

Jun Wu

List of Publications by Year in descending order

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96
papers

4,568
citations

117625

34
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110387

64
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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). New Zealand Journal of Crop and Horticultural Science, 2022, 50, 303-325.	1.3	5
2	Genome-wide genetic diversity and IBD analysis reveals historic dissemination routes of pear in China. Tree Genetics and Genomes, 2022, 18, 1.	1.6	3
3	Pear genetics: Recent advances, new prospects, and a roadmap for the future. Horticulture Research, 2022, 9, .	6.3	12
4	Alternative splicing analysis provides insight into the domestication and improvement of pear (<i>Pyrus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	3.6	3
5	Metabolomics Combined with Proteomics Provide a Novel Interpretation of the Changes in Flavonoid Glycosides during White Tea Processing. Foods, 2022, 11, 1226.	4.3	17
6	Taxonomic Uncertainty and Its Conservation Implications in Management, a Case from <i>Pyrus hopeiensis</i> (Rosaceae). Diversity, 2022, 14, 417.	1.7	4
7	The Variation of Stone Cell Content in 236 Germplasms of Sand Pear (<i>Pyrus pyrifolia</i>) and Identification of Related Candidate Genes. Horticultural Plant Journal, 2021, 7, 108-116.	5.0	25
8	Genome-wide association studies provide insights into the genetic determination of fruit traits of pear. Nature Communications, 2021, 12, 1144.	12.8	44
9	An accumulation of genetic variation and selection across the disease-related genes during apple domestication. Tree Genetics and Genomes, 2021, 17, 1.	1.6	10
10	Dynamic Diversity of NLR Genes in Triticum and Mining of Promising NLR Alleles for Disease Resistance. Current Issues in Molecular Biology, 2021, 43, 965-977.	2.4	0
11	The PyPIF5-PymiR156a-PySPL9-PyMYB114/MYB10 module regulates light-induced anthocyanin biosynthesis in red pear. Molecular Horticulture, 2021, 1, .	5.8	16
12	A systems genetics approach reveals PbrNSC as a regulator of lignin and cellulose biosynthesis in stone cells of pear fruit. Genome Biology, 2021, 22, 313.	8.8	32
13	Genome-wide comparative analysis of the BAHD superfamily in seven Rosaceae species and expression analysis in pear (<i>Pyrus bretschneideri</i>). BMC Plant Biology, 2020, 20, 14.	3.6	22
14	Contrasting genetic variation and positive selection followed the divergence of NBS-encoding genes in Asian and European pears. BMC Genomics, 2020, 21, 809.	2.8	7
15	Mining and evolution analysis of lateral organ boundaries domain (LBD) genes in Chinese white pear (<i>Pyrus bretschneideri</i>). BMC Genomics, 2020, 21, 644.	2.8	18
16	Pearprocess: A new phenotypic tool for stone cell trait evaluation in pear fruit. Journal of Integrative Agriculture, 2020, 19, 1625-1634.	3.5	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. Genomics, 2020, 112, 3484-3496.	2.9	20
18	Overexpression of sugar transporter gene PbSWEET4 of pear causes sugar reduce and early senescence in leaves. Gene, 2020, 743, 144582.	2.2	27

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19	PyWRKY26 and PybHLH3 cotargeted the PyMYB114 promoter to regulate anthocyanin biosynthesis and transport in red-skinned pears. Horticulture Research, 2020, 7, 37.	6.3	95
20	CRISPR-Cas12b enables efficient plant genome engineering. Nature Plants, 2020, 6, 202-208.	9.3	116
21	Identification of key genes related to seedlessness by genome-wide detection of structural variation and transcriptome analysis in "Shijiwuhe" pear. Gene, 2020, 738, 144480.	2.2	2
22	Comparison of multiple algorithms to reliably detect structural variants in pears. BMC Genomics, 2020, 21, 61.	2.8	15
23	Homozygosity Mapping Reveals Population History and Trait Architecture in Self-Incompatible Pear (Pyrus spp.). Frontiers in Plant Science, 2020, 11, 590846.	3.6	7
24	Genome-wide survey and expression analysis of the SLAC/SLAH gene family in pear (Pyrus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 542 Td	2.9	10
25	PbrmiR397a regulates lignification during stone cell development in pear fruit. Plant Biotechnology Journal, 2019, 17, 103-117.	8.3	114
26	The Î2-amylase PbrBAM3 from pear (Pyrus betulaefolia) regulates soluble sugar accumulation and ROS homeostasis in response to cold stress. Plant Science, 2019, 287, 110184.	3.6	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. Journal of Agricultural and Food Chemistry, 2019, 67, 8319-8331.	5.2	15
28	Marker-trait associations and genomic predictions of interspecific pear (Pyrus) fruit characteristics. Scientific Reports, 2019, 9, 9072.	3.3	38
29	The Genome of Pear. Compendium of Plant Genomes, 2019, , 133-143.	0.5	1
30	Single-pollen-cell sequencing for gamete-based phased diploid genome assembly in plants. Genome Research, 2019, 29, 1889-1899.	5.5	28
31	The bracteatus pineapple genome and domestication of clonally propagated crops. Nature Genetics, 2019, 51, 1549-1558.	21.4	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 (Pyrus). Plant Biotechnology Journal, 2019, 17, 1582-1594.	8.3	46
33	PbrMYB169 positively regulates lignification of stone cells in pear fruit. Journal of Experimental Botany, 2019, 70, 1801-1814.	4.8	73
34	Genome-wide identification, expression and functional analysis of the phosphofructokinase gene family in Chinese white pear (Pyrus bretschneideri). Gene, 2019, 702, 133-142.	2.2	15
35	Fine-mapping and validation of the genomic region underpinning pear red skin colour. Horticulture Research, 2019, 6, 29.	6.3	31
36	Comparative Transcriptomic Analysis Provides Insight into the Domestication and Improvement of Pear (P. pyrifolia) Fruit. Plant Physiology, 2019, 180, 435-452.	4.8	33

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37	The involvement of PybZIPa in light-induced anthocyanin accumulation via the activation of PyUFGT through binding to tandem G-boxes in its promoter. <i>Horticulture Research</i> , 2019, 6, 134.	6.3	61
38	The mining and evolutionary investigation of AP2/ERF genes in pear (<i>Pyrus</i>). <i>BMC Plant Biology</i> , 2018, 18, 46.	3.6	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.	1.9	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.	3.6	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 /Overclock 10	2.0	38
42	Diversification and independent domestication of Asian and European pears. <i>Genome Biology</i> , 2018, 19, 77.	8.8	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.	1.6	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.	1.6	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.	3.4	28
46	Fast diffusion of domesticated maize to temperate zones. <i>Scientific Reports</i> , 2017, 7, 2077.	3.3	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.	3.1	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.	5.7	279
49	An eFP browser for visualizing strawberry fruit and flower transcriptomes. <i>Horticulture Research</i> , 2017, 4, 17029.	6.3	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.	0.9	23
51	Genome-wide identification of the MADS-box transcription factor family in pear (<i>Pyrus</i>) Tj ETQq1 1 0.784314 rgBT /Overclock 10	2.0	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.	3.3	59
53	Overexpression of sucrose transporter gene PbSUT2 from <i>Pyrus bretschneideri</i> , enhances sucrose content in <i>Solanum lycopersicum</i> fruit. <i>Plant Physiology and Biochemistry</i> , 2016, 105, 150-161.	5.8	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.	3.1	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.	1.2	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.	1.6	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.	3.3	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.	3.6	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.	3.1	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.	1.6	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.	3.6	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.	1.6	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.	1.8	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.	2.5	86
65	Identification of miRNAs involved in pear fruit development and quality. <i>BMC Genomics</i> , 2014, 15, 953.	2.8	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.	1.8	28
68	Evidence for Apoplasmic Phloem Unloading in Pear Fruit. <i>Plant Molecular Biology Reporter</i> , 2014, 32, 931-939.	1.8	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.	4.8	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.	1.6	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.	5.8	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	1.6	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</i> L.). <i>Plant Molecular Biology Reporter</i> , 2013, 31, 678-687.	1.8	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	2.8	32
75	The genome of the pear (<i>Pyrus bretschneideri</i> Rehd.). <i>Genome Research</i> , 2013, 23, 396-408.	5.5	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.	5.7	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</i> L.). <i>Tree Genetics and Genomes</i> , 2013, 9, 1351-1360.	1.6	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	2.5	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.	3.6	6
80	Identification and Characterisation of SFBs in <i>Prunus mume</i> . <i>Plant Molecular Biology Reporter</i> , 2012, 30, 878-884.	1.8	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.	2.1	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.	4.2	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.	7.3	30
84	Self-compatibility of 'Zaoguan'™ (<i>Pyrus bretschneideri</i> Rehd.) is associated with style-part mutations. <i>Genetica</i> , 2011, 139, 1149-1158.	1.1	10
85	Recognition specificity of self-incompatibility in <i>Pyrus</i> and <i>Malus</i> . <i>Molecular Breeding</i> , 2011, 28, 549-557.	2.1	11
86	Heteroallelic diploid pollen led to self-compatibility in tetraploid cultivar 'Shaoli'™ (<i>Pyrus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 22	1.6	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.	1.6	7
88	Self-compatibility of 'Katy'™ apricot (<i>Prunus armeniaca</i> L.) 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.	5.6	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.	1.6	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.	5.7	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.	2.0	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.	5.7	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.	2.1	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.	3.8	41