

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

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Transferability of Newly Developed Pear SSR Markers to Other Rosaceae Species. <i>Plant Molecular Biology Reporter</i> , 2013, 31, 1271-1282.	1.0	70
2	An AFLP, SRAP, and SSR Genetic Linkage Map and Identification of QTLs for Fruit Traits in Pear ( <i>Pyrus L.</i> ). <i>Plant Molecular Biology Reporter</i> , 2013, 31, 678-687.	1.0	69
3	Quantitative proteomic investigation employing stable isotope labeling by peptide dimethylation on proteins of strawberry fruit at different ripening stages. <i>Journal of Proteomics</i> , 2013, 94, 219-239.	1.2	66
4	The Biochemistry and Molecular Biology of Volatile Messengers in Trees. <i>Tree Physiology</i> , 2013, , 47-93.	0.9	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. <i>Postharvest Biology and Technology</i> , 2013, 86, 212-220.	2.9	60
6	Identifying the candidate genes involved in the calyx abscission process of "Kuerlexiangli" ( <i>Pyrus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 502 Td	1.2	32
7	Transcriptome profiling of fruit development and maturation in Chinese white pear ( <i>Pyrus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 502 Td	1.2	50
8	A genome-wide identification and characterization of mircoRNAs and their targets in "Suli" pear ( <i>Pyrus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 502 Td	1.6	19
9	Arguments for standardizing transposable element annotation in plant genomes. <i>Trends in Plant Science</i> , 2013, 18, 367-376.	4.3	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. <i>Plant Physiology</i> , 2013, 163, 1419-1432.	2.3	25
11	Molecular Analysis of the Processes of Surface Brown Spot (SBS) Formation in Pear Fruit ( <i>Pyrus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 502 Td	1.1	16
12	Evidence for regulation of columnar habit in apple by a putative 2-oxoglutarate-dependent Fe(II) oxygenase. <i>New Phytologist</i> , 2013, 200, 993-999.	3.5	47
13	Expression and genomic structure of the dormancy-associated MADS box genes MADS13 in Japanese pears ( <i>Pyrus pyrifolia</i> Nakai) that differ in their chilling requirement for endodormancy release. <i>Tree Physiology</i> , 2013, 33, 654-667.	1.4	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. <i>Japanese Society for Horticultural Science</i> , 2013, 82, 301-311.	0.8	10
16	Using genomics to improve fruit quality. <i>Biological Research</i> , 2013, 46, 347-352.	1.5	28
17	The First 50 Plant Genomes. <i>Plant Genome</i> , 2013, 6, plantgenome2013.03.0001in.	1.6	228
18	Identification of <i>Pyrus</i> Single Nucleotide Polymorphisms (SNPs) and Evaluation for Genetic Mapping in European Pear and Interspecific <i>Pyrus</i> Hybrids. <i>PLoS ONE</i> , 2013, 8, e77022.	1.1	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.	0.3	35
20	Identification of miRNAs involved in pear fruit development and quality. <i>BMC Genomics</i> , 2014, 15, 953.	1.2	102
21	Genetic, metabolite and developmental determinism of fruit friction discolouration in pear. <i>BMC Plant Biology</i> , 2014, 14, 241.	1.6	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	0.9	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	0.9	64
24	The Evolution of Plant Gene and Genome Sequencing. <i>Advances in Botanical Research</i> , 2014, , 47-90.	0.5	6
25	Insights into the Common Ancestor of Eudicots. <i>Advances in Botanical Research</i> , 2014, 69, 137-174.	0.5	1
26	The complex jujube genome provides insights into fruit tree biology. <i>Nature Communications</i> , 2014, 5, 5315.	5.8	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.	4.1	53
28	Genomics and bioinformatics resources for translational science in Rosaceae. <i>Plant Biotechnology Reports</i> , 2014, 8, 49-64.	0.9	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.	2.0	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.	1.0	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.	1.2	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.	1.5	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.	1.7	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.	0.6	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.	2.4	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.	1.2	58

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37	Genomics and Functional Genomics of Winter Low Temperature Tolerance in Temperate Fruit Crops. <i>Critical Reviews in Plant Sciences</i> , 2014, 33, 125-140.	2.7	18
38	Analysis of 41 plant genomes supports a wave of successful genome duplications in association with the Cretaceous–Paleogene boundary. <i>Genome Research</i> , 2014, 24, 1334-1347.	2.4	381
39	Transcriptional control of fleshy fruit development and ripening. <i>Journal of Experimental Botany</i> , 2014, 65, 4527-4541.	2.4	296
40	Characterization of the lipoxygenase (LOX) gene family in the Chinese white pear ( <i>Pyrus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	1.2	49
41	Comparative population genomics reveals the domestication history of the peach, <i>Prunus persica</i> , and human influences on perennial fruit crops. <i>Genome Biology</i> , 2014, 15, 415.	3.8	134
42	Genetic mapping of polygenic scab ( <i>Venturia pirina</i> ) resistance in an interspecific pear family. <i>Molecular Breeding</i> , 2014, 34, 2179-2189.	1.0	24
43	Investment in plant research and development bears fruit in China. <i>Plant Cell Reports</i> , 2014, 33, 541-550.	2.8	7
44	F1 hybrid of cultivated apple ( <i>Malus domestica</i> ) and European pear ( <i>Pyrus communis</i> ) with fertile F2 offspring. <i>Molecular Breeding</i> , 2014, 34, 817-828.	1.0	14
45	Development of genic SSR markers from transcriptome sequencing of pear buds. <i>Journal of Zhejiang University: Science B</i> , 2014, 15, 303-312.	1.3	23
46	Transcriptome-based single nucleotide polymorphism markers for genome mapping in Japanese pear ( <i>Pyrus pyrifolia</i> Nakai). <i>Tree Genetics and Genomes</i> , 2014, 10, 853-863.	0.6	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	1.2	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. <i>DNA Research</i> , 2014, 21, 169-181.	1.5	201
50	Identification and characterization of <i>Colletotrichum fructicola</i> causing black spots on young fruits related to bitter rot of pear ( <i>Pyrus bretschneideri</i> Rehd.) in China. <i>Crop Protection</i> , 2014, 58, 41-48.	1.0	37
51	Proteomic analysis of ‘Zaosu’™ pear ( <i>Pyrus bretschneideri</i> Rehd.) and its early-maturing bud sport. <i>Plant Science</i> , 2014, 224, 120-135.	1.7	15
52	The <i>Brassica oleracea</i> genome reveals the asymmetrical evolution of polyploid genomes. <i>Nature Communications</i> , 2014, 5, 3930.	5.8	918
53	The bright side of transposons in crop evolution. <i>Briefings in Functional Genomics</i> , 2014, 13, 276-295.	1.3	106
54	Understanding development and ripening of fruit crops in an ‘omics’™ era. <i>Horticulture Research</i> , 2014, 1, 14034.	2.9	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.	0.7	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.	1.6	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.	1.6	55
59	An integrated database of wood-formation related genes in plants. <i>Scientific Reports</i> , 2015, 5, 11422.	1.6	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.	0.8	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.	1.2	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.	1.2	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.	1.6	13
64	MnTEdb, a collective resource for mulberry transposable elements. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, .	1.4	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.	1.2	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.	1.2	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.	0.3	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.	1.8	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.	1.5	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.	1.1	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.	1.1	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.	1.1	21
73	PyMYB10 and PyMYB10.1 Interact with bHLH to Enhance Anthocyanin Accumulation in Pears. <i>PLoS ONE</i> , 2015, 10, e0142112.	1.1	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.	1.7	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.	1.7	173
76	Whole Genome Sequencing of Fruit Tree Species. <i>Advances in Botanical Research</i> , 2015, , 1-37.	0.5	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.	1.1	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.	2.5	127
79	Genome-wide identification and characterization of R2R3-MYB transcription factors in pear. <i>Scientia Horticulturae</i> , 2015, 197, 176-182.	1.7	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.	1.2	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.	0.6	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.	1.0	34
84	Proteome analysis of pear reveals key genes associated with fruit development and quality. <i>Planta</i> , 2015, 241, 1363-1379.	1.6	42
85	Species-specific duplications driving the recent expansion of NBS-LRR genes in five Rosaceae species. <i>BMC Genomics</i> , 2015, 16, 77.	1.2	39
86	Progress, challenges and the future of crop genomes. <i>Current Opinion in Plant Biology</i> , 2015, 24, 71-81.	3.5	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.	0.5	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.	1.5	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.	0.6	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.	1.6	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.	1.6	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.	1.7	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.	0.6	6
96	A standard nomenclature for gene designation in the Rosaceae. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	0.6	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.	1.4	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.	2.7	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.	1.2	15
102	Molecular basis of angiosperm tree architecture. <i>New Phytologist</i> , 2015, 206, 541-556.	3.5	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.	1.7	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.	0.6	17
105	Genetic mapping and pyramiding of two new pear scab resistance QTLs. <i>Molecular Breeding</i> , 2015, 35, 1.	1.0	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.	0.6	17
107	Hybrid seedling inviability locus (HIs1) mapped on linkage group 4 of the Japanese flowering cherry, <i>Cerasus yedoensis</i> 'Somei-yoshino'. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	0.6	6
108	A taste of pineapple evolution through genome sequencing. <i>Nature Genetics</i> , 2015, 47, 1374-1376.	9.4	5
109	A major QTL controlling apple skin russeting maps on the linkage group 12 of 'Renetta Grigia di Torriana'. <i>BMC Plant Biology</i> , 2015, 15, 150.	1.6	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.	1.3	52
111	Genomic resources in fruit plants: an assessment of current status. <i>Critical Reviews in Biotechnology</i> , 2015, 35, 438-447.	5.1	16
112	Prediction of retrotransposons and assessment of genetic variability based on developed retrotransposon-based insertion polymorphism (RBIP) markers in <i>Pyrus L.</i> <i>Molecular Genetics and Genomics</i> , 2015, 290, 225-237.	1.0	17
113	Construction of a High-Density Simple Sequence Repeat Consensus Genetic Map for Pear ( <i>Pyrus spp.</i> ). <i>Plant Molecular Biology Reporter</i> , 2015, 33, 316-325.	1.0	47
114	Application of Genomic Technologies to the Breeding of Trees. <i>Frontiers in Genetics</i> , 2016, 7, 198.	1.1	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.	1.0	51
116	Genomics of pear and other Rosaceae fruit trees. <i>Breeding Science</i> , 2016, 66, 148-159.	0.9	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.	1.1	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.	1.7	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.	1.7	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.	1.7	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.	1.7	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.	1.7	83
123	Fine mapping of the gene for susceptibility to black spot disease in Japanese pear (&lt;i>Pyrus) Tj ETQq1 1 0.784314 rgBT /Overloc	0.9	20
124	The genome of black raspberry (<i>Rubus occidentalis</i>). <i>Plant Journal</i> , 2016, 87, 535-547.	2.8	111
125	Genome mapping of postzygotic hybrid necrosis in an interspecific pear population. <i>Horticulture Research</i> , 2016, 3, 15064.	2.9	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.	1.7	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.	0.9	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.	0.9	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.	1.7	42
134	Evolution and expression patterns of cytokinin oxidase genes in <i>Fragaria vesca</i> . <i>Scientia Horticulturae</i> , 2016, 212, 115-125.	1.7	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.	2.0	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.	1.0	44
137	Volatile profiling of two pear genotypes with different potential for white pear aroma improvement. <i>Scientia Horticulturae</i> , 2016, 209, 221-228.	1.7	11
138	The role of Ca <sup>2+</sup> and Ca <sup>2+</sup> channels in the gametophytic self-incompatibility of <i>Pyrus pyrifolia</i> . <i>Cell Calcium</i> , 2016, 60, 299-308.	1.1	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	0.6	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.	3.5	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.	1.4	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.	0.6	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.	1.6	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.	1.6	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.	2.8	233

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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.	1.2	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.	1.0	32
149	Advances in Genetic Diversity Analysis in Fruit Tree Crops. <i>Progress in Botany Fortschritte Der Botanik</i> , 2016, , 245-264.	0.1	4
150	Overexpression of sucrose transporter gene <i>PbSUT2</i> from <i>Pyrus bretschneideri</i> , enhances sucrose content in <i>Solanum lycopersicum</i> fruit. <i>Plant Physiology and Biochemistry</i> , 2016, 105, 150-161.	2.8	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.	1.7	15
152	Landscape and evolutionary dynamics of terminal repeat retrotransposons in miniature in plant genomes. <i>Genome Biology</i> , 2016, 17, 7.	3.8	50
153	Evolution of plant genome architecture. <i>Genome Biology</i> , 2016, 17, 37.	3.8	331
154	Isolation and characterization of putative functional long terminal repeat retrotransposons in the <i>Pyrus</i> genome. <i>Mobile DNA</i> , 2016, 7, 1.	1.3	25
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 62 137	1.7	16
156	Cloning, localization and expression analysis of two <i>fw2.2</i> -like genes in small- and large-fruited pear species. <i>Journal of Integrative Agriculture</i> , 2016, 15, 282-294.	1.7	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.	0.3	0
158	Genome-Wide Identification, Evolution and Functional Divergence of MYB Transcription Factors in Chinese White Pear ( <i>Pyrus bretschneideri</i> ). <i>Plant and Cell Physiology</i> , 2016, 57, 824-847.	1.5	89
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.	1.5	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.	0.3	11
161	The Genome of the Model Moss <i>Physcomitrella patens</i> . <i>Advances in Botanical Research</i> , 2016, 78, 97-140.	0.5	9
162	Characterization of DNA methyltransferase and demethylase genes in <i>Fragaria vesca</i> . <i>Molecular Genetics and Genomics</i> , 2016, 291, 1333-1345.	1.0	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 62 137	2.4	137

#	ARTICLE	IF	CITATIONS
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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.	0.3	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.	2.4	170
167	Construction of a high-density genetic linkage map in pear ( <i>Pyrus communis</i> — <i>Pyrus pyrifolia</i> nakai) using SSRs and SNPs developed by SLAF-seq. <i>Scientia Horticulturae</i> , 2017, 218, 198-204.	1.7	42
168	Genetic variation and population structure of <i>Pyrus</i> pear landraces in Tibet revealed by SSR markers. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	7
169	Novel Insights into Tree Biology and Genome Evolution as Revealed Through Genomics. <i>Annual Review of Plant Biology</i> , 2017, 68, 457-483.	8.6	64
170	Diversification of Rosaceae since the Late Cretaceous based on plastid phylogenomics. <i>New Phytologist</i> , 2017, 214, 1355-1367.	3.5	278
171	Phylogenetic analysis of 25 plant species representing 19 angiosperm families and one gymnosperm family based on 390 orthologous genes. <i>Plant Systematics and Evolution</i> , 2017, 303, 413-417.	0.3	9
172	Genotyping-by-sequencing of pear ( <i>Pyrus</i> spp.) accessions unravels novel patterns of genetic diversity and selection footprints. <i>Horticulture Research</i> , 2017, 4, 17015.	2.9	56
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.	1.3	25
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175	Nashi or Williams pear fruits? Use of volatile organic compounds, physicochemical parameters, and sensory evaluation to understand the consumer's preference. <i>European Food Research and Technology</i> , 2017, 243, 1917-1931.	1.6	18
176	Dormancy-Associated MADS-Box (DAM) and the Abscisic Acid Pathway Regulate Pear Endodormancy Through a Feedback Mechanism. <i>Plant and Cell Physiology</i> , 2017, 58, 1378-1390.	1.5	99
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.	1.8	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.	1.5	212
179	Genome-wide sequencing of longan ( <i>Dimocarpus longan</i> Lour.) provides insights into molecular basis of its polyphenol-rich characteristics. <i>GigaScience</i> , 2017, 6, 1-14.	3.3	103
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.	1.8	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.	1.5	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.	2.9	25
184	Comparative transcriptome analysis of <i>Ziziphus jujuba</i> infected by jujube witches' broom phytoplasmas. <i>Scientia Horticulturae</i> , 2017, 226, 50-58.	1.7	21
185	Interval mapping for red/green skin color in Asian pears using a modified QTL-seq method. <i>Horticulture Research</i> , 2017, 4, 17053.	2.9	52
186	Global Identification, Classification, and Expression Analysis of MAPKKK genes: Functional Characterization of MdRaf5 Reveals Evolution and Drought-Responsive Profile in Apple. <i>Scientific Reports</i> , 2017, 7, 13511.	1.6	21
187	Breeding Avenues in Fruit Crops for Imparting Resistance Against Insect Pests. , 2017, , 289-322.		0
188	Identification and expression patterns of alcohol dehydrogenase genes involving in ester volatile biosynthesis in pear fruit. <i>Journal of Integrative Agriculture</i> , 2017, 16, 1742-1750.	1.7	14
189	Differential expression analysis of genes related to graft union healing in <i>Pyrus ussuriensis</i> Maxim by cDNA-AFLP. <i>Scientia Horticulturae</i> , 2017, 225, 700-706.	1.7	6
190	Map-based cloning of the pear gene <i>MYB114</i> identifies an interaction with other transcription factors to coordinately regulate fruit anthocyanin biosynthesis. <i>Plant Journal</i> , 2017, 92, 437-451.	2.8	279
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192	Pearl millet genome sequence provides a resource to improve agronomic traits in arid environments. <i>Nature Biotechnology</i> , 2017, 35, 969-976.	9.4	356
193	Transcriptome and phytohormone analysis reveals a comprehensive phytohormone and pathogen defence response in pear self-/cross-pollination. <i>Plant Cell Reports</i> , 2017, 36, 1785-1799.	2.8	32
194	Genome re-sequencing reveals the history of apple and supports a two-stage model for fruit enlargement. <i>Nature Communications</i> , 2017, 8, 249.	5.8	286
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196	Characterization and analysis of <i>CCR</i> and <i>CAD</i> gene families at the whole-genome level for lignin synthesis of stone cells in pear ( <i>Pyrus bretschneideri</i> ) fruit. <i>Biology Open</i> , 2017, 6, 1602-1613.	0.6	71
197	PbCOL8 is a clock-regulated flowering time repressor in pear. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	7
198	Construction of high efficiency regeneration and transformation systems of <i>Pyrus ussuriensis</i> Maxim. <i>Plant Cell, Tissue and Organ Culture</i> , 2017, 131, 139-150.	1.2	15
199	High-quality de novo assembly of the apple genome and methylome dynamics of early fruit development. <i>Nature Genetics</i> , 2017, 49, 1099-1106.	9.4	693

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201	Draft Genome Sequence of <i>Mentha longifolia</i> and Development of Resources for Mint Cultivar Improvement. <i>Molecular Plant</i> , 2017, 10, 323-339.	3.9	79
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207	Two Highly Similar Poplar Paleo-subgenomes Suggest an Autotetraploid Ancestor of Salicaceae Plants. <i>Frontiers in Plant Science</i> , 2017, 08, 571.	1.7	20
208	Characterization and Phylogenetic Analysis of Ancient Italian Landraces of Pear. <i>Frontiers in Plant Science</i> , 2017, 8, 751.	1.7	38
209	Transcriptome Analysis of Differentially Expressed Genes Induced by Low and High Potassium Levels Provides Insight into Fruit Sugar Metabolism of Pear. <i>Frontiers in Plant Science</i> , 2017, 8, 938.	1.7	37
210	PLC-Mediated Signaling Pathway in Pollen Tubes Regulates the Gametophytic Self-incompatibility of <i>Pyrus</i> Species. <i>Frontiers in Plant Science</i> , 2017, 8, 1164.	1.7	29
211	Genome-wide characterization, evolution, and expression analysis of the leucine-rich repeat receptor-like protein kinase (LRR-RLK) gene family in Rosaceae genomes. <i>BMC Genomics</i> , 2017, 18, 763.	1.2	62
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213	The Effect of Different Pollination on the Expression of Dangshan Su Pear MicroRNA. <i>BioMed Research International</i> , 2017, 2017, 1-18.	0.9	13
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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.	0.2	61
216	Identification, classification, and transcription profiles of the B-type response regulator family in pear. <i>PLoS ONE</i> , 2017, 12, e0171523.	1.1	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	1.1	34
218	B-BOX genes: genome-wide identification, evolution and their contribution to pollen growth in pear ( <i>Pyrus bretschneideri</i> Rehd.). <i>BMC Plant Biology</i> , 2017, 17, 156.	1.6	56

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220	Characterization and Expression Profiling Analysis of Calmodulin Genes in Response to Salt and Osmotic Stresses in Pear ( <i>Pyrus bretschneideri</i> Rehd.) and in Comparison with <i>Arabidopsis</i> . <i>BioMed Research International</i> , 2017, 2017, 1-13.	0.9	3
221	Expansion and evolutionary patterns of cysteine-rich peptides in plants. <i>BMC Genomics</i> , 2017, 18, 610.	1.2	18
222	Overview of Next-generation Sequencing Platforms Used in Published Draft Plant Genomes in Light of Genotypization of Immortelle Plant ( <i>Helichrysum Arenarium</i> ). <i>Medicinski Arhiv = Medical Archives = Archives De Médecine</i> , 2017, 71, 288.	0.4	28
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224	Genome-wide identification, characterization, and expression analyses of the HAK/KUP/KT potassium transporter gene family reveals their involvement in K <sup>+</sup> deficient and abiotic stress responses in pear rootstock seedlings. <i>Plant Growth Regulation</i> , 2018, 85, 187-198.	1.8	33
225	Systematic analysis and comparison of the PHD-Finger gene family in Chinese pear ( <i>Pyrus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 507 Td 519-531.	1.4	21
226	Phylogenetic and expression analysis of protein disulfide isomerase unravels good reference genes for gene expression studies in pear and peach fruits. <i>Canadian Journal of Plant Science</i> , 2018, 98, 1045-1057.	0.3	1
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232	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.	1.6	6
233	The mining and evolutionary investigation of AP2/ERF genes in pear ( <i>Pyrus</i> ). <i>BMC Plant Biology</i> , 2018, 18, 46.	1.6	41
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235	The genetic architecture of floral traits in the woody plant <i>Prunus mume</i> . <i>Nature Communications</i> , 2018, 9, 1702.	5.8	73
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238	Genome-wide survey and analysis of the TIFY gene family and its potential role in anthocyanin synthesis in Chinese sand pear ( <i>Pyrus pyrifolia</i> ). <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	0.6	16
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.	1.7	25
240	The blue light signal transduction pathway is involved in anthocyanin accumulation in "Red Zaosu"™ pear. <i>Planta</i> , 2018, 248, 37-48.	1.6	97
241	Genome-wide identification, phylogenetic analysis, and expression profiling of the BBX family genes in pear. <i>Journal of Horticultural Science and Biotechnology</i> , 2018, 93, 37-50.	0.9	24
242	Phylogenetic and expression analysis of the magnesium transporter family in pear, and functional verification of <i>PbrMGT7</i> in pear pollen. <i>Journal of Horticultural Science and Biotechnology</i> , 2018, 93, 51-63.	0.9	14
243	Genome structure of <i>Rosa multiflora</i> , a wild ancestor of cultivated roses. <i>DNA Research</i> , 2018, 25, 113-121.	1.5	70
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245	Characterisation of the whole-genome wide hexokinase gene family unravels the functional divergence in pear ( <i>Pyrus bretschneideri</i> Rehd.). <i>Journal of Horticultural Science and Biotechnology</i> , 2018, 93, 244-254.	0.9	6
246	Characterization and expression analysis of PbEXP genes in the epidermis of pear ( <i>Pyrus bretschneideri</i> ) Tj ETQq1 1.0,784314 rgBT /Overlock 10 Tf 50	1.8	20
247	Transcriptome analysis unravels an ethylene response factor involved in regulating fruit ripening in pear. <i>Physiologia Plantarum</i> , 2018, 163, 124-135.	2.6	56
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249	ATMT transformation efficiencies with native promoters in <i>Botryosphaeria kuwatsukai</i> causing ring rot disease in pear. <i>World Journal of Microbiology and Biotechnology</i> , 2018, 34, 179.	1.7	1
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252	Leveraging Transcriptome Data for Enhanced Gene Expression Analysis in Apple. <i>Journal of the American Society for Horticultural Science</i> , 2018, 143, 333-346.	0.5	4
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	0.6	8
254	Genome-Wide Characterization of DNA Demethylase Genes and Their Association with Salt Response in <i>Pyrus</i> . <i>Genes</i> , 2018, 9, 398.	1.0	14

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257	Retrospective and perspective of plant epigenetics in China. <i>Journal of Genetics and Genomics</i> , 2018, 45, 621-638.	1.7	45
258	Dynamic transcriptome analysis of root nitrate starvation and re-supply provides insights into nitrogen metabolism in pear ( <i>Pyrus bretschneideri</i> ). <i>Plant Science</i> , 2018, 277, 322-333.	1.7	15
259	WaspBase: a genomic resource for the interactions among parasitic wasps, insect hosts and plants. Database: the <i>Journal of Biological Databases and Curation</i> , 2018, 2018, 1-9.	1.4	3
260	Draft genome sequence of wild <i>Prunus yedoensis</i> reveals massive inter-specific hybridization between sympatric flowering cherries. <i>Genome Biology</i> , 2018, 19, 127.	3.8	89
261	Postharvest metabolomic changes in <i>Pyrus ussuriensis</i> Maxim. wild accession "Zaoshu Shanli"™. <i>Journal of Separation Science</i> , 2018, 41, 4001-4013.	1.3	14
262	Genome-Wide Identification and Functional Prediction of Novel Drought-Responsive lncRNAs in <i>Pyrus betulifolia</i> . <i>Genes</i> , 2018, 9, 311.	1.0	27
263	Identification of QTLs Associated with Conversion of Sucrose to Hexose in Mature Fruit of Japanese Pear. <i>Plant Molecular Biology Reporter</i> , 2018, 36, 643-652.	1.0	12
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265	Transcriptome sequencing analysis of two different genotypes of Asian pear reveals potential drought stress genes. <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	0.6	9
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268	Draft genome sequence of Taiwanese pear ( <i>Pyrus pyrifolia</i> ). <i>Data in Brief</i> , 2018, 19, 1871-1873.	0.5	1
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271	Genome-Wide analysis of aluminum-activated malate transporter family genes in six rosaceae species, and expression analysis and functional characterization on malate accumulation in Chinese white pear. <i>Plant Science</i> , 2018, 274, 451-465.	1.7	26
272	Horizontal transfers of LTR retrotransposons in seven species of Rosales. <i>Genome</i> , 2018, 61, 587-594.	0.9	7

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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 /Overlock 10	1.8	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.	1.7	18
276	Quince ( <i>Cydonia oblonga</i> Mill.) Breeding. , 2018, , 277-304.		2
277	Characterizing the expression of translation elongation factor gene EF1 $\alpha$ in pear ( <i>Pyrus</i> ) fruit: evaluation of EF1 $\alpha$ as a housekeeping gene. <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	0.6	2
278	Diversification and independent domestication of Asian and European pears. <i>Genome Biology</i> , 2018, 19, 77.	3.8	149
279	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.	1.6	6
280	Woody Ornamentals of the Temperate Zone. <i>Handbook of Plant Breeding</i> , 2018, , 803-887.	0.1	9
281	Cherry Breeding: Sweet Cherry ( <i>Prunus avium</i> L.) and Sour Cherry ( <i>Prunus cerasus</i> L.). , 2018, , 31-88.		2
282	Pear ( <i>Pyrus</i> spp.) Breeding. , 2018, , 131-163.		10
283	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.	2.4	25
284	Genome-Wide Analysis Characterization and Evolution of SBP Genes in <i>Fragaria vesca</i> , <i>Pyrus bretschneideri</i> , <i>Prunus persica</i> and <i>Prunus mume</i> . <i>Frontiers in Genetics</i> , 2018, 9, 64.	1.1	33
285	Molecular Characterization, Evolution, and Expression Profiling of the Dirigent (DIR) Family Genes in Chinese White Pear ( <i>Pyrus bretschneideri</i> ). <i>Frontiers in Genetics</i> , 2018, 9, 136.	1.1	39
286	Draft genome sequence of Japanese pear ( <i>Pyrus pyrifolia</i> ). <i>Data in Brief</i> , 2018, 19, 2221-2223.	0.5	1
287	Genome Wide Identification, Evolutionary, and Expression Analysis of VQ Genes from Two <i>Pyrus</i> Species. <i>Genes</i> , 2018, 9, 224.	1.0	16
288	Abscisic Acid (ABA ) Promotes the Induction and Maintenance of Pear ( <i>Pyrus pyrifolia</i> White Pear) Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.8	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.	1.7	47
290	Comparative and Expression Analysis of Ubiquitin Conjugating Domain-Containing Genes in Two <i>Pyrus</i> Species. <i>Cells</i> , 2018, 7, 77.	1.8	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.	1.2	22
293	Transcriptome analyses provide new possible mechanisms of aroma ester weakening of "Nanguo" pear after cold storage. Scientia Horticulturae, 2018, 237, 247-256.	1.7	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.	1.8	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.	0.5	9
296	PbGLR3.3 Regulates Pollen Tube Growth in the Mediation of Ca <sup>2+</sup> Influx in <i>Pyrus bretschneideri</i> . Journal of Plant Biology, 2018, 61, 217-226.	0.9	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.	1.1	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	0.6	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 10.1	1.0	5
300	Genome-wide identification, evolution, and expression analysis of the <i>KT/HAK/KUP</i> family in pear. Genome, 2018, 61, 755-765.	0.9	25
301	Sequence and Analysis of the Black Raspberry ( <i>Rubus occidentalis</i> ) Genome. Compendium of Plant Genomes, 2018, , 185-197.	0.3	3
302	Expansion and evolutionary patterns of GDSL-type esterases/lipases in Rosaceae genomes. Functional and Integrative Genomics, 2018, 18, 673-684.	1.4	37
303	Genome survey sequencing of <i>Dioscorea zingiberensis</i> . Genome, 2018, 61, 567-574.	0.9	18
304	Genomic Resources for the Woodland Strawberry ( <i>Fragaria vesca</i> ). Compendium of Plant Genomes, 2018, , 25-33.	0.3	3
305	The effect of bagging on ascorbate in <i>Pyrus</i> fruit. New Zealand Journal of Crop and Horticultural Science, 2019, 47, 19-31.	0.7	4
306	<i>PbrmiR397a</i> regulates lignification during stone cell development in pear fruit. Plant Biotechnology Journal, 2019, 17, 103-117.	4.1	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.	1.0	13
308	Identification of miRNAs involved in fruit ripening by deep sequencing of <i>Olea europaea</i> L. transcriptome. PLoS ONE, 2019, 14, e0221460.	1.1	18

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310	Transcriptomic and Gas Chromatography-Mass Spectrometry Metabolomic Profiling Analysis of the Epidermis Provides Insights into Cuticular Wax Regulation in Developing ‘Yuluxiang’™ Pear Fruit. <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 8319-8331.	2.4	15
311	Differential retention of transposable element-derived sequences in outcrossing Arabidopsis genomes. <i>Mobile DNA</i> , 2019, 10, 30.	1.3	26
312	Reconstruction of Ancestral Chromosomes of the Family Rosaceae. <i>Compendium of Plant Genomes</i> , 2019, , 149-161.	0.3	0
313	Molecular Characterization, DNA Finger Printing, and Genomics in Horticultural Crops. , 2019, , 595-618.		1
314	Genetics and Breeding of Pear. <i>Compendium of Plant Genomes</i> , 2019, , 63-101.	0.3	1
315	Repetitive Sequences in Pear. <i>Compendium of Plant Genomes</i> , 2019, , 145-152.	0.3	0
316	Regulatory Sequences of Pear. <i>Compendium of Plant Genomes</i> , 2019, , 153-177.	0.3	0
317	Botany and Taxonomy of Pear. <i>Compendium of Plant Genomes</i> , 2019, , 1-33.	0.3	3
318	Functional Genomics. <i>Compendium of Plant Genomes</i> , 2019, , 265-277.	0.3	0
319	Whole-Genome Duplications in Pear and Apple. <i>Compendium of Plant Genomes</i> , 2019, , 279-299.	0.3	11
320	Genetic Diversity and Domestication History in <i>Pyrus</i> . <i>Compendium of Plant Genomes</i> , 2019, , 51-62.	0.3	5
321	Marker-trait associations and genomic predictions of interspecific pear ( <i>Pyrus</i> ) fruit characteristics. <i>Scientific Reports</i> , 2019, 9, 9072.	1.6	38
322	Stone Cell Development in Pear. <i>Compendium of Plant Genomes</i> , 2019, , 201-225.	0.3	5
323	Genetics, Genomics, and Breeding for Fire Blight Resistance in Pear. <i>Compendium of Plant Genomes</i> , 2019, , 243-264.	0.3	6
324	Molecular Mapping of Major Genes and QTLs in Pear. <i>Compendium of Plant Genomes</i> , 2019, , 113-131.	0.3	4
325	The Genome of Pear. <i>Compendium of Plant Genomes</i> , 2019, , 133-143.	0.3	1
326	PbrPCCP1 mediates the PbrTTS1 signaling to control pollen tube growth in pear. <i>Plant Science</i> , 2019, 289, 110244.	1.7	2

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329	Evolutionary Rate Heterogeneity and Functional Divergence of Orthologous Genes in <i>Pyrus</i> . <i>Biomolecules</i> , 2019, 9, 490.	1.8	10
330	Auxin regulates adventitious root formation in tomato cuttings. <i>BMC Plant Biology</i> , 2019, 19, 435.	1.6	69
331	Single-pollen-cell sequencing for gamete-based phased diploid genome assembly in plants. <i>Genome Research</i> , 2019, 29, 1889-1899.	2.4	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.	1.6	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.	0.7	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.	1.8	74
335	Integrative Analysis of the Core Fruit Lignification Toolbox in Pear Reveals Targets for Fruit Quality Bioengineering. <i>Biomolecules</i> , 2019, 9, 504.	1.8	28
336	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.	4.1	46
337	PbrMYB169 positively regulates lignification of stone cells in pear fruit. <i>Journal of Experimental Botany</i> , 2019, 70, 1801-1814.	2.4	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.	1.7	163
339	Origins of the Apple: The Role of Megafaunal Mutualism in the Domestication of <i>Malus</i> and Rosaceous Trees. <i>Frontiers in Plant Science</i> , 2019, 10, 617.	1.7	65
340	Screening for quantitative real-time PCR reference genes with high stable expression using the mRNA-sequencing data for pear. <i>Tree Genetics and Genomes</i> , 2019, 15, 1.	0.6	10
341	In Silico Genome-Wide Analysis of the Pear ( <i>Pyrus bretschneideri</i> ) KNOX Family and the Functional Characterization of PbKNOX1, an Arabidopsis BREVIPEDICELLUS Orthologue Gene, Involved in Cell Wall and Lignin Biosynthesis. <i>Frontiers in Genetics</i> , 2019, 10, 632.	1.1	28
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.	0.8	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.	0.9	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.	1.8	37

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346	Development of a highly efficient Axiom <sup>®</sup> , 70 K SNP array for <i>Pyrus</i> and evaluation for high-density mapping and germplasm characterization. <i>BMC Genomics</i> , 2019, 20, 331.	1.2	40
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.	1.6	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.	1.0	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.	1.0	9
350	Validation of SNP markers for fruit quality and disease resistance loci in apple ( <i>Malus domestica</i> ) Tj ETQq1 1 0.784314 rgBT /Overclock 10 If 50 422 T	2.9	50
351	Insight on Rosaceae Family with Genome Sequencing and Functional Genomics Perspective. <i>BioMed Research International</i> , 2019, 2019, 1-12.	0.9	21
352	Fine-mapping and validation of the genomic region underpinning pear red skin colour. <i>Horticulture Research</i> , 2019, 6, 29.	2.9	31
353	Unbiased subgenome evolution following a recent whole-genome duplication in pear ( <i>Pyrus</i> ) Tj ETQq0 0 0 rgBT /Overclock 10 If 50 422 T	2.9	54
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.	1.8	6
355	Comparative Transcriptomic Analysis Provides Insight into the Domestication and Improvement of Pear ( <i>P. pyrifolia</i> ) Fruit. <i>Plant Physiology</i> , 2019, 180, 435-452.	2.3	33
356	Construction of a high-density linkage map for bronze loquat using RAD-Seq. <i>Scientia Horticulturae</i> , 2019, 251, 59-64.	1.7	11
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.	4.1	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.	1.1	11
359	Gene duplication and evolution in recurring polyploidization–diploidization cycles in plants. <i>Genome Biology</i> , 2019, 20, 38.	3.8	542
360	Metacaspase gene family in Rosaceae genomes: Comparative genomic analysis and their expression during pear pollen tube and fruit development. <i>PLoS ONE</i> , 2019, 14, e0211635.	1.1	9
361	Genome-Wide Identification and Analysis of High-Copy-Number LTR Retrotransposons in Asian Pears. <i>Genes</i> , 2019, 10, 156.	1.0	4
362	Family-1 UDP glycosyltransferases in pear ( <i>Pyrus bretschneideri</i> ): Molecular identification, phylogenomic characterization and expression profiling during stone cell formation. <i>Molecular Biology Reports</i> , 2019, 46, 2153-2175.	1.0	22

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364	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.	2.3	6
365	Evolution and functional divergence of MADS-box genes in <i>Pyrus</i> . <i>Scientific Reports</i> , 2019, 9, 1266.	1.6	15
366	Comprehensive genome-wide analysis of the pear ( <i>Pyrus bretschneideri</i> ) laccase gene (PbLAC) family and functional identification of PbLAC1 involved in lignin biosynthesis. <i>PLoS ONE</i> , 2019, 14, e0210892.	1.1	30
367	Tung Tree ( <i>Vernicia fordii</i> ) Genome Provides A Resource for Understanding Genome Evolution and Improved Oil Production. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 558-575.	3.0	43
368	Genome-Wide Identification and Characterization of ABC Transporters in Nine Rosaceae Species Identifying MdABCG28 as a Possible Cytokinin Transporter linked to Dwarfing. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5783.	1.8	21
369	Pseudo-chromosome length genome assembly of a double haploid "Bartlett" pear ( <i>Pyrus communis</i> L.). <i>GigaScience</i> , 2019, 8, .	3.3	76
370	Genotyping-by-sequencing approaches using optimized two-enzyme combinations in Asian pears ( <i>Pyrus</i> ) Tj ETQq1 1.0.784314 rgBT / Ov	1.0	2
371	A de novo genome assembly of the dwarfing pear rootstock Zhongai 1. <i>Scientific Data</i> , 2019, 6, 281.	2.4	28
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373	TRANSNAP: a web database providing comprehensive information on Japanese pear transcriptome. <i>Scientific Reports</i> , 2019, 9, 18922.	1.6	10
374	Knockout of the S-acyltransferase Gene, PbPAT14, Confers the Dwarf Yellowing Phenotype in First Generation Pear by ABA Accumulation. <i>International Journal of Molecular Sciences</i> , 2019, 20, 6347.	1.8	14
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376	Decoding systems biology of plant stress for sustainable agriculture development and optimized food production. <i>Progress in Biophysics and Molecular Biology</i> , 2019, 145, 19-39.	1.4	15
377	Transcriptomic and evolutionary analyses of white pear ( <i>Pyrus bretschneideri</i> ) $\beta$ -amylase genes reveals their importance for cold and drought stress responses. <i>Gene</i> , 2019, 689, 102-113.	1.0	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.	1.0	29
379	Transcriptomic analysis of bagging-treated "Pingguo" pear shows that MYB4-like1, MYB4-like2, MYB1R1 and WDR involved in anthocyanin biosynthesis are up-regulated in fruit peels in response to light. <i>Scientia Horticulturae</i> , 2019, 244, 428-434.	1.7	22
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382	Identification and functional characterization of SOC1-like genes in <i>Pyrus bretschneideri</i> . <i>Genomics</i> , 2020, 112, 1622-1632.	1.3	13
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	4.2	32
384	<i>De novo</i> assembly of a wild pear ( <i>Pyrus betuleafolia</i> ) genome. <i>Plant Biotechnology Journal</i> , 2020, 18, 581-595.	4.1	72
385	Genome-wide analysis of coding and non-coding RNA reveals a conserved miR164-NAC regulatory pathway for fruit ripening. <i>New Phytologist</i> , 2020, 225, 1618-1634.	3.5	86
386	Ethylene mediates the branching of the jasmonate-induced flavonoid biosynthesis pathway by suppressing anthocyanin biosynthesis in red Chinese pear fruits. <i>Plant Biotechnology Journal</i> , 2020, 18, 1223-1240.	4.1	101
387	Transcriptome analysis of watercore in <i>Pyrus pyrifolia</i> by comparing pairs of susceptible and resistant F1 sibs. <i>Scientia Horticulturae</i> , 2020, 264, 109136.	1.7	10
388	Genome-wide comparative analysis of the BAHD superfamily in seven Rosaceae species and expression analysis in pear ( <i>Pyrus bretschneideri</i> ). <i>BMC Plant Biology</i> , 2020, 20, 14.	1.6	22
389	Genome wide identification and functional characterization of strawberry pectin methylesterases related to fruit softening. <i>BMC Plant Biology</i> , 2020, 20, 13.	1.6	41
390	RNA-Seq analysis of compatible and incompatible styles of <i>Pyrus</i> species at the beginning of pollination. <i>Plant Molecular Biology</i> , 2020, 102, 287-306.	2.0	6
391	Epigenetic patterns within the haplotype phased fig ( <i>Ficus carica</i> L.) genome. <i>Plant Journal</i> , 2020, 102, 600-614.	2.8	43
392	Genetic and ploidy diversity of pear ( <i>Pyrus</i> spp.) germplasm of Friuli Venezia Giulia, Italy. <i>Genetic Resources and Crop Evolution</i> , 2020, 67, 83-96.	0.8	14
393	Cloning and functional characterization of two cinnamate 4-hydroxylase genes from <i>Pyrus bretschneideri</i> . <i>Plant Physiology and Biochemistry</i> , 2020, 156, 135-145.	2.8	19
394	Characteristics and Expression Analyses of Trehalose-6-Phosphate Synthase Family in <i>Prunus mume</i> Reveal Genes Involved in Trehalose Biosynthesis and Drought Response. <i>Biomolecules</i> , 2020, 10, 1358.	1.8	9
395	Genome-wide identification and expression analysis of the MYB transcription factor in Japanese plum ( <i>Prunus salicina</i> ). <i>Genomics</i> , 2020, 112, 4875-4886.	1.3	25
396	A new species of <i>Malus</i> in China, <i>Malus shizongensis</i> Liu sp. nov. <i>Journal of Integrative Agriculture</i> , 2020, 19, 2451-2457.	1.7	2
397	Construction of high-resolution genetic linkage map in pear pseudo-BC1 (( <i>Pyrus pyrifolia</i> × <i>P.</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50,662 Td (si	0.7	7
398	Transcriptome Analysis of Low- and High-Sucrose Pear Cultivars Identifies Key Regulators of Sucrose Biosynthesis in Fruits. <i>Plant and Cell Physiology</i> , 2020, 61, 1493-1506.	1.5	13

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400	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.	1.3	27
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.	1.2	7
402	The Peptide PbrPSK2 From Phytosulfokine Family Induces Reactive Oxygen Species (ROS) Production to Regulate Pear Pollen Tube Growth. <i>Frontiers in Plant Science</i> , 2020, 11, 601993.	1.7	9
403	Advances in Genomic, Transcriptomic, and Metabolomic Analyses of Fruit Quality in Fruit Crops. <i>Horticultural Plant Journal</i> , 2020, 6, 361-371.	2.3	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.	1.2	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.	1.4	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.	0.8	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 Molecular Sciences</i> , 2020, 21, 4933.	1.8	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.	0.3	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>	1.1	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.	2.3	46
411	PbrPOE21 inhibits pear pollen tube growth in vitro by altering apical reactive oxygen species content. <i>Planta</i> , 2020, 252, 43.	1.6	3
412	Mining and evolution analysis of lateral organ boundaries domain (LBD) genes in Chinese white pear ( <i>Pyrus bretschneideri</i> ). <i>BMC Genomics</i> , 2020, 21, 644.	1.2	18
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.	1.2	9
414	Advances in cultivar and rootstock breeding: a case study in peach. <i>Acta Horticulturae</i> , 2020, , 1-8.	0.1	0
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