

The genome of the pear (<i>Pyrus bretschneideri</i> Re

Genome Research

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Transferability of Newly Developed Pear SSR Markers to Other Rosaceae Species. Plant Molecular Biology Reporter, 2013, 31, 1271-1282.	1.8	70
2	An AFLP, SRAP, and SSR Genetic Linkage Map and Identification of QTLs for Fruit Traits in Pear (Pyrus L.). Plant Molecular Biology Reporter, 2013, 31, 678-687.	1.8	69
3	Quantitative proteomic investigation employing stable isotope labeling by peptide dimethylation on proteins of strawberry fruit at different ripening stages. Journal of Proteomics, 2013, 94, 219-239.	2.4	66
4	The Biochemistry and Molecular Biology of Volatile Messengers in Trees. Tree Physiology, 2013, , 47-93.	2.5	25
5	Effect of cold storage and 1-MCP treatment on ethylene perception, signalling and synthesis: Influence on the development of the evergreen behaviour in "Conference" pears. Postharvest Biology and Technology, 2013, 86, 212-220.	6.0	60
6	Identifying the candidate genes involved in the calyx abscission process of 'Kuerlexiangli' (Pyrus) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 502 Td	2.8	32
7	Transcriptome profiling of fruit development and maturation in Chinese white pear (Pyrus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 502 Td	2.8	50
8	A genome-wide identification and characterization of mircoRNAs and their targets in "Suli" pear (Pyrus) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 502 Td	3.2	19
9	Arguments for standardizing transposable element annotation in plant genomes. Trends in Plant Science, 2013, 18, 367-376.	8.8	26
10	Selective Acquisition and Retention of Genomic Sequences by Pack- <i>mutator</i> -Like Elements Based on Guanine-Cytosine Content and the Breadth of Expression. Plant Physiology, 2013, 163, 1419-1432.	4.8	25
11	Molecular Analysis of the Processes of Surface Brown Spot (SBS) Formation in Pear Fruit (Pyrus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 502 Td	2.5	16
12	Evidence for regulation of columnar habit in apple by a putative 2-oxoglutarate-dependent dioxygenase. New Phytologist, 2013, 200, 993-999.	7.3	47
13	Expression and genomic structure of the dormancy-associated MADS box genes MADS13 in Japanese pears (Pyrus pyrifolia Nakai) that differ in their chilling requirement for endodormancy release. Tree Physiology, 2013, 33, 654-667.	3.1	91
14	Recent Advances in Temperate Fruit Crops. , 2013, , 251-284.		0
15	Transcriptome Analysis of Giant Pear Fruit with Fruit-specific DNA Reduplication on a Mutant Branch. Japanese Society for Horticultural Science, 2013, 82, 301-311.	0.8	10
16	Using genomics to improve fruit quality. Biological Research, 2013, 46, 347-352.	3.4	28
17	The First 50 Plant Genomes. Plant Genome, 2013, 6, plantgenome2013.03.0001in.	2.8	228
18	Identification of Pyrus Single Nucleotide Polymorphisms (SNPs) and Evaluation for Genetic Mapping in European Pear and Interspecific Pyrus Hybrids. PLoS ONE, 2013, 8, e77022.	2.5	64

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19	Origin, Domestication, and Dispersing of Pear (<i>Pyrus</i> spp.). <i>Advances in Agriculture</i> , 2014, 2014, 1-8.	0.9	35
20	Identification of miRNAs involved in pear fruit development and quality. <i>BMC Genomics</i> , 2014, 15, 953.	2.8	102
21	Genetic, metabolite and developmental determinism of fruit friction discolouration in pear. <i>BMC Plant Biology</i> , 2014, 14, 241.	3.6	16
22	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 50	1.5	64
23	Identification of QTLs controlling harvest time and fruit skin color in Japanese pear (<i>Pyrus pyrifolia</i>) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	1.9	64
24	The Evolution of Plant Gene and Genome Sequencing. <i>Advances in Botanical Research</i> , 2014, , 47-90.	1.1	6
25	Insights into the Common Ancestor of Eudicots. <i>Advances in Botanical Research</i> , 2014, 69, 137-174.	1.1	1
26	The complex jujube genome provides insights into fruit tree biology. <i>Nature Communications</i> , 2014, 5, 5315.	12.8	251
27	Genome-wide identification and expression analyses of cytochrome <i>P450</i> genes in mulberry (<i>Morus notabilis</i>). <i>Journal of Integrative Plant Biology</i> , 2014, 56, 887-901.	8.5	53
28	Genomics and bioinformatics resources for translational science in Rosaceae. <i>Plant Biotechnology Reports</i> , 2014, 8, 49-64.	1.5	18
29	Pigmentation in sand pear (<i>Pyrus pyrifolia</i>) fruit: biochemical characterization, gene discovery and expression analysis with exocarp pigmentation mutant. <i>Plant Molecular Biology</i> , 2014, 85, 123-134.	3.9	33
30	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
31	Heterologous gene silencing induced by tobacco rattle virus (TRV) is efficient for pursuing functional genomics studies in woody plants. <i>Plant Cell, Tissue and Organ Culture</i> , 2014, 116, 163-174.	2.3	24
32	Hypovirulence of the Phytopathogenic Fungus <i>Botryosphaeria dothidea</i> : Association with a Coinfecting Chrysovirus and a Partitivirus. <i>Journal of Virology</i> , 2014, 88, 7517-7527.	3.4	115
33	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.	3.6	48
34	Impact of tree training system, branch type and position in the canopy on the ripening homogeneity of 'Abb' pear fruit. <i>Tree Genetics and Genomes</i> , 2014, 10, 1477-1488.	1.6	14
35	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
36	Phylogeny and evolutionary histories of <i>Pyrus</i> L. revealed by phylogenetic trees and networks based on data from multiple DNA sequences. <i>Molecular Phylogenetics and Evolution</i> , 2014, 80, 54-65.	2.7	58

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37	Genomics and Functional Genomics of Winter Low Temperature Tolerance in Temperate Fruit Crops. Critical Reviews in Plant Sciences, 2014, 33, 125-140.	5.7	18
38	Analysis of 41 plant genomes supports a wave of successful genome duplications in association with the Cretaceous–Paleogene boundary. Genome Research, 2014, 24, 1334-1347.	5.5	381
39	Transcriptional control of fleshy fruit development and ripening. Journal of Experimental Botany, 2014, 65, 4527-4541.	4.8	296
40	Characterization of the lipoxygenase (LOX) gene family in the Chinese white pear (Pyrus) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	2.8	49
41	Comparative population genomics reveals the domestication history of the peach, <i>Prunus persica</i> , and human influences on perennial fruit crops. Genome Biology, 2014, 15, 415.	8.8	134
42	Genetic mapping of polygenic scab (<i>Venturia pirina</i>) resistance in an interspecific pear family. Molecular Breeding, 2014, 34, 2179-2189.	2.1	24
43	Investment in plant research and development bears fruit in China. Plant Cell Reports, 2014, 33, 541-550.	5.6	7
44	F1 hybrid of cultivated apple (<i>Malus domestica</i>) and European pear (<i>Pyrus communis</i>) with fertile F2 offspring. Molecular Breeding, 2014, 34, 817-828.	2.1	14
45	Development of genic SSR markers from transcriptome sequencing of pear buds. Journal of Zhejiang University: Science B, 2014, 15, 303-312.	2.8	23
46	Transcriptome-based single nucleotide polymorphism markers for genome mapping in Japanese pear (<i>Pyrus pyrifolia</i> Nakai). Tree Genetics and Genomes, 2014, 10, 853-863.	1.6	24
47	Comparative transcriptome analysis of eggplant (<i>Solanum melongena</i> L.) and turkey berry (<i>Solanum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 66	2.8	66
48	Genomics of <i>Erwinia amylovora</i> and Related <i>Erwinia</i> Species Associated with Pome Fruit Trees. , 2014, , 1-36.		13
49	Dissection of the Octoploid Strawberry Genome by Deep Sequencing of the Genomes of <i>Fragaria</i> Species. DNA Research, 2014, 21, 169-181.	3.4	201
50	Identification and characterization of <i>Colletotrichum fruticicola</i> causing black spots on young fruits related to bitter rot of pear (<i>Pyrus bretschneideri</i> Rehd.) in China. Crop Protection, 2014, 58, 41-48.	2.1	37
51	Proteomic analysis of “Zaosu” pear (<i>Pyrus bretschneideri</i> Rehd.) and its early-maturing bud sport. Plant Science, 2014, 224, 120-135.	3.6	15
52	The <i>Brassica oleracea</i> genome reveals the asymmetrical evolution of polyploid genomes. Nature Communications, 2014, 5, 3930.	12.8	918
53	The bright side of transposons in crop evolution. Briefings in Functional Genomics, 2014, 13, 276-295.	2.7	106
54	Understanding development and ripening of fruit crops in an “omics” era. Horticulture Research, 2014, 1, 14034.	6.3	53

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55	Biological and Molecular Characterization of Five <i>Phomopsis</i> Species Associated with Pear Shoot Canker in China. <i>Plant Disease</i> , 2015, 99, 1704-1712.	1.4	40
56	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	Genes Encoding Aluminum-Activated Malate Transporter II and their Association with Fruit Acidity in Apple. <i>Plant Genome</i> , 2015, 8, eplantgenome2015.03.0016.	2.8	55
59	An integrated database of wood-formation related genes in plants. <i>Scientific Reports</i> , 2015, 5, 11422.	3.3	3
60	Sequencing of plant genomes – a review. <i>Turk Tarim Ve Ormancilik Dergisi/Turkish Journal of Agriculture and Forestry</i> , 2015, 39, 361-376.	2.1	20
61	A dense SNP genetic map constructed using restriction site-associated DNA sequencing enables detection of QTLs controlling apple fruit quality. <i>BMC Genomics</i> , 2015, 16, 747.	2.8	83
62	Transcriptome sequencing and analysis of major genes involved in calcium signaling pathways in pear plants (<i>Pyrus calleryana</i> Decne.). <i>BMC Genomics</i> , 2015, 16, 738.	2.8	19
63	Developing expressed sequence tag libraries and the discovery of simple sequence repeat markers for two species of raspberry (<i>Rubus</i> L.). <i>BMC Plant Biology</i> , 2015, 15, 258.	3.6	13
64	MnTEdb, a collective resource for mulberry transposable elements. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, .	3.0	25
65	A transcriptome approach towards understanding the development of ripening capacity in ‘Bartlett’ pears (<i>Pyrus communis</i> L.). <i>BMC Genomics</i> , 2015, 16, 762.	2.8	25
66	Identification and characterization of microRNAs from in vitro-grown pear shoots infected with Apple stem grooving virus in response to high temperature using small RNA sequencing. <i>BMC Genomics</i> , 2015, 16, 945.	2.8	22
67	De novo assembly, functional annotation, and marker development of Asian pear (<i>Pyrus pyrifolia</i>) fruit transcriptome through massively parallel sequencing. <i>Genetics and Molecular Research</i> , 2015, 14, 18344-18355.	0.2	1
68	Genome-Wide Analysis of Sorbitol Dehydrogenase (SDH) Genes and Their Differential Expression in Two Sand Pear (<i>Pyrus pyrifolia</i>) Fruits. <i>International Journal of Molecular Sciences</i> , 2015, 16, 13065-13083.	4.1	16
69	A Zinc-Dependent Protease AMZ- <i>tk</i> from a Thermophilic Archaeon is a New Member of the Archaeometzincin Protein Family. <i>Frontiers in Microbiology</i> , 2015, 6, 1380.	3.5	13
70	Genome-Wide Characterization of Simple Sequence Repeat (SSR) Loci in Chinese Jujube and Jujube SSR Primer Transferability. <i>PLoS ONE</i> , 2015, 10, e0127812.	2.5	48
71	Metabolic Profiling of Developing Pear Fruits Reveals Dynamic Variation in Primary and Secondary Metabolites, Including Plant Hormones. <i>PLoS ONE</i> , 2015, 10, e0131408.	2.5	69
72	Candidate Resistant Genes of Sand Pear (<i>Pyrus pyrifolia</i> Nakai) to <i>Alternaria alternata</i> Revealed by Transcriptome Sequencing. <i>PLoS ONE</i> , 2015, 10, e0135046.	2.5	21
73	PyMYB10 and PyMYB10.1 Interact with bHLH to Enhance Anthocyanin Accumulation in Pears. <i>PLoS ONE</i> , 2015, 10, e0142112.	2.5	36

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74	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
75	Next Generation Sequencing Technologies: The Doorway to the Unexplored Genomics of Non-Model Plants. <i>Frontiers in Plant Science</i> , 2015, 6, 1074.	3.6	173
76	Whole Genome Sequencing of Fruit Tree Species. <i>Advances in Botanical Research</i> , 2015, , 1-37.	1.1	13
77	Karyotype and Gene Order Evolution from Reconstructed Extinct Ancestors Highlight Contrasts in Genome Plasticity of Modern Rosid Crops. <i>Genome Biology and Evolution</i> , 2015, 7, 735-749.	2.5	46
78	Quality assessment of pear juice under ultrasound and commercial pasteurization processing conditions. <i>LWT - Food Science and Technology</i> , 2015, 64, 452-458.	5.2	127
79	Genome-wide identification and characterization of R2R3-MYB transcription factors in pear. <i>Scientia Horticulturae</i> , 2015, 197, 176-182.	3.6	18
80	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.	2.8	76
81	Next-Generation Sequencing (NGS) Tools and Impact in Plant Breeding. , 2015, , 563-612.		8
82	Construction of a SNP-based high-density genetic map for pummelo using RAD sequencing. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	1.6	46
83	Systematic selection and validation of appropriate reference genes for gene expression studies by quantitative real-time PCR in pear. <i>Acta Physiologiae Plantarum</i> , 2015, 37, 1.	2.1	34
84	Proteome analysis of pear reveals key genes associated with fruit development and quality. <i>Planta</i> , 2015, 241, 1363-1379.	3.2	42
85	Species-specific duplications driving the recent expansion of NBS-LRR genes in five Rosaceae species. <i>BMC Genomics</i> , 2015, 16, 77.	2.8	39
86	Progress, challenges and the future of crop genomes. <i>Current Opinion in Plant Biology</i> , 2015, 24, 71-81.	7.1	197
87	Recent Advances in Genetics and Molecular Control of Bud Dormancy in Pipfruits. , 2015, , 107-122.		6
88	Acceleration of Forest and Fruit Tree Domestication by Genomic Selection. <i>Advances in Botanical Research</i> , 2015, , 93-124.	1.1	16
89	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
90	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
91	Columnar apple primary roots share some features of the columnar-specific gene expression profile of aerial plant parts as evidenced by RNA-Seq analysis. <i>BMC Plant Biology</i> , 2015, 15, 34.	3.6	17

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92	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.	3.6	138
93	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
94	Extreme expansion of NBS-encoding genes in Rosaceae. <i>BMC Genetics</i> , 2015, 16, 48.	2.7	84
95	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
96	A standard nomenclature for gene designation in the Rosaceae. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	1.6	17
97	DNA Sequencing, Other Omics and Synthetic Biology. , 2015, , 125-140.		0
98	An RNA-Seq analysis of the pear (<i>Pyrus communis</i> L.) transcriptome, with a focus on genes associated with dwarf. <i>Plant Gene</i> , 2015, 4, 69-77.	2.3	20
99	High resolution physical mapping of single gene fragments on pachytene chromosome 4 and 7 of <i>Rosa</i> . <i>BMC Genetics</i> , 2015, 16, 74.	2.7	9
100	Physiological and Molecular Regulation of Adventitious Root Formation. <i>Critical Reviews in Plant Sciences</i> , 2015, 34, 506-521.	5.7	71
101	Homologues of potato chromosome 5 show variable collinearity in the euchromatin, but dramatic absence of sequence similarity in the pericentromeric heterochromatin. <i>BMC Genomics</i> , 2015, 16, 374.	2.8	15
102	Molecular basis of angiosperm tree architecture. <i>New Phytologist</i> , 2015, 206, 541-556.	7.3	81
103	Early proteomic changes in pear (<i>Pyrus communis</i> L.) calli induced by co-culture on microcallus suspension of incompatible quince (<i>Cydonia oblonga</i> Mill.). <i>Scientia Horticulturae</i> , 2015, 194, 337-343.	3.6	7
104	Genetic mapping of <i>Cacopsylla pyri</i> resistance in an interspecific pear (<i>Pyrus</i> spp.) population. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	1.6	17
105	Genetic mapping and pyramiding of two new pear scab resistance QTLs. <i>Molecular Breeding</i> , 2015, 35, 1.	2.1	12
106	Genome-wide identification, characterization, and expression analysis of the dehydrin gene family in Asian pear (<i>Pyrus pyrifolia</i>). <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	1.6	17
107	Hybrid seedling inviability locus (Hls1) mapped on linkage group 4 of the Japanese flowering cherry, <i>Cerasus</i> — <i>yedoensis</i> ‘Somei-yoshino’™. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	1.6	6
108	A taste of pineapple evolution through genome sequencing. <i>Nature Genetics</i> , 2015, 47, 1374-1376.	21.4	5
109	A major QTL controlling apple skin russetting maps on the linkage group 12 of ‘Renetta Grigia di Torriana’™. <i>BMC Plant Biology</i> , 2015, 15, 150.	3.6	49

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110	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.	2.9	52
111	Genomic resources in fruit plants: an assessment of current status. <i>Critical Reviews in Biotechnology</i> , 2015, 35, 438-447.	9.0	16
112	Prediction of retrotransposons and assessment of genetic variability based on developed retrotransposon-based insertion polymorphism (RBIP) markers in <i>Pyrus</i> L. <i>Molecular Genetics and Genomics</i> , 2015, 290, 225-237.	2.1	17
113	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
114	Application of Genomic Technologies to the Breeding of Trees. <i>Frontiers in Genetics</i> , 2016, 7, 198.	2.3	45
115	Systematic Analysis of the 4-Coumarate:Coenzyme A Ligase (4CL) Related Genes and Expression Profiling during Fruit Development in the Chinese Pear. <i>Genes</i> , 2016, 7, 89.	2.4	51
116	Genomics of pear and other Rosaceae fruit trees. <i>Breeding Science</i> , 2016, 66, 148-159.	1.9	48
117	Primitive Genepools of Asian Pears and Their Complex Hybrid Origins Inferred from Fluorescent Sequence-Specific Amplification Polymorphism (SSAP) Markers Based on LTR Retrotransposons. <i>PLoS ONE</i> , 2016, 11, e0149192.	2.5	23
118	MYB Transcription Factors in Chinese Pear (<i>Pyrus bretschneideri</i> Rehd.): Genome-Wide Identification, Classification, and Expression Profiling during Fruit Development. <i>Frontiers in Plant Science</i> , 2016, 7, 577.	3.6	143
119	Genome-Wide Sequence Variation Identification and Floral-Associated Trait Comparisons Based on the Re-sequencing of the "Nagafu No. 2"™ and "Qinguan"™ Varieties of Apple (<i>Malus domestica</i> Borkh.). <i>Frontiers in Plant Science</i> , 2016, 7, 908.	3.6	33
120	Characterization of CIPK Family in Asian Pear (<i>Pyrus bretschneideri</i> Rehd) and Co-expression Analysis Related to Salt and Osmotic Stress Responses. <i>Frontiers in Plant Science</i> , 2016, 7, 1361.	3.6	26
121	Comparative Genomic Analysis of the GRF Genes in Chinese Pear (<i>Pyrus bretschneideri</i> Rehd), Poplar (<i>Populus</i>), Grape (<i>Vitis vinifera</i>), Arabidopsis and Rice (<i>Oryza sativa</i>). <i>Frontiers in Plant Science</i> , 2016, 7, 1750.	3.6	97
122	Structural, Evolutionary, and Functional Analysis of the Class III Peroxidase Gene Family in Chinese Pear (<i>Pyrus bretschneideri</i>). <i>Frontiers in Plant Science</i> , 2016, 7, 1874.	3.6	83
123	Fine mapping of the gene for susceptibility to black spot disease in Japanese pear (<i>Pyrus</i> Tj ETQq1 1 0.784314 rgBT /Overloc	1.9	20
124	The genome of black raspberry (<i>Rubus occidentalis</i>). <i>Plant Journal</i> , 2016, 87, 535-547.	5.7	111
125	Genome mapping of postzygotic hybrid necrosis in an interspecific pear population. <i>Horticulture Research</i> , 2016, 3, 15064.	6.3	15
126	Emerging Genomics of Angiosperm Trees. <i>Plant Genetics and Genomics: Crops and Models</i> , 2016, , 85-99.	0.3	0
127	Fruit Ripening in Melon. <i>Plant Genetics and Genomics: Crops and Models</i> , 2016, , 345-375.	0.3	4

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128	Structural Genomics of Angiosperm Trees: Genome Duplications, Ploidy, and Repeat Sequences. <i>Plant Genetics and Genomics: Crops and Models</i> , 2016, , 101-120.	0.3	0
129	Role of Genomics in Enhancing Nutrition Content of Cereals. , 2016, , 77-96.		1
130	Genome-wide analysis of the synonymous codon usage patterns in apple. <i>Journal of Integrative Agriculture</i> , 2016, 15, 983-991.	3.5	20
131	Transcriptome profiling reveals differentially expressed genes associated with wizened flower bud formation in Chinese pear (<i>Pyrus bretschneideri</i> Rehd.). <i>Journal of Horticultural Science and Biotechnology</i> , 2016, 91, 227-235.	1.9	4
132	Development of molecular markers for genetic and physical mapping of the <i>PcDw</i> locus in pear (<i>Pyrus communis</i> L.). <i>Journal of Horticultural Science and Biotechnology</i> , 2016, 91, 299-307.	1.9	7
133	F-box genes: Genome-wide expansion, evolution and their contribution to pollen growth in pear (<i>Pyrus bretschneideri</i>). <i>Plant Science</i> , 2016, 253, 164-175.	3.6	42
134	Evolution and expression patterns of cytokinin oxidase genes in <i>Fragaria vesca</i> . <i>Scientia Horticulturae</i> , 2016, 212, 115-125.	3.6	12
135	Mono- and sesquiterpene release from tomato (<i>Solanum lycopersicum</i>) leaves upon mild and severe heat stress and through recovery: From gene expression to emission responses. <i>Environmental and Experimental Botany</i> , 2016, 132, 1-15.	4.2	51
136	Construction of a high-density SNP genetic map in flue-cured tobacco based on SLAF-seq. <i>Molecular Breeding</i> , 2016, 36, 1.	2.1	44
137	Volatile profiling of two pear genotypes with different potential for white pear aroma improvement. <i>Scientia Horticulturae</i> , 2016, 209, 221-228.	3.6	11
138	The role of Ca ²⁺ and Ca ²⁺ channels in the gametophytic self-incompatibility of <i>Pyrus pyrifolia</i> . <i>Cell Calcium</i> , 2016, 60, 299-308.	2.4	15
139	Identification of russet-associated microRNAs in the exocarp of a Dangshansuli pear mutant (<i>Pyrus</i>) Tj ETQq1 1 0.784314 rgBT /Overl	1.6	4
140	Evolution of Rosaceae Fruit Types Based on Nuclear Phylogeny in the Context of Geological Times and Genome Duplication. <i>Molecular Biology and Evolution</i> , 2017, 34, msw242.	8.9	200
141	Characterization of virus-derived small interfering RNAs in Apple stem grooving virus-infected in vitro-cultured <i>Pyrus pyrifolia</i> shoot tips in response to high temperature treatment. <i>Virology Journal</i> , 2016, 13, 166.	3.4	16
142	Polygenic inheritance of resistance to <i>Cacopsylla pyri</i> in a <i>Pyrus communis</i> × <i>P. ussuriensis</i> progeny is explained by three QTLs involving an epistatic interaction. <i>Tree Genetics and Genomes</i> , 2016, 12, 1.	1.6	7
143	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.	3.3	16
144	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
145	The walnut (<i>Juglans regia</i>) genome sequence reveals diversity in genes coding for the biosynthesis of non-structural polyphenols. <i>Plant Journal</i> , 2016, 87, 507-532.	5.7	233

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146	A QTL detected in an interspecific pear population confers stable fire blight resistance across different environments and genetic backgrounds. <i>Molecular Breeding</i> , 2016, 36, 1.	2.1	25
147	Small RNA and PARE sequencing in flower bud reveal the involvement of sRNAs in endodormancy release of Japanese pear (<i>Pyrus pyrifolia</i> 'Kosui'). <i>BMC Genomics</i> , 2016, 17, 230.	2.8	25
148	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.	2.1	32
149	Advances in Genetic Diversity Analysis in Fruit Tree Crops. <i>Progress in Botany Fortschritte Der Botanik</i> , 2016, , 245-264.	0.3	4
150	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
151	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.	3.6	15
152	Landscape and evolutionary dynamics of terminal repeat retrotransposons in miniature in plant genomes. <i>Genome Biology</i> , 2016, 17, 7.	8.8	50
153	Evolution of plant genome architecture. <i>Genome Biology</i> , 2016, 17, 37.	8.8	331
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155	Quantitative Proteomics-Based Reconstruction and Identification of Metabolic Pathways and Membrane Transport Proteins Related to Sugar Accumulation in Developing Fruits of Pear (<i>Pyrus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 62	3.6	25
156	Cloning, localization and expression analysis of two fw2.2-like genes in small- and large-fruited pear species. <i>Journal of Integrative Agriculture</i> , 2016, 15, 282-294.	3.5	16
157	Molecular characterization of pear 14-3-3b gene regulated during fruit development. <i>Canadian Journal of Plant Science</i> , 2016, 96, 433-438.	0.9	0
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159	Involvement of <i>EARLY BUD-BREAK</i> , an AP2/ERF Transcription Factor Gene, in Bud Break in Japanese Pear (<i>Pyrus pyrifolia</i> Nakai) Lateral Flower Buds: Expression, Histone Modifications and Possible Target Genes. <i>Plant and Cell Physiology</i> , 2016, 57, 1038-1047.	3.1	49
160	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.	0.9	11
161	The Genome of the Model Moss <i>Physcomitrella patens</i> . <i>Advances in Botanical Research</i> , 2016, 78, 97-140.	1.1	9
162	Characterization of DNA methyltransferase and demethylase genes in <i>Fragaria vesca</i> . <i>Molecular Genetics and Genomics</i> , 2016, 291, 1333-1345.	2.1	37
163	Two MYB transcription factors regulate flavonoid biosynthesis in pear fruit (<i>Pyrus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 62	4.8	137

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165	Gene-expression profile of developing pollen tube of <i>Pyrus bretschneideri</i> . <i>Gene Expression Patterns</i> , 2016, 20, 11-21.	0.8	40
166	Dormancy-associated MADS-box genes and microRNAs jointly control dormancy transition in pear (<i>Pyrus pyrifolia</i> white pear group) flower bud. <i>Journal of Experimental Botany</i> , 2016, 67, 239-257.	4.8	170
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168	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
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173	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.	2.9	25
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177	Potassium enhances the sugar assimilation in leaves and fruit by regulating the expression of key genes involved in sugar metabolism of Asian pears. <i>Plant Growth Regulation</i> , 2017, 83, 287-300.	3.4	38
178	The genome sequence of sweet cherry (<i>Prunus avium</i>) for use in genomics-assisted breeding. <i>DNA Research</i> , 2017, 24, 499-508.	3.4	212
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180	Comprehensive analysis of differentially expressed genes under salt stress in pear (<i>Pyrus betulaefolia</i>) using RNA-Seq. <i>Plant Growth Regulation</i> , 2017, 82, 409-420.	3.4	13
181	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

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183	Differential gene expression analysis of “Chili”™ (<i>Pyrus bretschneideri</i>) fruit pericarp with two types of bagging treatments. <i>Horticulture Research</i> , 2017, 4, 17005.	6.3	25
184	Comparative transcriptome analysis of <i>Ziziphus jujuba</i> infected by jujube witches’ broom phytoplasmas. <i>Scientia Horticulturae</i> , 2017, 226, 50-58.	3.6	21
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215	Plant secondary metabolites and its dynamical systems of induction in response to environmental factors: A review. <i>African Journal of Agricultural Research Vol Pp</i> , 2017, 12, 71-84.	0.5	61
216	Identification, classification, and transcription profiles of the B-type response regulator family in pear. <i>PLoS ONE</i> , 2017, 12, e0171523.	2.5	28
217	Comparison of the transcriptomic analysis between two Chinese white pear (<i>Pyrus bretschneideri</i>) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	2.5	34
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231	Evolutionary diversification of galactinol synthases in Rosaceae: adaptive roles of galactinol and raffinose during apple bud dormancy. <i>Journal of Experimental Botany</i> , 2018, 69, 1247-1259.	4.8	33
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239	Phylogeny relationship among commercial and wild pear species based on morphological characteristics and SCoT molecular markers. <i>Scientia Horticulturae</i> , 2018, 235, 323-333.	3.6	25
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246	Characterization and expression analysis of PbEXP genes in the epidermis of pear (<i>Pyrus bretschneideri</i>) Tj ETQq1 1,0784314 rgBT /Overlock 10 Tf 50	3.4	20
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253	Characterization and expression of the ABC family (G group) in "Dangshansuli"™ pear (<i>Pyrus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.3	8
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274	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	4.1	74
275	Combined Analyses of Chloroplast DNA Haplotypes and Microsatellite Markers Reveal New Insights Into the Origin and Dissemination Route of Cultivated Pears Native to East Asia. <i>Frontiers in Plant Science</i> , 2018, 9, 591.	3.6	18
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277	Characterizing the expression of translation elongation factor gene EF1 α in pear (<i>Pyrus</i>) fruit: evaluation of EF1 α as a housekeeping gene. <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	1.6	2
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281	Cherry Breeding: Sweet Cherry (<i>Prunus avium</i> L.) and Sour Cherry (<i>Prunus cerasus</i> L.). , 2018, , 31-88.		2
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286	Draft genome sequence of Japanese pear (<i>Pyrus pyrifolia</i>). <i>Data in Brief</i> , 2018, 19, 2221-2223.	1.0	1
287	Genome Wide Identification, Evolutionary, and Expression Analysis of VQ Genes from Two <i>Pyrus</i> Species. <i>Genes</i> , 2018, 9, 224.	2.4	16
288	Absciscic Acid (ABA) Promotes the Induction and Maintenance of Pear (<i>Pyrus pyrifolia</i> White Pear) Tj ETQq1 1 0.784314 rgBT /Overclock 10	4.1	74
289	The Sucrose Synthase Gene Family in Chinese Pear (<i>Pyrus bretschneideri</i> Rehd.): Structure, Expression, and Evolution. <i>Molecules</i> , 2018, 23, 1144.	3.8	47
290	Comparative and Expression Analysis of Ubiquitin Conjugating Domain-Containing Genes in Two <i>Pyrus</i> Species. <i>Cells</i> , 2018, 7, 77.	4.1	24

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292	Genome-wide characterization of simple sequence repeats in <i>Pyrus bretschneideri</i> and their application in an analysis of genetic diversity in pear. BMC Genomics, 2018, 19, 473.	2.8	22
293	Transcriptome analyses provide new possible mechanisms of aroma ester weakening of "Nanguo" pear after cold storage. Scientia Horticulturae, 2018, 237, 247-256.	3.6	29
294	Comparative Analysis of Transcriptomes to Identify Genes Associated with Fruit Size in the Early Stage of Fruit Development in <i>Pyrus pyrifolia</i> . International Journal of Molecular Sciences, 2018, 19, 2342.	4.1	18
295	The genetic locus underlying red foliage and fruit skin traits is mapped to the same location in the two pear bud mutants "Red Zaosu" and "Max Red Bartlett". Hereditas, 2018, 155, 25.	1.4	9
296	PbGLR3.3 Regulates Pollen Tube Growth in the Mediation of Ca ²⁺ Influx in <i>Pyrus bretschneideri</i> . Journal of Plant Biology, 2018, 61, 217-226.	2.1	7
297	Selection and validation of suitable reference genes for qRT-PCR analysis in pear leaf tissues under distinct training systems. PLoS ONE, 2018, 13, e0202472.	2.5	9
298	Quantitative trait loci (QTL) mapping of blush skin and flowering time in a European pear (<i>Pyrus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.6	6
299	Network analysis reveals the co-expression of sugar and aroma genes in the Chinese white pear (<i>Pyrus</i>) Tj ETQq0 0 0 rgBT /Overlock 10	2.2	5
300	Genome-wide identification, evolution, and expression analysis of the <i>KT/HAK/KUP</i> family in pear. Genome, 2018, 61, 755-765.	2.0	25
301	Sequence and Analysis of the Black Raspberry (<i>Rubus occidentalis</i>) Genome. Compendium of Plant Genomes, 2018, , 185-197.	0.5	3
302	Expansion and evolutionary patterns of GDSL-type esterases/lipases in Rosaceae genomes. Functional and Integrative Genomics, 2018, 18, 673-684.	3.5	37
303	Genome survey sequencing of <i>Dioscorea zingiberensis</i> . Genome, 2018, 61, 567-574.	2.0	18
304	Genomic Resources for the Woodland Strawberry (<i>Fragaria vesca</i>). Compendium of Plant Genomes, 2018, , 25-33.	0.5	3
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306	<i>PbrmiR397a</i> regulates lignification during stone cell development in pear fruit. Plant Biotechnology Journal, 2019, 17, 103-117.	8.3	114
307	Genome-wide identification and analysis of the MADS-box gene family and its potential role in fruit development and ripening in red bayberry (<i>Morella rubra</i>). Gene, 2019, 717, 144045.	2.2	13
308	Identification of miRNAs involved in fruit ripening by deep sequencing of <i>Olea europaea</i> L. transcriptome. PLoS ONE, 2019, 14, e0221460.	2.5	18

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311	Differential retention of transposable element-derived sequences in outcrossing Arabidopsis genomes. Mobile DNA, 2019, 10, 30.	3.6	26
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319	Whole-Genome Duplications in Pear and Apple. Compendium of Plant Genomes, 2019, , 279-299.	0.5	11
320	Genetic Diversity and Domestication History in Pyrus. Compendium of Plant Genomes, 2019, , 51-62.	0.5	5
321	Marker-trait associations and genomic predictions of interspecific pear (Pyrus) fruit characteristics. Scientific Reports, 2019, 9, 9072.	3.3	38
322	Stone Cell Development in Pear. Compendium of Plant Genomes, 2019, , 201-225.	0.5	5
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324	Molecular Mapping of Major Genes and QTLs in Pear. Compendium of Plant Genomes, 2019, , 113-131.	0.5	4
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329	Evolutionary Rate Heterogeneity and Functional Divergence of Orthologous Genes in <i>Pyrus</i> . <i>Biomolecules</i> , 2019, 9, 490.	4.0	10
330	Auxin regulates adventitious root formation in tomato cuttings. <i>BMC Plant Biology</i> , 2019, 19, 435.	3.6	69
331	Single-pollen-cell sequencing for gamete-based phased diploid genome assembly in plants. <i>Genome Research</i> , 2019, 29, 1889-1899.	5.5	28
332	<i>Colletotrichum</i> species associated with anthracnose of <i>Pyrus</i> spp. in China. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2019, 42, 1-35.	4.4	113
333	Integrated genetic linkage maps for Korean pears (<i>Pyrus</i> hybrid) using GBS-based SNPs and SSRs. <i>Horticulture Environment and Biotechnology</i> , 2019, 60, 779-786.	2.1	9
334	MYB Gene Family in Potato (<i>Solanum tuberosum</i> L.): Genome-Wide Identification of Hormone-Responsive Reveals Their Potential Functions in Growth and Development. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4847.	4.1	74
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337	PbrMYB169 positively regulates lignification of stone cells in pear fruit. <i>Journal of Experimental Botany</i> , 2019, 70, 1801-1814.	4.8	73
338	Efficient Targeted Mutagenesis in Apple and First Time Edition of Pear Using the CRISPR-Cas9 System. <i>Frontiers in Plant Science</i> , 2019, 10, 40.	3.6	163
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342	Sequencing of a Wild Apple (<i>Malus baccata</i>) Genome Unravels the Differences Between Cultivated and Wild Apple Species Regarding Disease Resistance and Cold Tolerance. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2051-2060.	1.8	47
343	Genome Size Variation within Species of Chinese Jujube (<i>Ziziphus jujuba</i> Mill.) and Its Wild Ancestor Sour Jujube (<i>Z. acidujuba</i> Cheng et Liu). <i>Forests</i> , 2019, 10, 460.	2.1	14
344	In Silico Genome-Wide Analysis of Respiratory Burst Oxidase Homolog (RBOH) Family Genes in Five Fruit-Producing Trees, and Potential Functional Analysis on Lignification of Stone Cells in Chinese White Pear. <i>Cells</i> , 2019, 8, 520.	4.1	37

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347	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.	3.6	41
348	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
349	Phylogenetic and Expression Analysis of Mn-CDF Transporters in Pear (<i>Pyrus bretschneideri</i> Rehd.). <i>Plant Molecular Biology Reporter</i> , 2019, 37, 98-110.	1.8	9
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351	Insight on Rosaceae Family with Genome Sequencing and Functional Genomics Perspective. <i>BioMed Research International</i> , 2019, 2019, 1-12.	1.9	21
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354	Identifying Genome-Wide Sequence Variations and Candidate Genes Implicated in Self-Incompatibility by Resequencing <i>Fragaria viridis</i> . <i>International Journal of Molecular Sciences</i> , 2019, 20, 1039.	4.1	6
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357	BBX16, a B-box protein, positively regulates light-induced anthocyanin accumulation by activating MYB10 in red pear. <i>Plant Biotechnology Journal</i> , 2019, 17, 1985-1997.	8.3	184
358	Transcriptome sequencing of Himalayan Raspberry (<i>Rubus ellipticus</i>) and development of simple sequence repeat markers. <i>3 Biotech</i> , 2019, 9, 161.	2.2	11
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365	Evolution and functional divergence of MADS-box genes in <i>Pyrus</i> . <i>Scientific Reports</i> , 2019, 9, 1266.	3.3	15
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370	Genotyping-by-sequencing approaches using optimized two-enzyme combinations in Asian pears (<i>Pyrus</i>) Tj ETQq1 1 0.784314 rgBT /Qv	2.1	2
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377	Transcriptomic and evolutionary analyses of white pear (<i>Pyrus bretschneideri</i>) β -amylase genes reveals their importance for cold and drought stress responses. <i>Gene</i> , 2019, 689, 102-113.	2.2	22
378	Molecular identification, phylogenomic characterization and expression patterns analysis of the LIM (LIN-11, Isl1 and MEC-3 domains) gene family in pear (<i>Pyrus bretschneideri</i>) reveal its potential role in lignin metabolism. <i>Gene</i> , 2019, 686, 237-249.	2.2	29
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383	Investigations into the production of volatile compounds in Korla fragrant pears (<i>Pyrus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50,662 Td (si	8.2	32
384	<i>De novo</i> assembly of a wild pear (<i>Pyrus betuleafolia</i>) genome. Plant Biotechnology Journal, 2020, 18, 581-595.	8.3	72
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388	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
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390	RNA-Seq analysis of compatible and incompatible styles of <i>Pyrus</i> species at the beginning of pollination. Plant Molecular Biology, 2020, 102, 287-306.	3.9	6
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401	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
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403	Advances in Genomic, Transcriptomic, and Metabolomic Analyses of Fruit Quality in Fruit Crops. <i>Horticultural Plant Journal</i> , 2020, 6, 361-371.	5.0	33
404	Genome-wide survey of sucrose non-fermenting 1-related protein kinase 2 in Rosaceae and expression analysis of PbrSnRK2 in response to ABA stress. <i>BMC Genomics</i> , 2020, 21, 781.	2.8	11
405	Genome-wide characterization of the cellulose synthase gene superfamily in <i>Pyrus bretschneideri</i> and reveal its potential role in stone cell formation. <i>Functional and Integrative Genomics</i> , 2020, 20, 723-738.	3.5	13
406	Reconstruction of the Largest Pedigree Network for Pear Cultivars and Evaluation of the Genetic Diversity of the USDA-ARS National <i>Pyrus</i> Collection. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3285-3297.	1.8	18
407	Characterization and Comparison of Two Complete Plastomes of Rosaceae Species (<i>Potentilla dickinsii</i>) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf</i> <i>Molecular Sciences</i> , 2020, 21, 4933.	4.1	14
408	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.	0.9	7
409	Gene structure, evolution and expression analysis of the P-ATPase gene family in Chinese pear (<i>Pyrus</i>) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf</i>	2.5	21
410	Light-Induced Basic/Helix-Loop-Helix64 Enhances Anthocyanin Biosynthesis and Undergoes CONSTITUTIVELY PHOTOMORPHOGENIC1-Mediated Degradation in Pear. <i>Plant Physiology</i> , 2020, 184, 1684-1701.	4.8	46
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413	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.	2.8	9
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416	Multiomics analyses unveil the involvement of microRNAs in pear fruit senescence under high- or low-temperature conditions. <i>Horticulture Research</i> , 2020, 7, 196.	6.3	11

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418	Genome-Wide Identification of the Vacuolar H ⁺ -ATPase Gene Family in Five Rosaceae Species and Expression Analysis in Pear (<i>Pyrus bretschneideri</i>). Plants, 2020, 9, 1661.	3.5	3
419	Comparative physiological and transcriptomic analysis of pear leaves under distinct training systems. Scientific Reports, 2020, 10, 18892.	3.3	5
420	Pearprocess: A new phenotypic tool for stone cell trait evaluation in pear fruit. Journal of Integrative Agriculture, 2020, 19, 1625-1634.	3.5	10
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429	Molecular karyotypes of loquat (<i>Eriobotrya japonica</i>) aneuploids can be detected by using SSR markers combined with quantitative PCR irrespective of heterozygosity. Plant Methods, 2020, 16, 22.	4.3	9
430	Expression and evolutionary analysis of soluble inorganic pyrophosphatase gene family in pear and four other Rosaceae species. Plant Systematics and Evolution, 2020, 306, 1.	0.9	5
431	A high-quality genome provides insights into the new taxonomic status and genomic characteristics of <i>Cladopus chinensis</i> (Podostemaceae). Horticulture Research, 2020, 7, 46.	6.3	11
432	Characterization of the Auxin Efflux Transporter PIN Proteins in Pear. Plants, 2020, 9, 349.	3.5	19
433	REVEILLE Transcription Factors Contribute to the Nighttime Accumulation of Anthocyanins in 'Red Zaosu' (Pyrus Bretschneideri Rehd.) Pear Fruit Skin. International Journal of Molecular Sciences, 2020, 21, 1634.	4.1	14
434	A Chinese White Pear (<i>Pyrus bretschneideri</i>) BZR Gene PbBZR1 Act as a Transcriptional Repressor of Lignin Biosynthetic Genes in Fruits. Frontiers in Plant Science, 2020, 11, 1087.	3.6	16

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436	Characterization and Expression of KT/HAK/KUP Transporter Family Genes in Willow under Potassium Deficiency, Drought, and Salt Stresses. <i>BioMed Research International</i> , 2020, 2020, 1-12.	1.9	23
437	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.	3.6	7
438	PbGA20ox2 Regulates Fruit Set and Induces Parthenocarp by Enhancing GA4 Content. <i>Frontiers in Plant Science</i> , 2020, 11, 113.	3.6	26
439	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
440	Histone Acetylation at the Promoter for the Transcription Factor PuWRKY31 Affects Sucrose Accumulation in Pear Fruit. <i>Plant Physiology</i> , 2020, 182, 2035-2046.	4.8	84
441	EjFRI, FRIGIDA (FRI) Ortholog from <i>Eriobotrya japonica</i> , Delays Flowering in <i>Arabidopsis</i> . <i>International Journal of Molecular Sciences</i> , 2020, 21, 1087.	4.1	8
442	Genome size and chromosome ploidy identification in pear germplasm represented by Asian pears - Local pear varieties. <i>Scientia Horticulturae</i> , 2020, 265, 109202.	3.6	5
443	B-box Proteins in <i>Arachis duranensis</i> : Genome-Wide Characterization and Expression Profiles Analysis. <i>Agronomy</i> , 2020, 10, 23.	3.0	18
444	Analysis of Fruit Lignin Content, Composition, and Linkage Types in Pear Cultivars and Related Species. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 2493-2505.	5.2	13
445	Effects of Metaxenia on Stone Cell Formation in Pear (<i>Pyrus bretschneideri</i>) Based on Transcriptomic Analysis and Functional Characterization of the Lignin-Related Gene PbC4H2. <i>Forests</i> , 2020, 11, 53.	2.1	6
446	A constitutive and drought-responsive mRNA undergoes long-distance transport in pear (<i>Pyrus</i>) Tj ETQq1 1 0.784314 rgBT / Overlock 10	3.6	25
447	Comparison of multiple algorithms to reliably detect structural variants in pears. <i>BMC Genomics</i> , 2020, 21, 61.	2.8	15
448	Physiological and transcriptomic analysis of “Whangkeumbae” pear core browning during low-temperature storage. <i>Gene Expression Patterns</i> , 2020, 36, 119113.	0.8	9
449	Genome-wide DNA polymorphisms in four <i>Actinidia arguta</i> genotypes based on whole-genome re-sequencing. <i>PLoS ONE</i> , 2020, 15, e0219884.	2.5	3
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451	Genome-wide analysis of long noncoding RNAs affecting floral bud dormancy in pears in response to cold stress. <i>Tree Physiology</i> , 2021, 41, 771-790.	3.1	20
453	Physiological and transcriptional responses of <i>Alternaria alternata</i> induced abnormal leaf senescence in <i>Pyrus pyrifolia</i> . <i>Scientia Horticulturae</i> , 2021, 277, 109786.	3.6	3

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462	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
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483	Comparative Genomic Analysis of TCP Genes in Six Rosaceae Species and Expression Pattern Analysis in <i>Pyrus bretschneideri</i> . Frontiers in Genetics, 2021, 12, 669959.	2.3	8
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501	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.	3.6	11
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505	Genome-wide investigation and comparative analysis of <i>MATE</i> gene family in Rosaceae species and their regulatory role in abiotic stress responses in Chinese pear (<i>Pyrus</i>) Tj ETQq1 1 0.784314 rgBT / Overlock 10 Tf 50 21		
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518	A high-quality chromosome-level genome of wild <i>Rosa rugosa</i> . DNA Research, 2021, 28, .	3.4	10
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520	Development of Genome-Wide Functional Markers Using Draft Genome Assembly of Guava (<i>Psidium</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tff 708332.	3.6	8
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553	New Strategies to Overcome Present CRISPR/Cas9 Limitations in Apple and Pear: Efficient Dechimerization and Base Editing. <i>International Journal of Molecular Sciences</i> , 2021, 22, 319.	4.1	53
554	High diversity of <i>Diaporthe</i> species associated with pear shoot canker in China. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2020, 45, 132-162.	4.4	63
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558	The complete chloroplast genome sequence of strawberry (<i>Fragaria</i> — <i>Ananassa</i> Duch.) and comparison with related species of Rosaceae. <i>PeerJ</i> , 2017, 5, e3919.	2.0	68
559	Comparative genomic analysis of the IDD genes in five Rosaceae species and expression analysis in Chinese white pear (<i>Pyrus bretschneideri</i>). <i>PeerJ</i> , 2019, 7, e6628.	2.0	8
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572	Researches of pear tree (<i>Pyrus</i> spp.) genomics. Journal of Plant Biotechnology, 2015, 42, 290-297.	0.4	0
573	Analysis of Tissue Specific Expression of <i>SOT</i> Gene Family in White Pear. Botanical Research, 2018, 07, 496-506.	0.0	0
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#	ARTICLE	IF	CITATIONS
595	A Novel Pear Scab (<i>Venturia nashicola</i>) Resistance Gene, <i>Rvn3</i> , from Interspecific Hybrid Pear (<i>Pyrus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	3.5	3
596	Genome-wide identification and co-expression analysis of GDSL genes related to suberin formation during fruit russetting in pear. <i>Horticultural Plant Journal</i> , 2022, 8, 153-170.	5.0	7
597	Analysis of CcGASA family members in <i>Citrus clementina</i> (Hort. ex Tan.) by a genome-wide approach. <i>BMC Plant Biology</i> , 2021, 21, 565.	3.6	9
598	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
599	Anticipated Polymorphic SSRs and Their Application Based on Next Generation Sequencing of <i>Prunus Persica</i> . <i>Han'guk Yukchong Hakhoe Chi</i> , 2021, 53, 350-360.	0.5	1
600	Identification of bZIP transcription factors and their responses to brown spot in pear. <i>Genetics and Molecular Biology</i> , 2022, 45, e20210175.	1.3	5
601	Characterization and Functional Explorations of O-glycosylation Enzymes SECRET AGENT and SPINDLY in <i>Pyrus bretschneideri</i> . <i>Journal of Plant Biology</i> , 0, , 1.	2.1	0
602	Pear genetics: Recent advances, new prospects, and a roadmap for the future. <i>Horticulture Research</i> , 2022, 9, .	6.3	12
603	S1-bZIP Transcription Factors Play Important Roles in the Regulation of Fruit Quality and Stress Response. <i>Frontiers in Plant Science</i> , 2021, 12, 802802.	3.6	10
604	The CfMK1 Gene Regulates Reproduction, Appressorium Formation, and Pathogenesis in a Pear Anthracnose-Causing Fungus. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 77.	3.5	7
605	Perspectives and recent progress of genome-wide association studies (GWAS) in fruits. <i>Molecular Biology Reports</i> , 2022, 49, 5341-5352.	2.3	12
606	Morphological and Developmental Features of Stone Cells in <i>Eriobotrya</i> Fruits. <i>Frontiers in Plant Science</i> , 2022, 13, 823993.	3.6	3
607	Overexpression of apple <i>Ma12</i> , a mitochondrial pyrophosphatase pump gene, leads to malic acid accumulation and the upregulation of malate dehydrogenase in tomato and apple calli. <i>Horticulture Research</i> , 2022, 9, .	6.3	10
608	Codon usage patterns across seven <i>Rosales</i> species. <i>BMC Plant Biology</i> , 2022, 22, 65.	3.6	12
609	Multi-Omics Analysis Reveals the Dynamic Changes of RNA N6-Methyladenosine in Pear (<i>Pyrus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 18 <i>Microbiology</i> , 2021, 12, 803512.	3.5	3
610	Genome-Wide In Silico Analysis and Expression Profiling of Phosphoenolpyruvate Carboxylase Genes in Loquat, Apple, Peach, Strawberry and Pear. <i>Agronomy</i> , 2022, 12, 25.	3.0	7
611	Cryptochrome-Mediated Blue-Light Signal Contributes to Lignin Biosynthesis in Stone Cells in Pear Fruit. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
612	Chromosome-scale assembly and population diversity analyses provide insights into the evolution of <i>Sapindus mukorossi</i> . <i>Horticulture Research</i> , 2022, 9, .	6.3	4

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613	Biochemical characterization of an alcohol dehydrogenase from <i>Pyrus ussuriensis</i> "Nanguoli"™. <i>European Journal of Horticultural Science</i> , 2022, 87, .	0.7	0
614	Genome-wide analysis of the CCT gene family in Chinese white pear (<i>Pyrus bretschneideri</i> Rehd.) and characterization of PbPRR2 in response to varying light signals. <i>BMC Plant Biology</i> , 2022, 22, 81.	3.6	1
615	Transcriptome Analysis of the Molecular Patterns of Pear Plants Infected by Two <i>Colletotrichum fructicola</i> Pathogenic Strains Causing Contrasting Sets of Leaf Symptoms. <i>Frontiers in Plant Science</i> , 2022, 13, 761133.	3.6	7
616	Transcriptomics analysis of field-droughted pear (<i>Pyrus</i> spp.) reveals potential drought stress genes and metabolic pathways. <i>PeerJ</i> , 2022, 10, e12921.	2.0	5
617	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.	2.8	8
618	Whole-genome analysis of <i>CCS</i> , <i>SAHH</i> , <i>SAMS</i> gene families in five Rosaceae species and their expression analysis in <i>Pyrus bretschneideri</i> . <i>PeerJ</i> , 2022, 10, e13086.	2.0	1
619	Organization and regulation of the apple SUMOylation system under salt and ABA. <i>Plant Physiology and Biochemistry</i> , 2022, 182, 22-35.	5.8	2
620	Transposon insertions regulate genome-wide allele-specific expression and underpin flower colour variations in apple (<i>Malus</i> spp.). <i>Plant Biotechnology Journal</i> , 2022, 20, 1285-1297.	8.3	21
621	Alternative splicing analysis provides insight into the domestication and improvement of pear (<i>Pyrus</i>) Tj ETQq0 0 0 0 BT /Overlock 10 Tf 8.6	8.6	3
622	Genome-Wide Identification and Comparative Analysis of the ASR Gene Family in the Rosaceae and Expression Analysis of PbrASRs During Fruit Development. <i>Frontiers in Genetics</i> , 2021, 12, 792250.	2.3	4
623	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.	3.6	23
624	Deciphering Evolutionary Dynamics of WRKY I Genes in Rosaceae Species. <i>Frontiers in Ecology and Evolution</i> , 2021, 9, .	2.2	0
625	Chromosome-level genome assembly and characterization of <i>Sophora Japonica</i> . <i>DNA Research</i> , 2022, 29, .	3.4	3
626	Microsatellite Loci Reveal High Genetic Diversity, Mutation, and Migration Rates as Invasion Drivers of Callery Pear (<i>Pyrus calleryana</i>) in the Southeastern United States. <i>Frontiers in Genetics</i> , 2022, 13, 861398.	2.3	6
627	Comparative transcriptome analysis of candidate genes involved in chlorogenic acid biosynthesis during fruit development in three pear varieties of Xinjiang Uygur Autonomous Region. <i>Journal of Zhejiang University: Science B</i> , 2022, 23, 345-351.	2.8	2
628	Identification and testing of reference genes for qRT-PCR analysis during pear fruit development. , 2022, 77, 2763-2777.		3
673	Study on Supergenous <i>Rubus</i> L.: Edible, Medicinal, and Phylogenetic Characterization. <i>Plants</i> , 2022, 11, 1211.	3.5	9
674	Genomic and Bioinformatic Resources for Perennial Fruit Species. <i>Current Genomics</i> , 2022, 23, .	1.6	0

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675	Analysis of the Î²-Glucosidase Family Reveals Genes Involved in the Lignification of Stone Cells in Chinese White Pear (<i>Pyrus bretschneideri</i> Rehd.). <i>Frontiers in Plant Science</i> , 2022, 13, .	3.6	2
676	Cellulose accumulation mediated by <scp>PbrCSLD5</scp>, a cellulose synthase-like protein, results in cessation of pollen tube growth in <i>Pyrus bretschneideri</i>. <i>Physiologia Plantarum</i> , 2022, 174, e13700.	5.2	2
677	Rapid evolution of T2/S-RNase genes in <i>Fragaria</i> linked to multiple transitions from self-incompatibility to self-compatibility. <i>Plant Diversity</i> , 2023, 45, 219-228.	3.7	3
678	Transcriptome analysis to identify candidate genes related to chlorogenic acid biosynthesis during development of Korla fragrant pear in Xinjiang. <i>Food Science and Human Wellness</i> , 2022, 11, 854-864.	4.9	6
679	Genome-wide clonal variability in European pear "Rocha" using high-throughput sequencing. <i>Horticulture Research</i> , 2022, 9, .	6.3	1
680	Genome Assembly and Population Resequencing Reveal the Geographical Divergence of Shanmei (<i>Rubus</i>) Tj ETQq1.1.0.784314 rgBT /Overlock	6.9	3
681	Unexpected Low DNA Methylation in Transposable Elements at the 5â€²-CCGG Sites in Three Fruit Tree Cultivars. <i>Agronomy</i> , 2022, 12, 1347.	3.0	0
682	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
683	An Update on Progress and Challenges of Crop Genomes. <i>Springer Protocols</i> , 2022, , 1-11.	0.3	1
684	Construction of a high-density bin-map and identification of fruit quality-related quantitative trait loci and functional genes in pear. <i>Horticulture Research</i> , 2022, 9, .	6.3	6
685	The Origin and Evolution of RNase T2 Family and Gametophytic Self-incompatibility System in Plants. <i>Genome Biology and Evolution</i> , 2022, 14, .	2.5	5
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687	Genome-Wide Analysis of Genes Involved in the GA Signal Transduction Pathway in "Duli" Pear (<i>Pyrus</i>) Tj ETQq0.0.0 rgBT /Overlock	4.1	2
688	Integrative Analysis of the GRAS Genes From Chinese White Pear (<i>Pyrus bretschneideri</i>): A Critical Role in Leaf Regeneration. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	1
689	Molecular Approaches in Conservation and Restoration of Agrobiodiversity. , 2022, , 169-216.		1
690	PbrCalS5, a callose synthase protein, is involved in pollen tube growth in <i>Pyrus bretschneideri</i> . <i>Planta</i> , 2022, 256, .	3.2	4
691	Comparative Genomic Analysis of SAUR Gene Family, Cloning and Functional Characterization of Two Genes (PbrSAUR13 and PbrSAUR52) in <i>Pyrus bretschneideri</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 7054.	4.1	4
692	Highly efficient CRISPR systems for loss-of-function and gain-of-function research in pear calli. <i>Horticulture Research</i> , 2022, 9, .	6.3	12

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693	Genome-Wide Identification of MAPKK and MAPKKK Gene Family Members and Transcriptional Profiling Analysis during Bud Dormancy in Pear (<i>Pyrus x bretschneideri</i>). <i>Plants</i> , 2022, 11, 1731.	3.5	2
694	Genome-wide identification and comparative evolutionary analysis of sorbitol metabolism pathway genes in four Rosaceae species and three model plants. <i>BMC Plant Biology</i> , 2022, 22, .	3.6	5
695	PbUGT72AJ2-Mediated Glycosylation Plays an Important Role in Lignin Formation and Stone Cell Development in Pears (<i>Pyrus bretschneideri</i>). <i>International Journal of Molecular Sciences</i> , 2022, 23, 7893.	4.1	5
696	Comparative transcriptome analysis provides insights into the mechanism of pear dwarfing. <i>Journal of Integrative Agriculture</i> , 2022, 21, 1952-1967.	3.5	5
697	Comparative genomic analysis of the <i>COBRA</i> genes in six Rosaceae species and expression analysis in Chinese white pear (<i>Pyrus bretschneideri</i>). <i>PeerJ</i> , 0, 10, e13723.	2.0	1
698	Integrative Analysis of the DICER-like (DCL) Genes From Peach (<i>Prunus persica</i>): A Critical Role in Response to Drought Stress. <i>Frontiers in Ecology and Evolution</i> , 0, 10, .	2.2	4
699	Genome-wide identification and characterization of the abiotic-stress-responsive lipoxygenase gene family in diploid woodland strawberry (<i>Fragaria vesca</i>). <i>Journal of Integrative Agriculture</i> , 2022, 21, 1982-1996.	3.5	2
700	Computational analysis of potential candidate genes involved in the cold stress response of ten Rosaceae members. <i>BMC Genomics</i> , 2022, 23, .	2.8	1
701	Utilizing paralogues for phylogenetic reconstruction has the potential to increase species tree support and reduce gene tree discordance in target enrichment data. <i>Molecular Ecology Resources</i> , 2022, 22, 3018-3034.	4.8	8
702	Rearrangement and domestication as drivers of Rosaceae mitogenome plasticity. <i>BMC Biology</i> , 2022, 20, .	3.8	14
703	Evaluation of the early defoliation trait and identification of resistance genes through a comprehensive transcriptome analysis in pears. <i>Journal of Integrative Agriculture</i> , 2023, 22, 120-138.	3.5	1
704	Genomic characterisation, phylogenetic comparison and candidate gene identification of the lipid transfer proteins gene family in pear (<i>Pyrus bretschneideri</i> Rehd.) and other Rosaceae species. <i>Journal of Horticultural Science and Biotechnology</i> , 2023, 98, 178-193.	1.9	1
705	Transcriptome analysis reveals gene associated with fruit size during fruit development in pear. <i>Scientia Horticulturae</i> , 2022, 305, 111367.	3.6	5
706	Single-base resolution methylome of different ecotype from <i>Pyrus betulaefolia</i> reveals epigenomic changes in response to salt stress. <i>Scientia Horticulturae</i> , 2022, 306, 111437.	3.6	1
707	The role of gene duplication in the divergence of the sweet cherry. <i>Plant Gene</i> , 2022, 32, 100379.	2.3	0
708	Integrated transcriptome and metabolome analysis unveiled the mechanisms of xenia effect and the role of different pollens on aroma formation in 'Yali' pear (<i>Pyrus bretschneideri</i> Rehd.). <i>Scientia Horticulturae</i> , 2023, 307, 111503.	3.6	2
709	The role of invasive plant species in drought resilience in agriculture: the case of sweet briar (<i>Rosa rubiginosa</i> L.). <i>Journal of Experimental Botany</i> , 2023, 74, 2799-2810.	4.8	3
710	Genome-Wide Identification, Evolution, and Expression Analysis of CASA Gene Family in <i>Prunus mume</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 10923.	4.1	8

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711	Comparative genomic analysis of N6-methyladenosine regulators in nine rosaceae species and functional characterization in response to drought stress in pear. Horticultural Plant Journal, 2023, 9, 693-704.	5.0	2
712	An identical-by-descent segment harbors a 12-bp insertion determining fruit softening during domestication and speciation in <i>Pyrus</i> . BMC Biology, 2022, 20, .	3.8	3
713	The Apricot Genome. Compendium of Plant Genomes, 2022, , 41-67.	0.5	0
714	Molecular characterization of intergeneric hybrids between <i>Malus</i> and <i>Pyrus</i> . Horticulture Research, 2023, 10, .	6.3	2
715	SNP-based high-density linkage map construction and QTL mapping of black spot disease resistance in Chinese sand pear. Journal of Applied Genetics, 0, , .	1.9	0
716	Transcriptome changes associated with boron applications in fruits of watercore-susceptible pear cultivar. Molecular Biology Reports, 2022, 49, 12055-12061.	2.3	1
717	Haplotype-phased genome assembly for <i>Ficus carica</i> breeding. Acta Horticulturae, 2022, , 13-18.	0.2	0
718	Stoneless fruit cultivars: past, present and future perspectives with special reference to economically important <i>Ziziphus</i> species. Acta Horticulturae, 2022, , 79-90.	0.2	1
719	Genome-wide identification of calcium-dependent protein kinases (CDPKs) in pear (<i>Pyrus bretschneideri</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Environment and Biotechnology, 2022, 63, 903-915.	2.1	2
720	Genome-wide identification of the mitogen-activated protein kinase kinase kinase (MAPKKK) in pear (<i>Pyrus bretschneideri</i>) and their functional analysis in response to black spot. Planta, 2023, 257, .	3.2	1
721	QTL Analysis and CAPS Marker Development Linked with Russet in Pear (<i>Pyrus</i> spp.). Plants, 2022, 11, 3196.	3.5	0
722	The application of fatty acid synthesis inhibitors regulates the suberin biosynthesis in the exocarp of the russet mutant of "Dangshansuli" (<i>Pyrus bretschneideri</i> Rehd.). Acta Physiologiae Plantarum, 2023, 45, .	2.1	0
723	Bio-Organic Fertilizer Promotes Pear Yield by Shaping the Rhizosphere Microbiome Composition and Functions. Microbiology Spectrum, 2022, 10, .	3.0	7
724	Construction of High-Density Genetic Linkage Map Using GBS-SNPs and SSRs in Interspecific Hybrid Derived from the Cross Between "Manpungbae" and "Oharabeni" Pear (<i>Pyrus</i> spp.). Han'guk Yukchong Hakhoe Chi, 2022, 54, 285-293.	0.5	0
725	Genome assembly of wild loquat (<i>Eriobotrya japonica</i>) and resequencing provide new insights into the genomic evolution and fruit domestication in loquat. Horticulture Research, 2023, 10, .	6.3	12
726	Multi-omics analyses reveal stone cell distribution pattern in pear fruit. Plant Journal, 2023, 113, 626-642.	5.7	9
727	Self Sâ€Nase inhibits ABFâ€LRX signaling to arrest pollen tube growth to achieve selfâ€incompatibility in pear. Plant Journal, 2023, 113, 595-609.	5.7	3
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731	The miR156xâ€™+â€™p/SPL13-6 module responds to ABA, IAA, and ethylene, and SPL13-6 participates in the juvenileâ€™adult phase transition in Pyrus. Horticulture Environment and Biotechnology, 2023, 64, 437-448.	2.1	1
732	Phenotypic and transcriptomic analyses reveal major differences between apple and pear scab nonhost resistance. , 0, 3, .		0
733	Integrating genomics and genome editing for orphan crop improvement: a bridge between orphan crops and modern agriculture system. GM Crops and Food, 2023, 14, 1-20.	3.8	22
734	Genome-wide characterization of Ficus carica MADS-box transcription factors with a focus on their roles during fruit development. Horticulture Environment and Biotechnology, 0, , .	2.1	0
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736	Bearing Fruit: Miocene Apes and Rosaceous Fruit Evolution. Biological Theory, 0, , .	1.5	0
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739	Characterization of the REVEILLE family in Rosaceae and role of PblHY in flowering time regulation. BMC Genomics, 2023, 24, .	2.8	7
740	The transcription factor PbrMYB24 regulates lignin and cellulose biosynthesis in stone cells of pear fruits. Plant Physiology, 2023, 192, 1997-2014.	4.8	13
741	Identification and genetic mapping of novel resistance gene, Rvn4, for pear scab in Chinese pear. Scientia Horticulturae, 2023, 317, 112032.	3.6	0
742	New insights into aroma regulation in pear peel and flesh under methyl jasmonate treatment obtained by metabolite and whole-transcriptome RNA sequencing analyses. Postharvest Biology and Technology, 2023, 201, 112347.	6.0	3
743	The involvement of Ein3-binding F-box protein PbrEBF3 in regulating ethylene signaling during Cuiguan pear fruit ripening. Plant Science, 2023, 329, 111600.	3.6	3
744	A large-scale proteogenomic atlas of pear. Molecular Plant, 2023, 16, 599-615.	8.3	7
745	Chromosome-Level Assembly of Flowering Cherry (Prunus campanulata) Provides Insight into Anthocyanin Accumulation. Genes, 2023, 14, 389.	2.4	1
746	Identification and functional analysis of arabinogalactan protein expressed in pear pollen tubes. Journal of Integrative Agriculture, 2023, 22, 776-789.	3.5	0
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749	Stepwise Optimization of the RT-qPCR Protocol and the Evaluation of Housekeeping Genes in Pears (<i>Pyrus bretschneideri</i>) under Various Hormone Treatments and Stresses. <i>Horticulturae</i> , 2023, 9, 275.	2.8	2
750	Elucidation of the GAUT gene family in eight Rosaceae species and function analysis of PbrGAUT22 in pear pollen tube growth. <i>Planta</i> , 2023, 257, .	3.2	1
751	Comprehensive genomic analysis of the Rho GTPases regulators in seven Rosaceae species revealed that PbrGDI1 controls pollen tube growth in <i>Pyrus</i> via mediating cellulose deposition. <i>International Journal of Biological Macromolecules</i> , 2023, 235, 123860.	7.5	0
752	Secondary Metabolites and Bioprospecting. , 2023, , 229-255.		0
753	Autotetraploidization Alters Morphology, Photosynthesis, Cytological Characteristics and Fruit Quality in Sour Jujube (<i>Ziziphus acidojujuba</i> Cheng et Liu). <i>Plants</i> , 2023, 12, 1106.	3.5	0
754	QTL mapping and transcriptome analysis of sugar content during fruit ripening of <i>Pyrus pyrifolia</i> . <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	1
755	Reciprocal regulation of flower induction by <i>ELF3</i> and <i>ELF3</i> generated via alternative promoter usage. <i>Plant Cell</i> , 2023, 35, 2095-2113.	6.6	2
756	Time-Series Transcriptome Analysis Reveals the Molecular Mechanism of Ethylene Reducing Cold Sensitivity of Postharvest 'Huangguan'™ Pear. <i>International Journal of Molecular Sciences</i> , 2023, 24, 5326.	4.1	1
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759	Genome-Wide Identification and Expression Analysis of the fw2.2-like Gene Family in Pear. <i>Horticulturae</i> , 2023, 9, 429.	2.8	0
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761	Auxin inhibits lignin and cellulose biosynthesis in stone cells of pear fruit via the <i>PbrARF13</i> – <i>PbrNSC</i> – <i>PbrMYB132</i> transcriptional regulatory cascade. <i>Plant Biotechnology Journal</i> , 2023, 21, 1408-1425.	8.3	4
762	Genome-Wide Identification and Expression Analysis of CAMTA Gene Family Implies PbrCAMTA2 Involved in Fruit Softening in Pear. <i>Horticulturae</i> , 2023, 9, 467.	2.8	3
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764	Genome-Wide Identification and Expression Analysis of NCED Gene Family in Pear and Its Response to Exogenous Gibberellin and Paclobutrazol. <i>International Journal of Molecular Sciences</i> , 2023, 24, 7566.	4.1	3
765	PbrATL18, an E3 ubiquitin ligase identified by genome-wide identification, is a positive factor in pear resistance to drought and <i>Colletotrichum fructicola</i> infection. <i>Horticultural Plant Journal</i> , 2023, , .	5.0	3

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768	Multi-omics analysis of green- and russet skin pear cultivars identify key regulators of skin russetting. <i>Scientia Horticulturae</i> , 2023, 318, 112116.	3.6	0
769	Role of integrative omics and bioinformatics approaches in berries research and genetic improvement. , 2023, , 159-192.		0
770	Induction and characterization of tetraploid pear from the seeds of 'Dangshansuli' (<i>Pyrus) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	2.0	0
771	Insights into the dwarfing mechanism of pear (<i>Pyrus betulaefolia</i>) based on anatomical and structural analysis using X-ray scanning. <i>Horticultural Plant Journal</i> , 2024, 10, 355-366.	5.0	1
772	Transcriptome analysis reveals that <scp>PbMYB61</scp> and <scp>PbMYB308</scp> are involved in the regulation of lignin biosynthesis in pear fruit stone cells. <i>Plant Journal</i> , 2023, 116, 217-233.	5.7	2
774	Genomic insights into domestication and genetic improvement of fruit crops. <i>Plant Physiology</i> , 2023, 192, 2604-2627.	4.8	4
775	Genome-wide identification and characterization of the PbrATG family in <i>Pyrus bretschneideri</i> and functional analysis of PbrATG1a in response to <i>Botryosphaeria dothidea</i> . <i>Horticultural Plant Journal</i> , 2024, 10, 327-340.	5.0	0
776	The PcERF5 promotes anthocyanin biosynthesis in red-fleshed pear (<i>Pyrus communis</i>) through both activating and interacting with PcMYB transcription factors. <i>Journal of Integrative Agriculture</i> , 2023, 22, 2687-2704.	3.5	1
777	PearMODB: a multiomics database forÂpear (<i>Pyrus</i>) genomics, genetics andÂbreeding study. Database: the Journal of Biological Databases and Curation, 2023, 2023, .	3.0	2
778	The PcHY5 methylation is associated with anthocyanin biosynthesis and transport in â€˜Max red Bartlettâ€™ and â€˜Bartlettâ€™ pears1. <i>Journal of Integrative Agriculture</i> , 2023, , .	3.5	1
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780	Genome-wide identification and expression analysis of U-box gene family in <i>Juglans regia</i> L.. <i>Genetic Resources and Crop Evolution</i> , 0, , .	1.6	0
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803	Plant phenolics: neglected secondary metabolites in plant stress tolerance. <i>Revista Brasileira De Botanica</i> , 0, , .	1.3	1
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