

Jun Wu

List of Publications by Year in descending order

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96
papers

4,568
citations

117625

34
h-index

110387

64
g-index

97
all docs

97
docs citations

97
times ranked

3789
citing authors

#	ARTICLE	IF	CITATIONS
1	The genome of the pear (<i>Pyrus bretschneideri</i> Rehd.). <i>Genome Research</i> , 2013, 23, 396-408.	5.5	832
2	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
3	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
4	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
5	Diversification and independent domestication of Asian and European pears. <i>Genome Biology</i> , 2018, 19, 77.	8.8	149
6	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
7	CRISPR-Cas12b enables efficient plant genome engineering. <i>Nature Plants</i> , 2020, 6, 202-208.	9.3	116
8	<i>PbrmiR397a</i> regulates lignification during stone cell development in pear fruit. <i>Plant Biotechnology Journal</i> , 2019, 17, 103-117.	8.3	114
9	Identification of miRNAs involved in pear fruit development and quality. <i>BMC Genomics</i> , 2014, 15, 953.	2.8	102
10	PyWRKY26 and PybHLH3 cotargeted the PyMYB114 promoter to regulate anthocyanin biosynthesis and transport in red-skinned pears. <i>Horticulture Research</i> , 2020, 7, 37.	6.3	95
11	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
12	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
13	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
14	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>). <i>Journal of Experimental Botany</i> , 2017, 68, 1075-1086.	10.7	217
15	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
16	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
17	<i>PbrMYB169</i> positively regulates lignification of stone cells in pear fruit. <i>Journal of Experimental Botany</i> , 2019, 70, 1801-1814.	4.8	73
18	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

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19	An eFP browser for visualizing strawberry fruit and flower transcriptomes. <i>Horticulture Research</i> , 2017, 4, 17029.	6.3	63
20	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
21	The bracteatus pineapple genome and domestication of clonally propagated crops. <i>Nature Genetics</i> , 2019, 51, 1549-1558.	21.4	60
22	Distinct transcriptome profiles reveal gene expression patterns during fruit development and maturation in five main cultivated species of pear (<i>Pyrus L.</i>). <i>Scientific Reports</i> , 2016, 6, 28130.	3.3	59
23	Transcriptome profiling reveals differential gene expression in proanthocyanidin biosynthesis associated with red/green skin color mutant of pear (<i>Pyrus communis L.</i>). <i>Frontiers in Plant Science</i> , 2015, 6, 795.	3.6	53
24	The β -amylase PbrBAM3 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.	3.6	52
25	Identification of differentially expressed genes related to coloration in red/green mutant pear (<i>Pyrus</i>) Tj ETQq1 1 0.784314 rgBT /Overbo	1.6	50
26	Construction of a High-Density Simple Sequence Repeat Consensus Genetic Map for Pear (<i>Pyrus spp.</i>). <i>Plant Molecular Biology Reporter</i> , 2015, 33, 316-325.	1.8	47
27	Development of an integrated 200K <i>SNP</i> 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.	8.3	46
28	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.	1.6	45
29	Genetic diversity and population structure of pear (<i>Pyrus spp.</i>) collections revealed by a set of core genome-wide SSR markers. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	1.6	45
30	Genome-wide association studies provide insights into the genetic determination of fruit traits of pear. <i>Nature Communications</i> , 2021, 12, 1144.	12.8	44
31	Analysis of the role of LinA and LinB in biodegradation of γ -hexachlorocyclohexane. <i>Environmental Microbiology</i> , 2007, 9, 2331-2340.	3.8	41
32	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
33	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
34	Evidence for Apoplasmic Phloem Unloading in Pear Fruit. <i>Plant Molecular Biology Reporter</i> , 2014, 32, 931-939.	1.8	39
35	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
36	Marker-trait associations and genomic predictions of interspecific pear (<i>Pyrus</i>) fruit characteristics. <i>Scientific Reports</i> , 2019, 9, 9072.	3.3	38

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37	Genome-wide identification of the <i>MADS-box</i> transcription factor family in pear (<i>Pyrus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 5	2.0	38
38	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
39	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.	4.8	33
40	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
41	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.	8.8	32
42	Fine-mapping and validation of the genomic region underpinning pear red skin colour. <i>Horticulture Research</i> , 2019, 6, 29.	6.3	31
43	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
44	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
45	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
46	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
47	Single-pollen-cell sequencing for gamete-based phased diploid genome assembly in plants. <i>Genome Research</i> , 2019, 29, 1889-1899.	5.5	28
48	Overexpression of sugar transporter gene PbSWEET4 of pear causes sugar reduce and early senescence in leaves. <i>Gene</i> , 2020, 743, 144582.	2.2	27
49	Comparative Genomic Analysis Reveals Multiple Long Terminal Repeats, Lineage-Specific Amplification, and Frequent Interelement Recombination for Cassandra Retrotransposon in Pear (<i>Pyrus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 5	2.4	26
50	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.	5.0	25
51	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
52	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
53	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
54	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.	3.6	22

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55	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
56	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
57	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.	2.9	20
58	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.	2.8	18
59	Metabolomics Combined with Proteomics Provide a Novel Interpretation of the Changes in Flavonoid Glycosides during White Tea Processing. <i>Foods</i> , 2022, 11, 1226.	4.3	17
60	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
61	Heteroallelic diploid pollen led to self-compatibility in tetraploid cultivar "Sha 01" (<i>Pyrus</i>) Tj ETQq1 1 0.784314 rgBT / Overlock 10 T	1.6	16
62	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
63	The PyPIF5-PymiR156a-PySPL9-PyMYB114/MYB10 module regulates light-induced anthocyanin biosynthesis in red pear. <i>Molecular Horticulture</i> , 2021, 1, .	5.8	16
64	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
65	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.	5.2	15
66	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.	2.2	15
67	Comparison of multiple algorithms to reliably detect structural variants in pears. <i>BMC Genomics</i> , 2020, 21, 61.	2.8	15
68	Inheritance of Hetero-Diploid Pollen S-Haplotype in Self-Compatible Tetraploid Chinese Cherry (<i>Prunus</i>) Tj ETQq0 0 0 rgBT / Overlock 10 T	2.5	12
69	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
70	Pear genetics: Recent advances, new prospects, and a roadmap for the future. <i>Horticulture Research</i> , 2022, 9, .	6.3	12
71	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
72	Recognition specificity of self-incompatibility in <i>Pyrus</i> and <i>Malus</i> . <i>Molecular Breeding</i> , 2011, 28, 549-557.	2.1	11

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73	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
74	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 50 702 Td	2.9	10
75	Pearprocess: A new phenotypic tool for stone cell trait evaluation in pear fruit. <i>Journal of Integrative Agriculture</i> , 2020, 19, 1625-1634.	3.5	10
76	An accumulation of genetic variation and selection across the disease-related genes during apple domestication. <i>Tree Genetics and Genomes</i> , 2021, 17, 1.	1.6	10
77	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
78	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
79	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
80	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
81	Fast diffusion of domesticated maize to temperate zones. <i>Scientific Reports</i> , 2017, 7, 2077.	3.3	7
82	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.	2.8	7
83	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.	3.6	7
84	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
85	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
86	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
87	Genome-wide comparison of the GRAS protein family in eight Rosaceae species and GRAS 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.	1.3	5
88	Taxonomic Uncertainty and Its Conservation Implications in Management, a Case from <i>Pyrus hopeiensis</i> (Rosaceae). <i>Diversity</i> , 2022, 14, 417.	1.7	4
89	Identification and Characterisation of SFBs in <i>Prunus mume</i> . <i>Plant Molecular Biology Reporter</i> , 2012, 30, 878-884.	1.8	3
90	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

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91	Genome-wide genetic diversity and IBD analysis reveals historic dissemination routes of pear in China. <i>Tree Genetics and Genomes</i> , 2022, 18, 1.	1.6	3
92	Alternative splicing analysis provides insight into the domestication and improvement of pear (<i>Pyrus</i>) Tj ETQq0 0 0 ggBT /Overclock 10 Tf	3.6	3
93	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.	2.2	2
94	The Genome of Pear. <i>Compendium of Plant Genomes</i> , 2019, , 133-143.	0.5	1
95	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.	2.4	0
96	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