i> , 2017, 24, dsw063.	1.5	28
46	Fast diffusion of domesticated maize to temperate zones. <i>Scientific Reports</i> , 2017, 7, 2077.	1.6	7
47	A New Insight into the Evolution and Functional Divergence of SWEET Transporters in Chinese White Pear (<i>Pyrus bretschneideri</i>). <i>Plant and Cell Physiology</i> , 2017, 58, 839-850.	1.5	87
48	Map-based cloning of the pear gene <i>MYB114</i> identifies an interaction with other transcription factors to coordinately regulate fruit anthocyanin biosynthesis. <i>Plant Journal</i> , 2017, 92, 437-451.	2.8	279
49	An eFP browser for visualizing strawberry fruit and flower transcriptomes. <i>Horticulture Research</i> , 2017, 4, 17029.	2.9	63
50	Genome-wide analysis and characterization of molecular evolution of the HCT gene family in pear (<i>Pyrus bretschneideri</i>). <i>Plant Systematics and Evolution</i> , 2017, 303, 71-90.	0.3	23
51	Genome-wide identification of the MADS-box transcription factor family in pear (<i>Pyrus</i>) Tj ETQq1 1 0.784314 rgBT /Overdock 10	0.9	38
52	Distinct transcriptome profiles reveal gene expression patterns during fruit development and maturation in five main cultivated species of pear (<i>Pyrus</i> L.). <i>Scientific Reports</i> , 2016, 6, 28130.	1.6	59
53	Overexpression of sucrose transporter gene <i>PbSUT2</i> from <i>Pyrus bretschneideri</i> , enhances sucrose content in <i>Solanum lycopersicum</i> fruit. <i>Plant Physiology and Biochemistry</i> , 2016, 105, 150-161.	2.8	38
54	Genome-Wide Identification, Evolution and Functional Divergence of MYB Transcription Factors in Chinese White Pear (<i>Pyrus bretschneideri</i>). <i>Plant and Cell Physiology</i> , 2016, 57, 824-847.	1.5	89

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55	Maternal inheritance has impact on organic acid content in progeny of pear (<i>Pyrus</i> spp.) fruit. <i>Euphytica</i> , 2016, 209, 305-321.	0.6	23
56	Genetic diversity and population structure of pear (<i>Pyrus</i> spp.) collections revealed by a set of core genome-wide SSR markers. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	0.6	45
57	Genome-wide Annotation and Comparative Analysis of Long Terminal Repeat Retrotransposons between Pear Species of <i>P. bretschneideri</i> and <i>P. Communis</i> . <i>Scientific Reports</i> , 2015, 5, 17644.	1.6	16
58	Transcriptome profiling reveals differential gene expression in proanthocyanidin biosynthesis associated with red/green skin color mutant of pear (<i>Pyrus communis</i> L.). <i>Frontiers in Plant Science</i> , 2015, 6, 795.	1.7	53
59	Genome-Wide Function, Evolutionary Characterization and Expression Analysis of Sugar Transporter Family Genes in Pear (<i>Pyrus bretschneideri</i> Rehd). <i>Plant and Cell Physiology</i> , 2015, 56, 1721-1737.	1.5	74
60	Evaluation of new IRAP markers of pear and their potential application in differentiating bud sports and other Rosaceae species. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	0.6	9
61	Identification and testing of reference genes for gene expression analysis in pollen of <i>Pyrus bretschneideri</i> . <i>Scientia Horticulturae</i> , 2015, 190, 43-56.	1.7	34
62	Identification of differentially expressed genes using digital gene expression profiles in <i>Pyrus pyrifolia</i> Nakai cv. Hosui bud release following early defoliation. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	0.6	6
63	Construction of a High-Density Simple Sequence Repeat Consensus Genetic Map for Pear (<i>Pyrus</i> spp.). <i>Plant Molecular Biology Reporter</i> , 2015, 33, 316-325.	1.0	47
64	Hydrogen Sulfide Prolongs Postharvest Storage of Fresh-Cut Pears (<i>Pyrus pyrifolia</i>) by Alleviation of Oxidative Damage and Inhibition of Fungal Growth. <i>PLoS ONE</i> , 2014, 9, e85524.	1.1	86
65	Identification of miRNAs involved in pear fruit development and quality. <i>BMC Genomics</i> , 2014, 15, 953.	1.2	102
66	Comparative Genomic Analysis Reveals Multiple Long Terminal Repeats, Lineage-Specific Amplification, and Frequent Interelement Recombination for Cassandra Retrotransposon in Pear (<i>Pyrus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 297 Td (
67	A Novel Set of EST-Derived SSR Markers for Pear and Cross-Species Transferability in Rosaceae. <i>Plant Molecular Biology Reporter</i> , 2014, 32, 290-302.	1.0	28
68	Evidence for Apoplasmic Phloem Unloading in Pear Fruit. <i>Plant Molecular Biology Reporter</i> , 2014, 32, 931-939.	1.0	39
69	High-density genetic linkage map construction and identification of fruit-related QTLs in pear using SNP and SSR markers. <i>Journal of Experimental Botany</i> , 2014, 65, 5771-5781.	2.4	171
70	Hetero-diploid pollen grains that represent self-compatibility are incompatible with non-self receptors in tetraploid Chinese cherry (<i>Prunus pseudocerasus</i> Lindl). <i>Tree Genetics and Genomes</i> , 2014, 10, 619-625.	0.6	7
71	Low temperature inhibits pollen tube growth by disruption of both tip-localized reactive oxygen species and endocytosis in <i>Pyrus bretschneideri</i> Rehd.. <i>Plant Physiology and Biochemistry</i> , 2014, 74, 255-262.	2.8	30
72	Identification of differentially expressed genes related to coloration in red/green mutant pear (<i>Pyrus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.6	50

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73	An AFLP, SRAP, and SSR Genetic Linkage Map and Identification of QTLs for Fruit Traits in Pear (<i>Pyrus L.</i>). <i>Plant Molecular Biology Reporter</i> , 2013, 31, 678-687.	1.0	69
74	Identifying the candidate genes involved in the calyx abscission process of 'Kuerlexiangli'™ (<i>Pyrus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.2	32
75	The genome of the pear (<i>Pyrus bretschneideri</i> Rehd.). <i>Genome Research</i> , 2013, 23, 396-408.	2.4	832
76	Molecular Determinants and Mechanisms of Gametophytic Self-Incompatibility in Fruit Trees of Rosaceae. <i>Critical Reviews in Plant Sciences</i> , 2013, 32, 53-68.	2.7	39
77	Molecular cloning and gene expression differences of the anthocyanin biosynthesis-related genes in the red/green skin color mutant of pear (<i>Pyrus communis L.</i>). <i>Tree Genetics and Genomes</i> , 2013, 9, 1351-1360.	0.6	45
78	Inheritance of Hetero-Diploid Pollen S-Haplotype in Self-Compatible Tetraploid Chinese Cherry (<i>Prunus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.1	12
79	Characterization of the S-RNase genomic DNA allele sequence in <i>Prunus speciosa</i> and <i>P. pseudocerasus</i> . <i>Scientia Horticulturae</i> , 2012, 144, 93-101.	1.7	6
80	Identification and Characterisation of SFBs in <i>Prunus mume</i> . <i>Plant Molecular Biology Reporter</i> , 2012, 30, 878-884.	1.0	3
81	The activity of plasma membrane hyperpolarization-activated Ca ²⁺ channels during pollen development of <i>Pyrus pyrifolia</i> . <i>Acta Physiologiae Plantarum</i> , 2012, 34, 969-975.	1.0	3
82	Low temperature inhibits pollen viability by alteration of actin cytoskeleton and regulation of pollen plasma membrane ion channels in <i>Pyrus pyrifolia</i> . <i>Environmental and Experimental Botany</i> , 2012, 78, 70-75.	2.0	20
83	Reciprocal regulation of Ca ²⁺ -activated outward K ⁺ channels of <i>Pyrus pyrifolia</i> pollen by heme and carbon monoxide. <i>New Phytologist</i> , 2011, 189, 1060-1068.	3.5	30
84	Self-compatibility of 'Zaoguan'™ (<i>Pyrus bretschneideri</i> Rehd.) is associated with style-part mutations. <i>Genetica</i> , 2011, 139, 1149-1158.	0.5	10
85	Recognition specificity of self-incompatibility in <i>Pyrus</i> and <i>Malus</i> . <i>Molecular Breeding</i> , 2011, 28, 549-557.	1.0	11
86	Heteroallelic diploid pollen led to self-compatibility in tetraploid cultivar 'Sha 01'™ (<i>Pyrus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 22	0.6	16
87	Molecular analysis of eight SFB alleles and a new SFB-like gene in <i>Prunus pseudocerasus</i> and <i>Prunus speciosa</i> . <i>Tree Genetics and Genomes</i> , 2011, 7, 891-902.	0.6	7
88	Self-compatibility of 'Katy'™ apricot (<i>Prunus armeniaca L.</i>) is associated with pollen-part mutations. <i>Sexual Plant Reproduction</i> , 2011, 24, 23-35.	2.2	21
89	cAMP activates hyperpolarization-activated Ca ²⁺ channels in the pollen of <i>Pyrus pyrifolia</i> . <i>Plant Cell Reports</i> , 2011, 30, 1193-1200.	2.8	23
90	Identification of S-genotypes in Chinese cherry cultivars (<i>Prunus pseudocerasus</i> Lindl.). <i>Tree Genetics and Genomes</i> , 2010, 6, 579-590.	0.6	16

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91	Spermidine oxidase-derived H ₂ O ₂ regulates pollen plasma membrane hyperpolarization-activated Ca ²⁺ -permeable channels and pollen tube growth. <i>Plant Journal</i> , 2010, 63, 1042-1053.	2.8	182
92	S-RNase disrupts tip-localized reactive oxygen species and induces nuclear DNA degradation in incompatible pollen tubes of <i>Pyrus pyrifolia</i> . <i>Journal of Cell Science</i> , 2010, 123, 4301-4309.	1.2	116
93	S-RNase triggers mitochondrial alteration and DNA degradation in the incompatible pollen tube of <i>Pyrus pyrifolia</i> in vitro. <i>Plant Journal</i> , 2009, 57, 220-229.	2.8	73
94	S genotyping and S screening utilizing SFB gene polymorphism in Japanese plum and sweet cherry by dot-blot analysis. <i>Molecular Breeding</i> , 2008, 21, 339-349.	1.0	11
95	Construction of a genetically engineered and stable strain of degrading gamma-hexachlorocyclohexane and carbendazim by transposon mini-Tn5. <i>Wei Sheng Wu Xue Bao = Acta Microbiologica Sinica</i> , 2008, 48, 45-50.	0.2	0
96	Analysis of the role of LinA and LinB in biodegradation of γ -hexachlorocyclohexane. <i>Environmental Microbiology</i> , 2007, 9, 2331-2340.	1.8	41