

Shaoling Zhang

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

164
papers

3,338
citations

28
h-index

52
g-index

182
ext. papers

4,938
ext. citations

4.9
avg, IF

5.38
L-index

#	Paper	IF	Citations
164	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. <i>Environmental and Experimental Botany</i> , 2022 , 196, 104782	5.9	2
163	Cryptochrome-mediated blue-light signal contributes to lignin biosynthesis in stone cells in pear fruit.. <i>Plant Science</i> , 2022 , 318, 111211	5.3	1
162	Genome-wide genetic diversity and IBD analysis reveals historic dissemination routes of pear in China. <i>Tree Genetics and Genomes</i> , 2022 , 18, 1	2.1	1
161	Revealing the early response of pear (<i>Pyrus bretschneideri</i> Rehd) leaves during <i>Botryosphaeria dothidea</i> infection by transcriptome analysis.. <i>Plant Science</i> , 2022 , 315, 111146	5.3	0
160	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	4.5	0
159	Alternative splicing analysis provides insight into the domestication and improvement of pear (<i>Pyrus pyrifolia</i>) fruit. <i>Scientia Horticulturae</i> , 2022 , 297, 110976	4.1	
158	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	4.1	1
157	Cellulose accumulation mediated by PbrCSLD5, a cellulose synthase-like protein, results in cessation of pollen tube growth in <i>Pyrus bretschneideri</i> .. <i>Physiologia Plantarum</i> , 2022 , e13700	4.6	0
156	Multi-Omics Analysis Reveals the Dynamic Changes of RNA N -Methyladenosine in Pear () Defense Responses to Pathogen Infection.. <i>Frontiers in Microbiology</i> , 2021 , 12, 803512	5.7	0
155	Transcriptome provides potential insights into how calcium affects the formation of stone cell in <i>Pyrus</i> . <i>BMC Genomics</i> , 2021 , 22, 831	4.5	
154	Genome-wide Identification and Evolution of the Gene Family in Eight Rosaceae Species and Expression Analysis Under Stress in. <i>Frontiers in Genetics</i> , 2021 , 12, 770014	4.5	2
153	PbrRALF2-elicited reactive oxygen species signaling is mediated by the PbrCrRLK1L13-PbrMPK18 module in pear pollen tubes. <i>Horticulture Research</i> , 2021 , 8, 222	7.7	1
152	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>). <i>BMC Plant Biology</i> , 2021 , 21, 235	5.3	3
151	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	4.3	3
150	PbCSE1 promotes lignification during stone cell development in pear (<i>Pyrus bretschneideri</i>) fruit. <i>Scientific Reports</i> , 2021 , 11, 9450	4.9	0
149	Genome-Wide Analysis of RAV Transcription Factors and Functional Characterization of Anthocyanin-Biosynthesis-Related Genes in Pear. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	2
148	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	4.7	3

147	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	5.3	0
146	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	1.3	0
145	Timing of meristem initiation and maintenance determines the morphology of fern gametophytes. <i>Journal of Experimental Botany</i> , 2021 , 72, 6990-7001	7	3
144	Characterization of genes involved in pear ascorbic acid metabolism and their response to bagging treatment during fruit development. <i>Scientia Horticulturae</i> , 2021 , 285, 110178	4.1	1
143	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	7	6
142	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	4.3	3
141	Transcriptome Analysis of Pear Leaves in Response to Calcium Treatment During Infection. <i>Phytopathology</i> , 2021 , PHYTO10200458R	3.8	1
140	Genome-wide association studies provide insights into the genetic determination of fruit traits of pear. <i>Nature Communications</i> , 2021 , 12, 1144	17.4	12
139	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	5.3	12
138	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	2.6	2
137	Genes: Genome-Wide Identification, Evolution, and Their Contribution to Lignin Biosynthesis in Pear (). <i>Plants</i> , 2021 , 10,	4.5	1
136	High-Resolution Microstructure Analysis of Cork Spot Disordered Pear Fruit "Akizuki" (Nakai) Using X-Ray CT. <i>Frontiers in Plant Science</i> , 2021 , 12, 715124	6.2	1
135	Analysis of Gene Family and Its Function on Cell Lignification in Pears (). <i>Plants</i> , 2021 , 10,	4.5	1
134	Investigation of proline in superficial scald development during low temperature storage of Dangshansuli pear fruit. <i>Postharvest Biology and Technology</i> , 2021 , 181, 111643	6.2	2
133	Establishment of efficient callus genetic transformation system for <i>Pyrus armeniacaefolia</i> . <i>Scientia Horticulturae</i> , 2021 , 289, 110429	4.1	1
132	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	4.7	2
131	Genome-Wide Identification and Comparative Analysis of the Gene Family in the Rosaceae and Expression Analysis of During Fruit Development.. <i>Frontiers in Genetics</i> , 2021 , 12, 792250	4.5	1
130	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	5.3	2

129	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	4.3	9
128	Candidate proteins involved in the calyx abscission process of 啤uerlexiangli (Pyrus sinkiangensis Yu) identified by iTRAQ analysis. <i>Acta Physiologiae Plantarum</i> , 2020 , 42, 1	2.6	1
127	Phylogenetic and Expression Analyses of Cullin Family Members Unveil the Role of PbCUL1.C1 in Pollen Tube Growth Underlying Non-self S-RNase in Pear. <i>Plant Molecular Biology Reporter</i> , 2020 , 38, 601-612	1.7	
126	Overexpression of sugar transporter gene PbSWEET4 of pear causes sugar reduce and early senescence in leaves. <i>Gene</i> , 2020 , 743, 144582	3.8	3
125	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	1.3	1
124	Characterization of the Auxin Efflux Transporter PIN Proteins in Pear. <i>Plants</i> , 2020 , 9,	4.5	9
123	SPLs-mediated flowering regulation and hormone biosynthesis and signaling accompany juvenile-adult phase transition in <i>Pyrus</i> . <i>Scientia Horticulturae</i> , 2020 , 272, 109584	4.1	0
122	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	3.8	0
121	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	4.3	7
120	Comparison of multiple algorithms to reliably detect structural variants in pears. <i>BMC Genomics</i> , 2020 , 21, 61	4.5	4
119	regulates lignification during stone cell development in pear () fruit. <i>Horticulture Research</i> , 2020 , 7, 59	7.7	4
118	Exogenous Calcium Improved Resistance to by Increasing Autophagy Activity and Salicylic Acid Level in Pear. <i>Molecular Plant-Microbe Interactions</i> , 2020 , 33, 1150-1160	3.6	12
117	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	5.3	10
116	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	4.9	4
115	Characterization of the pectin methyl-esterase gene family and its function in controlling pollen tube growth in pear (<i>Pyrus bretschneideri</i>). <i>Genomics</i> , 2020 , 112, 2467-2477	4.3	10
114	Comprehensive genomic analysis of the RNase T2 gene family in Rosaceae and expression analysis in <i>Pyrus bretschneideri</i> . <i>Plant Systematics and Evolution</i> , 2020 , 306, 1	1.3	4
113	Effects of palmitic acid (16:0), hexacosanoic acid (26:0), ethephon and methyl jasmonate on the cuticular wax composition, structure and expression of key gene in the fruits of three pear cultivars. <i>Functional Plant Biology</i> , 2020 , 47, 156-169	2.7	2
112	PbrPOE21 inhibits pear pollen tube growth in vitro by altering apical reactive oxygen species content. <i>Planta</i> , 2020 , 252, 43	4.7	1

111	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	4.5	8
110	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	4.5	4
109	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	4.3	10
108	Identification and functional characterization of SOC1-like genes in <i>Pyrus bretschneideri</i> . <i>Genomics</i> , 2020 , 112, 1622-1632	4.3	5
107	Investigations into the production of volatile compounds in Korla fragrant pears (<i>Pyrus sinkiangensis</i> Yu). <i>Food Chemistry</i> , 2020 , 302, 125337	8.5	19
106	Single-pollen-cell sequencing for gamete-based phased diploid genome assembly in plants. <i>Genome Research</i> , 2019 , 29, 1889-1899	9.7	15
105	The bracteatus pineapple genome and domestication of clonally propagated crops. <i>Nature Genetics</i> , 2019 , 51, 1549-1558	36.3	32
104	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	11.6	24
103	Soil chemical properties and geographical distance exerted effects on arbuscular mycorrhizal fungal community composition in pear orchards in Jiangsu Province, China. <i>Applied Soil Ecology</i> , 2019 , 142, 18-24	5	17
102	Identification of hexokinase family members in pear (<i>Pyrus bretschneideri</i>) and functional exploration of PbHXK1 in modulating sugar content and plant growth. <i>Gene</i> , 2019 , 711, 143932	3.8	9
101	PbrSLAH3 is a nitrate-selective anion channel which is modulated by calcium-dependent protein kinase 32 in pear. <i>BMC Plant Biology</i> , 2019 , 19, 190	5.3	3
100	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	5.3	11
99	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	5.3	21
98	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	3.8	6
97	Unbiased subgenome evolution following a recent whole-genome duplication in pear (Rehd.). <i>Horticulture Research</i> , 2019 , 6, 34	7.7	31
96	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,	4.8	35
95	Comparative Transcriptomic Analysis Provides Insight into the Domestication and Improvement of Pear () Fruit. <i>Plant Physiology</i> , 2019 , 180, 435-452	6.6	20
94	Gene duplication and evolution in recurring polyploidization-diploidization cycles in plants. <i>Genome Biology</i> , 2019 , 20, 38	18.3	180

93	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	11.6	35
92	Phylogenetic and Expression Analyses of With-No-Lysine Kinase Genes Reveal Novel Gene Family Diversity in Fruit Trees. <i>Horticultural Plant Journal</i> , 2019 , 5, 47-58	4.3	4
91	Genome-wide survey and expression analysis of the SLAC/SLAH gene family in pear (<i>Pyrus bretschneideri</i>) and other members of the Rosaceae. <i>Genomics</i> , 2019 , 111, 1097-1107	4.3	7
90	A novel MYB transcription factor regulates ascorbic acid synthesis and affects cold tolerance. <i>Plant, Cell and Environment</i> , 2019 , 42, 832-845	8.4	45
89	The α -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	5.3	22
88	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	5.7	6
87	Self-incompatibility in Pear. <i>Compendium of Plant Genomes</i> , 2019 , 179-200	0.8	
86	The Genome of Pear. <i>Compendium of Plant Genomes</i> , 2019 , 133-143	0.8	
85	PbrPCCP1 mediates the PbrTTS1 signaling to control pollen tube growth in pear. <i>Plant Science</i> , 2019 , 289, 110244	5.3	2
84	Identification of Shaker K channel family members in Rosaceae and a functional exploration of PbrKAT1. <i>Planta</i> , 2019 , 250, 1911-1925	4.7	11
83	Genome-wide analysis of polygalacturonase gene family from pear genome and identification of the member involved in pear softening. <i>BMC Plant Biology</i> , 2019 , 19, 587	5.3	12
82	The involvement of in light-induced anthocyanin accumulation via the activation of through binding to tandem G-boxes in its promoter. <i>Horticulture Research</i> , 2019 , 6, 134	7.7	13
81	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	3.8	11
80	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	4.1	12
79	The gene PbtMT4 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	4.6	15
78	The unique evolutionary pattern of the Hydroxyproline-rich glycoproteins superfamily in Chinese white pear (<i>Pyrus bretschneideri</i>). <i>BMC Plant Biology</i> , 2018 , 18, 36	5.3	4
77	The mining and evolutionary investigation of AP2/ERF genes in pear (<i>Pyrus</i>). <i>BMC Plant Biology</i> , 2018 , 18, 46	5.3	28
76	Phosphatidic Acid Counteracts S-RNase Signaling in Pollen by Stabilizing the Actin Cytoskeleton. <i>Plant Cell</i> , 2018 , 30, 1023-1039	11.6	47

75	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 ^{1.9}	5
74	ViewBS: a powerful toolkit for visualization of high-throughput bisulfite sequencing data. <i>Bioinformatics</i> , 2018 , 34, 708-709	7.2 18
73	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>Frontiers in Plant Science</i> , 2018 , 9, 161	6.2 35
72	Chemical Composition and Crystal Morphology of Epicuticular Wax in Mature Fruits of 35 Pear (spp.) Cultivars. <i>Frontiers in Plant Science</i> , 2018 , 9, 679	6.2 19
71	Diversification and independent domestication of Asian and European pears. <i>Genome Biology</i> , 2018 , 19, 77	18.3 75
70	Identification and comparative analysis of the MCU gene family in pear and its functions during fruit ripening. <i>Journal of Plant Physiology</i> , 2018 , 229, 53-62	3.6 5
69	Characterization of the Genes Involved in Malic Acid Metabolism from Pear Fruit and Their Expression Profile after Postharvest 1-MCP/Ethrel Treatment. <i>Journal of Agricultural and Food Chemistry</i> , 2018 , 66, 8772-8782	5.7 12
68	PbGLR3.3 Regulates Pollen Tube Growth in the Mediation of Ca ²⁺ Influx in <i>Pyrus bretschneideri</i> 2018 , 61, 217-226	4
67	Network analysis reveals the co-expression of sugar and aroma genes in the Chinese white pear (<i>Pyrus bretschneideri</i>). <i>Gene</i> , 2018 , 677, 370-377	3.8 2
66	Genome-wide identification, evolution, and expression analysis of the KT/HAK/KUP family in pear. <i>Genome</i> , 2018 , 61, 755-765	2.4 18
65	Comparative analysis of the volatile organic compounds in mature fruits of 12 Occidental pear (<i>Pyrus communis</i> L.) cultivars. <i>Scientia Horticulturae</i> , 2018 , 240, 239-248	4.1 14
64	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	3.8 4
63	Physiological and Nutritional Responses of Pear Seedlings to Nitrate Concentrations. <i>Frontiers in Plant Science</i> , 2018 , 9, 1679	6.2 12
62	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	5.3 8
61	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	1 5
60	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 ^{3.2}	16
59	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	4.1 19
58	Evolution, expression analysis, and functional verification of <i>Catharanthus roseus</i> RLK1-like kinase (CrRLK1L) family proteins in pear (<i>Pyrus bretschneideri</i>). <i>Genomics</i> , 2017 , 109, 290-301	4.3 13

57	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, 289-301	4.5	22
56	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	6.2	28
55	Calcium treatments promote the aroma volatiles emission of pear (<i>Pyrus ussuriensis</i> [Languoli]) fruit during post-harvest ripening process. <i>Scientia Horticulturae</i> , 2017 , 215, 102-111	4.1	18
54	and : two transcriptionally active LTR retrotransposon subfamilies with a specific LTR structure and horizontal transfer in four Rosaceae species. <i>Mobile DNA</i> , 2017 , 8, 14	4.4	2
53	Expansion and evolutionary patterns of cysteine-rich peptides in plants. <i>BMC Genomics</i> , 2017 , 18, 610	4.5	6
52	Map-based cloning of the pear gene MYB114 identifies an interaction with other transcription factors to coordinately regulate fruit anthocyanin biosynthesis. <i>Plant Journal</i> , 2017 , 92, 437-451	6.9	147
51	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	5.1	19
50	Characterization of the MAPK Gene Family and PbrMAPK13 Response to Hormone and Temperature Stresses via Different Expression Pattern in <i>Pyrus bretschneideri</i> Pollen. <i>Journal of the American Society for Horticultural Science</i> , 2017 , 142, 163-174	2.3	0
49	PbCOL8 is a clock-regulated flowering time repressor in pear. <i>Tree Genetics and Genomes</i> , 2017 , 13, 1	2.1	2
48	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	1.3	14
47	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	4.5	27
46	Genome-wide identification of the transcription factor family in pear () reveals evolution and functional divergence. <i>PeerJ</i> , 2017 , 5, e3776	3.1	19
45	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	4.9	9
44	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	4.9	36
43	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, 1727-42	3.1	23
42	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	4.1	8
41	Phylogenetic and Expression Analysis of Pear Yellow Stripe-Like Transporters and Functional Verification of PbrYSL4 in Pear Pollen. <i>Plant Molecular Biology Reporter</i> , 2016 , 34, 737-747	1.7	2
40	Molecular characterization and expression pattern of sorbitol transporter gene PbSOT2 in Pear (<i>Pyrus bretschneideri</i> Rehd.) fruit. <i>Canadian Journal of Plant Science</i> , 2016 , 96, 128-137	1	7

39	Gene-expression profile of developing pollen tube of <i>Pyrus bretschneideri</i> . <i>Gene Expression Patterns</i> , 2016 , 20, 11-21	1.5	25
38	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	2.1	7
37	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	5.3	88
36	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	4.1	25
35	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	4.3	34
34	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	2.1	30
33	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	4.9	55
32	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	4.9	13
31	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	6.2	42
30	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	4.5	50
29	Mitochondrial dysfunction mediated by cytoplasmic acidification results in pollen tube growth cessation in <i>Pyrus pyrifolia</i> . <i>Physiologia Plantarum</i> , 2015 , 153, 603-15	4.6	15
28	Overexpression of PbDCHAR2 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	2.4	9
27	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	2.3	10
26	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	4.1	36
25	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, 255-63	5.1	25
24	Characterization of the lipoxygenase (LOX) gene family in the Chinese white pear (<i>Pyrus bretschneideri</i>) and comparison with other members of the Rosaceae. <i>BMC Genomics</i> , 2014 , 15, 444	4.5	33
23	Long-chain base phosphates modulate pollen tube growth via channel-mediated influx of calcium. <i>Plant Journal</i> , 2014 , 79, 507-16	6.9	15
22	Evolution of the aroma volatiles of pear fruits supplemented with fatty acid metabolic precursors. <i>Molecules</i> , 2014 , 19, 20183-96	4.8	26

21	Identification of miRNAs involved in pear fruit development and quality. <i>BMC Genomics</i> , 2014 , 15, 953	4.5	66
20	Comparative genomic analysis reveals multiple long terminal repeats, lineage-specific amplification, and frequent interelement recombination for Cassandra retrotransposon in pear (<i>Pyrus bretschneideri</i> Rehd.). <i>Genome Biology and Evolution</i> , 2014 , 6, 1423-36	3.9	20
19	Identifying the candidate genes involved in the calyx abscission process of 'Kuerlexiangli' (<i>Pyrus sinkiangensis</i> Yu) by digital transcript abundance measurements. <i>BMC Genomics</i> , 2013 , 14, 727	4.5	25
18	The genome of the pear (<i>Pyrus bretschneideri</i> Rehd.). <i>Genome Research</i> , 2013 , 23, 396-408	9.7	615
17	Molecular Determinants and Mechanisms of Gametophytic Self-Incompatibility in Fruit Trees of Rosaceae. <i>Critical Reviews in Plant Sciences</i> , 2013 , 32, 53-68	5.6	22
16	Molecular cloning and expression analysis of a gene for sucrose transporter from pear (<i>Pyrus bretschneideri</i> Rehd.) fruit. <i>Plant Physiology and Biochemistry</i> , 2013 , 73, 63-9	5.4	22
15	TARE1, a mutated Copia-like LTR retrotransposon followed by recent massive amplification in tomato. <i>PLoS ONE</i> , 2013 , 8, e68587	3.7	18
14	Fast loading ester fluorescent Ca ²⁺ and pH indicators into pollen of <i>Pyrus pyrifolia</i> . <i>Journal of Plant Research</i> , 2012 , 125, 185-95	2.6	21
13	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	2.6	3
12	Evaluation of the volatile profile of 33 <i>Pyrus ussuriensis</i> cultivars by HS-SPME with GC-MS. <i>Food Chemistry</i> , 2012 , 134, 2367-82	8.5	60
11	cAMP activates hyperpolarization-activated Ca ²⁺ channels in the pollen of <i>Pyrus pyrifolia</i> . <i>Plant Cell Reports</i> , 2011 , 30, 1193-200	5.1	21
10	Changes in germinability, lipid peroxidation, and antioxidant enzyme activities in pear stock (<i>Pyrus betulaefolia</i> Bge.) seeds during room- and low-temperature storage. <i>Acta Physiologiae Plantarum</i> , 2011 , 33, 2035-2040	2.6	9
9	Self-incompatibility in <i>Papaver rhoeas</i> activates nonspecific cation conductance permeable to Ca ²⁺ and K ⁺ . <i>Plant Physiology</i> , 2011 , 155, 963-73	6.6	43
8	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, 1042-53	6.9	152
7	In vitro antifungal activity and mode of action of selected polyphenolic antioxidants on <i>Botrytis cinerea</i> . <i>Archives of Phytopathology and Plant Protection</i> , 2010 , 43, 1564-1578	1	18
6	Anatomy, ultrastructure and lignin distribution of stone cells in two <i>Pyrus</i> species. <i>Plant Science</i> , 2009 , 176, 413-419	5.3	90
5	PROFILE OF ANTIOXIDANT ACTIVITIES OF SELECTED STRAWBERRY GENOTYPES. <i>Acta Horticulturae</i> , 2009 , 551-556	0.3	4
4	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	2.6	6

- 3 The effect of temperature, polyamines and polyamine synthesis inhibitor on in vitro pollen germination and pollen tube growth of *Prunus mume*. *Scientia Horticulturae*, **2004**, 99, 289-299 4.1 33
- 2 Characterization and Functional Explorations of O-glycosylation Enzymes SECRET AGENT and SPINDLY in *Pyrus bretschneideri*
- 1 Identification and testing of reference genes for qRT-PCR analysis during pear fruit development1 1