

Shaoling Zhang

List of Publications by Year in descending order

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179
papers

6,210
citations

94269

37
h-index

95083

68
g-index

182
all docs

182
docs citations

182
times ranked

5184
citing authors

#	ARTICLE	IF	CITATIONS
1	The genome of the pear (<i>Pyrus bretschneideri</i> Rehd.). <i>Genome Research</i> , 2013, 23, 396-408.	2.4	832
2	Gene duplication and evolution in recurring polyploidization–diploidization cycles in plants. <i>Genome Biology</i> , 2019, 20, 38.	3.8	542
3	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
4	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
5	Diversification and independent domestication of Asian and European pears. <i>Genome Biology</i> , 2018, 19, 77.	3.8	149
6	Anatomy, ultrastructure and lignin distribution of stone cells in two <i>Pyrus</i> species. <i>Plant Science</i> , 2009, 176, 413-419.	1.7	138
7	Genome-wide identification and comparative analysis of the heat shock transcription factor family in Chinese white pear (<i>Pyrus bretschneideri</i>) and five other Rosaceae species. <i>BMC Plant Biology</i> , 2015, 15, 12.	1.6	138
8	Identification of miRNAs involved in pear fruit development and quality. <i>BMC Genomics</i> , 2014, 15, 953.	1.2	102
9	Phosphatidic Acid Counteracts S-RNase Signaling in Pollen by Stabilizing the Actin Cytoskeleton. <i>Plant Cell</i> , 2018, 30, 1023-1039.	3.1	101
10	A novel MYB transcription factor regulates ascorbic acid synthesis and affects cold tolerance. <i>Plant, Cell and Environment</i> , 2019, 42, 832-845.	2.8	98
11	ICE1 of <i>Pyrus ussuriensis</i> functions in cold tolerance by enhancing PuDREBa transcriptional levels through interacting with PuHHP1. <i>Scientific Reports</i> , 2015, 5, 17620.	1.6	94
12	A WRKY transcription factor PbrWRKY53 from <i>Pyrus betulaefolia</i> is involved in drought tolerance and AsA accumulation. <i>Plant Biotechnology Journal</i> , 2019, 17, 1770-1787.	4.1	93
13	Evaluation of the volatile profile of 33 <i>Pyrus ussuriensis</i> cultivars by HS-SPME with GC-MS. <i>Food Chemistry</i> , 2012, 134, 2367-2382.	4.2	83
14	Genome-wide analysis of WRKY transcription factors in white pear (<i>Pyrus bretschneideri</i>) reveals evolution and patterns under drought stress. <i>BMC Genomics</i> , 2015, 16, 1104.	1.2	76
15	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 0.784314rgBT /Overdock 10 T		
16	Genome-wide characterization, evolution, and expression analysis of the leucine-rich repeat receptor-like protein kinase (LRR-RLK) gene family in Rosaceae genomes. <i>BMC Genomics</i> , 2017, 18, 763.	1.2	62
17	Characterization and Quantification of Polyphenols and Triterpenoids in Thinned Young Fruits of Ten Pear Varieties by UPLC-Q TRAP-MS/MS. <i>Molecules</i> , 2019, 24, 159.	1.7	62
18	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.	2.9	61

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19	The bracteatus pineapple genome and domestication of clonally propagated crops. <i>Nature Genetics</i> , 2019, 51, 1549-1558.	9.4	60
20	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
21	Self-Incompatibility in <i>Papaver rhoeas</i> Activates Nonspecific Cation Conductance Permeable to Ca ²⁺ and K ⁺ . <i>Plant Physiology</i> , 2011, 155, 963-973.	2.3	58
22	Unbiased subgenome evolution following a recent whole-genome duplication in pear (<i>Pyrus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 622 Td (2.9	54
23	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
24	Genomic characterization, phylogenetic comparison and differential expression of the cyclic nucleotide-gated channels gene family in pear (<i>Pyrus bretschneideri</i> Rehd.). <i>Genomics</i> , 2015, 105, 39-52.	1.3	52
25	Chemical Composition and Crystal Morphology of Epicuticular Wax in Mature Fruits of 35 Pear (<i>Pyrus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 382 Td (1.7	52
26	The Î ² -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.	1.7	52
27	Chemical composition, crystal morphology and key gene expression of cuticular waxes of Asian pears at harvest and after storage. <i>Postharvest Biology and Technology</i> , 2017, 132, 71-80.	2.9	51
28	Characterization of the lipoxygenase (LOX) gene family in the Chinese white pear (<i>Pyrus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 382 Td (1.2	49
29	Identifying genetic diversity and a preliminary core collection of <i>Pyrus pyrifolia</i> cultivars by a genome-wide set of SSR markers. <i>Scientia Horticulturae</i> , 2014, 167, 5-16.	1.7	48
30	Development of an integrated 200K <sc>SNP</sc> 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
31	The effect of temperature, polyamines and polyamine synthesis inhibitor on in vitro pollen germination and pollen tube growth of <i>Prunus mume</i> . <i>Scientia Horticulturae</i> , 2004, 99, 289-299.	1.7	45
32	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
33	ViewBS: a powerful toolkit for visualization of high-throughput bisulfite sequencing data. <i>Bioinformatics</i> , 2018, 34, 708-709.	1.8	44
34	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
35	Construction of a high-density genetic linkage map in pear (<i>Pyrus communis</i> — <i>Pyrus pyrifolia</i> nakai) using SSRs and SNPs developed by SLAF-seq. <i>Scientia Horticulturae</i> , 2017, 218, 198-204.	1.7	42
36	Evolution of the Aroma Volatiles of Pear Fruits Supplemented with Fatty Acid Metabolic Precursors. <i>Molecules</i> , 2014, 19, 20183-20196.	1.7	41

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37	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
38	Genome-wide analyses and expression patterns under abiotic stress of NAC transcription factors in white pear (<i>Pyrus bretschneideri</i>). <i>BMC Plant Biology</i> , 2019, 19, 161.	1.6	41
39	Apoplastic calmodulin promotes self-incompatibility pollen tube growth by enhancing calcium influx and reactive oxygen species concentration in <i>Pyrus pyrifolia</i> . <i>Plant Cell Reports</i> , 2014, 33, 255-263.	2.8	40
40	Gene-expression profile of developing pollen tube of <i>Pyrus bretschneideri</i> . <i>Gene Expression Patterns</i> , 2016, 20, 11-21.	0.3	40
41	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
42	Genome-wide identification of PbrbHLH family genes, and expression analysis in response to drought and cold stresses in pear (<i>Pyrus bretschneideri</i>). <i>BMC Plant Biology</i> , 2021, 21, 86.	1.6	39
43	Genome-wide identification of the MADS-box transcription factor family in pear (<i>Pyrus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 222	0.9	38
44	Characterization of the glutathione S-transferase (GST) gene family in <i>Pyrus bretschneideri</i> and their expression pattern upon superficial scald development. <i>Plant Growth Regulation</i> , 2018, 86, 211-222.	1.8	36
45	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
46	The gene <i>PbTMT4</i> from pear (<i>Pyrus bretschneideri</i>) mediates vacuolar sugar transport and strongly affects sugar accumulation in fruit. <i>Physiologia Plantarum</i> , 2018, 164, 307-319.	2.6	33
47	Physiological and Nutritional Responses of Pear Seedlings to Nitrate Concentrations. <i>Frontiers in Plant Science</i> , 2018, 9, 1679.	1.7	33
48	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
49	Identifying the candidate genes involved in the calyx abscission process of 'Kuerlexiangli'™ (<i>Pyrus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 222	1.2	32
50	Molecular cloning and expression analysis of a gene for sucrose transporter from pear (<i>Pyrus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 222	2.8	32
51	Genome-wide identification and comparative analysis of the cation proton antiporters family in pear and four other Rosaceae species. <i>Molecular Genetics and Genomics</i> , 2016, 291, 1727-1742.	1.0	32
52	Transcriptome and phytohormone analysis reveals a comprehensive phytohormone and pathogen defence response in pear self-/cross-pollination. <i>Plant Cell Reports</i> , 2017, 36, 1785-1799.	2.8	32
53	Comparative analysis of the volatile organic compounds in mature fruits of 12 Occidental pear (<i>Pyrus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 222	1.7	32
54	Identification of hexokinase family members in pear (<i>Pyrus</i> $\tilde{}$ bretschneideri) and functional exploration of <i>PbHXX1</i> in modulating sugar content and plant growth. <i>Gene</i> , 2019, 711, 143932.	1.0	32

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55	Investigations into the production of volatile compounds in Korla fragrant pears (<i>Pyrus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 7	4.2	32
56	<i>In vitro</i> antifungal activity and mode of action of selected polyphenolic antioxidants on <i>Botrytis cinerea</i> . Archives of Phytopathology and Plant Protection, 2010, 43, 1564-1578.	0.6	30
57	Soil chemical properties and geographical distance exerted effects on arbuscular mycorrhizal fungal community composition in pear orchards in Jiangsu Province, China. Applied Soil Ecology, 2019, 142, 18-24.	2.1	30
58	A WRKY transcription factor PbWRKY40 from <i>Pyrus betulaefolia</i> functions positively in salt tolerance and modulating organic acid accumulation by regulating PbVHA-B1 expression. Environmental and Experimental Botany, 2022, 196, 104782.	2.0	30
59	Genome-wide analysis of polygalacturonase gene family from pear genome and identification of the member involved in pear softening. BMC Plant Biology, 2019, 19, 587.	1.6	29
60	Integrated high-density consensus genetic map of <i>Pyrus</i> and anchoring of the "Bartlett" v1.0 (<i>Pyrus communis</i>) genome. DNA Research, 2017, 24, dsw063.	1.5	28
61	Single-pollen-cell sequencing for gamete-based phased diploid genome assembly in plants. Genome Research, 2019, 29, 1889-1899.	2.4	28
62	Calcium treatments promote the aroma volatiles emission of pear (<i>Pyrus ussuriensis</i> "Nanguoli" fruit during post-harvest ripening process. Scientia Horticulturae, 2017, 215, 102-111.	1.7	27
63	Characterization of the pectin methyl-esterase gene family and its function in controlling pollen tube growth in pear (<i>Pyrus bretschneideri</i>). Genomics, 2020, 112, 2467-2477.	1.3	27
64	Overexpression of sugar transporter gene PbSWEET4 of pear causes sugar reduce and early senescence in leaves. Gene, 2020, 743, 144582.	1.0	27
65	Fast loading ester fluorescent Ca ²⁺ and pH indicators into pollen of <i>Pyrus pyrifolia</i> . Journal of Plant Research, 2012, 125, 185-195.	1.2	26
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	Genome-wide identification and functional analysis of U-box E3 ubiquitin ligases gene family related to drought stress response in Chinese white pear (<i>Pyrus bretschneideri</i>). BMC Plant Biology, 2021, 21, 235.	1.6	26
68	Evolution, expression analysis, and functional verification of <i>Catharanthus roseus</i> RLK1-like kinase (CrRLK1L) family proteins in pear (<i>Pyrus bretschneideri</i>). Genomics, 2017, 109, 290-301.	1.3	25
69	Characterization of the Genes Involved in Malic Acid Metabolism from Pear Fruit and Their Expression Profile after Postharvest 1-MCP/Ethrel Treatment. Journal of Agricultural and Food Chemistry, 2018, 66, 8772-8782.	2.4	25
70	Genome-wide identification, evolution, and expression analysis of the <i>KT/HAK/KUP</i> family in pear. Genome, 2018, 61, 755-765.	0.9	25
71	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.	2.3	25
72	cAMP activates hyperpolarization-activated Ca ²⁺ channels in the pollen of <i>Pyrus pyrifolia</i> . Plant Cell Reports, 2011, 30, 1193-1200.	2.8	23

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73	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
74	Genome-wide identification and expression analysis of the bZIP transcription factors, and functional analysis in response to drought and cold stresses in pear (<i>Pyrus breschneideri</i>). <i>BMC Plant Biology</i> , 2021, 21, 583.	1.6	23
75	Transcriptomic and evolutionary analyses of white pear (<i>Pyrus bretschneideri</i>) α -amylase genes reveals their importance for cold and drought stress responses. <i>Gene</i> , 2019, 689, 102-113.	1.0	22
76	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
77	TARE1, a Mutated Copia-Like LTR Retrotransposon Followed by Recent Massive Amplification in Tomato. <i>PLoS ONE</i> , 2013, 8, e68587.	1.1	20
78	Genome-wide identification and expression analysis of genes associated with peach (<i>Prunus persica</i>) fruit ripening. <i>Scientia Horticulturae</i> , 2019, 246, 317-327.	1.7	20
79	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
80	Timing of meristem initiation and maintenance determines the morphology of fern gametophytes. <i>Journal of Experimental Botany</i> , 2021, 72, 6990-7001.	2.4	20
81	PbMC1a/1b regulates lignification during stone cell development in pear (<i>Pyrus bretschneideri</i>) fruit. <i>Horticulture Research</i> , 2020, 7, 59.	2.9	20
82	Exogenous Calcium Improved Resistance to <i>Botryosphaeria dothidea</i> by Increasing Autophagy Activity and Salicylic Acid Level in Pear. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 1150-1160.	1.4	20
83	Characterization of the Auxin Efflux Transporter PIN Proteins in Pear. <i>Plants</i> , 2020, 9, 349.	1.6	19
84	Mitochondrial dysfunction mediated by cytoplasmic acidification results in pollen tube growth cessation in <i>Pyrus pyrifolia</i> . <i>Physiologia Plantarum</i> , 2015, 153, 603-615.	2.6	18
85	Expansion and evolutionary patterns of cysteine-rich peptides in plants. <i>BMC Genomics</i> , 2017, 18, 610.	1.2	18
86	Characterization of Dof family in <i>Pyrus bretschneideri</i> and role of PbDof9.2 in flowering time regulation. <i>Genomics</i> , 2020, 112, 712-720.	1.3	18
87	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
88	Long-chain base phosphates modulate pollen tube growth via channel-mediated influx of calcium. <i>Plant Journal</i> , 2014, 79, 507-516.	2.8	17
89	Cryptochrome-mediated blue-light signal contributes to lignin biosynthesis in stone cells in pear fruit. <i>Plant Science</i> , 2022, 318, 111211.	1.7	17
90	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

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91	Evolutionary and Expression Analysis Provides Evidence for the Plant Glutamate-like Receptors Family is Involved in Woody Growth-related Function. <i>Scientific Reports</i> , 2016, 6, 32013.	1.6	16
92	Overexpression of PbrNHX2 gene, a Na ⁺ /H ⁺ antiporter gene isolated from <i>Pyrus betulaefolia</i> , confers enhanced tolerance to salt stress via modulating ROS levels. <i>Plant Science</i> , 2019, 285, 14-25.	1.7	16
93	Transcriptome profiling reveals the candidate genes associated with aroma metabolites and emission of pear (<i>Pyrus ussuriensis</i> cv.). <i>Scientia Horticulturae</i> , 2016, 206, 33-42.	1.7	15
94	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
95	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
96	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
97	Comparison of multiple algorithms to reliably detect structural variants in pears. <i>BMC Genomics</i> , 2020, 21, 61.	1.2	15
98	Phylogenetic and expression analysis of the magnesium transporter family in pear, and functional verification of PbrMGT7 in pear pollen. <i>Journal of Horticultural Science and Biotechnology</i> , 2018, 93, 51-63.	0.9	14
99	Identification of Shaker K ⁺ channel family members in Rosaceae and a functional exploration of PbrKAT1. <i>Planta</i> , 2019, 250, 1911-1925.	1.6	14
100	Comparative analysis of the P-type ATPase gene family in seven Rosaceae species and an expression analysis in pear (<i>Pyrus bretschneideri</i> Rehd.). <i>Genomics</i> , 2020, 112, 2550-2563.	1.3	14
101	Genome-wide Identification and Evolution of the PP2C Gene Family in Eight Rosaceae Species and Expression Analysis Under Stress in <i>Pyrus bretschneideri</i> . <i>Frontiers in Genetics</i> , 2021, 12, 770014.	1.1	14
102	Variation of organic acids in mature fruits of 193 pear (<i>Pyrus</i> spp.) cultivars. <i>Journal of Food Composition and Analysis</i> , 2022, 109, 104483.	1.9	14
103	Identification and functional characterization of SOC1-like genes in <i>Pyrus bretschneideri</i> . <i>Genomics</i> , 2020, 112, 1622-1632.	1.3	13
104	Transcriptome Analysis of Low- and High-Sucrose Pear Cultivars Identifies Key Regulators of Sucrose Biosynthesis in Fruits. <i>Plant and Cell Physiology</i> , 2020, 61, 1493-1506.	1.5	13
105	Characterization of the pectin methylesterase inhibitor gene family in Rosaceae and role of PbrPMEI23/39/41 in methylesterified pectin distribution in pear pollen tube. <i>Planta</i> , 2021, 253, 118.	1.6	13
106	Cell growth dynamics in two types of apical meristems in fern gametophytes. <i>Plant Journal</i> , 2022, , .	2.8	13
107	Genome-wide identification and expression analysis of the OSCA gene family in <i>Pyrus bretschneideri</i> . <i>Canadian Journal of Plant Science</i> , 2018, 98, 918-929.	0.3	12
108	Establishment of efficient callus genetic transformation system for <i>Pyrus armeniacaefolia</i> . <i>Scientia Horticulturae</i> , 2021, 289, 110429.	1.7	12

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109	Overexpression of PbDHAR2 from <i>Pyrus sinkiangensis</i> in Transgenic Tomato Confers Enhanced Tolerance to Salt and Chilling Stresses. <i>Hortscience: A Publication of the American Society for Horticultural Science</i> , 2015, 50, 789-796.	0.5	12
110	Cinnamate-4-Hydroxylase Gene Is Involved in the Step of Lignin Biosynthesis in Chinese White Pear. <i>Journal of the American Society for Horticultural Science</i> , 2015, 140, 573-579.	0.5	12
111	PbrRALF2-elicited reactive oxygen species signaling is mediated by the PbrCrRLK1L13-PbrMPK18 module in pear pollen tubes. <i>Horticulture Research</i> , 2021, 8, 222.	2.9	12
112	Pear genetics: Recent advances, new prospects, and a roadmap for the future. <i>Horticulture Research</i> , 2022, 9, .	2.9	12
113	Molecular characterization and expression pattern of sorbitol transporter gene <i>PbSOT2</i> in Pear (<i>Pyrus bretschneideri</i> Rehd.) fruit. <i>Canadian Journal of Plant Science</i> , 2016, 96, 128-137.	0.3	11
114	Characterization of genes involved in pear ascorbic acid metabolism and their response to bagging treatment during 'Yali' fruit development. <i>Scientia Horticulturae</i> , 2021, 285, 110178.	1.7	11
115	Changes in germinability, lipid peroxidation, and antioxidant enzyme activities in pear stock (<i>Pyrus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 33, 2035-2040.	1.0	10
116	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 50 462 Td	1.3	10
117	Metabolome analysis reveals important compounds related to dwarfing effect of interstock on scion in pear. <i>Annals of Applied Biology</i> , 2021, 179, 108-122.	1.3	10
118	Identification and characterization of invertase family genes reveal their roles in vacuolar sucrose metabolism during <i>Pyrus bretschneideri</i> Rehd. fruit development. <i>Genomics</i> , 2021, 113, 1087-1097.	1.3	10
119	PbCSE1 promotes lignification during stone cell development in pear (<i>Pyrus bretschneideri</i>) fruit. <i>Scientific Reports</i> , 2021, 11, 9450.	1.6	10
120	Genome-wide identification and expression analysis of the pear autophagy-related gene PbrATG8 and functional verification of PbrATG8c in <i>Pyrus bretschneideri</i> Rehd. <i>Planta</i> , 2021, 253, 32.	1.6	10
121	Pervasive genome duplications across the plant tree of life and their links to major evolutionary innovations and transitions. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 3248-3256.	1.9	10
122	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
123	A MADS-box transcription factor of 'Kuerlexiangli' (<i>Pyrus sinkiangensis</i> Yu) PsJOINTLESS gene functions in floral organ abscission. <i>Gene</i> , 2018, 642, 163-171.	1.0	9
124	The Peptide PbrPSK2 From Phytosulfokine Family Induces Reactive Oxygen Species (ROS) Production to Regulate Pear Pollen Tube Growth. <i>Frontiers in Plant Science</i> , 2020, 11, 601993.	1.7	9
125	Genome-wide identification of lysin motif containing protein family genes in eight rosaceae species, and expression analysis in response to pathogenic fungus <i>Botryosphaeria dothidea</i> in Chinese white pear. <i>BMC Genomics</i> , 2020, 21, 612.	1.2	9
126	Pear metal transport protein PbMTP8.1 confers manganese tolerance when expressed in yeast and <i>Arabidopsis thaliana</i> . <i>Ecotoxicology and Environmental Safety</i> , 2021, 208, 111687.	2.9	9

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127	Investigation of proline in superficial scald development during low temperature storage of ‘Dangshansuli’ pear fruit. <i>Postharvest Biology and Technology</i> , 2021, 181, 111643.	2.9	9
128	Influence of endogenous and exogenous RNases on the variation of pollen cytosolic-free Ca ²⁺ in <i>Pyrus serotina</i> Rehd. <i>Acta Physiologiae Plantarum</i> , 2008, 30, 233-241.	1.0	8
129	Exogenous Melatonin Improves Pear Resistance to <i>Botryosphaeria dothidea</i> by Increasing Autophagic Activity and Sugar/Organic Acid Levels. <i>Phytopathology</i> , 2022, 112, 1335-1344.	1.1	8
130	PbrROP1/2-elicited imbalance of cellulose deposition is mediated by a CrRLK1L-ROPGEF module in the pollen tube of <i>Pyrus</i> . <i>Horticulture Research</i> , 2022, 9, .	2.9	8
131	Genome-wide identification and comparative analysis of the PYL gene family in eight Rosaceae species and expression analysis of seeds germination in pear. <i>BMC Genomics</i> , 2022, 23, 233.	1.2	8
132	<i>PpybZIP43</i> contributes to sucrose synthesis in pear fruits by activating <i>PpySPS3</i> expression and interacts with <i>PpySTOP1</i> . <i>Physiologia Plantarum</i> , 2022, 174, .	2.6	8
133	PbCOL8 is a clock-regulated flowering time repressor in pear. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	7
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#	ARTICLE	IF	CITATIONS
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146	Expression and evolutionary analysis of soluble inorganic pyrophosphatase gene family in pear and four other Rosaceae species. <i>Plant Systematics and Evolution</i> , 2020, 306, 1.	0.3	5
147	High-Resolution Microstructure Analysis of Cork Spot Disordered Pear Fruit "Akizuki" (<i>Pyrus</i>) Tj ETQq1 1 0.784314 rgBT /Overloc	1.7	5
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162	Study on the differences of gene expression between pear and apple wild cultivation materials based on RNA-seq technique. <i>BMC Plant Biology</i> , 2021, 21, 256.	1.6	3

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163	Identification and function analysis of fasciclin-like arabinogalactan protein family genes in pear (<i>Pyrus bretschneideri</i>). <i>Plant Systematics and Evolution</i> , 2021, 307, 1.	0.3	3
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167	Identification and testing of reference genes for qRT-PCR analysis during pear fruit development. , 2022, 77, 2763-2777.		3
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170	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
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