The genome of the domesticated apple (Malus Ã— dome

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Citation Report

#	Article	IF	Citations
1	Use of homologous and heterologous gene expression profiling tools to characterize transcription dynamics during apple fruit maturation and ripening. BMC Plant Biology, 2010, 10, 229.	1.6	79
2	Harvesting the apple genome. Nature Genetics, 2010, 42, 822-823.	9.4	9
3	Apple FLOWERING LOCUS T proteins interact with transcription factors implicated in cell growth and organ development. Tree Physiology, 2011, 31, 555-566.	1.4	62
4	Differential expression in RNA-seq: A matter of depth. Genome Research, 2011, 21, 2213-2223.	2.4	1,456
5	From forest to field: Perennial fruit crop domestication. American Journal of Botany, 2011, 98, 1389-1414.	0.8	348
6	Revision of the Nomenclature of the Differential Host-Pathogen Interactions of<i>Venturia inaequalis</i>and<i>Malus</i>. Annual Review of Phytopathology, 2011, 49, 391-413.	3.5	176
7	Effects of<i>Ginkgo biloba</i>Constituents on Fruit-Infesting Behavior of Codling Moth (<i>Cydia) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	2.4	15
8	Phylogenomic networks. Trends in Microbiology, 2011, 19, 483-491.	3.5	66
9	Recent advances on the regulation of anthocyanin synthesis in reproductive organs. Plant Science, 2011, 181, 219-229.	1.7	715
10	Crop genome sequencing: lessons and rationales. Trends in Plant Science, 2011, 16, 77-88.	4.3	222
11	What Next? The Next Transit from Biology to Diagnostics: Next Generation Sequencing for Immunogenetics. Transfusion Medicine and Hemotherapy, 2011, 38, 308-317.	0.7	9
12	Assessing molecular and morpho-agronomical diversity and identification of ISSR markers associated with fruit traits in quince (Cydonia oblonga). Genetics and Molecular Research, 2011, 10, 2729-2746.	0.3	21
13	Simple Sequence Repeat Marker Development and Mapping Targeted to Previously Unmapped Regions of the Strawberry Genome Sequence. Plant Genome, 2011, 4, 165-177.	1.6	28
14	Cell Death Mediated by the N-Terminal Domains of a Unique and Highly Conserved Class of NB-LRR Protein. Molecular Plant-Microbe Interactions, 2011, 24, 918-931.	1.4	319
15	Inheritance of and Molecular Markers for Susceptibility of <i>Malus domestica</i> to Fruit Ring Rot (<i>Botryosphaeria dothidea</i>). Journal of Phytopathology, 2011, 159, 782-788.	0.5	7
16	High temperature reduces apple fruit colour via modulation of the anthocyanin regulatory complex. Plant, Cell and Environment, 2011, 34, 1176-1190.	2.8	330
17	Journey through the past: 150 million years of plant genome evolution. Plant Journal, 2011, 66, 58-65.	2.8	91
18	Sequencing crop genomes: approaches and applications. New Phytologist, 2011, 191, 915-925.	3.5	101

#	ARTICLE	IF	CITATIONS
19	Application of a high-speed breeding technology to apple (Malusâ€ƒÃ—â€ƒdomestica) based on transgenic early flowering plants and marker-assisted selection. New Phytologist, 2011, 192, 364-377.	3.5	141
20	Deciphering the genetic determinism of bud phenology in apple progenies: a new insight into chilling and heat requirement effects on flowering dates and positional candidate genes. New Phytologist, 2011, 192, 378-392.	3.5	76
21	An unusual plant triterpene synthase with predominant Î±â€amyrinâ€producing activity identified by characterizing oxidosqualene cyclases from <i>Malus</i>â€ƒÃ—â€ƒ<i>domestica</i>. FEBS Journal, 2011, 278, 2485-2499.	2.2	67
22	The genome of woodland strawberry (Fragaria vesca). Nature Genetics, 2011, 43, 109-116.	9.4	1,091
23	Chocolate and strawberries. Nature Genetics, 2011, 43, 85-85.	9.4	0
24	Where systems biology meets postharvest. Postharvest Biology and Technology, 2011, 62, 223-237.	2.9	49
25	Comprehensive analysis of tandem amino acid repeats from ten angiosperm genomes. BMC Genomics, 2011, 12, 632.	1.2	12
26	Dissecting the genome of the polyploid crop oilseed rape by transcriptome sequencing. Nature Biotechnology, 2011, 29, 762-766.	9.4	187
27	Exploring giant plant genomes with next-generation sequencing technology. Chromosome Research, 2011, 19, 939-953.	1.0	56
28	Molecular characterization of novel Ty1-copia-like retrotransposons in pear (Pyrus pyrifolia). Tree Genetics and Genomes, 2011, 7, 845-856.	0.6	10
29	Genetic diversity of the genus Malus and implications for linkage mapping with SNPs. Tree Genetics and Genomes, 2011, 7, 857-868.	0.6	51
30	Differential transcript abundance and genotypic variation of four putative allergen-encoding gene families in melting peach. Tree Genetics and Genomes, 2011, 7, 903-916.	0.6	20
31	S-genotyping of old apple cultivars from the Carpathian basin: methodological, breeding and evolutionary aspects. Tree Genetics and Genomes, 2011, 7, 1135-1145.	0.6	19
32	Ectopic expression of a novel peach (Prunus persica) CBF transcription factor in apple (MalusÂÃ—Âdomestica) results in short-day induced dormancy and increased cold hardiness. Planta, 2011, 233, 971-983.	1.6	172
33	Genome-wide analysis of the RING finger gene family in apple. Molecular Genetics and Genomics, 2011, 286, 81-94.	1.0	55
34	DNA sequencing leads to genomics progress in China. Science China Life Sciences, 2011, 54, 290-292.	2.3	10
35	An introduction to the medicinal plant genome project. Frontiers of Medicine, 2011, 5, 178-184.	1.5	25
36	Transcriptomics of shading-induced and NAA-induced abscission in apple (Malus domestica) reveals a shared pathway involving reduced photosynthesis, alterations in carbohydrate transport and signaling and hormone crosstalk. BMC Plant Biology, 2011, 11, 138.	1.6	104

#	ARTICLE	IF	CITATIONS
37	Conservation and loss of ribosomal RNA gene sites in diploid and polyploid Fragaria (Rosaceae). BMC Plant Biology, 2011, 11, 157.	1.6	43
38	Apple skin patterning is associated with differential expression of MYB10. BMC Plant Biology, 2011, 11, 93.	1.6	227
39	Efficient virus-induced gene silencing in apple, pear and Japanese pear using Apple latent spherical virus vectors. Plant Methods, 2011, 7, 15.	1.9	107
40	SNP discovery in apple cultivars using next generation sequencing. BMC Proceedings, 2011, 5, .	1.8	5
41	Comparative analysis of rosaceous genomes and the reconstruction of a putative ancestral genome for the family. BMC Evolutionary Biology, 2011, 11, 9.	3.2	103
42	Physical mapping and BAC-end sequence analysis provide initial insights into the flax (Linum) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf	1.2	64
43	Analysis of expressed sequence tags generated from full-length enriched cDNA libraries of melon. BMC Genomics, 2011, 12, 252.	1.2	49
44	Analysis of BAC end sequences in oak, a keystone forest tree species, providing insight into the composition of its genome. BMC Genomics, 2011, 12, 292.	1.2	33
45	Metabolite profiling on apple volatile content based on solid phase microextraction and gas-chromatography time of flight mass spectrometry. Journal of Chromatography A, 2011, 1218, 4517-4524.	1.8	100
46	Arabidopsis paves the way: genomic and network analyses in crops. Current Opinion in Biotechnology, 2011, 22, 260-270.	3.3	55
47	Integration of physical and genetic maps in apple confirms whole-genome and segmental duplications in the apple genome. Journal of Experimental Botany, 2011, 62, 5117-5130.	2.4	78
48	Signaling Pathways Mediating the Induction of Apple Fruitlet Abscission Â Â Â. Plant Physiology, 2011, 155, 185-208.	2.3	163
49	Artemisia annuaextracts, artemisinin and 1,8-cineole, prevent fruit infestation by a major, cosmopolitan pest of apples. Pharmaceutical Biology, 2011, 49, 563-568.	1.3	17
50	Targeted Identification of Short Interspersed Nuclear Element Families Shows Their Widespread Existence and Extreme Heterogeneity in Plant Genomes. Plant Cell, 2011, 23, 3117-3128.	3.1	116
51	The Emerging Importance of Type I MADS Box Transcription Factors for Plant Reproduction. Plant Cell, 2011, 23, 865-872.	3.1	177
52	On the evolutionary history of the domesticated apple. Nature Genetics, 2011, 43, 1043-1044.	9.4	24
53	On the evolutionary history of the domesticated apple. Nature Genetics, 2011, 43, 1044-1045.	9.4	11
54	Widespread Endogenization of Genome Sequences of Non-Retroviral RNA Viruses into Plant Genomes. PLoS Pathogens, 2011, 7, e1002146.	2.1	173

#	ARTICLE	IF	CITATIONS
55	OrysPSSP: a comparative Platform for Small Secreted Proteins from rice and other plants. Nucleic Acids Research, 2012, 41, D1192-D1198.	6.5	18
56	Genetic control of biennial bearing in apple. Journal of Experimental Botany, 2012, 63, 131-149.	2.4	144
57	High-Throughput SNP Discovery and Genotyping for Constructing a Saturated Linkage Map of Chickpea (Cicer arietinum L.). DNA Research, 2012, 19, 357-373.	1.5	137
58	Molecular Tools for Exploring Polyploid Genomes in Plants. International Journal of Molecular Sciences, 2012, 13, 10316-10335.	1.8	40
59	Worldwide Core Collection of Olive Cultivars Based on Simple Sequence Repeat and Morphological Markers. Crop Science, 2012, 52, 211-221.	0.8	73
60	Isolation, Molecular Characterization, and Mapping of Four Rose MLO Orthologs. Frontiers in Plant Science, 2012, 3, 244.	1.7	30
61	Distribution of <i>MdACS3</i> null alleles in apple (<i>Malus</i> Ã— <i>domestica</i> Borkh.) and its relevance to the fruit ripening characters. Breeding Science, 2012, 62, 46-52.	0.9	13
62	Differential Expression of Biphenyl Synthase Gene Family Members in Fire-Blight-Infected Apple â€˜Holsteiner Coxâ€™. Plant Physiology, 2012, 158, 864-875.	2.3	42
63	The genome of Prunus mume. Nature Communications, 2012, 3, 1318.	5.8	441
64	i-ADHoRe 3.0â€"fast and sensitive detection of genomic homology in extremely large data sets. Nucleic Acids Research, 2012, 40, e11-e11.	6.5	192
65	Introduction of apple ANR genes into tobacco inhibits expression of both CHI and DFR genes in flowers, leading to loss of anthocyanin. Journal of Experimental Botany, 2012, 63, 2437-2447.	2.4	126
66	Expression Patterns of Genes Involved in Sugar Metabolism and Accumulation during Apple Fruit Development. PLoS ONE, 2012, 7, e33055.	1.1	231
67	Dissecting Plant Genomes with the PLAZA Comparative Genomics Platform Â. Plant Physiology, 2012, 158, 590-600.	2.3	238
68	Transcriptional analysis of apple fruit proanthocyanidin biosynthesis. Journal of Experimental Botany, 2012, 63, 5437-5450.	2.4	74
69	Nextâ€generation sequencing applications for wheat crop improvement. American Journal of Botany, 2012, 99, 365-371.	0.8	98
70	Genetic analysis of metabolites in apple fruits indicates an mQTL hotspot for phenolic compounds on linkage group 16. Journal of Experimental Botany, 2012, 63, 2895-2908.	2.4	74
71	Phytozome: a comparative platform for green plant genomics. Nucleic Acids Research, 2012, 40, D1178-D1186.	6.5	4,204
72	Analysis of cellulose synthase genes from domesticated apple identifies collinear genes WDR53 and CesA8A: partial co-expression, bicistronic mRNA, and alternative splicing of CESA8A. Journal of Experimental Botany, 2012, 63, 6045-6056.	2.4	8

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73	Dynamics and Adaptive Benefits of Protein Domain Emergence and Arrangements during Plant Genome Evolution. Genome Biology and Evolution, 2012, 4, 316-329.	1.1	66
74	A gene expression analysis of cell wall biosynthetic genes in Malus x domestica infected by 'Candidatus Phytoplasma mali'. Tree Physiology, 2012, 32, 1365-1377.	1.4	15
75	Decoding Plant and Animal Genome Plasticity from Differential Paleo-Evolutionary Patterns and Processes. Genome Biology and Evolution, 2012, 4, 917-928.	1.1	69
76	New Insight into the History of Domesticated Apple: Secondary Contribution of the European Wild Apple to the Genome of Cultivated Varieties. PLoS Genetics, 2012, 8, e1002703.	1.5	334
77	Metabolic and gene expression analysis of apple (Malus Ã— domestica) carotenogenesis. Journal of Experimental Botany, 2012, 63, 4497-4511.	2.4	75
78	Allelic Variation in Paralogs of GDP-l-Galactose Phosphorylase Is a Major Determinant of Vitamin C Concentrations in Apple Fruit Â Â Â. Plant Physiology, 2012, 160, 1613-1629.	2.3	81
79	Challenges in Feasible Problem Construction in Nutritional Genomics: An Empirical Study. , 2012, , 136-157.		4
80	Functional analysis of the isopentenyltransferase gene<i>MdIPT3a</i>from apple (<i>Malus) Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.9	8
82	Apple EIN3 BINDING F-box 1 inhibits the activity of three apple EIN3-like transcription factors. AoB PLANTS, 2012, 2012, pls034.	1.2	18
83	LARGE-SCALE STANDARDIZED PHENOTYPING OF APPLE IN ROSBREED. Acta Horticulturae, 2012, , 233-238.	0.1	17
84	Gamma Paleohexaploidy in the Stem Lineage of Core Eudicots: Significance for MADS-Box Gene and Species Diversification. Molecular Biology and Evolution, 2012, 29, 3793-3806.	3.5	127
85	Paternity and ploidy segregation of progenies derived from tetraploid Malus xiaojinensis. Tree Genetics and Genomes, 2012, 8, 1469-1476.	0.6	7
86	Nextâ€generation sequencingâ€based transcriptomic and proteomic analysis of the common reed, <i>Phragmites australis</i> (Poaceae), reveals genes involved in invasiveness and rhizome specificity. American Journal of Botany, 2012, 99, 232-247.	0.8	49
88	The genome of flax (<i>Linum usitatissimum</i>) assembled <i>de novo</i> from short shotgun sequence reads. Plant Journal, 2012, 72, 461-473.	2.8	415
89	Functional Genomics of Flowering Time in Trees. , 2012, , 39-69.		5
90	Genetic transformation of fruit trees: current status and remaining challenges. Transgenic Research, 2012, 21, 1163-1181.	1.3	74
91	Specific Detection of Potentially Allergenic Peach and Apple in Foods Using Polymerase Chain Reaction. Journal of Agricultural and Food Chemistry, 2012, 60, 2108-2115.	2.4	8
92	Genomics of Temperate Fruit Trees. , 2012, , 155-208.		0

#	ARTICLE	IF	CITATIONS
93	Gene duplication within the Green Lineage: the case of TEL genes. Journal of Experimental Botany, 2012, 63, 5061-5077.	2.4	35
94	Fine mapping of <i>Co</i>, a gene controlling columnar growth habit located on apple (<i>Malus</i>Ã—<i>domestica</i> Borkh.) linkage group 10. Plant Breeding, 2012, 131, 641-647.	1.0	42
95	Quantitative Real-Time PCR Analysis of â€˜Candidatus Phytoplasma maliâ€™ Without External Standard Curves. Erwerbs-Obstbau, 2012, 54, 147-153.	0.5	6
96	Genetic characterization of the Ma locus with pH and titratable acidity in apple. Molecular Breeding, 2012, 30, 899-912.	1.0	83
97	Cloning and Characterization of MxVHA-c, a Vacuolar H+-ATPase Subunit C Gene Related to Fe Efficiency from Malus xiaojinensis. Plant Molecular Biology Reporter, 2012, 30, 1149-1157.	1.0	11
98	A genetic linkage map of an apple rootstock progeny anchored to the Malus genome sequence. Tree Genetics and Genomes, 2012, 8, 991-1002.	0.6	17
99	Multiple plant hormones and cell wall metabolism regulate apple fruit maturation patterns and texture attributes. Tree Genetics and Genomes, 2012, 8, 1389-1406.	0.6	28
100	Trends in genomics and molecular marker systems for the development of some underutilized crops. Genes and Genomics, 2012, 34, 451-466.	0.5	12
101	Illusion or reality, abstract or concrete art? Models in health: do they answer the questions?. Revista Da AssociaÃ§Ã£o MÃ©dica Brasileira (English Edition), 2012, 58, 269-271.	0.1	0
102	The MdTFL1 gene of apple (Malus x domestica Borkh.) reduces vegetative growth and generation time. Tree Physiology, 2012, 32, 1288-1301.	1.4	91
103	Parthenocarpic genetic resources and gene expression related to parthenocarpy among four species in pear (Pyrus spp.). Scientia Horticulturae, 2012, 136, 101-109.	1.7	13
104	Functional characterization of an apple apomixis-related MhFIE gene in reproduction development. Plant Science, 2012, 185-186, 105-111.	1.7	17
105	Malus x domestica. , 2012, , 413-436.		1
106	The role of Schmidt â€˜Antonovkaâ€™ in apple scab resistance breeding. Tree Genetics and Genomes, 2012, 8, 627-642.	0.6	14
107	Rosaceae conserved orthologous set (RosCOS) markers as a tool to assess genome synteny between Malus and Fragaria. Tree Genetics and Genomes, 2012, 8, 643-658.	0.6	13
108	Aligned genetic linkage maps of apple rootstock cultivar â€˜JM7â€™ and Malus sieboldii â€˜Sanashi 63â€™ constructed with novel EST-SSRs. Tree Genetics and Genomes, 2012, 8, 709-723.	0.6	26
109	Fire Blight: Applied Genomic Insights of the Pathogen and Host. Annual Review of Phytopathology, 2012, 50, 475-494.	3.5	118
110	Comparative analysis of algorithms for whole-genome assembly of pyrosequencing data. Briefings in Bioinformatics, 2012, 13, 269-280.	3.2	23

#	ARTICLE	IF	CITATIONS
111	Use of a transgenic early flowering approach in apple (MalusÂÃ—Âdomestica Borkh.) to introgress fire blight resistance from cultivar Evereste. Molecular Breeding, 2012, 30, 857-874.	1.0	39
112	Translational plant proteomics: A perspective. Journal of Proteomics, 2012, 75, 4588-4601.	1.2	63
113	A high-throughput apple SNP genotyping platform using the GoldenGateâ„¢ assay. Gene, 2012, 494, 196-201.	1.0	29
114	The transcriptomes of columnar and standard type apple trees (Malus x domestica) â€" A comparative study. Gene, 2012, 498, 223-230.	1.0	35
115	Raspberry. , 2012, , 263-304.		7
116	Genetic diversity and structure of local apple cultivars from Northeastern Spain assessed by microsatellite markers. Tree Genetics and Genomes, 2012, 8, 1163-1180.	0.6	89
117	Association mapping in forest trees and fruit crops. Journal of Experimental Botany, 2012, 63, 4045-4060.	2.4	134
118	Genetic structure of East Asian cultivated pears (Pyrus spp.) and their reclassification in accordance with the nomenclature of cultivated plants. Plant Systematics and Evolution, 2012, 298, 1689-1700.	0.3	26
119	The tomato genome: implications for plant breeding, genomics and evolution. Genome Biology, 2012, 13, 167.	13.9	37
120	Argot2: a large scale function prediction tool relying on semantic similarity of weighted Gene Ontology terms. BMC Bioinformatics, 2012, 13, S14.	1.2	137
121	Putative resistance gene markers associated with quantitative trait loci for fire blight resistance in Malus â€˜Robusta 5â€™ accessions. BMC Genetics, 2012, 13, 25.	2.7	88
122	Whole genome comparisons of Fragaria, Prunus and Malus reveal different modes of evolution between Rosaceous subfamilies. BMC Genomics, 2012, 13, 129.	1.2	77
123	Rapid gene-based SNP and haplotype marker development in non-model eukaryotes using 3'UTR sequencing. BMC Genomics, 2012, 13, 18.	1.2	31
124	Development of a dense SNP-based linkage map of an apple rootstock progeny using the Malus Infinium whole genome genotyping array. BMC Genomics, 2012, 13, 203.	1.2	77
125	Transcriptome sequencing for SNP discovery across Cucumis melo. BMC Genomics, 2012, 13, 280.	1.2	86
126	Evolution of the Rdr1 TNL-cluster in roses and other Rosaceous species. BMC Genomics, 2012, 13, 409.	1.2	19
127	Toward allotetraploid cotton genome assembly: integration of a high-density molecular genetic linkage map with DNA sequence information. BMC Genomics, 2012, 13, 539.	1.2	95
128	Identification, characterization and distribution of transposable elements in the flax (Linum) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf	1.2	30

#	ARTICLE	IF	CITATIONS
129	Small RNA and transcriptome deep sequencing proffers insight into floral gene regulation in Rosa cultivars. BMC Genomics, 2012, 13, 657.	1.2	49
130	Rootstock-regulated gene expression patterns associated with fire blight resistance in apple. BMC Genomics, 2012, 13, 9.	1.2	84
131	Intraspecific sequence comparisons reveal similar rates of non-collinear gene insertion in the B and D genomes of bread wheat. BMC Plant Biology, 2012, 12, 155.	1.6	18
132	The AINTEGUMENTA genes, MdANT1 and MdANT2, are associated with the regulation of cell production during fruit growth in apple (Malus Ã— domestica Borkh.). BMC Plant Biology, 2012, 12, 98.	1.6	46
133	Apple. , 2012, , 329-367.		34
134	An Ancient Duplication of Apple MYB Transcription Factors Is Responsible for Novel Red Fruit-Flesh Phenotypes Â Â. Plant Physiology, 2012, 161, 225-239.	2.3	272
136	Utility of Metabolomics toward Assessing the Metabolic Basis of Quality Traits in Apple Fruit with an Emphasis on Antioxidants. Journal of Agricultural and Food Chemistry, 2012, 60, 8552-8560.	2.4	73
138	Apple Hypanthium Firmness: New Insights from Comparative Proteomics. Applied Biochemistry and Biotechnology, 2012, 168, 306-326.	1.4	26
140	Comprehensive QTL mapping survey dissects the complex fruit texture physiology in apple (Malus x) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	2.4	97
141	A natural mutation-led truncation in one of the two aluminum-activated malate transporter-like genes at the Ma locus is associated with low fruit acidity in apple. Molecular Genetics and Genomics, 2012, 287, 663-678.	1.0	124
142	Plant Genome Diversity Volume 1. , 2012, , .		15
145	Heat shock transcriptional factors in Malus domestica: identification, classification and expression analysis. BMC Genomics, 2012, 13, 639.	1.2	81
146	Identification, characterization, and utilization of genome-wide simple sequence repeats to identify a QTL for acidity in apple. BMC Genomics, 2012, 13, 537.	1.2	61
147	Sunburn of Apple Fruit: Historical Background, Recent Advances and Future Perspectives. Critical Reviews in Plant Sciences, 2012, 31, 455-504.	2.7	135
148	The mQTL hotspot on linkage group 16 for phenolic compounds in apple fruits is probably the result of a leucoanthocyanidin reductase gene at that locus. BMC Research Notes, 2012, 5, 618.	0.6	14
149	Genome-Wide SNP Detection, Validation, and Development of an 8K SNP Array for Apple. PLoS ONE, 2012, 7, e31745.	1.1	249
150	Molecular Genetic Features of Polyploidization and Aneuploidization Reveal Unique Patterns for Genome Duplication in Diploid Malus. PLoS ONE, 2012, 7, e29449.	1.1	27
151	A High Resolution Genetic Map Anchoring Scaffolds of the Sequenced Watermelon Genome. PLoS ONE, 2012, 7, e29453.	1.1	127

#	ARTICLE	IF	CITATIONS
152	Deconstruction of the (Paleo)Polyploid Grapevine Genome Based on the Analysis of Transposition Events Involving NBS Resistance Genes. PLoS ONE, 2012, 7, e29762.	1.1	38
153	Diversification of Genes Encoding Granule-Bound Starch Synthase in Monocots and Dicots Is Marked by Multiple Genome-Wide Duplication Events. PLoS ONE, 2012, 7, e30088.	1.1	37
154	A Genome-Wide Survey of Switchgrass Genome Structure and Organization. PLoS ONE, 2012, 7, e33892.	1.1	50
155	Genomic Selection for Fruit Quality Traits in Apple (MalusÃ—domestica Borkh.). PLoS ONE, 2012, 7, e36674.	1.1	218
156	A Multi-Population Consensus Genetic Map Reveals Inconsistent Marker Order among Maps Likely Attributed to Structural Variations in the Apple Genome. PLoS ONE, 2012, 7, e47864.	1.1	59
157	Apple Can Act as Anti-Aging on Yeast Cells. Oxidative Medicine and Cellular Longevity, 2012, 2012, 1-8.	1.9	23
158	Sequencing Technologies and Their Use in Plant Biotechnology and Breeding. , 2012, , .		5
159	Characterization of Two Orthologs of REVERSION-TO-ETHYLENE SENSITIVITY1 in Apple. Journal of Molecular Biology Research, 2012, 2, .	0.1	12
160	Genomics-Assisted Plant Breeding in the 21st Century: Technological Advances and Progress. , 0, , .		16
161	The First Ten Years of Plant Genome Sequencing and Prospects for the Next Decade. , 2012, , 1-15.		4
162	Divergence of TERMINAL FLOWER1-like genes in Rosaceae. Biologia Plantarum, 2012, 56, 465-472.	1.9	13
163	The <i>TvPirin</i> Gene Is Necessary for Haustorium Development in the Parasitic Plant <i>Triphysaria versicolor</i> Â Â Â Â. Plant Physiology, 2012, 158, 1046-1053.	2.3	31
164	Co-evolution of Genes for Specification in Arthropod-Plant Interactions: A Bioinformatic Analysis in Plant and Arthropod Genomes. , 2012, , 1-14.		0
165	Identification of interspecific hybrids among domesticated apple and its wild relatives. Tree Genetics and Genomes, 2012, 8, 1223-1235.	0.6	32
166	Genome sequence of foxtail millet (Setaria italica) provides insights into grass evolution and biofuel potential. Nature Biotechnology, 2012, 30, 549-554.	9.4	636
167	Coalescent-Based Analysis Distinguishes between Allo- and Autopolyploid Origin in Shepherd's Purse (Capsella bursa-pastoris). Molecular Biology and Evolution, 2012, 29, 1721-1733.	3.5	29
168	A microsatellite linkage map for the cultivated strawberry (FragariaÂÃ—Âananassa) suggests extensive regions of homozygosity in the genome that may have resulted from breeding and selection. Theoretical and Applied Genetics, 2012, 124, 1229-1240.	1.8	80
169	Construction of black (Rubus occidentalis) and red (R. idaeus) raspberry linkage maps and their comparison to the genomes of strawberry, apple, and peach. Theoretical and Applied Genetics, 2012, 125, 311-327.	1.8	51

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170	Molecular cloning and functional characterization of a novel apple MdCIPK6L gene reveals its involvement in multiple abiotic stress tolerance in transgenic plants. Plant Molecular Biology, 2012, 79, 123-135.	2.0	89
171	Physical mapping of a pollen modifier locus controlling self-incompatibility in apricot and synteny analysis within the Rosaceae. Plant Molecular Biology, 2012, 79, 229-242.	2.0	24
172	Evaluation of Genetic Diversity in Chinese Wild Apple Species Along with Apple Cultivars Using SSR Markers. Plant Molecular Biology Reporter, 2012, 30, 539-546.	1.0	75
173	Characterization of Transcriptional Differences Between Columnar and Standard Apple Trees Using RNA-Seq. Plant Molecular Biology Reporter, 2012, 30, 957-965.	1.0	27
174	Genomic Structure, Sub-Cellular Localization, and Promoter Analysis of the Gene Encoding Sorbitol-6-Phosphate Dehydrogenase from Apple. Plant Molecular Biology Reporter, 2012, 30, 904-914.	1.0	16
175	Apple, from genome to breeding. Tree Genetics and Genomes, 2012, 8, 509-529.	0.6	49
176	The peach genome. Tree Genetics and Genomes, 2012, 8, 531-547.	0.6	120
177	Development of a transgenic early flowering pear (Pyrus communis L.) genotype by RNAi silencing of PcTFL1-1 and PcTFL1-2. Planta, 2012, 235, 1239-1251.	1.6	112
178	Genome-wide analysis and expression profiling of the DREB transcription factor gene family in Malus under abiotic stress. Molecular Genetics and Genomics, 2012, 287, 423-436.	1.0	112
179	Fine genetic mapping of the Co locus controlling columnar growth habit in apple. Molecular Genetics and Genomics, 2012, 287, 437-450.	1.0	47
180	Towards the onset of fruit tree growing north of the Alps: Ancient DNA from waterlogged apple (Malus sp.) seed fragments. Annals of Anatomy, 2012, 194, 157-162.	1.0	13
181	Evolution of pathogenicity traits in the apple scab fungal pathogen in response to the domestication of its host. Evolutionary Applications, 2012, 5, 694-704.	1.5	28
182	Recent Progress Using Highâ€throughput Sequencing Technologies in Plant Molecular Breeding^F. Journal of Integrative Plant Biology, 2012, 54, 215-227.	4.1	40
183	In silico archeogenomics unveils modern plant genome organisation, regulation and evolution. Current Opinion in Plant Biology, 2012, 15, 122-130.	3.5	68
184	Formation of biphenyl and dibenzofuran phytoalexins in the transition zones of fire blight-infected stems of Malus domestica cv. â€˜Holsteiner Coxâ€™ and Pyrus communis cv. â€˜Conferenceâ€™. Phytochemistry, 2012, 77, 179-185.	1.4	57
185	Silencing of flavanone-3-hydroxylase in apple (MalusÂÃ—Âdomestica Borkh.) leads to accumulation of flavanones, but not to reduced fire blight susceptibility. Plant Physiology and Biochemistry, 2012, 51, 18-25.	2.8	32
186	Mining the apple genome reveals a family of nine ethylene receptor genes. Postharvest Biology and Technology, 2012, 72, 42-46.	2.9	20
187	The dynamic nature of bud dormancy in trees: environmental control and molecular mechanisms. Plant, Cell and Environment, 2012, 35, 1707-1728.	2.8	520

#	ARTICLE	IF	CITATIONS
188	A genomeâ€•wide phylogenetic reconstruction of family 1 UDPâ€•glycosyltransferases revealed the expansion of the family during the adaptation of plants to life on land. Plant Journal, 2012, 69, 1030-1042.	2.8	270
189	Advances in plant genome sequencing. Plant Journal, 2012, 70, 177-190.	2.8	156
190	The mitochondrial genome of <i>Malus domestica</i> and the importâ€•driven hypothesis of mitochondrial genome expansion in seed plants. Plant Journal, 2012, 71, 615-626.	2.8	76
191	QTL and candidate gene mapping for polyphenolic composition in apple fruit. BMC Plant Biology, 2012, 12, 12.	1.6	117
192	A genomics approach to understanding the role of auxin in apple (Malus x domestica)fruit size control. BMC Plant Biology, 2012, 12, 7.	1.6	170
193	Emerging Knowledge from Genome Sequencing of Crop Species. Molecular Biotechnology, 2012, 50, 250-266.	1.3	35
194	The first draft of the pigeonpea genome sequence. Journal of Plant Biochemistry and Biotechnology, 2012, 21, 98-112.	0.9	167
195	Examination of expansin genes as related to apple fruit crispness. Tree Genetics and Genomes, 2012, 8, 27-38.	0.6	14
196	Towards genomic selection in apple (Malus Ã— domestica Borkh.) breeding programmes: Prospects, challenges and strategies. Tree Genetics and Genomes, 2012, 8, 1-14.	0.6	108
197	Characterizing the walnut genome through analyses of BAC end sequences. Plant Molecular Biology, 2012, 78, 95-107.	2.0	27
198	Kiwifruit floral gene APETALA2 is alternatively spliced and accumulates in aberrant indeterminate flowers in the absence of miR172. Plant Molecular Biology, 2012, 78, 417-429.	2.0	51
199	Sexual incompatibility in Rosaceae fruit tree species: molecular interactions and evolutionary dynamics. Biologia Plantarum, 2012, 56, 201-209.	1.9	25
200	EST contig-based SSR linkage maps for MalusÂÃ—Âdomestica cv Royal Gala and an apple scab resistant accession of M. sieversii, the progenitor species of domestic apple. Molecular Breeding, 2012, 29, 379-397.	1.0	31
201	Functional allelic diversity of the apple alcohol acyl-transferase gene MdAAT1 associated with fruit ester volatile contents in apple cultivars. Molecular Breeding, 2012, 29, 609-625.	1.0	69
202	Diversity arrays technology (DArT) markers in apple for genetic linkage maps. Molecular Breeding, 2012, 29, 645-660.	1.0	41
203	Exploiting expressed sequence tag databases for mapping markers associated with fruit development and fruit quality in apple. Molecular Breeding, 2012, 29, 699-715.	1.0	7
204	Genomic organisation of the Mal d 1 gene cluster on linkage group 16 in apple. Molecular Breeding, 2012, 29, 759-778.	1.0	19
205	A candidate gene for fire blight resistance in Malus Ã— robusta 5 is coding for a CCâ€“NBSâ€“LRR. Tree Genetics and Genomes, 2013, 9, 237-251.	0.6	67

#	ARTICLE	IF	CITATIONS
206	Computational identification of microRNAs and their targets in apple. Genes and Genomics, 2013, 35, 377-385.	0.5	14
207	Transferability of Newly Developed Pear SSR Markers to Other Rosaceae Species. Plant Molecular Biology Reporter, 2013, 31, 1271-1282.	1.0	70
208	Genome-wide Analysis of the Distribution of AP2/ERF Transcription Factors Reveals Duplication and Elucidates their Potential Function in Chinese Cabbage (Brassica rapa ssp. pekinensis). Plant Molecular Biology Reporter, 2013, 31, 1002-1011.	1.0	32
209	Genome-Wide Analysis of the AP2/ERF Gene Family in Prunus mume. Plant Molecular Biology Reporter, 2013, 31, 741-750.	1.0	77
211	Carotenoid Cleavage Dioxygenase Genes from Fruit. ACS Symposium Series, 2013, , 11-19.	0.5	3
212	Tracing a key player in the regulation of plant architecture: the columnar growth habit of apple trees (MalusÂÃ—Âdomestica). Planta, 2013, 238, 1-22.	1.6	53
213	Novel genomic approaches unravel genetic architecture of complex traits in apple. BMC Genomics, 2013, 14, 393.	1.2	115
214	Frequent loss of lineages and deficient duplications accounted for low copy number of disease resistance genes in Cucurbitaceae. BMC Genomics, 2013, 14, 335.	1.2	74
215	Genome-wide analysis of the GH3 family in apple (Malus Ã— domestica). BMC Genomics, 2013, 14, 297.	1.2	69
216	Saturated linkage map construction in Rubus idaeus using genotyping by sequencing and genome-independent imputation. BMC Genomics, 2013, 14, 2.	1.2	171
217	A qRT-PCR assay for the expression of all Mal d 1 isoallergen genes. BMC Plant Biology, 2013, 13, 51.	1.6	39
218	A candidate gene based approach validates Md-PG1 as the main responsible for a QTL impacting fruit texture in apple (Malus x domesticaBorkh). BMC Plant Biology, 2013, 13, 37.	1.6	70
219	Functions of the apple TFL1/FT orthologs in phase transition. Scientia Horticulturae, 2013, 156, 106-112.	1.7	20
220	Biology, Controls and Models of Tree Volatile Organic Compound Emissions. Tree Physiology, 2013, , .	0.9	38
221	The molecular network regulating the coloration in apple. Scientia Horticulturae, 2013, 163, 1-9.	1.7	32
222	One hundred years of research at East Malling: science into practice for perennial fruit crops. Annals of Applied Biology, 2013, 163, 1-11.	1.3	6
223	Engineering NLR immune receptors for broad-spectrum disease resistance. Trends in Plant Science, 2013, 18, 469-472.	4.3	21
224	Nucleotide Composition of the Nelumbo nucifera Genome. Tropical Plant Biology, 2013, 6, 85-97.	1.0	2

#	ARTICLE	IF	CITATIONS
225	Phytoalexin formation in fire blight-infected apple. Trees - Structure and Function, 2013, 27, 477-484.	0.9	27
226	QTL involved in the modification of cyanidin compounds in black and red raspberry fruit. Theoretical and Applied Genetics, 2013, 126, 847-865.	1.8	17
227	Conservation and Functional Element Discovery in 20 Angiosperm Plant Genomes. Molecular Biology and Evolution, 2013, 30, 1729-1744.	3.5	60
228	A proteomic investigation of apple fruit during ripening and in response to ethylene treatment. Journal of Proteomics, 2013, 93, 276-294.	1.2	75
229	Sorbitol dehydrogenase is a cytosolic protein required for sorbitol metabolism in Arabidopsis thaliana. Plant Science, 2013, 205-206, 63-75.	1.7	45
230	Insights into phylogeny, sex function and age of Fragaria based on whole chloroplast genome sequencing. Molecular Phylogenetics and Evolution, 2013, 66, 17-29.	1.2	144
231	Functional Genomics Reveals That a Compact Terpene Synthase Gene Family Can Account for Terpene Volatile Production in Apple Â. Plant Physiology, 2013, 161, 787-804.	2.3	107
232	Horizontal Transfer of Entire Genomes via Mitochondrial Fusion in the Angiosperm <i>Amborella</i>. Science, 2013, 342, 1468-1473.	6.0	322
233	Assembly and Validation of the Genome of the Nonmodel Basal Angiosperm <i>Amborella</i>. Science, 2013, 342, 1516-1517.	6.0	89
234	Identification of lipoxygenase (LOX) genes putatively involved in fruit flavour formation in apple (Malus Ã— domestica). Tree Genetics and Genomes, 2013, 9, 1493-1511.	0.6	68
235	The Biochemistry and Molecular Biology of Volatile Messengers in Trees. Tree Physiology, 2013, , 47-93.	0.9	25
236	Sensory profiling of apple: Methodological aspects, cultivar characterisation and postharvest changes. Postharvest Biology and Technology, 2013, 77, 111-120.	2.9	49
237	Phylogenetic Analysis of 47 Chloroplast Genomes Clarifies the Contribution of Wild Species to the Domesticated Apple Maternal Line. Molecular Biology and Evolution, 2013, 30, 1751-1760.	3.5	112
238	Genome-wide identification and expression analysis of MAPK and MAPKK gene family in Malus domestica. Gene, 2013, 531, 377-387.	1.0	92
239	From ozone depletion to agriculture: understanding the role of <scp>UV</scp> radiation in sustainable crop production. New Phytologist, 2013, 197, 1058-1076.	3.5	159
240	Calmodulin-dependent and calmodulin-independent glutamate decarboxylases in apple fruit. BMC Plant Biology, 2013, 13, 144.	1.6	47
241	Whole genome duplication events in plant evolution reconstructed and predicted using myosin motor proteins. BMC Evolutionary Biology, 2013, 13, 202.	3.2	51
242	Assessment of phenotypic variation of Malus orientalis in the North Caucasus region. Genetic Resources and Crop Evolution, 2013, 60, 1463-1477.	0.8	23

#	ARTICLE	IF	CITATIONS
243	Phenotypic changes associated with <scp>RNA</scp> interference silencing of chalcone synthase in apple (<i>Malus</i> Ã— <i>domestica</i>). Plant Journal, 2013, 74, 398-410.	2.8	78
244	Geneâ€forâ€gene relationship in the hostâ€“pathogen system <i><scp>M</scp>alusÂ</i>Ã—Â<i>robusta</i> 5â€“<i><scp>E</scp>rwinia amylovora</i>. New Phytologist, 2013, 197, 1262-1275.	3.5	88
245	The genome of the pear (<i>Pyrus bretschneideri</i> Rehd.). Genome Research, 2013, 23, 396-408.	2.4	832
246	Genomics reveals new landscapes for crop improvement. Genome Biology, 2013, 14, 206.	3.8	99
247	Genome-wide analysis of the AP2/ERF superfamily in apple and transcriptional evidence of ERF involvement in scab pathogenesis. Scientia Horticulturae, 2013, 151, 112-121.	1.7	59
248	Regulation of ripening and opportunities for control in tomato and other fruits. Plant Biotechnology Journal, 2013, 11, 269-278.	4.1	156
249	The draft genome of watermelon (Citrullus lanatus) and resequencing of 20 diverse accessions. Nature Genetics, 2013, 45, 51-58.	9.4	731
250	Evolution of GOLDEN2-LIKE gene function in C3 and C4 plants. Planta, 2013, 237, 481-495.	1.6	98
251	Evaluation of the hormonal state of columnar apple trees (Malus x domestica) based on high throughput gene expression studies. Plant Molecular Biology, 2013, 81, 211-220.	2.0	34
252	Apple 1-Aminocyclopropane-1-Carboxylic Acid Synthase Genes, MdACS1 and MdACS3a, are Expressed in Different Systems of Ethylene Biosynthesis. Plant Molecular Biology Reporter, 2013, 31, 204-209.	1.0	58
253	Convergent gene loss following gene and genome duplications creates single-copy families in flowering plants. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 2898-2903.	3.3	351
254	Exploring the apple genome reveals six ACC synthase genes expressed during fruit ripening. Scientia Horticulturae, 2013, 157, 119-123.	1.7	31
255	Genome-wide analysis and identification of stress-responsive genes of the NAMâ€“ATAF1,2â€“CUC2 transcription factor family in apple. Plant Physiology and Biochemistry, 2013, 71, 11-21.	2.8	81
256	Genome-wide identification and analysis of the SBP-box family genes in apple (MalusÂÃ—Âdomestica) Tj ETQq1 1 0.784314 rgBT /Overl	2.8	145
257	Molecular cloning, polyclonal antibody preparation, and characterization ofÂaÂfunctional iron-related transcription factor IRO2 from Malus xiaojinensis. Plant Physiology and Biochemistry, 2013, 67, 63-70.	2.8	14
258	Genome-wide identification and analysis of the aldehyde dehydrogenase (ALDH) gene superfamily in apple (MalusÂÃ—Âdomestica Borkh.). Plant Physiology and Biochemistry, 2013, 71, 268-282.	2.8	36
259	Significance and Biological Consequences of Polyploidization in Land Plant Evolution. , 2013, , 277-293.		34
260	Differences in acidity of apples are probably mainly caused by a malic acid transporter gene on LG16. Tree Genetics and Genomes, 2013, 9, 475-487.	0.6	47

#	ARTICLE	IF	CITATIONS
261	Genetic and physical characterisation of the locus controlling columnar habit in apple (MalusÂÃ—Âdomestica Borkh.). Molecular Breeding, 2013, 31, 429-440.	1.0	45
262	The Evolution of Fruit Tree Productivity: A Review. Economic Botany, 2013, 67, 51-62.	0.8	77
263	Apple <scp><i>SEPALLATA1/2</i></scp>â€•like genes control fruit flesh development and ripening. Plant Journal, 2013, 73, 1044-1056.	2.8	124
264	Genome-wide identification, molecular evolution and expression analyses of the phospholipase D gene family in three Rosaceae species. Scientia Horticulturae, 2013, 153, 13-21.	1.7	20
265	Fruit Development and Ripening. Annual Review of Plant Biology, 2013, 64, 219-241.	8.6	492
266	SEPALLATA1/2-suppressed mature apples have low ethylene, high auxin and reduced transcription of ripening-related genes. AoB PLANTS, 2013, 5, pls047.	1.2	56
267	Miniature inverted-repeat transposable elements: discovery, distribution, and activity. Genome, 2013, 56, 475-486.	0.9	76
268	The draft genome of sweet orange (Citrus sinensis). Nature Genetics, 2013, 45, 59-66.	9.4	837
270	Differential expression of flavonoid 3â€²-hydroxylase during fruit development establishes the different B-ring hydroxylation patterns of flavonoids in FragariaÂÃ— ananassa and Fragaria vesca. Plant Physiology and Biochemistry, 2013, 72, 72-78.	2.8	25
271	A decade of plant proteomics and mass spectrometry: Translation of technical advancements to food security and safety issues. Mass Spectrometry Reviews, 2013, 32, 335-365.	2.8	70
272	Effects of preharvest nitric oxide treatment on ethylene biosynthesis and soluble sugars metabolism in â€˜Golden Deliciousâ€™ apples. Postharvest Biology and Technology, 2013, 84, 9-15.	2.9	44
273	Characterization of the <scp>LTR</scp> retrotransposon repertoire of a plant clade of six diploid and one tetraploid species. Plant Journal, 2013, 75, 699-709.	2.8	42
274	Arguments for standardizing transposable element annotation in plant genomes. Trends in Plant Science, 2013, 18, 367-376.	4.3	26
275	The high-quality draft genome of peach (Prunus persica) identifies unique patterns of genetic diversity, domestication and genome evolution. Nature Genetics, 2013, 45, 487-494.	9.4	1,031
276	Apple gene function and gene family database: an integrated bioinformatics database for apple research. Plant Growth Regulation, 2013, 70, 199-206.	1.8	15
277	DNA marker applications to molecular genetics and genomics in tomato. Breeding Science, 2013, 63, 21-30.	0.9	35
278	Transformation of apple (Malus Ã— domestica) using mutants of apple acetolactate synthase as a selectable marker and analysis of the T-DNA integration sites. Plant Cell Reports, 2013, 32, 703-714.	2.8	26
279	Functional Annotation of Plant Genomes. , 2013, , 155-176.		0

#	Article	IF	Citations
280	Combined Morphological and Molecular Phylogeny of the Clusioid Clade (Malpighiales) and the Placement of the Ancient Rosid MacrofossilPaleoclusia. International Journal of Plant Sciences, 2013, 174, 910-936.	0.6	39
281	Impacts of Resistance Gene Genetics, Function, and Evolution on a Durable Future. Annual Review of Phytopathology, 2013, 51, 291-319.	3.5	131
282	Identification of genetic loci associated with fire blight resistance in <i>Malus</i> through combined use of QTL and association mapping. Physiologia Plantarum, 2013, 148, 344-353.	2.6	42
283	Plant Organogenesis. Methods in Molecular Biology, 2013, , .	0.4	4
284	Tapping the Promise of Genomics in Species with Complex, Nonmodel Genomes. Annual Review of Plant Biology, 2013, 64, 89-110.	8.6	53
285	Adventitious Root Induction in Arabidopsis thaliana as a Model for In Vitro Root Organogenesis. Methods in Molecular Biology, 2013, 959, 159-175.	0.4	35
286	The chloroplast protein import system: From algae to trees. Biochimica Et Biophysica Acta - Molecular Cell Research, 2013, 1833, 314-331.	1.9	158
287	Catabolism of GABA in apple fruit: Subcellular localization and biochemical characterization of two Î³-aminobutyrate transaminases. Postharvest Biology and Technology, 2013, 75, 106-113.	2.9	38
288	Differential expression of CPKs and cytosolic Ca2+ variation in resistant and susceptible apple cultivars (Malus x domestica) in response to the pathogen Erwinia amylovora and mechanical wounding. BMC Genomics, 2013, 14, 760.	1.2	38
289	Candidate genes of cuticle formation show characteristic expression in the fruit skin of apple. Plant Growth Regulation, 2013, 70, 71-78.	1.8	34
290	Development of a seedling clone with high regeneration capacity and susceptibility to Agrobacterium in apple. Scientia Horticulturae, 2013, 164, 202-208.	1.7	140
291	Biology and biotechnology of fruit flavor and aroma volatiles. Stewart Postharvest Review, 0, 9, 1-13.	0.7	1
292	Addition of a breeding database in the Genome Database for Rosaceae. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat078.	1.4	19
293	Potential assessment of genome-wide association study and genomic selection in Japanese pear <i>Pyrus pyrifolia</i>. Breeding Science, 2013, 63, 125-140.	0.9	68
294	A Genome-Wide Expression Profile of Salt-Responsive Genes in the Apple Rootstock Malus zumi. International Journal of Molecular Sciences, 2013, 14, 21053-21070.	1.8	25
295	Malus Ã—oxysepala (M. domestica Borkh. Ã— M. sylvestris Mill.) â€“ a new spontaneous apple hybrid. Acta Societatis Botanicorum Poloniae, 2013, 82, 147-156.	0.8	4
296	The history of mapping the apple genome. Folia Horticulturae, 2013, 25, 161-168.	0.6	5
297	Orthology <scp>G</scp>uided <scp>A</scp>ssembly in highly heterozygous crops: creating a reference transcriptome to uncover genetic diversity in <i><scp>L</scp>olium perenne</i>. Plant Biotechnology Journal, 2013, 11, 605-617.	4.1	23

#	Article	IF	Citations
298	Evidence for regulation of columnar habit in apple by a putative 2<scp>OG</scp>â€Fe(<scp>II</scp>) oxygenase. New Phytologist, 2013, 200, 993-999.	3.5	47
299	Cropâ€toâ€wild gene flow and spatial genetic structure in the closest wild relatives of the cultivated apple. Evolutionary Applications, 2013, 6, 737-748.	1.5	54
300	Early Induction of Apple Fruitlet Abscission Is Characterized by an Increase of Both Isoprene Emission and Abscisic Acid Content Â Â Â. Plant Physiology, 2013, 161, 1952-1969.	2.3	59
301	Draft genome sequence of the mulberry tree Morus notabilis. Nature Communications, 2013, 4, 2445.	5.8	277
302	Biomarker development for external CO2 injury prediction in apples through exploration of both transcriptome and DNA methylation changes. AoB PLANTS, 2013, 5, plt021.	1.2	28
303	PlantRNA, a database for tRNAs of photosynthetic eukaryotes. Nucleic Acids Research, 2013, 41, D273-D279.	6.5	66
304	Recent Advances in Temperate Fruit Crops. , 2013, , 251-284.		0
305	A Major QTL Controlling Earliness of Fruit Maturity Linked to the Red leaf/Red flesh Trait in Apple cv. ^|^lsquo;Maypole^|^rsquo;. Japanese Society for Horticultural Science, 2013, 82, 97-105.	0.8	12
306	Apple SSRs present in coding and noncoding regions of expressed sequence tags show differences in transferability to other fruit species in Rosaceae. Canadian Journal of Plant Science, 2013, 93, 183-190.	0.3	3
307	Breeding in peach, cherry and plum: from a tissue culture, genetic, transcriptomic and genomic perspective. Biological Research, 2013, 46, 219-230.	1.5	40
308	Cracking in sweet cherries: A comprehensive review from a physiological, molecular, and genomic perspective. Chilean Journal of Agricultural Research, 2013, 73, 66-72.	0.4	62
309	Using genomics to improve fruit quality. Biological Research, 2013, 46, 347-352.	1.5	28
310	THE POTENTIAL IMPACTS OF GENETICS, GENOMICS AND BREEDING ON ORGANIC FRUIT PRODUCTION. Acta Horticulturae, 2013, , 155-160.	0.1	2
311	De Novo Transcriptome Sequencing and Analysis for Venturia inaequalis, the Devastating Apple Scab Pathogen. PLoS ONE, 2013, 8, e53937.	1.1	32
312	Evaluation of SNP Data from the Malus Infinium Array Identifies Challenges for Genetic Analysis of Complex Genomes of Polyploid Origin. PLoS ONE, 2013, 8, e67407.	1.1	17
313	Characterization and Evolution of Conserved MicroRNA through Duplication Events in Date Palm (Phoenix dactylifera). PLoS ONE, 2013, 8, e71435.	1.1	22
314	Identification of Pyrus Single Nucleotide Polymorphisms (SNPs) and Evaluation for Genetic Mapping in European Pear and Interspecific Pyrus Hybrids. PLoS ONE, 2013, 8, e77022.	1.1	64
315	The AP2-Like Gene OitaAP2 Is Alternatively Spliced and Differentially Expressed in Inflorescence and Vegetative Tissues of the Orchid Orchis italica. PLoS ONE, 2013, 8, e77454.	1.1	20

#	Article	IF	Citations
316	RNA-Seq Analysis Reveals Candidate Genes for Ontogenic Resistance in Malus-Venturia Pathosystem. PLoS ONE, 2013, 8, e78457.	1.1	57
317	Genome Wide Analysis of the Apple MYB Transcription Factor Family Allows the Identification of MdoMYB121 Gene Confering Abiotic Stress Tolerance in Plants. PLoS ONE, 2013, 8, e69955.	1.1	174
318	Phenolic Compounds in Apple (Malus x domestica Borkh.): Compounds Characterization and Stability during Postharvest and after Processing. Antioxidants, 2013, 2, 181-193.	2.2	146
319	Phylogenomics of MADS-Box Genes in Plants â€" Two Opposing Life Styles in One Gene Family. Biology, 2013, 2, 1150-1164.	1.3	70
320	POST-HARVEST CONTROL OF APPLE BLUE MOLD UNDER COLD STORAGE CONDITIONS. American Journal of Agricultural and Biological Science, 2014, 9, 167-173.	0.9	4
321	Infection of Apple by Apple Stem Grooving Virus Leads to Extensive Alterations in Gene Expression Patterns but No Disease Symptoms. PLoS ONE, 2014, 9, e95239.	1.1	22
322	ANALYSIS OF THE TIME-DEPENDENT PROTEIN CHANGES IN WOUNDED APPLES ('GOLDEN DELICIOUS'). Acta Horticulturae, 2014, , 171-176.	0.1	0
323	Extending the sRNAome of Apple by Next-Generation Sequencing. PLoS ONE, 2014, 9, e95782.	1.1	17
324	Wild European Apple (Malus sylvestris (L.) Mill.) Population Dynamics: Insight from Genetics and Ecology in the Rhine Valley. Priorities for a Future Conservation Programme. PLoS ONE, 2014, 9, e96596.	1.1	29
325	Construction and Analysis of High-Density Linkage Map Using High-Throughput Sequencing Data. PLoS ONE, 2014, 9, e98855.	1.1	319
326	Development and Validation of a 20K Single Nucleotide Polymorphism (SNP) Whole Genome Genotyping Array for Apple (Malus Ã— domestica Borkh). PLoS ONE, 2014, 9, e110377.	1.1	200
327	IDENTIFICATION OF A QTL FOR POSTHARVEST DISEASE RESISTANCE TO PENICILLIUM EXPANSUM IN MALUS SIEVERSII. Acta Horticulturae, 2014, , 199-203.	0.1	10
328	Molecular mechanism in apple fruit ripening. Ikushugaku Kenkyu, 2014, 16, 169-174.	0.1	0
330	Fruit Quality Traits Have Played Critical Roles in Domestication of the Apple. Plant Genome, 2014, 7, plantgenome2014.04.0018.	1.6	67
331	Fine-mapping of the apple scab resistance locus Rvi12 (Vb) derived from â€˜Hansenâ€™s baccata #2â€™. Molecular Breeding, 2014, 34, 2119-2129.	1.0	19
332	The Long-Term Investment Strategy: Orchardists Observing and Reacting to Change. Journal of Ethnobiology, 2014, 34, 335-358.	0.8	2
334	Fast and Cost-Effective Genetic Mapping in Apple Using Next-Generation Sequencing. G3: Genes, Genomes, Genetics, 2014, 4, 1681-1687.	0.8	123
335	Multiscale investigation of mealiness in apple: an atypical role for a pectin methylesterase during fruit maturation. BMC Plant Biology, 2014, 14, 375.	1.6	50

#	ARTICLE	IF	CITATIONS
336	Transcriptomic events associated with internal browning of apple during postharvest storage. BMC Plant Biology, 2014, 14, 328.	1.6	76
337	The 2-C-methylerythritol 4-phosphate pathway in melon is regulated by specialized isoforms for the first and last steps. Journal of Experimental Botany, 2014, 65, 5077-5092.	2.4	54
338	An apple B-box protein, MdCOL11, is involved in UV-B- and temperature-induced anthocyanin biosynthesis. Planta, 2014, 240, 1051-1062.	1.6	123
339	Genomewide identification and expression analysis of the ARF gene family in apple. Journal of Genetics, 2014, 93, 785-797.	0.4	40
340	Genetic, metabolite and developmental determinism of fruit friction discolouration in pear. BMC Plant Biology, 2014, 14, 241.	1.6	16
341	Comparative Genomic Analysis Reveals Multiple Long Terminal Repeats, Lineage-Specific Amplification, and Frequent Interelement Recombination for Cassandra Retrotransposon in Pear (Pyrus) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	1.1	26
342	Reactive oxygen species produced via plasma membrane NADPH oxidase regulate anthocyanin synthesis in apple peel. Planta, 2014, 240, 1023-1035.	1.6	40
343	Gene expression profiling by cDNA-AFLP reveals potential candidate genes for partial resistance of â€˜PrÃ©sident Roulinâ€™ against Venturia inaequalis. BMC Genomics, 2014, 15, 1043.	1.2	10
344	Genomewide analysis of TCP transcription factor gene family in Malus domestica. Journal of Genetics, 2014, 93, 733-746.	0.4	57
345	Molecular-level and trait-level differentiation between the cultivated apple (<i>Malus</i>Ã—Â<i>domestica</i>Borkh.) and its main progenitor<i>Malus</i><i>sieversii</i>. Plant Genetic Resources: Characterisation and Utilisation, 2014, 12, 330-340.	0.4	22
346	Effect of extending the photoperiod with low-intensity red or far-red light on the timing of shoot elongation and flower-bud formation of 1-year-old Japanese pear (Pyrus pyrifolia). Tree Physiology, 2014, 34, 534-546.	1.4	25
347	A novel gene, MdSSK1, as a component of the SCF complex rather than MdSBP1 can mediate the ubiquitination of S-RNase in apple. Journal of Experimental Botany, 2014, 65, 3121-3131.	2.4	59
348	Evolution of the fruit endocarp: molecular mechanisms underlying adaptations in seed protection and dispersal strategies. Frontiers in Plant Science, 2014, 5, 284.	1.7	121
349	Identification of QTLs controlling harvest time and fruit skin color in Japanese pear (Pyrus pyrifolia) Tj ETQq1 1 0.784314 rgBT /Overlock	0.9	64
350	The Evolution of Plant Gene and Genome Sequencing. Advances in Botanical Research, 2014, , 47-90.	0.5	6
351	Insights into the Common Ancestor of Eudicots. Advances in Botanical Research, 2014, 69, 137-174.	0.5	1
352	The Malus domestica sugar transporter gene family: identifications based on genome and expression profiling related to the accumulation of fruit sugars. Frontiers in Plant Science, 2014, 5, 569.	1.7	125
353	Light-controlled flavonoid biosynthesis in fruits. Frontiers in Plant Science, 2014, 5, 534.	1.7	353

#	ARTICLE	IF	CITATIONS
354	P-MITE: a database for plant miniature inverted-repeat transposable elements. Nucleic Acids Research, 2014, 42, D1176-D1181.	6.5	121
355	Fruit Self-Thinning: A Trait to Consider for Genetic Improvement of Apple Tree. PLoS ONE, 2014, 9, e91016.	1.1	29
356	Identification of QTLs for fruit quality traits in Japanese apples: QTLs for early ripening are tightly related to preharvest fruit drop. Breeding Science, 2014, 64, 240-251.	0.9	77
357	Characterisation of two genes encoding cytochrome P450 mono-oxygenases involved in gibberellin biosynthesis in apple (<i>Malus</i>Ã—<i>domestica</i>Borkh.). Journal of Horticultural Science and Biotechnology, 2014, 89, 329-337.	0.9	0
358	The complex jujube genome provides insights into fruit tree biology. Nature Communications, 2014, 5, 5315.	5.8	251
359	Molecular characterization of cisgenic lines of apple â€˜Galaâ€™ carrying the <i>Rvi6</i> scab resistance gene. Plant Biotechnology Journal, 2014, 12, 2-9.	4.1	50
360	Fine mapping of the gene Rvi18 (V25) for broad-spectrum resistance to apple scab, and development of a linked SSR marker suitable for marker-assisted breeding. Molecular Breeding, 2014, 34, 2021-2032.	1.0	16
361	The still mysterious roles of cysteine-containing glutathione transferases in plants. Frontiers in Pharmacology, 2014, 5, 192.	1.6	98
362	Genetic regulation and structural changes during tomato fruit development and ripening. Frontiers in Plant Science, 2014, 5, 124.	1.7	94
363	Breeding for Apple (Malusâ€‰Ã—â€‰domestica Borkh.) Fruit Quality Traits in the Genomics Era. , 2014, , 387-416.		10
364	Genetic identification of apple cultivars bred in Korea using simple sequence repeat markers. Horticulture Environment and Biotechnology, 2014, 55, 531-539.	0.7	16
365	The Genome Database for Rosaceae (GDR): year 10 update. Nucleic Acids Research, 2014, 42, D1237-D1244.	6.5	195
366	Interspecific polymorphism of the glucosyltransferase domain of the sucrose synthase gene in Malus and related Rosaceae species. Russian Journal of Genetics, 2014, 50, 1339-1342.	0.2	2
367	Genome-wide identification and characterisation of R2R3-MYB genes in sugar beet (Beta vulgaris). BMC Plant Biology, 2014, 14, 249.	1.6	95
368	Insights into the evolution and diversification of the AT-hook Motif Nuclear Localized gene family in land plants. BMC Plant Biology, 2014, 14, 266.	1.6	61
370	Begin at the beginning: A BAC-end view of the passion fruit (Passiflora) genome. BMC Genomics, 2014, 15, 816.	1.2	34
371	Molecular evidence for natural hybridization between wild loquat (Eriobotrya japonica) and its relative E. prinoides. BMC Plant Biology, 2014, 14, 275.	1.6	13
372	Analysis of changes in protein abundance after wounding in â€˜Golden Deliciousâ€™ apples. Postharvest Biology and Technology, 2014, 87, 51-60.	2.9	23

#	ARTICLE	IF	CITATIONS
373	Plant genome sequencing â€" applications for crop improvement. Current Opinion in Biotechnology, 2014, 26, 31-37.	3.3	164
374	Transcriptome profiling to identify genes involved in pathogenicity of Valsa mali on apple tree. Fungal Genetics and Biology, 2014, 68, 31-38.	0.9	87
375	Improving the identification rate of data independent label-free quantitative proteomics experiments on non-model crops: A case study on apple fruit. Journal of Proteomics, 2014, 105, 31-45.	1.2	44
376	Development of an efficient regeneration and Agrobacterium-mediated transformation system in crab apple (Malus micromalus) using cotyledons as explants. In Vitro Cellular and Developmental Biology - Plant, 2014, 50, 1-8.	0.9	11
377	Genomics and bioinformatics resources for translational science in Rosaceae. Plant Biotechnology Reports, 2014, 8, 49-64.	0.9	18
378	Sequencing and Assembly of the Transgenic Papaya Genome. , 2014, , 187-203.		2
379	Identification of Quantitative Trait Loci (QTLs) for Fruit Quality Traits in Apple. Plant Molecular Biology Reporter, 2014, 32, 109-116.	1.0	26
380	Whole genome comparison between table and wine grapes reveals a comprehensive catalog of structural variants. BMC Plant Biology, 2014, 14, 7.	1.6	115
381	A segmental duplication encompassing S-haplotype triggers pollen-part self-compatibility in Japanese pear (Pyrus pyrifolia). Molecular Breeding, 2014, 33, 117-128.	1.0	18
382	Callose and cellulose synthase gene expression analysis from the tight cluster to the full bloom stage and during early fruit development in MalusÂÃ—Âdomestica. Journal of Plant Research, 2014, 127, 173-183.	1.2	6
383	The columnar mutation (â€œCo geneâ€) of apple (MalusÂÃ—Âdomestica) is associated with an integration of a Gypsy-like retrotransposon. Molecular Breeding, 2014, 33, 863-880.	1.0	52
384	Differential Transcriptional Profiles of Dormancy-Related Genes in Apple Buds. Plant Molecular Biology Reporter, 2014, 32, 796-813.	1.0	51
385	Cloning and characterization of MxHA7, a plasma membrane H+-ATPase gene related to high tolerance of Malus xiaojinensis to iron deficiency. Acta Physiologiae Plantarum, 2014, 36, 955-962.	1.0	9
386	Towards an improved apple reference transcriptome using RNA-seq. Molecular Genetics and Genomics, 2014, 289, 427-438.	1.0	33
387	Tree immunity: growing old without antibodies. Trends in Plant Science, 2014, 19, 367-370.	4.3	33
388	Screening and characterization of apple Rho-like GTPase (MdROPs) genes related to S-RNase mediated self-incompatibility. Plant Cell, Tissue and Organ Culture, 2014, 117, 465-476.	1.2	10
389	Isolation, classification and transcription profiles of the AP2/ERF transcription factor superfamily in citrus. Molecular Biology Reports, 2014, 41, 4261-4271.	1.0	80
390	Identification of a major quantitative trait locus for resistance to fire blight in the wild apple species Malus fusca. Molecular Breeding, 2014, 34, 407-419.	1.0	50

#	Article	IF	Citations
391	Characterisation of the virescent locus controlling a recessive phenotype in apple rootstocks (Malus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.0	4
392	A genome-wide analysis of the expansin genes in MalusÂÃ—ÂDomestica. Molecular Genetics and Genomics, 2014, 289, 225-236.	1.0	39
393	The <i><scp>AAT</scp>1</i> locus is critical for the biosynthesis of esters contributing to â€˜ripe appleâ€™ flavour in â€˜Royal Galaâ€™ and â€˜Granny Smithâ€™ apples. Plant Journal, 2014, 78, 903-915.	2.8	76
394	Genome-wide identification and expression profiling of the cystatin gene family in apple (MalusÂÃ—Âdomestica Borkh.). Plant Physiology and Biochemistry, 2014, 79, 88-97.	2.8	25
395	Genome-wide identification of members in the YTH domain-containing RNA-binding protein family in apple and expression analysis of their responsiveness to senescence and abiotic stresses. Gene, 2014, 538, 292-305.	1.0	38
396	TRVâ€“GFP: a modified Tobacco rattle virus vector for efficient and visualizable analysis of gene function. Journal of Experimental Botany, 2014, 65, 311-322.	2.4	126
397	Widespread antiâ€sense transcription in apple is correlated with si<scp>RNA</scp> production and indicates a large potential for transcriptional and/or postâ€transcriptional control. New Phytologist, 2014, 203, 287-299.	3.5	72
398	Profiling of extensively diversified plant <scp>LINE</scp>s reveals distinct plantâ€specific subclades. Plant Journal, 2014, 79, 385-397.	2.8	35
399	Key flowering genes including FT-like genes are upregulated in the vasculature of apple dwarfing rootstocks. Tree Genetics and Genomes, 2014, 10, 189-202.	0.6	43
400	Cloning and functional characterization of the Rvi15 (Vr2) gene for apple scab resistance. Tree Genetics and Genomes, 2014, 10, 251-260.	0.6	44
401	Evolution of a symbiotic receptor through gene duplications in the legumeâ€“rhizobium mutualism. New Phytologist, 2014, 201, 961-972.	3.5	71
402	Advances in QTL mapping for ethylene production in apple (MalusÃ—domestica Borkh.). Postharvest Biology and Technology, 2014, 87, 126-132.	2.9	28
403	The domestication and evolutionary ecology of apples. Trends in Genetics, 2014, 30, 57-65.	2.9	261
404	Genomics of Plant Genetic Resources. , 2014, , .		16
405	Transcriptome analysis of the exocarp of apple fruit identifies light-induced genes involved in red color pigmentation. Gene, 2014, 534, 78-87.	1.0	48
406	Natural Variations and Genome-Wide Association Studies in Crop Plants. Annual Review of Plant Biology, 2014, 65, 531-551.	8.6	567
407	Plant speciation through chromosome instability and ploidy change: Cellular mechanisms, molecular factors and evolutionary relevance. Current Plant Biology, 2014, 1, 10-33.	2.3	205
408	High-throughput Sequencing Technology and Its Application. The Journal of Northeast Agricultural University, 2014, 21, 84-96.	0.1	16

#	ARTICLE	IF	CITATIONS
409	Genome-wide identification and expression profiling of the SnRK2 gene family in Malus prunifolia. Gene, 2014, 552, 87-97.	1.0	51
410	Apple (<i>Malus domestica</i>L. Borkh) as an emerging model for fruit development. Plant Biosystems, 2014, 148, 157-168.	0.8	37
411	Metabolic diversity in apple germplasm. Plant Breeding, 2014, 133, 281-290.	1.0	6
412	Genomics of Cold Hardiness in Woody Plants. Critical Reviews in Plant Sciences, 2014, 33, 92-124.	2.7	104
413	Genomics and Functional Genomics of Winter Low Temperature Tolerance in Temperate Fruit Crops. Critical Reviews in Plant Sciences, 2014, 33, 125-140.	2.7	18
414	Transcriptional control of fleshy fruit development and ripening. Journal of Experimental Botany, 2014, 65, 4527-4541.	2.4	296
415	Doubling down on genomes: Polyploidy and crop plants. American Journal of Botany, 2014, 101, 1711-1725.	0.8	336
416	Wood biosynthesis and typologies: a molecular rhapsody. Tree Physiology, 2014, 34, 839-855.	1.4	44
417	Identification and cloning of an NADPH-dependent hydroxycinnamoyl-CoA double bond reductase involved in dihydrochalcone formation in MalusÃ—domestica Borkh.. Phytochemistry, 2014, 107, 24-31.	1.4	31
418	Genetic Mechanisms of Allopolyploid Speciation Through Hybrid Genome Doubling. International Review of Cell and Molecular Biology, 2014, 309, 199-258.	1.6	13
419	Paleo-evolutionary plasticity of plant disease resistance genes. BMC Genomics, 2014, 15, 187.	1.2	51
420	Characterization of the lipoxygenase (LOX) gene family in the Chinese white pear (Pyrus) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	1.2	49
421	Characterization of the MLO gene family in Rosaceae and gene expression analysis in Malus domestica. BMC Genomics, 2014, 15, 618.	1.2	97
422	The American cranberry: first insights into the whole genome of a species adapted to bog habitat. BMC Plant Biology, 2014, 14, 165.	1.6	105
424	Characterization of an apple TT2-type R2R3 MYB transcription factor functionally similar to the poplar proanthocyanidin regulator PtMYB134. Planta, 2014, 240, 497-511.	1.6	61
425	One-step reconstruction of multi-generation pedigree networks in apple (MalusÂÃ—Âdomestica Borkh.) and the parentage of Golden Delicious. Molecular Breeding, 2014, 34, 511-524.	1.0	21
426	F1 hybrid of cultivated apple (MalusÂÃ—Âdomestica) and European pear (Pyrus communis) with fertile F2 offspring. Molecular Breeding, 2014, 34, 817-828.	1.0	14
427	Reference genes for transcriptional analysis of flowering and fruit ripening stages in apple (MalusÂÃ—Âdomestica Borkh.). Molecular Breeding, 2014, 34, 829-842.	1.0	83

#	Article	IF	Citations
429	Apple ring rot-responsive putative microRNAs revealed by high-throughput sequencing in MalusÂÃ—Âdomestica Borkh.. Molecular Biology Reports, 2014, 41, 5273-5286.	1.0	10
430	The transcriptional response of apple alcohol acyltransferase (MdAAT2) to salicylic acid and ethylene is mediated through two apple MYB TFs in transgenic tobacco. Plant Molecular Biology, 2014, 85, 627-638.	2.0	17
431	A genealogy of the citrus family. Nature Biotechnology, 2014, 32, 640-642.	9.4	50
432	Micro<scp>RNA</scp>s in fruit trees: discovery, diversity and future research directions. Plant Biology, 2014, 16, 856-865.	1.8	26
433	Genome sequence of the cultivated cotton Gossypium arboreum. Nature Genetics, 2014, 46, 567-572.	9.4	883
434	Next-generation wearable electronics. Nature Biotechnology, 2014, 32, 642-643.	9.4	150
435	Transcriptomic analysis demonstrates the early responses of local ethylene and redox signaling to low iron stress in Malus xiaojinensis. Tree Genetics and Genomes, 2014, 10, 573-584.	0.6	15
436	A consensus â€˜Honeycrispâ€™ apple (Malus Ã— domestica) genetic linkage map from three full-sib progeny populations. Tree Genetics and Genomes, 2014, 10, 627-639.	0.6	27
437	Selection of low-variance expressed Malus x domestica (apple) genes for use as quantitative PCR reference genes (housekeepers). Tree Genetics and Genomes, 2014, 10, 751-759.	0.6	25
438	Transcriptome-based single nucleotide polymorphism markers for genome mapping in Japanese pear (Pyrus pyrifolia Nakai). Tree Genetics and Genomes, 2014, 10, 853-863.	0.6	24
439	Genetic mapping of the loquat canker resistance locus in bronze loquat (Eriobotrya deflexa). Tree Genetics and Genomes, 2014, 10, 875-883.	0.6	12
440	Isolation, Characterization, and Structure Analysis of a Vacuolar Processing Enzyme Gene (MhVPEÎ³) from Malus hupehensis (Pamp) Rehd. Applied Biochemistry and Biotechnology, 2014, 173, 579-595.	1.4	9
441	Mapping in an apple (Malus x domestica) F1 segregating population based on physical clustering of differentially expressed genes. BMC Genomics, 2014, 15, 261.	1.2	12
442	Downregulation of Carnitine Acyl-Carnitine Translocase by miRNAs 132 and 212 Amplifies Glucose-Stimulated Insulin Secretion. Diabetes, 2014, 63, 3805-3814.	0.3	45
443	Genomics: A potential panacea for the perennial problem. American Journal of Botany, 2014, 101, 1780-1790.	0.8	49
444	Genomics of Erwinia amylovora and Related Erwinia Species Associated with Pome Fruit Trees. , 2014, , 1-36.		13
445	Dissection of the Octoploid Strawberry Genome by Deep Sequencing of the Genomes of Fragaria Species. DNA Research, 2014, 21, 169-181.	1.5	201
446	Grouping and characterization of putative glycosyltransferase genes from Panax ginseng Meyer. Gene, 2014, 536, 186-192.	1.0	29

#	Article	IF	Citations
447	Mining and comparison of the genes encoding the key enzymes involved in sugar biosynthesis in apple, grape, and sweet orange. Scientia Horticulturae, 2014, 165, 311-318.	1.7	27
448	Characterization of MxFIT, an iron deficiency induced transcriptional factor in Malus xiaojinensis. Plant Physiology and Biochemistry, 2014, 75, 89-95.	2.8	12
449	Elimination of the nptII marker gene in transgenic apple and pear with a chemically inducible R/Rs recombinase. Plant Cell, Tissue and Organ Culture, 2014, 117, 335-348.	1.2	32
450	The bright side of transposons in crop evolution. Briefings in Functional Genomics, 2014, 13, 276-295.	1.3	106
451	Role of MicroRNAs in Biotic and Abiotic Stress Responses in Crop Plants. Applied Biochemistry and Biotechnology, 2014, 174, 93-115.	1.4	175
452	Glucitol Dehydrogenase from Peach (Prunus persica) Fruits is Regulated by Thioredoxin h. Plant and Cell Physiology, 2014, 55, 1157-1168.	1.5	11
453	Elucidating the molecular responses of apple rootstock resistant to ARD pathogens: challenges and opportunities for development of genomics-assisted breeding tools. Horticulture Research, 2014, 1, 14043.	2.9	57
454	BREEDING APPLE ROOTSTOCKS IN THE TWENTY-FIRST CENTURY - WHAT CAN WE EXPECT THEM TO DO TO INCREASE PRODUCTIVITY IN THE ORCHARD?. Acta Horticulturae, 2014, , 421-428.	0.1	7
455	EVIDENCE OF A MAJOR QTL FOR FIRE BLIGHT RESISTANCE IN THE APPLE WILD SPECIES MALUS FUSCA. Acta Horticulturae, 2014, , 289-293.	0.1	14
456	Transcriptional regulation of ethylene and jasmonate mediated defense response in apple (Malus) Tj ETQq1 1 0.784314 rgBT /Overlock	2.9	47
457	MOLECULAR CHARACTERIZATION OF THE CO GENE REGION IN MALUS Ã— DOMESTICA. Acta Horticulturae, 2014, , 87-95.	0.1	2
458	Genetic and environmental control of fruit maturation, dry matter and firmness in apple (Malus Ã—) Tj ETQq1 1 0.784314 rgBT /Overloc	2.9	50
460	Genomic variants of genes associated with three horticultural traits in apple revealed by genome re-sequencing. Horticulture Research, 2014, 1, 14045.	2.9	36
461	Understanding development and ripening of fruit crops in an â€˜omicsâ€™ era. Horticulture Research, 2014, 1, 14034.	2.9	53
462	Transcriptional dynamics of the developing sweet cherry (Prunus avium L.) fruit: sequencing, annotation and expression profiling of exocarp-associated genes. Horticulture Research, 2014, 1, 11.	2.9	82
463	Genetic control of juvenile growth and botanical architecture in an ornamental woody plant, Prunus mumeSieb. et Zucc. as revealed by a high-density linkage map. BMC Genetics, 2014, 15, S1.	2.7	26
464	Assessment of genetic diversity and genetic relationships among 46 Iranian and non-Iranian dwarfing rootstocks of apple (<i>Malus</i>Ã—<i>domestica</i>Borkh.) using microsatellite markers. Journal of Horticultural Science and Biotechnology, 2014, 89, 121-129.	0.9	1
466	AFLP analysis of genetic diversity in the genus Mallus Mill. (Apple). Russian Journal of Genetics, 2015, 51, 966-973.	0.2	9

#	Article	IF	Citations
467	Fine mapping of the Rvi5 (Vm) apple scab resistance locus in the â€˜Murrayâ€™ apple genotype. Molecular Breeding, 2015, 35, 1.	1.0	15
468	Pale green lethal disorder in apple (Malus) is caused by a mutation in the PHYLLO gene which is essential for phylloquinone (vitamin K1) biosynthesis. Tree Genetics and Genomes, 2015, 11, 1.	0.6	9
469	Genomic basis of the differences between cider and dessert apple varieties. Evolutionary Applications, 2015, 8, 650-661.	1.5	33
472	Two quantitative trait loci, Dw1 and Dw2, are primarily responsible for rootstock-induced dwarfing in apple. Horticulture Research, 2015, 2, 15001.	2.9	62
473	THE PEACH GENOME: INSIGHTS ON GENETIC DIVERSITY AND DOMESTICATION. Acta Horticulturae, 2015, , 63-68.	0.1	0
474	ROSE GENOMICS: CHALLENGES AND PERSPECTIVES. Acta Horticulturae, 2015, , 35-40.	0.1	1
475	Genome-wide Annotation and Comparative Analysis of Long Terminal Repeat Retrotransposons between Pear Species of P. bretschneideri and P. Communis. Scientific Reports, 2015, 5, 17644.	1.6	16
477	Genes Encoding Aluminumâ€Activated Malate Transporter II and their Association with Fruit Acidity in Apple. Plant Genome, 2015, 8, eplantgenome2015.03.0016.	1.6	55
478	An integrated database of wood-formation related genes in plants. Scientific Reports, 2015, 5, 11422.	1.6	3
479	Transcriptome changes in apple peel tissues during CO2 injuryÂsymptom development under controlled atmosphere storage regimens. Horticulture Research, 2015, 2, 15061.	2.9	9
480	Sequencing of plant genomes â€“ a review. Turk Tarim Ve Ormancilik Dergisi/Turkish Journal of Agriculture and Forestry, 2015, 39, 361-376.	0.8	20
481	High density linkage mapping of genomic and transcriptomic SNPs for synteny analysis and anchoring the genome sequence of chickpea. Scientific Reports, 2015, 5, 13387.	1.6	41
482	A dense SNP genetic map constructed using restriction site-associated DNA sequencing enables detection of QTLs controlling apple fruit quality. BMC Genomics, 2015, 16, 747.	1.2	83
483	A high-density genetic map for anchoring genome sequences and identifying QTLs associated with dwarf vine in pumpkin (Cucurbita maxima Duch.). BMC Genomics, 2015, 16, 1101.	1.2	84
484	Genetic control of pear rootstock-induced dwarfing and precocity is linked to a chromosomal region syntenic to the apple Dw1 loci. BMC Plant Biology, 2015, 15, 230.	1.6	37
485	Developing expressed sequence tag libraries and the discovery of simple sequence repeat markers for two species of raspberry (Rubus L.). BMC Plant Biology, 2015, 15, 258.	1.6	13
486	Synteny analysis in Rosids with a walnut physical map reveals slow genome evolution in long-lived woody perennials. BMC Genomics, 2015, 16, 707.	1.2	83
487	The distribution and impact of common copy-number variation in the genome of the domesticated apple, Malus x domestica Borkh. BMC Genomics, 2015, 16, 848.	1.2	21

#	Article	IF	Citations
488	MnTEdb, a collective resource for mulberry transposable elements. Database: the Journal of Biological Databases and Curation, 2015, 2015, .	1.4	25
489	Identification of a QTL for psylla resistance in pear via genome scanning approach. Scientia Horticulturae, 2015, 197, 568-572.	1.7	8
490	Cnidaria: fast, reference-free clustering of raw and assembled genome and transcriptome NGS data. BMC Bioinformatics, 2015, 16, 352.	1.2	11
491	Chemodiversity in the Fingerprint Analysis of Volatile Organic Compounds (VOCs) of 35 Old and 7 Modern Apple Cultivars Determined by Protonâ€Transferâ€Reaction Mass Spectrometry (PTRâ€MS) in Two Different Seasons. Chemistry and Biodiversity, 2015, 12, 800-812.	1.0	16
492	The <i><scp>O</scp></i>â€methyltransferase gene <i><scp>M</scp>do<scp>OMT</scp>1</i> is required for biosynthesis of methylated phenylpropenes in ripe apple fruit. Plant Journal, 2015, 82, 937-950.	2.8	35
493	<i>O</i>â€Methyltransferases involved in biphenyl and dibenzofuran biosynthesis. Plant Journal, 2015, 83, 263-276.	2.8	27
494	A <i>micro<scp>RNA</scp></i> allele that emerged prior to apple domestication may underlie fruit size evolution. Plant Journal, 2015, 84, 417-427.	2.8	95
495	A GENOMICS APPROACH TO UNDERSTANDING FRUIT CHARACTERS. Acta Horticulturae, 2015, , 199-205.	0.1	0
497	LinkImpute: Fast and Accurate Genotype Imputation for Nonmodel Organisms. G3: Genes, Genomes, Genetics, 2015, 5, 2383-2390.	0.8	407
498	Recent Progress in Genomic Analysis of Ornamental Plants, with a Focus on Carnation. Horticulture Journal, 2015, 84, 3-13.	0.3	17
499	Characterization of Ty1/copia-like retrotransposon families from pigeonpea genome. Genetics and Molecular Research, 2015, 14, 5812-5822.	0.3	1
500	Application of genomics-assisted breeding for generation of climate resilient crops: progress and prospects. Frontiers in Plant Science, 2015, 6, 563.	1.7	243
501	Fire Blight Control: The Struggle Goes On. A Comparison of Different Fire Blight Control Methods in Switzerland with Respect to Biosafety, Efficacy and Durability. International Journal of Environmental Research and Public Health, 2015, 12, 11422-11447.	1.2	45
502	Convergent Evolution at the Gametophytic Self-Incompatibility System in Malus and Prunus. PLoS ONE, 2015, 10, e0126138.	1.1	63
503	Identification of Genetic Loci Associated with Quality Traits in Almond via Association Mapping. PLoS ONE, 2015, 10, e0127656.	1.1	36
504	Genome-Wide Characterization of Simple Sequence Repeat (SSR) Loci in Chinese Jujube and Jujube SSR Primer Transferability. PLoS ONE, 2015, 10, e0127812.	1.1	48
505	De Novo Regulatory Motif Discovery Identifies Significant Motifs in Promoters of Five Classes of Plant Dehydrin Genes. PLoS ONE, 2015, 10, e0129016.	1.1	27
506	Comparative Transcriptomes Analysis of Red- and White-Fleshed Apples in an F1 Population of Malus sieversii f. niedzwetzkyana Crossed with M. domestica â€˜Fujiâ€™. PLoS ONE, 2015, 10, e0133468.	1.1	29

#	ARTICLE	IF	CITATIONS
507	Comprehensive Evolutionary and Expression Analysis of FCS-Like Zinc finger Gene Family Yields Insights into Their Origin, Expansion and Divergence. PLoS ONE, 2015, 10, e0134328.	1.1	22
508	Development of the First Cisgenic Apple with Increased Resistance to Fire Blight. PLoS ONE, 2015, 10, e0143980.	1.1	71
509	Association mapping for kernel phytosterol content in almond. Frontiers in Plant Science, 2015, 6, 530.	1.7	20
510	Massive sequencing of Ulmus minorâ€™s transcriptome provides new molecular tools for a genus under the constant threat of Dutch elm disease. Frontiers in Plant Science, 2015, 6, 541.	1.7	19
511	Identification, isolation, and expression analysis of heat shock transcription factors in the diploid woodland strawberry Fragaria vesca. Frontiers in Plant Science, 2015, 6, 736.	1.7	72
512	Dynamic transcription profiles of â€œQinguanâ€•apple (Malus Ã— domestica) leaves in response to Marssonina coronaria inoculation. Frontiers in Plant Science, 2015, 6, 842.	1.7	16
513	Divergence of the bZIP Gene Family in Strawberry, Peach, and Apple Suggests Multiple Modes of Gene Evolution after Duplication. International Journal of Genomics, 2015, 2015, 1-11.	0.8	21
514	Unlimited Thirst for Genome Sequencing, Data Interpretation, and Database Usage in Genomic Era: The Road towards Fast-Track Crop Plant Improvement. Genetics Research International, 2015, 2015, 1-15.	2.0	18
515	Genetics in Genomic Era. Genetics Research International, 2015, 2015, 1-2.	2.0	10
516	Is There Room for Improving the Nutraceutical Composition of Apple?. Journal of Agricultural and Food Chemistry, 2015, 63, 2750-2759.	2.4	64
517	Low expression of PIN gene family members is involved in triggering the dwarfing effect in M9 interstem but not in M9 rootstock apple trees. Acta Physiologiae Plantarum, 2015, 37, 1.	1.0	21
518	Whole Genome Sequencing of Fruit Tree Species. Advances in Botanical Research, 2015, , 1-37.	0.5	13
519	Karyotype and Gene Order Evolution from Reconstructed Extinct Ancestors Highlight Contrasts in Genome Plasticity of Modern Rosid Crops. Genome Biology and Evolution, 2015, 7, 735-749.	1.1	46
520	High quality reference genome of drumstick tree (Moringa oleifera Lam.), a potential perennial crop. Science China Life Sciences, 2015, 58, 627-638.	2.3	53
521	Genetics and Genomics of Tree Architecture. Advances in Botanical Research, 2015, , 157-200.	0.5	13
522	Next-Generation Sequencing and Assembly of Plant Genomes. , 2015, , 53-64.		1
523	Expression of flowering locus T2 transgene from Pyrus communis L. delays dormancy and leaf senescence in Malus Ã— domestica Borkh, and causes early flowering in tobacco. Plant Science, 2015, 241, 164-176.	1.7	30
524	Genome-wide identification and characterization of R2R3-MYB transcription factors in pear. Scientia Horticulturae, 2015, 197, 176-182.	1.7	18

#	Article	IF	Citations
525	Sorbitol-6-phosphate dehydrogenase (S6PDH) gene polymorphism in Malus Mill. (Rosaceae). Russian Journal of Genetics, 2015, 51, 1069-1074.	0.2	1
526	A Time-Calibrated Road Map of Brassicaceae Species Radiation and Evolutionary History. Plant Cell, 2015, 27, tpc.15.00482.	3.1	200
527	Mutant-Based Reverse Genetics for Functional Genomics of Non-model Crops. , 2015, , 473-487.		1
528	Apple fruit texture QTLs: year and cold storage effects on sensory and instrumental traits. Tree Genetics and Genomes, 2015, 11, 1.	0.6	23
529	Integration of <i>Bp<scp>MADS</scp>4</i> on various linkage groups improves the utilization of the rapid cycle breeding system in apple. Plant Biotechnology Journal, 2015, 13, 246-258.	4.1	20
530	Targeted mutagenesis using zinc-finger nucleases in perennial fruit trees. Planta, 2015, 241, 941-951.	1.6	63
531	MetaQTL analysis provides a compendium of genomic loci controlling fruit quality traits in apple. Tree Genetics and Genomes, 2015, 11, 1.	0.6	25
532	Identification and validation of a QTL influencing bitter pit symptoms in apple (MalusÂÃ—Âdomestica). Molecular Breeding, 2015, 35, 1.	1.0	19
533	Genome-wide analysis of the GRAS gene family in Prunus mume. Molecular Genetics and Genomics, 2015, 290, 303-317.	1.0	74
534	Identification of SNPs linked to eight apple disease resistance loci. Molecular Breeding, 2015, 35, 1.	1.0	41
535	Metabolite-based genome-wide association studies in plants. Current Opinion in Plant Biology, 2015, 24, 31-38.	3.5	204
536	High-resolution genetic and physical map of the Rvi1 (Vg) apple scab resistance locus. Molecular Breeding, 2015, 35, 1.	1.0	14
537	Abiotic Stress Biology in Horticultural Plants. , 2015, , .		17
538	Genome-wide identification and analysis of the apple (Malus Ã— domestica Borkh.) TIFY gene family. Tree Genetics and Genomes, 2015, 11, 1.	0.6	51
539	Heat shock transcription factors expression during fruit development and under hot air stress in Ponkan (Citrus reticulata Blanco cv. Ponkan) fruit. Gene, 2015, 559, 129-136.	1.0	17
540	Proteome analysis of pear reveals key genes associated with fruit development and quality. Planta, 2015, 241, 1363-1379.	1.6	42
541	Discovery of Novel Genes Derived from Transposable Elements Using Integrative Genomic Analysis. Molecular Biology and Evolution, 2015, 32, 1487-1506.	3.5	49
542	High frequency of chromosome deletions in regenerated and mutagenized apple (MalusÂÃ—Âdomestica) Tj ETQq1 1 0.784314 rgBT /O	1.0	6

#	Article	IF	Citations
543	Species-specific duplications driving the recent expansion of NBS-LRR genes in five Rosaceae species. BMC Genomics, 2015, 16, 77.	1.2	39
544	Apple allergens genomics and biotechnology. , 2015, , 35-54.		8
545	Progress, challenges and the future of crop genomes. Current Opinion in Plant Biology, 2015, 24, 71-81.	3.5	197
546	Comprehensive genomic analysis and expression profiling of diacylglycerol kinase gene family in Malus prunifolia (Willd.) Borkh. Gene, 2015, 561, 225-234.	1.0	22
547	Use of targeted SNP selection for an improved anchoring of the melon (Cucumis melo L.) scaffold genome assembly. BMC Genomics, 2015, 16, 4.	1.2	67
548	Genome-wide identification and characterization of the DREB transcription factor gene family in mulberry. Biologia Plantarum, 2015, 59, 253-265.	1.9	42
549	Identification and genetic characterization of a quantitative trait locus for adventitious rooting from apple hardwood cuttings. Tree Genetics and Genomes, 2015, 11, 1.	0.6	22
550	Ultra-high density intra-specific genetic linkage maps accelerate identification of functionally relevant molecular tags governing important agronomic traits in chickpea. Scientific Reports, 2015, 5, 9468.	1.6	74
551	Candidate gene prediction via quantitative trait locus analysis of fruit shape index traits in apple. Euphytica, 2015, 206, 381-391.	0.6	12
552	Suppressing Sorbitol Synthesis Substantially Alters the Global Expression Profile of Stress Response Genes in Apple (<i>Malus domestica</i>) Leaves. Plant and Cell Physiology, 2015, 56, 1748-1761.	1.5	29
553	QTLs detected for individual sugars and soluble solids content in apple. Molecular Breeding, 2015, 35, 1.	1.0	75
554	Chloroplast heterogeneity and historical admixture within the genus <i>Malus</i>. American Journal of Botany, 2015, 102, 1198-1208.	0.8	36
555	Recent Advances in Genetics and Molecular Control of Bud Dormancy in Pipfruits. , 2015, , 107-122.		6
556	Acceleration of Forest and Fruit Tree Domestication by Genomic Selection. Advances in Botanical Research, 2015, , 93-124.	0.5	16
557	Genome-Wide Function, Evolutionary Characterization and Expression Analysis of Sugar Transporter Family Genes in Pear (<i>Pyrus bretschneideri</i>Rehd). Plant and Cell Physiology, 2015, 56, 1721-1737.	1.5	74
558	Population and Conservation Genomics in Forest and Fruit Trees. Advances in Botanical Research, 2015, , 125-155.	0.5	8
559	Sequencing consolidates molecular markers with plant breeding practice. Theoretical and Applied Genetics, 2015, 128, 779-795.	1.8	96
560	Genome-wide characterization and analysis of F-box protein-encoding genes in the Malus domestica genome. Molecular Genetics and Genomics, 2015, 290, 1435-1446.	1.0	38

#	Article	IF	Citations
561	Expression of DORMANCY-ASSOCIATED MADS-BOX (DAM)-like genes in apple. Biologia Plantarum, 2015, 59, 237-244.	1.9	71
562	The vulnerability of US apple (Malus) genetic resources. Genetic Resources and Crop Evolution, 2015, 62, 765-794.	0.8	74
563	Apple russeting as seen through the RNA-seq lens: strong alterations in the exocarp cell wall. Plant Molecular Biology, 2015, 88, 21-40.	2.0	94
564	RNA-Seq analysis and transcriptome assembly for blackberry (Rubus sp. Var. Lochness) fruit. BMC Genomics, 2015, 16, 5.	1.2	62
565	Development and preliminary evaluation of a 90ÂK AxiomÂ® SNP array for the allo-octoploid cultivated strawberry Fragaria Ã— ananassa. BMC Genomics, 2015, 16, 155.	1.2	179
566	Columnar apple primary roots share some features of the columnar-specific gene expression profile of aerial plant parts as evidenced by RNA-Seq analysis. BMC Plant Biology, 2015, 15, 34.	1.6	17
567	Genome-wide identification and comparative analysis of the heat shock transcription factor family in Chinese white pear (Pyrus bretschneideri) and five other Rosaceae species. BMC Plant Biology, 2015, 15, 12.	1.6	138
568	The draft genome of Primula veris yields insights into the molecular basis of heterostyly. Genome Biology, 2015, 16, 12.	3.8	96
569	Genome-wide identification and analysis of the MADS-box gene family in sesame. Gene, 2015, 569, 66-76.	1.0	37
570	New insights into the evolutionary history of plant sorbitol dehydrogenase. BMC Plant Biology, 2015, 15, 101.	1.6	26
571	Transcription profiling of the chilling requirement for bud break in apples: a putative role for FLC-like genes. Journal of Experimental Botany, 2015, 66, 2659-2672.	2.4	78
572	Apple SVP Family MADS-Box Proteins and the Tomato Pedicel Abscission Zone Regulator JOINTLESS have Similar Molecular Activities. Plant and Cell Physiology, 2015, 56, 1097-1106.	1.5	23
573	Application of multiplexed cysteineâ€labeled complex protein sample for 2D electrophoretic gel alignment. Proteomics, 2015, 15, 1777-1780.	1.3	6
574	Extreme expansion of NBS-encoding genes in Rosaceae. BMC Genetics, 2015, 16, 48.	2.7	84
575	Molecular characterization of genes encoding leucoanthocyanidin reductase involved in proanthocyanidin biosynthesis in apple. Frontiers in Plant Science, 2015, 6, 243.	1.7	58
576	A CBL gene, MdCBL5, controls the calcium signal and influences pollen tube growth in apple. Tree Genetics and Genomes, 2015, 11, 1.	0.6	11
577	Improving resistance of different apple cultivars using the Rvi6 scab resistance gene in a cisgenic approach based on the Flp/FRT recombinase system. Molecular Breeding, 2015, 35, 1.	1.0	44
578	Functional diversification of the dehydrin gene family in apple and its contribution to cold acclimation during dormancy. Physiologia Plantarum, 2015, 155, 315-329.	2.6	18

#	ARTICLE	IF	CITATIONS
579	A standard nomenclature for gene designation in the Rosaceae. Tree Genetics and Genomes, 2015, 11, 1.	0.6	17
580	DNA Sequencing, Other Omics and Synthetic Biology. , 2015, , 125-140.		0
581	A Conserved Cytochrome P450 Evolved in Seed Plants Regulates Flower Maturation. Molecular Plant, 2015, 8, 1751-1765.	3.9	36
582	Controlled atmosphere-related injury in â€˜Honeycrispâ€™ apples is associated with Î³-aminobutyrate accumulation. Canadian Journal of Plant Science, 2015, 95, 879-886.	0.3	15
583	Genetic diversity of Malus cultivars and wild relatives in the Chinese National Repository of Apple Germplasm Resources. Tree Genetics and Genomes, 2015, 11, 1.	0.6	30
584	Ethylene negatively regulates transcript abundance of ROP-GAP rheostat-encoding genes and affects apoplastic reactive oxygen species homeostasis in epicarps of cold stored apple fruits. Journal of Experimental Botany, 2015, 66, 7255-7270.	2.4	42
585	High resolution physical mapping of single gene fragments on pachytene chromosome 4 and 7 of Rosa. BMC Genetics, 2015, 16, 74.	2.7	9
586	Physiological and Molecular Regulation of Adventitious Root Formation. Critical Reviews in Plant Sciences, 2015, 34, 506-521.	2.7	71
587	The Phytoene synthase gene family of apple (Malus x domestica) and its role in controlling fruit carotenoid content. BMC Plant Biology, 2015, 15, 185.	1.6	65
588	Homologues of potato chromosome 5 show variable collinearity in the euchromatin, but dramatic absence of sequence similarity in the pericentromeric heterochromatin. BMC Genomics, 2015, 16, 374.	1.2	15
589	Molecular basis of angiosperm tree architecture. New Phytologist, 2015, 206, 541-556.	3.5	81
590	Biphenyl 4-Hydroxylases Involved in Aucuparin Biosynthesis in Rowan and Apple Are Cytochrome P450 736A Proteins. Plant Physiology, 2015, 168, 428-442.	2.3	39
591	Genetic mapping and pyramiding of two new pear scab resistance QTLs. Molecular Breeding, 2015, 35, 1.	1.0	12
592	Transcription Profiles Reveal Sugar and Hormone Signaling Pathways Mediating Flower Induction in Apple (<i>Malus domestica</i>Borkh.). Plant and Cell Physiology, 2015, 56, 2052-2068.	1.5	118
593	Genome investigation suggests<i>MdSHN3</i>, an APETALA2-domain transcription factor gene, to be a positive regulator of apple fruit cuticle formation and an inhibitor of russet development. Journal of Experimental Botany, 2015, 66, 6579-6589.	2.4	76
594	Multispectral airborne imagery in the field reveals genetic determinisms of morphological and transpiration traits of an apple tree hybrid population in response to water deficit. Journal of Experimental Botany, 2015, 66, 5453-5465.	2.4	31
595	Hybrid seedling inviability locus (HIs1) mapped on linkage group 4 of the Japanese flowering cherry, Cerasusâ€‰Ã—â€‰yedoensis â€˜Somei-yoshinoâ€™. Tree Genetics and Genomes, 2015, 11, 1.	0.6	6
596	Characterization of a spermidine hydroxycinnamoyltransferase in<i>Malus domestica</i>highlights the evolutionary conservation of trihydroxycinnamoyl spermidines in pollen coat of core Eudicotyledons. Journal of Experimental Botany, 2015, 66, 7271-7285.	2.4	62

#	Article	IF	Citations
597	Plant Breeding in the Omics Era. , 2015, , .		46
598	Polyploid and aneuploid detection in apple using a single nucleotide polymorphism array. Tree Genetics and Genomes, 2015, 11, 1.	0.6	27
599	Candidate defense genes as predictors of partial resistance in â€˜PrÃ©sident Roulinâ€™ against apple scab caused by Venturia inaequalis. Tree Genetics and Genomes, 2015, 11, 1.	0.6	7
600	A major QTL controlling apple skin russeting maps on the linkage group 12 of â€˜Renetta Grigia di Torrianaâ€™. BMC Plant Biology, 2015, 15, 150.	1.6	49
601	Oxidative stress associated with rootstockâ€“scion interactions in pear/quince combinations during early stages of graft development. Journal of Plant Physiology, 2015, 176, 25-35.	1.6	63
602	Dynamic evolution of NBSâ€“LRR genes in bread wheat and its progenitors. Molecular Genetics and Genomics, 2015, 290, 727-738.	1.0	79
603	Identification of a xyloglucan-specific endo-(1-4)-beta-d-glucanase inhibitor protein from apple (MalusÃ—domestica Borkh.) as a potential defense gene against Botryosphaeria dothidea. Plant Science, 2015, 231, 11-19.	1.7	25
604	Climateâ€resilient agroforestry: physiological responses to climate change and engineering of crassulacean acid metabolism (<scp>CAM</scp>) as a mitigation strategy. Plant, Cell and Environment, 2015, 38, 1833-1849.	2.8	59
605	Genome-wide identification and analysis of the MADS-box gene family in apple. Gene, 2015, 555, 277-290.	1.0	95
606	Genome-wide identification of jasmonate biosynthetic genes and characterization of their expression profiles during apple (MalusÂÃ—Âdomestica) fruit maturation. Plant Growth Regulation, 2015, 75, 355-364.	1.8	13
607	Genome, Transcriptome, and Functional Analyses of <i>Penicillium expansum</i> Provide New Insights Into Secondary Metabolism and Pathogenicity. Molecular Plant-Microbe Interactions, 2015, 28, 232-248.	1.4	183
608	Plant Genotyping. Methods in Molecular Biology, 2015, , .	0.4	14
609	New Insights into Fruit Firmness and Weight Control in Sweet Cherry. Plant Molecular Biology Reporter, 2015, 33, 783-796.	1.0	39
610	Virulence Characterization of <i>Venturia inaequalis</i> Reference Isolates on the Differential Set of <i>Malus</i> Hosts. Plant Disease, 2015, 99, 370-375.	0.7	27
611	Genomic resources in fruit plants: an assessment of current status. Critical Reviews in Biotechnology, 2015, 35, 438-447.	5.1	16
612	Prediction of retrotransposons and assessment of genetic variability based on developed retrotransposon-based insertion polymorphism (RBIP) markers in Pyrus L. Molecular Genetics and Genomics, 2015, 290, 225-237.	1.0	17
613	Effect of auxin, cytokinin and nitrogen on anthocyanin biosynthesis in callus cultures of red-fleshed apple (Malus sieversii f.niedzwetzkyana). Plant Cell, Tissue and Organ Culture, 2015, 120, 325-337.	1.2	101
614	QTL Analysis Coupled with PTR-ToF-MS and Candidate Gene-Based Association Mapping Validate the Role of Md-AAT1 as a Major Gene in the Control of Flavor in Apple Fruit. Plant Molecular Biology Reporter, 2015, 33, 239-252.	1.0	19

#	ARTICLE	IF	CITATIONS
615	Construction of a High-Density Simple Sequence Repeat Consensus Genetic Map for Pear (Pyrus spp.). Plant Molecular Biology Reporter, 2015, 33, 316-325.	1.0	47
616	Genome-wide analysis of TCP family in tobacco. Genetics and Molecular Research, 2016, 15, .	0.3	23
617	Biochemistry of apple aroma: A review. Food Technology and Biotechnology, 2016, 54, 375-397.	0.9	116
618	Genome to Phenome Mapping in Apple Using Historical Data. Plant Genome, 2016, 9, plantgenome2015.11.0113.	1.6	102
619	Molecular and Genomic Tools Provide Insights on Crop Domestication and Evolution. Advances in Agronomy, 2016, 135, 181-223.	2.4	4
620	Analysis of â€˜Fujiâ€™ apple somatic variants from next-generation sequencing. Genetics and Molecular Research, 2016, 15, .	0.3	24
621	Profile of Compounds in Different Cultivars of Apple (Malus x domestica). , 2016, , 1-18.		5
622	Application of Genomic Technologies to the Breeding of Trees. Frontiers in Genetics, 2016, 7, 198.	1.1	45
623	Systematic Analysis of the 4-Coumarate:Coenzyme A Ligase (4CL) Related Genes and Expression Profiling during Fruit Development in the Chinese Pear. Genes, 2016, 7, 89.	1.0	51
624	Genomics of pear and other Rosaceae fruit trees. Breeding Science, 2016, 66, 148-159.	0.9	48
625	Genomic dissection of a â€˜Fujiâ€™ apple cultivar: re-sequencing, SNP marker development, definition of haplotypes, and QTL detection. Breeding Science, 2016, 66, 499-515.	0.9	26
626	The Jujube Genome Provides Insights into Genome Evolution and the Domestication of Sweetness/Acidity Taste in Fruit Trees. PLoS Genetics, 2016, 12, e1006433.	1.5	136
627	Primitive Genepools of Asian Pears and Their Complex Hybrid Origins Inferred from Fluorescent Sequence-Specific Amplification Polymorphism (SSAP) Markers Based on LTR Retrotransposons. PLoS ONE, 2016, 11, e0149192.	1.1	23
628	CisSERS: Customizable In Silico Sequence Evaluation for Restriction Sites. PLoS ONE, 2016, 11, e0152404.	1.1	11
629	Transgenic Suppression of AGAMOUS Genes in Apple Reduces Fertility and Increases Floral Attractiveness. PLoS ONE, 2016, 11, e0159421.	1.1	28
630	Evolutionary and Expression Analyses of the Apple Basic Leucine Zipper Transcription Factor Family. Frontiers in Plant Science, 2016, 7, 376.	1.7	64
631	MYB Transcription Factors in Chinese Pear (Pyrus bretschneideri Rehd.): Genome-Wide Identification, Classification, and Expression Profiling during Fruit Development. Frontiers in Plant Science, 2016, 7, 577.	1.7	143
632	Genome-Wide Sequence Variation Identification and Floral-Associated Trait Comparisons Based on the Re-sequencing of the â€˜Nagafu No. 2â€™ and â€˜Qinguanâ€™ Varieties of Apple (Malus domestica Borkh.). Frontiers in Plant Science, 2016, 7, 908.	1.7	33

#	Article	IF	Citations
633	Application of Somatic Embryogenesis in Woody Plants.. Frontiers in Plant Science, 2016, 07, 938.	1.7	146
634	Genome-Wide Comparative Analyses Reveal the Dynamic Evolution of Nucleotide-Binding Leucine-Rich Repeat Gene Family among Solanaceae Plants. Frontiers in Plant Science, 2016, 7, 1205.	1.7	75
635	Characterization of CIPK Family in Asian Pear (Pyrus bretschneideri Rehd) and Co-expression Analysis Related to Salt and Osmotic Stress Responses. Frontiers in Plant Science, 2016, 7, 1361.	1.7	26
636	Variation in Host and Pathogen in the Neonectria/Malus Interaction; toward an Understanding of the Genetic Basis of Resistance to European Canker. Frontiers in Plant Science, 2016, 7, 1365.	1.7	38
637	Genome-Wide Identification and Expression Analysis of the Tubby-Like Protein Family in the Malus domestica Genome. Frontiers in Plant Science, 2016, 7, 1693.	1.7	35
638	Comparative Genomic Analysis of the GRF Genes in Chinese Pear (Pyrus bretschneideri Rehd), Poplar (Populous), Grape (Vitis vinifera), Arabidopsis and Rice (Oryza sativa). Frontiers in Plant Science, 2016, 7, 1750.	1.7	97
639	Identification and Transcript Analysis of the TCP Transcription Factors in the Diploid Woodland Strawberry Fragaria vesca. Frontiers in Plant Science, 2016, 07, 1937.	1.7	75
640	Fine mapping of the gene for susceptibility to black spot disease in Japanese pear (<i>Pyrus) Tj ETQq1 1 0.784314 rgBT /Overlock	0.9	20
641	A New Plant Breeding Technique Using ALSV Vectors to Shorten the Breeding Periods of Fruit Trees. , 2016, , .		0
642	Use of Microsatellites to Study Agricultural Biodiversity and Food Traceability. , 2016, , .		1
643	The genome of black raspberry (<i>Rubus occidentalis</i>). Plant Journal, 2016, 87, 535-547.	2.8	111
644	Influence of preâ€harvest calcium, potassium and triazole application on the proteome of apple at harvest. Journal of the Science of Food and Agriculture, 2016, 96, 4984-4993.	1.7	8
645	Cyclic voltammetry of apple fruits: Memristors in vivo. Bioelectrochemistry, 2016, 112, 9-15.	2.4	22
646	HAPI-Gen. , 2016, , .		2
647	A high-density genetic linkage map of bronze loquat based on SSR and RAPD markers. Tree Genetics and Genomes, 2016, 12, 1.	0.6	6
648	Old Apple (Malus domestica L. Borkh) Varieties with Hypoallergenic Properties: An Integrated Approach for Studying Apple Allergenicity. Journal of Agricultural and Food Chemistry, 2016, 64, 9224-9236.	2.4	20
649	Giving fruit a nutritional boost. Nature Plants, 2016, 2, 16191.	4.7	4
650	Comparative phylogenetic analysis and transcriptional profiling of MADS-box gene family identified DAM and FLC-like genes in apple (Malusx domestica). Scientific Reports, 2016, 6, 20695.	1.6	80

#	Article	IF	Citations
651	Genome mapping of postzygotic hybrid necrosis in an interspecific pear population. Horticulture Research, 2016, 3, 15064.	2.9	15
652	Genomic tools for developing markers for postharvest disease resistance inRosaceaefruit crops. Acta Horticulturae, 2016, , 7-16.	0.1	4
653	NBS-LRR resistance genes polymorphism in apple (Malus domestica Borkh.) varieties inferred from NBS-profiling. Russian Journal of Genetics, 2016, 52, 1291-1295.	0.2	3
654	Emerging Genomics of Angiosperm Trees. Plant Genetics and Genomics: Crops and Models, 2016, , 85-99.	0.3	0
655	Evolutionary Histories of Gene Families in Angiosperm Trees. Plant Genetics and Genomics: Crops and Models, 2016, , 121-137.	0.3	0
656	Genome survey of pistachio (Pistacia vera L.) by next generation sequencing: Development of novel SSR markers and genetic diversity in Pistacia species. BMC Genomics, 2016, 17, 998.	1.2	78
657	Fruit Ripening in Melon. Plant Genetics and Genomics: Crops and Models, 2016, , 345-375.	0.3	4
658	Inhibition of Recombinant Aldose-6-Phosphate Reductase from Peach Leaves by Hexose-Phosphates, Inorganic Phosphate and Oxidants. Plant and Cell Physiology, 2016, 58, pcw180.	1.5	9
659	Structural Genomics of Angiosperm Trees: Genome Duplications, Ploidy, and Repeat Sequences. Plant Genetics and Genomics: Crops and Models, 2016, , 101-120.	0.3	0
660	QTL analysis of soft scald in two apple populations. Horticulture Research, 2016, 3, 16043.	2.9	21
661	Divergent Evolutionary Pattern of Sugar Transporter Genes is Associated with the Difference in Sugar Accumulation between Grasses and Eudicots. Scientific Reports, 2016, 6, 29153.	1.6	27
662	Gene expression and metabolism preceding soft scald, a chilling injury of â€˜Honeycrispâ€™ apple fruit. BMC Genomics, 2016, 17, 798.	1.2	28
663	The Watermelon Genome. Plant Genetics and Genomics: Crops and Models, 2016, , 199-210.	0.3	4
665	Fire blight disease reactome: RNA-seq transcriptional profile of apple host plant defense responses to Erwinia amylovora pathogen infection. Scientific Reports, 2016, 6, 21600.	1.6	38
666	Development of efficient transformation systems for functional genomic research in apple. Acta Horticulturae, 2016, , 191-198.	0.1	0
667	Technological progress in Japanese horticultural production and its academic aspects. Acta Horticulturae, 2016, , 9-18.	0.1	0
668	Role of Genomics in Enhancing Nutrition Content of Cereals. , 2016, , 77-96.		1
669	Computational analysis of atpB gene promoter from different Pakistani apple varieties. Computational Biology and Chemistry, 2016, 64, 1-8.	1.1	1

#	ARTICLE	IF	CITATIONS
670	Progress in Botany 77. Progress in Botany Fortschritte Der Botanik, 2016, , .	0.1	2
671	Genome-wide analysis of the synonymous codon usage patterns in apple. Journal of Integrative Agriculture, 2016, 15, 983-991.	1.7	20
672	Transcriptome analysis reveals the effects of sugar metabolism and auxin and cytokinin signaling pathways on root growth and development of grafted apple. BMC Genomics, 2016, 17, 150.	1.2	52
673	Detecting QTLs and putative candidate genes involved in budbreak and flowering time in an apple multiparental population. Journal of Experimental Botany, 2016, 67, 2875-2888.	2.4	91
674	Differential expression of phenylalanine ammonia lyase (PAL) genes implies distinct roles in development of graft incompatibility symptoms in Prunus.. Scientia Horticulturae, 2016, 204, 16-24.	1.7	39
675	The evolutionary landscape of PRC1 core components in green lineage. Planta, 2016, 243, 825-846.	1.6	20
676	Genomewide analysis of ABCBs with a focus on ABCB1 and ABCB19 in Malus domestica. Journal of Genetics, 2016, 95, 141-149.	0.4	10
677	Development of molecular markers for genetic and physical mapping of the <i>PcDw</i> locus in pear (<i>Pyrus communis</i> L.). Journal of Horticultural Science and Biotechnology, 2016, 91, 299-307.	0.9	7
678	Expression Profiling of Several Gene Families Involved in Anthocyanin Biosynthesis in Apple (Malus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 449-464.	2.8	36
679	Comparative analysis of plant immune receptor architectures uncovers host proteins likely targeted by pathogens. BMC Biology, 2016, 14, 8.	1.7	293
680	Transcriptome changes specifically associated with apple (Malus domestica) root defense response during Pythium ultimum infection. Physiological and Molecular Plant Pathology, 2016, 94, 16-26.	1.3	70
681	Molecular aspects in pathogen-fruit interactions: Virulence and resistance. Postharvest Biology and Technology, 2016, 122, 11-21.	2.9	136
682	Epigenetic regulation of MdMYB1 is associated with paper bagging-induced red pigmentation of apples. Planta, 2016, 244, 573-586.	1.6	47
683	Structural genomics and transcriptional characterization of the Dormancy-Associated MADS-box genes during bud dormancy progression in apple. Tree Genetics and Genomes, 2016, 12, 1.	0.6	35
684	Ethnobotany of Mexico. Ethnobiology, 2016, , .	0.4	36
685	Phylogeographical Approaches to the Study of Plant Domestication, with Special Emphasis on Perennial Plants. Ethnobiology, 2016, , 319-366.	0.4	8
686	Analysis of basic leucine zipper genes and their expression during bud dormancy in peach (Prunus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	2.8	16
687	Structure analysis and expression pattern of the ERF transcription factor family in poplar. Acta Physiologiae Plantarum, 2016, 38, 1.	1.0	4

#	Article	IF	Citations
688	Construction of a high-density, high-quality genetic map of cultivated lotus (Nelumbo nucifera) using next-generation sequencing. BMC Genomics, 2016, 17, 466.	1.2	22
689	Towards integration of population and comparative genomics in forest trees. New Phytologist, 2016, 212, 338-344.	3.5	31
690	To Have and to Hold. Current Topics in Developmental Biology, 2016, 119, 63-109.	1.0	53
691	Expression Analysis of the MdCIbHLH1 Gene in Apple Flower Buds and Seeds in the Process of Dormancy. Horticultural Plant Journal, 2016, 2, 61-66.	2.3	15
692	A droplet-vitrification protocol enabled cryopreservation of doubled haploid explants of Malus x domestica Borkh. â€˜Golden Deliciousâ€™. Scientia Horticulturae, 2016, 209, 187-191.	1.7	10
693	Widespread natural variation of DNA methylation within angiosperms. Genome Biology, 2016, 17, 194.	3.8	436
694	Genetics and Molecular Marker Identification of a Resistance to Glomerella Leaf Spot in Apple. Horticultural Plant Journal, 2016, 2, 121-125.	2.3	14
695	Exploiting genotyping by sequencing to characterize the genomic structure of the American cranberry through high-density linkage mapping. BMC Genomics, 2016, 17, 451.	1.2	45
696	F-box genes: Genome-wide expansion, evolution and their contribution to pollen growth in pear (Pyrus bretschneideri). Plant Science, 2016, 253, 164-175.	1.7	42
697	Expression of a putative dioxygenase gene adjacent to an insertion mutation is involved in the short internodes of columnar apples (Malus Ã— domestica). Journal of Plant Research, 2016, 129, 1109-1126.	1.2	33
698	Rapid Cycle Breeding: Application of Transgenic Early Flowering for Perennial Trees. , 2016, , 299-334.		10
699	Genome-wide identification and expression analysis of the bZIP gene family in apple (Malus domestica). Tree Genetics and Genomes, 2016, 12, 1.	0.6	58
700	Global identification and expression analysis of stress-responsive genes of the Argonaute family in apple. Molecular Genetics and Genomics, 2016, 291, 2015-2030.	1.0	4
701	Genome-wide identification and characterization of R2R3MYB family in Rosaceae. Genomics Data, 2016, 9, 50-57.	1.3	12
702	Mono- and sesquiterpene release from tomato (Solanum lycopersicum) leaves upon mild and severe heat stress and through recovery: From gene expression to emission responses. Environmental and Experimental Botany, 2016, 132, 1-15.	2.0	51
703	Genomics and expression analysis of DHHC-cysteine-rich domain S-acyl transferase protein family in apple. Genes and Genomics, 2016, 38, 671-684.	0.5	0
704	Spreading Winge and flying high: The evolutionary importance of polyploidy after a century of study. American Journal of Botany, 2016, 103, 1139-1145.	0.8	81
705	Fine mapping of the rosy apple aphid resistance locus Dp-fl on linkage group 8 of the apple cultivar â€˜Florinaâ€™. Tree Genetics and Genomes, 2016, 12, 1.	0.6	14

#	Article	IF	Citations
706	Improved hybrid de novo genome assembly of domesticated apple (Malus x domestica). GigaScience, 2016, 5, 35.	3.3	56
707	Are We There Yet? Reliably Estimating the Completeness of Plant Genome Sequences. Plant Cell, 2016, 28, 1759-1768.	3.1	89
708	Proteomic analysis reveals dynamic regulation of fruit development and sugar and acid accumulation in apple. Journal of Experimental Botany, 2016, 67, 5145-5157.	2.4	84
709	AÂUnique haplotype found in apple accessions exhibiting early bud-break could serve as a marker for breeding apples with low chilling requirements. Molecular Breeding, 2016, 36, 1.	1.0	13
710	A high-density, multi-parental SNP genetic map on apple validates a new mapping approach for outcrossing species. Horticulture Research, 2016, 3, 16057.	2.9	68
711	MdMyb93 is a regulator of suberin deposition in russeted apple fruit skins. New Phytologist, 2016, 212, 977-991.	3.5	113
712	The Case of the Missing Ancient Fungal Polyploids. American Naturalist, 2016, 188, 602-614.	1.0	38
713	Evolution of Rosaceae Fruit Types Based on Nuclear Phylogeny in the Context of Geological Times and Genome Duplication. Molecular Biology and Evolution, 2017, 34, msw242.	3.5	200
714	Evolutionary and Expression Analysis Provides Evidence for the Plant Glutamate-like Receptors Family is Involved in Woody Growth-related Function. Scientific Reports, 2016, 6, 32013.	1.6	16
715	Comprehensive genomic analysis and expression profiling of Argonaute gene family and examination of their regulatory roles in water-use efficiency and abiotic stress responses in apple. Acta Physiologiae Plantarum, 2016, 38, 1.	1.0	5
716	Efficient Genome Editing in Apple Using a CRISPR/Cas9 system. Scientific Reports, 2016, 6, 31481.	1.6	270
717	Distinct transcriptome profiles reveal gene expression patterns during fruit development and maturation in five main cultivated species of pear (Pyrus L.). Scientific Reports, 2016, 6, 28130.	1.6	59
718	Cell wall dynamics during apple development and storage involves hemicellulose modifications and related expressed genes. BMC Plant Biology, 2016, 16, 201.	1.6	83
719	Biotechnology and apple breeding in Japan. Breeding Science, 2016, 66, 18-33.	0.9	33
720	Scab resistance in â€˜<scp>G</scp>enevaâ€™ apple is conditioned by a resistance gene cluster with complex genetic control. Molecular Plant Pathology, 2016, 17, 159-172.	2.0	19
721	The walnut (<i>Juglans regia</i>) genome sequence reveals diversity in genes coding for the biosynthesis of nonâ€structural polyphenols. Plant Journal, 2016, 87, 507-532.	2.8	233
722	Database of predicted SCAR markers in five fruit and three vegetable crops. Journal of Genetics, 2016, 95, 171-175.	0.4	0
723	Abscission-related genes revealed by RNA-Seq analysis using self-abscising apple (<i>Malus</i> Ã—) Tj ETQq1 1 0.784314 rgBT /Overlo	0.9	6

#	Article	IF	Citations
724	Most Compositae (Asteraceae) are descendants of a paleohexaploid and all share a paleotetraploid ancestor with the Calyceraceae. American Journal of Botany, 2016, 103, 1203-1211.	0.8	98
725	Genetics of Fruit Softening. Compendium of Plant Genomes, 2016, , 205-217.	0.3	20
726	Evolution of Gene Duplication in Plants. Plant Physiology, 2016, 171, 2294-2316.	2.3	1,094
727	Advances in Genetic Diversity Analysis in Fruit Tree Crops. Progress in Botany Fortschritte Der Botanik, 2016, , 245-264.	0.1	4
728	Analysis of transcripts differentially expressed between fruited and deflowered â€˜Galaâ€™ adult trees: a contribution to biennial bearing understanding in apple. BMC Plant Biology, 2016, 16, 55.	1.6	42
729	Landscape and evolutionary dynamics of terminal repeat retrotransposons in miniature in plant genomes. Genome Biology, 2016, 17, 7.	3.8	50
730	Evolution of plant genome architecture. Genome Biology, 2016, 17, 37.	3.8	331
731	Genotyping-by-sequencing in an orphan plant species Physocarpus opulifolius helps identify the evolutionary origins of the genus Prunus. BMC Research Notes, 2016, 9, 268.	0.6	4
732	An optimized TRV-based virus-induced gene silencing protocol for Malus crabapple. Plant Cell, Tissue and Organ Culture, 2016, 126, 499-509.	1.2	29
733	Isolation and characterization of putative functional long terminal repeat retrotransposons in the Pyrus genome. Mobile DNA, 2016, 7, 1.	1.3	25
734	Genomeâ€wide association links candidate genes to resistance to <i>Plum Pox Virus</i> in apricot (<i>Prunus armeniaca</i>). New Phytologist, 2016, 209, 773-784.	3.5	55
735	Multifunctional oxidosqualene cyclases and cytochrome P450 involved in the biosynthesis of apple fruit triterpenic acids. New Phytologist, 2016, 211, 1279-1294.	3.5	66
736	Development and validation of the Axiom^{Â®}Apple480K <scp>SNP</scp> genotyping array. Plant Journal, 2016, 86, 62-74.	2.8	156
737	Major Chromosomal Rearrangements Distinguish Willow and Poplar After the Ancestral â€œSalicoidâ€• Genome Duplication. Genome Biology and Evolution, 2016, 8, 1868-1875.	1.1	30
738	Genomics-based strategies for the use of natural variation in the improvement of crop metabolism. Plant Science, 2016, 242, 47-64.	1.7	60
739	Evolutionary Dynamics of the Leucine-Rich Repeat Receptor-Like Kinase (LRR-RLK) Subfamily in Angiosperms. Plant Physiology, 2016, 170, 1595-1610.	2.3	114
740	Comprehensive genomic identification and expression analysis of the nucleobase-ascorbate transporter (NAT) gene family in apple. Scientia Horticulturae, 2016, 198, 473-481.	1.7	18
741	Elm defence against herbivores and pathogens: morphological, chemical and molecular regulation aspects. Phytochemistry Reviews, 2016, 15, 961-983.	3.1	27

#	ARTICLE	IF	CITATIONS
742	Quantitative Proteomics-Based Reconstruction and Identification of Metabolic Pathways and Membrane Transport Proteins Related to Sugar Accumulation in Developing Fruits of Pear (<i>Pyrus) Tj ETQq0 0 0 rg BT /Overlock 10 Tf 5	1.3	27
743	Characterization of apple NADPH oxidase genes and their expression associated with oxidative stress in shoot culture in vitro. Plant Cell, Tissue and Organ Culture, 2016, 124, 621-633.	1.2	20
744	Phylogenetic and Expression Analysis of Pear Yellow Stripe-Like Transporters and Functional Verification of PbrYSL4 in Pear Pollen. Plant Molecular Biology Reporter, 2016, 34, 737-747.	1.0	3
745	Ancestors of modern plant crops. Current Opinion in Plant Biology, 2016, 30, 134-142.	3.5	54
746	Molecular characterization of pear 14-3-3b gene regulated during fruit development. Canadian Journal of Plant Science, 2016, 96, 433-438.	0.3	0
747	GREENC: a Wiki-based database of plant lncRNAs. Nucleic Acids Research, 2016, 44, D1161-D1166.	6.5	196
748	Transcriptional Regulation of Auxin Metabolism and Ethylene Biosynthesis Activation During Apple (MalusÂÃ—Âdomestica) Fruit Maturation. Journal of Plant Growth Regulation, 2016, 35, 655-666.	2.8	28
749	Climate-related adaptive genetic variation and population structure in natural stands of Norway spruce in the South-Eastern Alps. Tree Genetics and Genomes, 2016, 12, 1.	0.6	25
750	Comprehensive Phylogenetic Analysis Sheds Light on the Diversity and Origin of the MLO Family of Integral Membrane Proteins. Genome Biology and Evolution, 2016, 8, 878-895.	1.1	79
751	Genetic mapping of the loquat canker resistance gene pse-c in loquat (Eriobotrya japonica). Scientia Horticulturae, 2016, 200, 19-24.	1.7	4
752	Oxidative metabolism is associated with physiological disorders in fruits stored under multiple environmental stresses. Plant Science, 2016, 245, 143-152.	1.7	50
753	A new three-locus model for rootstock-induced dwarfing in apple revealed by genetic mapping of root bark percentage. Journal of Experimental Botany, 2016, 67, 1871-1881.	2.4	41
754	Candidate gene expression profiling reveals a time specific activation among different harvesting dates in â€˜Golden Deliciousâ€™ and â€˜Fujiâ€™ apple cultivars. Euphytica, 2016, 208, 401-413.	0.6	14
755	Genome-wide identification and characterization of WRKY transcriptional factor family in apple and analysis of their responses to waterlogging and drought stress. Plant Physiology and Biochemistry, 2016, 103, 71-83.	2.8	87
756	What makes up plant genomes: The vanishing line between transposable elements and genes. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2016, 1859, 366-380.	0.9	67
757	Genetic Diversity, Population Structure, Parentage Analysis, and Construction of Core Collections in the French Apple Germplasm Based on SSR Markers. Plant Molecular Biology Reporter, 2016, 34, 827-844.	1.0	110
758	Homologs of the FB_MR5 fire blight resistance gene of Malus Ã—robusta 5 are present in other Malus wild species accessions. Tree Genetics and Genomes, 2016, 12, 1.	0.6	5
759	Construction of a high density linkage map and its application in the identification of QTLs for soluble sugar and organic acid components in apple. Tree Genetics and Genomes, 2016, 12, 1.	0.6	95

#	Article	IF	Citations
760	Expression analysis of candidate cell wall-related genes associated with changes in pectin biochemistry during postharvest apple softening. Postharvest Biology and Technology, 2016, 112, 176-185.	2.9	61
761	Effects of genome structure variation, homeologous genes and repetitive DNA on polyploid crop research in the age of genomics. Plant Science, 2016, 242, 37-46.	1.7	33
762	Emergence of new virulent populations of apple scab from nonagricultural disease reservoirs. New Phytologist, 2016, 209, 1220-1229.	3.5	42
763	A review of genetic resources of pome fruits in Iran. Genetic Resources and Crop Evolution, 2016, 63, 151-172.	0.8	25
764	Genome-wide identification and characterization of the apple (Malus domestica) HECT ubiquitin-protein ligase family and expression analysis of their responsiveness to abiotic stresses. Molecular Genetics and Genomics, 2016, 291, 635-646.	1.0	21
765	EARLY BUD-BREAK1 (EBB1) defines a conserved mechanism for control of bud-break in woody perennials. Plant Signaling and Behavior, 2016, 11, e1073873.	1.2	35
766	Influence of Cultivar, Antiâ€Browning Solutions, Packaging Gasses, and Advanced Technology on Browning in Freshâ€Cut Apples During Storage. Journal of Food Process Engineering, 2017, 40, e12400.	1.5	26
767	Benchmark Dataset for Whole Genome Sequence Compression. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 1228-1236.	1.9	10
768	Influence of Respiration on Predictive Microbial Growth of <i>Aerobic Mesophilic Bacteria</i> and <i>Enterobacteriaceae</i> in Freshâ€Cut Apples Packaged Under Modified Atmosphere. Journal of Food Safety, 2017, 37, e12284.	1.1	19
769	MYB12 and MYB22 play essential roles in proanthocyanidin and flavonol synthesis in redâ€fleshed apple (<i>Malus sieversii</i> f<i>. niedzwetzkyana</i>). Plant Journal, 2017, 90, 276-292.	2.8	235
770	Functional Characterization of the Apple RING E3 Ligase MdMIEL1 in Transgenic Arabidopsis. Horticultural Plant Journal, 2017, 3, 53-59.	2.3	8
771	Unravelling genetic diversity and cultivar parentage in the Danish apple gene bank collection. Tree Genetics and Genomes, 2017, 13, 1.	0.6	42
772	Methylation effect on IPT5b gene expression determines cytokinin biosynthesis in apple rootstock. Biochemical and Biophysical Research Communications, 2017, 482, 604-609.	1.0	28
773	The Epigenome and Transcriptional Dynamics of Fruit Ripening. Annual Review of Plant Biology, 2017, 68, 61-84.	8.6	335
774	Analysis of the apple rubbery wood disease by next generation sequencing of total RNA. European Journal of Plant Pathology, 2017, 148, 637-646.	0.8	11
775	Reduced representation genome sequencing reveals patterns of genetic diversity and selection in apple. Journal of Integrative Plant Biology, 2017, 59, 190-204.	4.1	30
776	Novel Insights into Tree Biology and Genome Evolution as Revealed Through Genomics. Annual Review of Plant Biology, 2017, 68, 457-483.	8.6	64
777	Abiotic Stress. Plant Genetics and Genomics: Crops and Models, 2017, , 275-302.	0.3	0

#	Article	IF	Citations
778	High-throughput sequencing reveals that pale green lethal disorder in apple (Malus) stimulates stress responses and affects senescence. Tree Genetics and Genomes, 2017, 13, 1.	0.6	4
779	McMYB12 Transcription Factors Co-regulate Proanthocyanidin and Anthocyanin Biosynthesis in Malus Crabapple. Scientific Reports, 2017, 7, 43715.	1.6	64
780	Diversification of Rosaceae since the Late Cretaceous based on plastid phylogenomics. New Phytologist, 2017, 214, 1355-1367.	3.5	278
781	Phylogenetic analysis of 25 plant species representing 19 angiosperm families and one gymnosperm family based on 390 orthologous genes. Plant Systematics and Evolution, 2017, 303, 413-417.	0.3	9
782	To what extent do wild apples in Kazakhstan retain their genetic integrity?. Tree Genetics and Genomes, 2017, 13, 1.	0.6	26
783	Apple RING finger E3 ubiquitin ligase MdMIEL1 negatively regulates salt and oxidative stresses tolerance. Journal of Plant Biology, 2017, 60, 137-145.	0.9	26
784	Transcriptomic analysis of molecular responses in Malus domestica â€˜M26â€™ roots affected by apple replant disease. Plant Molecular Biology, 2017, 94, 303-318.	2.0	55
785	Genome-wide identification, characterization of the MADS-box gene family in Chinese jujube and their involvement in flower development. Scientific Reports, 2017, 7, 1025.	1.6	42
786	Bioinformatic identification and expression analysis of the Malus domestica DREB2 transcription factors in different tissues and abiotic stress. Journal of Plant Biochemistry and Biotechnology, 2017, 26, 436-443.	0.9	12
787	The Structure and Methylation Level of the McMYB10 Promoter Determine the Leaf Color of Malus Crabapple. Hortscience: A Publication of the American Society for Hortcultural Science, 2017, 52, 520-526.	0.5	8
788	Integrated high-density consensus genetic map of<i>Pyrus</i>and anchoring of the â€˜Bartlettâ€™ v1.0 (<i>Pyrus communis</i>) genome. DNA Research, 2017, 24, dsw063.	1.5	28
789	Single-Copy Genes as Molecular Markers for Phylogenomic Studies in Seed Plants. Genome Biology and Evolution, 2017, 9, 1130-1147.	1.1	75
790	Antioxidant and cytotoxic activity of bioactive phenolic metabolites isolated from the yeast-extract treated cell culture of apple. Plant Cell, Tissue and Organ Culture, 2017, 130, 641-649.	1.2	33
791	Transcriptome profiling in leaves representing aboveground parts of apple replant disease affected Malus domestica â€˜M26â€™ plants. Scientia Horticulturae, 2017, 222, 111-125.	1.7	29
792	Biochemical Profile of Heritage and Modern Apple Cultivars and Application of Machine Learning Methods To Predict Usage, Age, and Harvest Season. Journal of Agricultural and Food Chemistry, 2017, 65, 5339-5356.	2.4	25
793	The genome sequence of sweet cherry (Prunus avium) for use in genomics-assisted breeding. DNA Research, 2017, 24, 499-508.	1.5	212
794	Insertion of a solo LTR retrotransposon associates with spur mutations in â€˜Red Deliciousâ€™ apple (MalusÂÃ—Âdomestica). Plant Cell Reports, 2017, 36, 1375-1385.	2.8	17
795	Genome-wide sequencing of longan (Dimocarpus longan Lour.) provides insights into molecular basis of its polyphenol-rich characteristics. GigaScience, 2017, 6, 1-14.	3.3	103

#	ARTICLE	IF	CITATIONS
796	Differential susceptibility and suitability of domestic and wild apple species for a florivorous weevil and its parasitoids. Journal of Applied Entomology, 2017, 141, 285-299.	0.8	7
797	DNA-informed breeding of rosaceous crops: promises, progress and prospects. Horticulture Research, 2017, 4, 17006.	2.9	63
798	A New Insight into the Evolution and Functional Divergence of SWEET Transporters in Chinese White Pear (Pyrus bretschneideri). Plant and Cell Physiology, 2017, 58, 839-850.	1.5	87
799	Identification and expression analysis of WRKY transcription factor genes in response to fungal pathogen and hormone treatments in apple (Malus domestica). Journal of Plant Biology, 2017, 60, 215-230.	0.9	36
800	Virus-induced gene silencing of the two squalene synthase isoforms of apple tree (MalusÂÃ—Âdomestica) Tj ETQq0 0 0 rgBT /Overlock 1 45-60.	1.6	15
801	The Peach v2.0 release: high-resolution linkage mapping and deep resequencing improve chromosome-scale assembly and contiguity. BMC Genomics, 2017, 18, 225.	1.2	342
802	Investigation and genetic mapping of a Glomerella leaf spot resistance locus in apple. Plant Breeding, 2017, 136, 119-125.	1.0	8
803	Elucidation of the â€˜Honeycrispâ€™ pedigree through haplotype analysis with a multi-family integrated SNP linkage map and a large apple (MalusÃ—domestica) pedigree-connected SNP data set. Horticulture Research, 2017, 4, 17003.	2.9	54
804	The molecular mechanism underlying anthocyanin metabolism in apple using the MdMYB16 and MdbHLH33 genes. Plant Molecular Biology, 2017, 94, 149-165.	2.0	151
805	Phylogenetic analysis of IDD gene family and characterization of its expression in response to flower induction in Malus. Molecular Genetics and Genomics, 2017, 292, 755-771.	1.0	29
806	Evaluation of multiple approaches to identify genome-wide polymorphisms in closely related genotypes of sweet cherry (Prunus avium L.). Computational and Structural Biotechnology Journal, 2017, 15, 290-298.	1.9	10
807	Molecular cloning and functional characterization of MdNHX1 reveals its involvement in salt tolerance in apple calli and Arabidopsis. Scientia Horticulturae, 2017, 215, 126-133.	1.7	17
808	Nuclear proteome analysis of apple cultivar â€˜Antonovkaâ€™ accessions in response to apple scab (Venturia inaequalis). European Journal of Plant Pathology, 2017, 148, 771-784.	0.8	6
809	Genetics and Genomics of Cucurbitaceae. Plant Genetics and Genomics: Crops and Models, 2017, , .	0.3	22
810	Comparative analysis of allergen genes and pro-inflammatory factors in pollen and fruit of apple varieties. Plant Science, 2017, 264, 57-68.	1.7	21
811	Comparative transcriptome analysis of Ziziphus jujuba infected by jujube witchesâ€™ broom phytoplasmas. Scientia Horticulturae, 2017, 226, 50-58.	1.7	21
812	Genome expression profile analysis of two types of new roots in apple rootstock via Solexa sequencing. Plant Gene, 2017, 12, 105-113.	1.4	0
813	Genome-wide identification of glycosyltransferases converting phloretin to phloridzin in Malus species. Plant Science, 2017, 265, 131-145.	1.7	53

#	ARTICLE	IF	CITATIONS
814	Global Identification, Classification, and Expression Analysis of MAPKKK genes: Functional Characterization of MdRaf5 Reveals Evolution and Drought-Responsive Profile in Apple. Scientific Reports, 2017, 7, 13511.	1.6	21
815	Breeding Avenues in Fruit Crops for Imparting Resistance Against Insect Pests. , 2017, , 289-322.		0
816	Patterns of low temperature induced accumulation of dehydrins in Rosaceae cropsâ€"Evidence for post-translational modification in apple. Journal of Plant Physiology, 2017, 218, 175-181.	1.6	14
817	Electrochemistry of Gala apples: Memristors in vivo. Russian Journal of Electrochemistry, 2017, 53, 1011-1018.	0.3	6
818	Apple genes involved in the response to Venturia inaequalis and salicylic acid treatment. Scientia Horticulturae, 2017, 226, 157-172.	1.7	10
819	Genome re-sequencing reveals the history of apple and supports a two-stage model for fruit enlargement. Nature Communications, 2017, 8, 249.	5.8	286
820	Genome-wide identification of the radiation sensitivity protein-23 (RAD23) family members in apple (MalusÃ—domestica Borkh.) and expression analysis of their stress responsiveness. Journal of Integrative Agriculture, 2017, 16, 820-827.	1.7	6
821	Mdoryco1-1 , a bidirectionally transcriptional Ty1 -copia retrotransposon from Malus Ã— domestica. Scientia Horticulturae, 2017, 220, 283-290.	1.7	2
822	Comparative transcripome data for commercial maturity and physiological maturity of â€˜Royal Galaâ€™ apple fruit under room temperature storage condition. Scientia Horticulturae, 2017, 225, 386-393.	1.7	8
823	Genome-wide identification and expression profiling analysis of brassinolide signal transduction genes regulating apple tree architecture. Acta Physiologiae Plantarum, 2017, 39, 1.	1.0	11
824	Rapid location of Glomerella leaf spot resistance gene locus in apple by whole genome re-sequencing. Molecular Breeding, 2017, 37, 1.	1.0	7
825	MdMYB4, an R2R3-Type MYB Transcription Factor, Plays a Crucial Role in Cold and Salt Stress in Apple Calli. Journal of the American Society for Horticultural Science, 2017, 142, 209-216.	0.5	14
826	PCPPI: a comprehensive database for the prediction of Penicilliumâ€“crop proteinâ€“protein interactions. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	1.4	10
828	Identification of the SRO gene family in apples (MalusÃ—domestica) with a functional characterization of MdRCD1. Tree Genetics and Genomes, 2017, 13, 1.	0.6	13
829	MdMYB4 enhances apple callus salt tolerance by increasing MdNHX1 expression levels. Plant Cell, Tissue and Organ Culture, 2017, 131, 283-293.	1.2	19
830	Identification of potential geneâ€associated major traits using <scp>GBS</scp>â€<scp>GWAS</scp> for Korean apple germplasm collections. Plant Breeding, 2017, 136, 977-986.	1.0	17
831	Genetic diversity, population structure, and linkage disequilibrium of elite and local apple accessions from Belgium using the IRSC array. Tree Genetics and Genomes, 2017, 13, 1.	0.6	31
832	Fire blight resistance of Malus Ã—arnoldiana is controlled by a quantitative trait locus located at the distal end of linkage group 12. European Journal of Plant Pathology, 2017, 148, 1011-1018.	0.8	32

#	ARTICLE	IF	CITATIONS
833	Allelic composition of MdMYB1 drives red skin color intensity in apple (MalusÂÃ—Âdomestica Borkh.) and its application to breeding. Euphytica, 2017, 213, 1.	0.6	13
834	Origin of the Domesticated Horticultural Species and Molecular Bases of Fruit Shape and Size Changes during the Domestication, Taking Tomato as an Example. Horticultural Plant Journal, 2017, 3, 125-132.	2.3	18
835	Comparative landscape of alternative splicing in fruit plants. Current Plant Biology, 2017, 9-10, 29-36.	2.3	16
836	Genome-wide identification, evolution, and expression analysis of GATA transcription factors in apple (Malus Ã— domestica Borkh.). Gene, 2017, 627, 460-472.	1.0	26
837	High-quality de novo assembly of the apple genome and methylome dynamics of early fruit development. Nature Genetics, 2017, 49, 1099-1106.	9.4	693
838	Identification and expression analysis of the apple (Malus Ã— domestica) basic helix-loop-helix transcription factor family. Scientific Reports, 2017, 7, 28.	1.6	43
839	Development of SNP markers using genotyping-by-sequencing for cultivar identification in rose (Rosa) Tj ETQq0 0 0 rgBT /Overlock 10 T	0.7	15
840	The pomegranate (<i>Punica granatum</i> L.) genome and the genomics of punicalagin biosynthesis. Plant Journal, 2017, 91, 1108-1128.	2.8	109
841	Retrotransposon-based sequence-specific amplified polymorphism markers for the analysis of genetic diversity and phylogeny in Malus Mill. (Rosaceae). Genetic Resources and Crop Evolution, 2017, 64, 1499-1511.	0.8	4
842	Genome-wide analysis and characterization of molecular evolution of the HCT gene family in pear (Pyrus bretschneideri). Plant Systematics and Evolution, 2017, 303, 71-90.	0.3	23
843	TATA Box Insertion Provides a Selection Mechanism Underpinning Adaptations to Fe Deficiency. Plant Physiology, 2017, 173, 715-727.	2.3	27
844	Reverse transcriptase sequences from mulberry LTR retrotransposons: characterization analysis. Open Life Sciences, 2017, 12, 266-276.	0.6	0
845	Transcriptomic analysis of aerial and root organs in two apple tree cultivars under soil water deprivation. Acta Horticulturae, 2017, , 283-288.	0.1	0
846	Novel genetic marker technologies revolutionize apple breedingÂ©. Acta Horticulturae, 2017, , 23-30.	0.1	4
847	Genome-wide association study unravels the genetic control of the apple volatilome and its interplay with fruit texture. Journal of Experimental Botany, 2017, 68, 1467-1478.	2.4	63
848	A disulfide bond A-like oxidoreductase is a strong candidate gene for self-incompatibility in apricot (Prunus armeniaca) pollen. Journal of Experimental Botany, 2017, 68, 5069-5078.	2.4	22
849	Genome Sequence-Based Marker Development and Genotyping in Potato. Compendium of Plant Genomes, 2017, , 307-326.	0.3	3
850	ALSV Vector Substantially Shortens Generation Time of Horticultural Plants. , 2017, , .		1

#	ARTICLE	IF	CITATIONS
851	Comprehensive analysis of GASA family members in the Malus domestica genome: identification, characterization, and their expressions in response to apple flower induction. BMC Genomics, 2017, 18, 827.	1.2	64
852	Identification, Classification, and Expression Analysis of GRAS Gene Family in Malus domestica. Frontiers in Physiology, 2017, 8, 253.	1.3	45
853	Overexpression of MpCYS4, A Phytocystatin Gene from Malus prunifolia (Willd.) Borkh., Enhances Stomatal Closure to Confer Drought Tolerance in Transgenic Arabidopsis and Apple. Frontiers in Plant Science, 2017, 8, 33.	1.7	48
854	New Insights on Leucine-Rich Repeats Receptor-Like Kinase Orthologous Relationships in Angiosperms. Frontiers in Plant Science, 2017, 08, 381.	1.7	54
855	Comprehensive Genomic Identification and Expression Analysis of the Phosphate Transporter (PHT) Gene Family in Apple. Frontiers in Plant Science, 2017, 8, 426.	1.7	48
856	SVP-like MADS Box Genes Control Dormancy and Budbreak in Apple. Frontiers in Plant Science, 2017, 08, 477.	1.7	121
857	Genome Wide Identification and Characterization of Apple bHLH Transcription Factors and Expression Analysis in Response to Drought and Salt Stress. Frontiers in Plant Science, 2017, 8, 480.	1.7	148
858	Two Highly Similar Poplar Paleo-subgenomes Suggest an Autotetraploid Ancestor of Salicaceae Plants. Frontiers in Plant Science, 2017, 08, 571.	1.7	20
859	Predicting Flowering Behavior and Exploring Its Genetic Determinism in an Apple Multi-family Population Based on Statistical Indices and Simplified Phenotyping. Frontiers in Plant Science, 2017, 8, 858.	1.7	16
860	Transcriptome Analysis of Differentially Expressed Genes Induced by Low and High Potassium Levels Provides Insight into Fruit Sugar Metabolism of Pear. Frontiers in Plant Science, 2017, 8, 938.	1.7	37
861	Two FERONIA-Like Receptor Kinases Regulate Apple Fruit Ripening by Modulating Ethylene Production. Frontiers in Plant Science, 2017, 8, 1406.	1.7	27
862	CHASE-Containing Histidine Kinase Receptors in Apple Tree: From a Common Receptor Structure to Divergent Cytokinin Binding Properties and Specific Functions. Frontiers in Plant Science, 2017, 8, 1614.	1.7	27
863	Genome-Wide Identification and Expression, Proteinâ€"Protein Interaction and Evolutionary Analysis of the Seed Plant-Specific BIG GRAIN and BIG GRAIN LIKE Gene Family. Frontiers in Plant Science, 2017, 8, 1812.	1.7	11
864	Multiple Copies of a Simple MYB-Binding Site Confers Trans-regulation by Specific Flavonoid-Related R2R3 MYBs in Diverse Species. Frontiers in Plant Science, 2017, 8, 1864.	1.7	38
865	Transcriptomic Response of Resistant (PI613981â€"Malus sieversii) and Susceptible (â€œRoyal Galaâ€) Genotypes of Apple to Blue Mold (Penicillium expansum) Infection. Frontiers in Plant Science, 2017, 8, 1981.	1.7	40
866	Role of the type VI secretion systems during disease interactions of Erwinia amylovora with its plant host. BMC Genomics, 2017, 18, 628.	1.2	26
867	Genome-wide characterization, evolution, and expression analysis of the leucine-rich repeat receptor-like protein kinase (LRR-RLK) gene family in Rosaceae genomes. BMC Genomics, 2017, 18, 763.	1.2	62
868	Draft Sequencing of the Heterozygous Diploid Genome of Satsuma (Citrus unshiu Marc.) Using a Hybrid Assembly Approach. Frontiers in Genetics, 2017, 8, 180.	1.1	49

#	ARTICLE	IF	CITATIONS
869	Rapid identification of apple (<i>Malus</i>Ã—<i>domestica</i> Borkh.) <i>S</i> alleles using sequencing-based DNA marker <i>APPLid</i>. Plant Biotechnology, 2017, 34, 97-106.	0.5	6
870	Comparative transcriptomic analysis reveals a series of single nucleotide polymorphism between red- and white-fleshed loquats (Eriobotrya japonica). Czech Journal of Genetics and Plant Breeding, 2017, 53, 97-106.	0.4	2
871	Comparative Transcriptome Analysis Reveals a Preformed Defense System in Apple Root of a Resistant Genotype of G.935 in the Absence of Pathogen. International Journal of Plant Genomics, 2017, 2017, 1-14.	2.2	17
872	Genome-wide identification and analysis of the MADS-box gene family in bread wheat (Triticum) Tj ETQq1 1 0.784314 rgBT /Overlock 1	1.1	69
873	Using RNA-seq data to select reference genes for normalizing gene expression in apple roots. PLoS ONE, 2017, 12, e0185288.	1.1	52
874	LinkImputeR: user-guided genotype calling and imputation for non-model organisms. BMC Genomics, 2017, 18, 523.	1.2	48
875	Parallel loss of introns in the ABCB1 gene in angiosperms. BMC Evolutionary Biology, 2017, 17, 238.	3.2	3
876	TGTT and AACA: two transcriptionally active LTR retrotransposon subfamilies with a specific LTR structure and horizontal transfer in four Rosaceae species. Mobile DNA, 2017, 8, 14.	1.3	2
877	Wild Apple Growth and Climate Change in Southeast Kazakhstan. Forests, 2017, 8, 406.	0.9	15
878	Identification of QTLs for Flesh Mealiness in Apple (<i>Malus</i> Ã—) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 382 Td (	0.3	23
879	New biotechnological tools to accelerate scab-resistance trait transfer to apple. Genetics and Molecular Biology, 2017, 40, 305-311.	0.6	12
880	RNA-seq-based genome annotation and identification of long-noncoding RNAs in the grapevine cultivar â€˜Rieslingâ€™. BMC Genomics, 2017, 18, 937.	1.2	15
881	In Silico Approach for Characterization and Comparison of Repeats in the Genomes of Oil and Date Palms. Bioinformatics and Biology Insights, 2017, 11, 117793221770238.	1.0	3
882	Overview of Next-generation Sequencing Platforms Used in Published Draft Plant Genomes in Light of Genotypization of Immortelle Plant (Helichrysium Arenarium). Medicinski Arhiv = Medical Archives = Archives De MÃ©decine, 2017, 71, 288.	0.4	28
883	Evolution of genes associated with gynoecium patterning and fruit development in Solanaceae. Annals of Botany, 2018, 121, 1211-1230.	1.4	37
884	The Use of RNA Sequencing and Correlation Network Analysis to Study Potential Regulators of Crabapple Leaf Color Transformation. Plant and Cell Physiology, 2018, 59, 1027-1042.	1.5	28
885	First insight into genetic diversity and population structure of the Caucasian wild apple (Malus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 10 Genetic Resources and Crop Evolution, 2018, 65, 1255-1268.	0.8	13
887	An integrated approach for increasing breeding efficiency in apple and peach in Europe. Horticulture Research, 2018, 5, 11.	2.9	98

#	ARTICLE	IF	CITATIONS
888	Identification and expression of the CEP gene family in apple (MalusÃ—domestica). Journal of Integrative Agriculture, 2018, 17, 348-358.	1.7	9
889	Systematic analysis and comparison of the PHD-Finger gene family in Chinese pear (Pyrus) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 519-531.	1.4	21
890	Memory and Learning in Plants. Signaling and Communication in Plants, 2018, , .	0.5	25
891	Structure and expression analysis of the sucrose synthase gene family in apple. Journal of Integrative Agriculture, 2018, 17, 847-856.	1.7	24
892	An annotated transcriptome of highly inbred Thuja plicata (Cupressaceae) and its utility for gene discovery of terpenoid biosynthesis and conifer defense. Tree Genetics and Genomes, 2018, 14, 1.	0.6	17
893	Identifying evolutionarily significant units for conservation of the endangered <i>Malus sieversii</i> using genomeâ€wide RADseq data. Nordic Journal of Botany, 2018, 36, e01733.	0.2	10
894	Genetic diversity of dihydrochalcone content in Malus germplasm. Genetic Resources and Crop Evolution, 2018, 65, 1485-1502.	0.8	15
895	Chromosome-scale scaffolding of the black raspberry (Rubus occidentalis L.) genome based on chromatin interaction data. Horticulture Research, 2018, 5, 8.	2.9	50
896	Genomic Selection. Population Genomics, 2018, , 427-480.	0.2	4
897	QTLs for susceptibility to Stemphylium vesicarium in pear. Molecular Breeding, 2018, 38, 1.	1.0	7
898	Morphological and biochemical diversity among the Malus species including indigenous Himalayan wild apples. Scientia Horticulturae, 2018, 233, 204-219.	1.7	19
899	Natural Variation Underlies Differences in ETHYLENE RESPONSE FACTOR17 Activity in Fruit Peel Degreening. Plant Physiology, 2018, 176, 2292-2304.	2.3	47
900	Genetics of resistance in apple against Venturia inaequalis (Wint.) Cke. Tree Genetics and Genomes, 2018, 14, 1.	0.6	43
901	Inferences on specificity recognition at the MalusÃ—domestica gametophytic self-incompatibility system. Scientific Reports, 2018, 8, 1717.	1.6	30
902	Evolutionary diversification of galactinol synthases in Rosaceae: adaptive roles of galactinol and raffinose during apple bud dormancy. Journal of Experimental Botany, 2018, 69, 1247-1259.	2.4	33
903	Expression of MdCCD7 in the scion determines the extent of sylleptic branching and the primary shoot growth rate of apple trees. Journal of Experimental Botany, 2018, 69, 2379-2390.	2.4	18
904	Identification of candidate genes at the Dp-fl locus conferring resistance against the rosy apple aphid Dysaphis plantaginea. Tree Genetics and Genomes, 2018, 14, 1.	0.6	3
905	Exploring DNA variant segregation types in pooled genome sequencing enables effective mapping of weeping trait in Malus. Journal of Experimental Botany, 2018, 69, 1499-1516.	2.4	33

#	Article	IF	Citations
906	Discovery of Negative-Sense RNA Viruses in Trees Infected with Apple Rubbery Wood Disease by Next-Generation Sequencing. Plant Disease, 2018, 102, 1254-1263.	0.7	59
907	Genome-wide searches and molecular analyses highlight the unique evolutionary path of flavone synthase I (FNSI) in Apiaceae. Genome, 2018, 61, 103-109.	0.9	7
908	Functional Divergence between Subgenomes and Gene Pairs after Whole Genome Duplications. Molecular Plant, 2018, 11, 388-397.	3.9	73
909	Widespread Whole Genome Duplications Contribute to Genome Complexity and Species Diversity in Angiosperms. Molecular Plant, 2018, 11, 414-428.	3.9	251
910	An atypical R2R3 <scp>MYB</scp> transcription factor increases cold hardiness by <scp>CBF</scp>â€dependent and <scp>CBF</scp>â€independent pathways in apple. New Phytologist, 2018, 218, 201-218.	3.5	217
911	CYSTM, a Novel Non-Secreted Cysteine-Rich Peptide Family, Involved in Environmental Stresses in Arabidopsis thaliana. Plant and Cell Physiology, 2018, 59, 423-438.	1.5	40
912	Epistatic fire blight resistance QTL alleles in the apple cultivar â€˜Enterpriseâ€™ and selection X-6398 discovered and characterized through pedigree-informed analysis. Molecular Breeding, 2018, 38, 1.	1.0	51
913	A manually annotated Actinidia chinensis var. chinensis (kiwifruit) genome highlights the challenges associated with draft genomes and gene prediction in plants. BMC Genomics, 2018, 19, 257.	1.2	167
914	The unique evolutionary pattern of the Hydroxyproline-rich glycoproteins superfamily in Chinese white pear (Pyrus bretschneideri). BMC Plant Biology, 2018, 18, 36.	1.6	6
915	Genome-wide expression analysis suggests a role for jasmonates in the resistance to blue mold in apple. Plant Growth Regulation, 2018, 85, 375-387.	1.8	8
916	Two QTL characterized for soft scald and soggy breakdown in apple (Malus Ã— domestica) through pedigree-based analysis of a large population of interconnected families. Tree Genetics and Genomes, 2018, 14, 1.	0.6	26
917	Genome-wide survey and analysis of the TIFY gene family and its potential role in anthocyanin synthesis in Chinese sand pear (Pyrus pyrifolia). Tree Genetics and Genomes, 2018, 14, 1.	0.6	16
918	Post-polyploid diploidization and diversification through dysploid changes. Current Opinion in Plant Biology, 2018, 42, 55-65.	3.5	171
919	The effect of polyploidization on tree hydraulic functioning. American Journal of Botany, 2018, 105, 161-171.	0.8	28
920	Genome-wide Identification and Expression Analysis of Half-size ABCG Genes in Malusâ€¯Ã—â€¯domestica. Horticultural Plant Journal, 2018, 4, 45-54.	2.3	4
921	Food safety evaluation for R-proteins introduced by biotechnology: A case study of VNT1 in late blight protected potatoes. Regulatory Toxicology and Pharmacology, 2018, 95, 66-74.	1.3	12
922	Assessment of genetic structure among different pear species (<i>Pyrus</i>spp.) using apple-derived SSR and evidence of duplications in the pear genome. Biotechnology and Biotechnological Equipment, 2018, 32, 591-601.	0.5	7
923	Genetic Diversity of Apple Cultivars Growing in Kazakhstan. Russian Journal of Genetics, 2018, 54, 176-187.	0.2	9

#	ARTICLE	IF	CITATIONS
924	Functional characterisation of <i>MdMYB44</i> as a negative regulator in the response to cold and salt stress in apple calli. Journal of Horticultural Science and Biotechnology, 2018, 93, 347-355.	0.9	12
925	Genome structure of Rosa multiflora, a wild ancestor of cultivated roses. DNA Research, 2018, 25, 113-121.	1.5	70
926	Genome-wide identification and expression analysis of the B-box gene family in the Apple (Malus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 6	1.0	70
927	Genome-wide analysis of antioxidant enzyme gene families involved in drought and low-temperature responses in Apple (<i>Malus domestica</i>). Journal of Horticultural Science and Biotechnology, 2018, 93, 337-346.	0.9	8
928	Evolution analysis of Dof transcription factor family and their expression in response to multiple abiotic stresses in Malus domestica. Gene, 2018, 639, 137-148.	1.0	31
929	Convergent adaptive evolution in marginal environments: unloading transposable elements as a common strategy among mangrove genomes. New Phytologist, 2018, 217, 428-438.	3.5	69
930	<i>In silico</i> and expression analysis of the tonoplast monosaccharide transporter (TMT) gene family in <i>Pyrus bretschneideri</i>. Journal of Horticultural Science and Biotechnology, 2018, 93, 366-376.	0.9	8
931	Browning in apples: Exploring the biochemical basis of an easilyâ€observable phenotype. Biochemistry and Molecular Biology Education, 2018, 46, 76-82.	0.5	20
932	Characterisation of the whole-genome wide hexokinase gene family unravels the functional divergence in pear (Pyrus bretschneideri Rehd.). Journal of Horticultural Science and Biotechnology, 2018, 93, 244-254.	0.9	6
933	Comparative epigenomics reveals evolution of duplicated genes in potato and tomato. Plant Journal, 2018, 93, 460-471.	2.8	33
934	Genome-wide analysis of carotenoid cleavage oxygenase genes and their responses to various phytohormones and abiotic stresses in apple (Malus domestica). Plant Physiology and Biochemistry, 2018, 123, 81-93.	2.8	40
935	Biological effects of ion beam irradiation on perennial gentian and apple. Plant Biotechnology, 2018, 35, 249-257.	0.5	9
936	Acibenzolar-S-Methyl Reprograms Apple Transcriptome Toward Resistance to Rosy Apple Aphid. Frontiers in Plant Science, 2018, 9, 1795.	1.7	17
937	Empirical Research on Domestic Violence in Contemporary China: Continuity and Advances. International Journal of Offender Therapy and Comparative Criminology, 2018, 62, 4879-4887.	0.8	18
938	Marker development and applications in the University of Minnesota apple and grape breeding programs. Acta Horticulturae, 2018, , 93-98.	0.1	1
942	Chromosome level high-density integrated genetic maps improve the Pyrus bretschneideri â€˜DangshanSuliâ€™ v1.0 genome. BMC Genomics, 2018, 19, 833.	1.2	34
943	Leveraging Transcriptome Data for Enhanced Gene Expression Analysis in Apple. Journal of the American Society for Horticultural Science, 2018, 143, 333-346.	0.5	4
944	Comprehensive genomic analysis of the TYROSINE AMINOTRANSFERASE (TAT) genes in apple (Malus) Tj ETQq1 1 0.784314 rgBT /Overl stresses in plants. Plant Physiology and Biochemistry, 2018, 133, 81-91.	2.8	16

#	ARTICLE	IF	CITATIONS
945	Large scale study of anti-sense regulation by differential network analysis. BMC Systems Biology, 2018, 12, 95.	3.0	1
946	Sex and Rosaceae apomicts. Taxon, 2018, 67, 1093-1107.	0.4	12
947	Evaluation and Recommendations for Routine Genotyping Using Skim Whole Genome Re-sequencing in Canola. Frontiers in Plant Science, 2018, 9, 1809.	1.7	24
948	Genome-Wide Identification and Expression Analysis of the CrRLK1L Gene Family in Apple (Malus) Tj ETQq1 1 0.784314 rgBT /Overlock	1.0	18
950	The Draft Genome of theÂMD-2 Pineapple. Plant Genetics and Genomics: Crops and Models, 2018, , 109-129.	0.3	0
951	Genome-wide analyses of genes encoding FK506-binding proteins reveal their involvement in abiotic stress responses in apple. BMC Genomics, 2018, 19, 707.	1.2	16
952	Genome-Wide Identification, Molecular Evolution, and Expression Divergence of Aluminum-Activated Malate Transporters in Apples. International Journal of Molecular Sciences, 2018, 19, 2807.	1.8	22
953	Fast construction of a reference genome: challenges and opportunities using â€˜Royal Galaâ€™ apple as a case study. Acta Horticulturae, 2018, , 35-40.	0.1	0
954	Expression analysis of apple DORMANCY-ASSOCIATED MADS-box genes in buds during dormancy release. Acta Horticulturae, 2018, , 39-46.	0.1	1
955	Genome-wide identification and characterization of apple long-chain Acyl-CoA synthetases and expression analysis under different stresses. Plant Physiology and Biochemistry, 2018, 132, 320-332.	2.8	41
956	Development and Characterization of Novel Genic-SSR Markers in Apple-Juniper Rust Pathogen Gymnosporangium yamadae (Pucciniales: Pucciniaceae) Using Next-Generation Sequencing. International Journal of Molecular Sciences, 2018, 19, 1178.	1.8	10
957	Transcriptome Profiling Reveals Transcriptional Regulation by DNA Methyltransferase Inhibitor 5-Aza-2â€²-Deoxycytidine Enhancing Red Pigmentation in Bagged â€œGranny Smithâ€•Apples (Malus domestica). International Journal of Molecular Sciences, 2018, 19, 3133.	1.8	19
958	Genome-wide Identification, Classification, Molecular Evolution and Expression Analysis of Malate Dehydrogenases in Apple. International Journal of Molecular Sciences, 2018, 19, 3312.	1.8	15
959	CRISPRâ€“Cas9-mediated genome editing in apple and grapevine. Nature Protocols, 2018, 13, 2844-2863.	5.5	142
960	Genetic analysis of a major international collection of cultivated apple varieties reveals previously unknown historic heteroploid and inbred relationships. PLoS ONE, 2018, 13, e0202405.	1.1	29
961	Determination of Predominant Organic Acid Components in Malus Species: Correlation with Apple Domestication. Metabolites, 2018, 8, 74.	1.3	46
962	Malus sieversii: the origin, flavonoid synthesis mechanism, and breeding of red-skinned and red-fleshed apples. Horticulture Research, 2018, 5, 70.	2.9	63
963	Genome-wide identification, characterization, and evolutionary analysis of NBS-encoding resistance genes in barley. 3 Biotech, 2018, 8, 453.	1.1	9

#	Article	IF	Citations
964	WaspBase: a genomic resource for the interactions among parasitic wasps, insect hosts and plants. Database: the Journal of Biological Databases and Curation, 2018, 2018, 1-9.	1.4	3
965	Draft genome sequence of wild Prunus yedoensis reveals massive inter-specific hybridization between sympatric flowering cherries. Genome Biology, 2018, 19, 127.	3.8	89
966	Towards map-based cloning of FB_Mfu10: identification of a receptor-like kinase candidate gene underlying the Malus fusca fire blight resistance locus on linkage group 10. Molecular Breeding, 2018, 38, 106.	1.0	28
967	Genetic Characterization of the Apple Germplasm Collection in Central Italy: The Value of Local Varieties. Frontiers in Plant Science, 2018, 9, 1460.	1.7	36
968	Identification and Characterization of miRNAs in Self-Rooted and Grafted Malus Reveals Critical Networks Associated with Flowering. International Journal of Molecular Sciences, 2018, 19, 2384.	1.8	13
969	Identification of QTLs Associated with Conversion of Sucrose to Hexose in Mature Fruit of Japanese Pear. Plant Molecular Biology Reporter, 2018, 36, 643-652.	1.0	12
970	Structural and functional apple genomics and its application in breeding. Czech Journal of Genetics and Plant Breeding, 2018, 54, 147-153.	0.4	0
971	Identification of transposons near predicted lncRNA and mRNA pools of Prunus mume using an integrative transposable element database constructed from Rosaceae plant genomes. Molecular Genetics and Genomics, 2018, 293, 1301-1316.	1.0	3
972	Anthocyanin Biosynthesis in Apple Fruit. Horticulture Journal, 2018, 87, 305-314.	0.3	72
973	Identification of a leucine-rich repeat receptor-like serine/threonine-protein kinase as a candidate gene for Rvi12 (Vb)-based apple scab resistance. Molecular Breeding, 2018, 38, 1.	1.0	8
974	RADseq approaches and applications for forest tree genetics. Tree Genetics and Genomes, 2018, 14, 1.	0.6	58
975	Characterization of 25 full-length S-RNase alleles, including flanking regions, from a pool of resequenced apple cultivars. Plant Molecular Biology, 2018, 97, 279-296.	2.0	17
976	Ectopic expression of the <i><scp>PISTILLATA</scp></i> homologous <i>Md<scp>PI</scp></i> inhibits fruit tissue growth and changes fruit shape in apple. Plant Direct, 2018, 2, e00051.	0.8	24
977	The isolation of the IGT family genes in Malusâ€‰Ã—â€‰domestica and their expressions in four idiotype apple cultivars. Tree Genetics and Genomes, 2018, 14, 1.	0.6	12
978	Genome-wide identification and expression analysis of GRF genes regulating apple tree architecture. Tree Genetics and Genomes, 2018, 14, 1.	0.6	18
979	Genetic engineering of trees: progress and new horizons. In Vitro Cellular and Developmental Biology - Plant, 2018, 54, 341-376.	0.9	47
980	Elucidating the contribution of wild related species on autochthonous pear germplasm: A case study from Mount Etna. PLoS ONE, 2018, 13, e0198512.	1.1	15
981	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. Plant Science, 2018, 274, 451-465.	1.7	26

#	ARTICLE	IF	CITATIONS
982	Phylogeny of Maleae (Rosaceae) Based on Multiple Chloroplast Regions: Implications to Genera Circumscription. BioMed Research International, 2018, 2018, 1-10.	0.9	23
983	Horizontal transfers of LTR retrotransposons in seven species of Rosales. Genome, 2018, 61, 587-594.	0.9	7
984	A study of gene expression changes at the Bp-2 locus associated with bitter pit symptom expression in apple (Malus pumila). Molecular Breeding, 2018, 38, 1.	1.0	6
985	Mapping QTLs for water-use efficiency reveals the potential candidate genes involved in regulating the trait in apple under drought stress. BMC Plant Biology, 2018, 18, 136.	1.6	42
986	Morphometrics Reveals Complex and Heritable Apple Leaf Shapes. Frontiers in Plant Science, 2017, 8, 2185.	1.7	46
987	An Updated Functional Annotation of Protein-Coding Genes in the Cucumber Genome. Frontiers in Plant Science, 2018, 9, 325.	1.7	2
988	A DREB-Like Transcription Factor From Maize (Zea mays), ZmDREB4.1, Plays a Negative Role in Plant Growth and Development. Frontiers in Plant Science, 2018, 9, 395.	1.7	57
989	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. Frontiers in Plant Science, 2018, 9, 591.	1.7	18
990	Comparative Genomics, Whole-Genome Re-sequencing and Expression Profile Analysis of Nucleobase:Cation Symporter 2 (NCS2) Genes in Maize. Frontiers in Plant Science, 2018, 9, 856.	1.7	6
991	Endophytic Bacillus and Pseudomonas spp. Modulate Apple Shoot Growth, Cellular Redox Balance, and Protein Expression Under in Vitro Conditions. Frontiers in Plant Science, 2018, 9, 889.	1.7	49
992	Quince (Cydonia oblonga Mill.) Breeding. , 2018, , 277-304.		2
993	Fresh Fruit. Practical Issues in Geriatrics, 2018, , 231-261.	0.3	0
994	Characterizing the expression of translation elongation factor gene EF1Î± in pear (Pyrus) fruit: evaluation of EF1Î± as a housekeeping gene. Tree Genetics and Genomes, 2018, 14, 1.	0.6	2
995	Diversification and independent domestication of Asian and European pears. Genome Biology, 2018, 19, 77.	3.8	149
996	Selection and evaluation of reference genes for qRT-PCR analysis in Euscaphis konishii Hayata based on transcriptome data. Plant Methods, 2018, 14, 42.	1.9	42
997	Genome-Wide Identification and Characterization of CIPK Family and Analysis Responses to Various Stresses in Apple (Malus domestica). International Journal of Molecular Sciences, 2018, 19, 2131.	1.8	30
998	Woody Ornamentals of the Temperate Zone. Handbook of Plant Breeding, 2018, , 803-887.	0.1	9
999	Cherry Breeding: Sweet Cherry (Prunus avium L.) and Sour Cherry (Prunus cerasus L.). , 2018, , 31-88.		2

#	ARTICLE	IF	CITATIONS
1000	Genome-Wide Analysis Characterization and Evolution of SBP Genes in Fragaria vesca, Pyrus bretschneideri, Prunus persica and Prunus mume. Frontiers in Genetics, 2018, 9, 64.	1.1	33
1001	RNA-sequencing Analysis Identifies Genes Associated with Chilling-mediated Endodormancy Release in Apple. Journal of the American Society for Horticultural Science, 2018, 143, 194-206.	0.5	21
1002	Genome Sequencing and Assembly by Long Reads in Plants. Genes, 2018, 9, 6.	1.0	97
1003	The proanthocyanidinâ€specific transcription factor Md<scp>MYBPA</scp>1 initiates anthocyanin synthesis under lowâ€temperature conditions in redâ€fleshed apples. Plant Journal, 2018, 96, 39-55.	2.8	127
1004	Regulation and Evolution of NLR Genes: A Close Interconnection for Plant Immunity. International Journal of Molecular Sciences, 2018, 19, 1662.	1.8	68
1005	Comparative Transcriptome Analysis of Genes Involved in Anthocyanin Biosynthesis in Red and Green Walnut (Juglans regia L.). Molecules, 2018, 23, 25.	1.7	36
1006	The Sucrose Synthase Gene Family in Chinese Pear (Pyrus bretschneideri Rehd.): Structure, Expression, and Evolution. Molecules, 2018, 23, 1144.	1.7	47
1007	Genome Identification of B-BOX Gene Family Members in Seven Rosacea Species and Their Expression Analysis in Response to Flower Induction in Malus domestica. Molecules, 2018, 23, 1763.	1.7	32
1008	Apple (Malus spp.) Breeding: Present and Future. , 2018, , 3-29.		16
1009	Antioxidant Phytochemicals in Fresh Produce: Exploitation of Genotype Variation and Advancements in Analytical Protocols. Frontiers in Chemistry, 2018, 5, 95.	1.8	12
1010	Systematic Chemical Analysis Approach Reveals Superior Antioxidant Capacity via the Synergistic Effect of Flavonoid Compounds in Red Vegetative Tissues. Frontiers in Chemistry, 2018, 6, 9.	1.8	31
1011	Genome-wide identification, characterization and expression analysis of long non-coding RNAs in different tissues of apple. Gene, 2018, 666, 44-57.	1.0	28
1012	Memristors and Electrical Memory in Plants. Signaling and Communication in Plants, 2018, , 139-161.	0.5	4
1013	Developing gene-tagged molecular markers for evaluation of genetic association of apple SWEET genes with fruit sugar accumulation. Horticulture Research, 2018, 5, 14.	2.9	73
1014	Sequencing Plant Genomes. Progress in Botany Fortschritte Der Botanik, 2018, , 109-193.	0.1	4
1015	Structural and functional analyses of genes encoding VQ proteins in apple. Plant Science, 2018, 272, 208-219.	1.7	46
1016	Comparative genomics of the nonlegume <i>Parasponia</i> reveals insights into evolution of nitrogen-fixing rhizobium symbioses. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E4700-E4709.	3.3	253
1017	Diversity and evolution of the repetitive genomic content in Cannabis sativa. BMC Genomics, 2018, 19, 156.	1.2	31

#	ARTICLE	IF	CITATIONS
1018	Genome-Wide Analysis and Cloning of the Apple Stress-Associated Protein Gene Family Reveals MdSAP15, Which Confers Tolerance to Drought and Osmotic Stresses in Transgenic Arabidopsis. International Journal of Molecular Sciences, 2018, 19, 2478.	1.8	40
1019	Genetic Engineering of Temperate Fruit Crops. , 2018, , 89-119.		1
1020	Quantitative trait loci (QTL) mapping of blush skin and flowering time in a European pear (Pyrus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 6	0.6	6
1021	A Genomeâ€Wide Association Study of Apple Quality and Scab Resistance. Plant Genome, 2018, 11, 170075.	1.6	61
1022	Ethylene receptors and related proteins in climacteric and non-climacteric fruits. Plant Science, 2018, 276, 63-72.	1.7	79
1023	Identification and characterization of histone modification gene family reveal their critical responses to flower induction in apple. BMC Plant Biology, 2018, 18, 173.	1.6	21
1024	Seed morphometry is suitable for apple-germplasm diversity-analyses. Computers and Electronics in Agriculture, 2018, 151, 118-125.	3.7	16
1025	Sequence and Analysis of the Black Raspberry (Rubus occidentalis) Genome. Compendium of Plant Genomes, 2018, , 185-197.	0.3	3
1026	Expansion and evolutionary patterns of GDSL-type esterases/lipases in Rosaceae genomes. Functional and Integrative Genomics, 2018, 18, 673-684.	1.4	37
1027	Identification of MdDof genes in apple and analysis of their response to biotic or abiotic stress. Functional Plant Biology, 2018, 45, 528.	1.1	15
1028	The Genomes of Rosaceous Berries and Their Wild Relatives. Compendium of Plant Genomes, 2018, , .	0.3	17
1029	Genomic Resources for the Woodland Strawberry (Fragaria vesca). Compendium of Plant Genomes, 2018, , 25-33.	0.3	3
1030	Transcriptomic Analysis of Red-Fleshed Apples Reveals the Novel Role of MdWRKY11 in Flavonoid and Anthocyanin Biosynthesis. Journal of Agricultural and Food Chemistry, 2018, 66, 7076-7086.	2.4	109
1031	Genetic diversity and core collection of Malusâ€¯Ã—â€¯domestica in northwestern Spain, Portugal and the Canary Islands by SSRs. Scientia Horticulturae, 2018, 240, 49-56.	1.7	20
1032	The use of a fertile doubled haploid apple line for QTL analysis of fruit traits. Breeding Science, 2019, 69, 410-419.	0.9	7
1033	Place, food practices, and scientific knowledge. Cultural Studies of Science Education, 2019, 14, 1037-1043.	0.9	0
1034	A novel miRNA negatively regulates resistance to Glomerella leaf spot by suppressing expression of an NBS gene in apple. Horticulture Research, 2019, 6, 93.	2.9	30
1035	Differential Chloroplast Proteomics of Temperature Adaptation in Apple (Malus x domestica Borkh.) Microshoots. Proteomics, 2019, 19, e1800142.	1.3	2

#	Article	IF	Citations
1036	Comparative analysis of the complete chloroplast genome among Prunus mume, P. armeniaca, and P. salicina. Horticulture Research, 2019, 6, 89.	2.9	91
1037	Cinnamateâ€CoA ligase is involved in biosynthesis of benzoateâ€derived biphenyl phytoalexin in MalusÂ Ã—Â domestica â€˜Golden Deliciousâ€™ cell cultures. Plant Journal, 2019, 100, 1176-1192.	2.8	13
1038	The first transcriptome sequencing and analysis of the endangered plant species Picea neoveitchii Mast. and potential EST-SSR markers development. Biotechnology and Biotechnological Equipment, 2019, 33, 967-973.	0.5	5
1039	Loquat Is a New Natural Host of Apple Stem Grooving Virus and Apple Chlorotic Leaf Spot Virus in China. Plant Disease, 2019, 103, 3290-3290.	0.7	16
1040	Tracing the origin and evolution history of methylation-related genes in plants. BMC Plant Biology, 2019, 19, 307.	1.6	59
1041	The infiltration efficiency of Agrobacterium-mediated transient transformation in four apple cultivars. Scientia Horticulturae, 2019, 256, 108597.	1.7	15
1042	A Multifaceted Overview of Apple Tree Domestication. Trends in Plant Science, 2019, 24, 770-782.	4.3	46
1043	High-quality, genome-wide SNP genotypic data for pedigreed germplasm of the diploid outbreeding species apple, peach, and sweet cherry through a common workflow. PLoS ONE, 2019, 14, e0210928.	1.1	67
1044	Validation of MADS-box genes from apple fruit pedicels during early fruit abscission by transcriptome analysis and real-time PCR. Genes and Genomics, 2019, 41, 1241-1251.	0.5	4
1045	Reconstruction of Ancestral Chromosomes of the Family Rosaceae. Compendium of Plant Genomes, 2019, , 149-161.	0.3	0
1046	Molecular Characterization, DNA Finger Printing, and Genomics in Horticultural Crops. , 2019, , 595-618.		1
1047	Predicting Specificities Under the Non-self Gametophytic Self-Incompatibility Recognition Model. Frontiers in Plant Science, 2019, 10, 879.	1.7	6
1048	Pseudomolecule-level assembly of the Chinese oil tree yellowhorn (Xanthoceras sorbifolium) genome. GigaScience, 2019, 8, .	3.3	47
1049	The Pear Genome. Compendium of Plant Genomes, 2019, , .	0.3	5
1050	Common and specific responses to iron and phosphorus deficiencies in roots of apple tree (Malus Ã—) Tj ETQq0 0 0 rgBT /Overlock 10 T	2.6	15
1051	Repetitive Sequences in Pear. Compendium of Plant Genomes, 2019, , 145-152.	0.3	0
1052	Whole-Genome Duplications in Pear and Apple. Compendium of Plant Genomes, 2019, , 279-299.	0.3	11
1053	The Genome of Pear. Compendium of Plant Genomes, 2019, , 133-143.	0.3	1

#	Article	IF	Citations
1054	Mo1363 â€“ Gaba Inhibited Nerve-Activity-Mediated Insulin Secretion: A Potential Negative Feedback Messenger from Pancreatic Islets to Pancreatic Ganglia. Gastroenterology, 2019, 156, S-752.	0.6	0
1055	Genetic and genomic resources for Rubus breeding: a roadmap for the future. Horticulture Research, 2019, 6, 116.	2.9	47
1056	Genome sequences of horticultural plants: past, present, and future. Horticulture Research, 2019, 6, 112.	2.9	108
1057	SSR analysis reveals molecular variation and genetic diversity in Malus sieversii with different stress resistance levels in China. Horticulture Environment and Biotechnology, 2019, 60, 935-943.	0.7	3
1058	Electronic structures, magnetic properties and lattice strain effects of quaternary Heusler alloys RuMnCrZ (Zâ€‰â€‰=â€‰â€‰P, As, Sb). Journal Physics D: Applied Physics, 2019, 52, 505003.	1.3	3
1059	A new Al₁₄Co₂₈Cr₂₈Ni₃₀ hypoeutectic high entropy alloy with excellent tensile property. Materials Research Express, 2019, 6, 116575.	0.8	1
1060	Genome-wide identification and transcript analysis of TCP transcription factors in grapevine. BMC Genomics, 2019, 20, 786.	1.2	47
1061	AppleMDO: A Multi-Dimensional Omics Database for Apple Co-Expression Networks and Chromatin States. Frontiers in Plant Science, 2019, 10, 1333.	1.7	44
1062	Auxin regulates adventitious root formation in tomato cuttings. BMC Plant Biology, 2019, 19, 435.	1.6	69
1063	Genome-Wide Analysis of NAC Gene Family in Betula pendula. Forests, 2019, 10, 741.	0.9	44
1064	gFACs: Gene Filtering, Analysis, and Conversion to Unify Genome Annotations Across Alignment and Gene Prediction Frameworks. Genomics, Proteomics and Bioinformatics, 2019, 17, 305-310.	3.0	37
1065	Genetic control of Î±â€•farnesene production in apple fruit and its role in fungal pathogenesis. Plant Journal, 2019, 100, 1148-1162.	2.8	26
1066	Identification and characterization of the MADS-box genes highly expressed in the laticifer cells of Hevea brasiliensis. Scientific Reports, 2019, 9, 12673.	1.6	2
1067	Nanoscale UV Absorber Boosting Coloration of Apple Skin. ACS Sustainable Chemistry and Engineering, 2019, 7, 16295-16300.	3.2	1
1068	Differential gene expression in non-transgenic and transgenic â€œM.26â€•apple overexpressing a peach CBF gene during the transition from eco-dormancy to bud break. Horticulture Research, 2019, 6, 86.	2.9	18
1069	Hybrid de novo genome assembly of Chinese chestnut (Castanea mollissima). GigaScience, 2019, 8, .	3.3	55
1070	Characterization and Expression Analysis of ERF Genes in Fragaria vesca Suggest Different Divergences of Tandem ERF Duplicates. Frontiers in Genetics, 2019, 10, 805.	1.1	8
1071	Effect of exogenous ATP treatment on sucrose metabolism and quality of Nanguo pear fruit. Scientia Horticulturae, 2019, 249, 71-76.	1.7	26

#	ARTICLE	IF	CITATIONS
1072	Identification of new regulators through transcriptome analysis that regulate anthocyanin biosynthesis in apple leaves at low temperatures. PLoS ONE, 2019, 14, e0210672.	1.1	34
1073	MdCOL4 Interaction Mediates Crosstalk Between UV-B and High Temperature to Control Fruit Coloration in Apple. Plant and Cell Physiology, 2019, 60, 1055-1066.	1.5	50
1074	Identification of zygotic and nucellar seedlings inCitrus limon: the search for molecular markers. Acta Horticulturae, 2019, , 35-42.	0.1	0
1075	I Want to (Bud) Break Free: The Potential Role of DAM and SVP-Like Genes in Regulating Dormancy Cycle in Temperate Fruit Trees. Frontiers in Plant Science, 2018, 9, 1990.	1.7	129
1076	De Novo Sequencing and Hybrid Assembly of the Biofuel Crop Jatropha curcas L.: Identification of Quantitative Trait Loci for Geminivirus Resistance. Genes, 2019, 10, 69.	1.0	20
1077	Efficient Targeted Mutagenesis in Apple and First Time Edition of Pear Using the CRISPR-Cas9 System. Frontiers in Plant Science, 2019, 10, 40.	1.7	163
1078	Genetic diversity and population structure analysis of wild Malus genotypes including the crabapples (M. baccata (L.) Borkh. & M. sikkimensis (Wenzig) Koehne ex C. Schneider) collected from the Indian Himalayan region using microsatellite markers. Genetic Resources and Crop Evolution, 2019, 66, 1311-1326.	0.8	11
1079	Origins of the Apple: The Role of Megafaunal Mutualism in the Domestication of Malus and Rosaceous Trees. Frontiers in Plant Science, 2019, 10, 617.	1.7	65
1080	Genome-Wide Analysis of the MADS-Box Transcription Factor Family in Solanum lycopersicum. International Journal of Molecular Sciences, 2019, 20, 2961.	1.8	69
1081	Genome-wide analysis of zinc- and iron-regulated transporter-like protein family members in apple and functional validation of ZIP10. BioMetals, 2019, 32, 657-669.	1.8	8
1082	Contribution of methylation regulation of MpDREB2A promoter to drought resistance of Mauls prunifolia. Plant and Soil, 2019, 441, 15-32.	1.8	16
1083	Integrated metatranscriptome and transcriptome reveals the microbial community composition and physiological function of xylem sap on grapevine during bleeding period. Genes and Genomics, 2019, 41, 1095-1111.	0.5	9
1084	Genomeâ€Wide Association Studies in Apple Reveal Loci for Aroma Volatiles, Sugar Composition, and Harvest Date. Plant Genome, 2019, 12, 180104.	1.6	70
1085	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. G3: Genes, Genomes, Genetics, 2019, 9, 2051-2060.	0.8	47
1086	Genome-wide identification, expression profiling, and protein-protein interaction properties of ovate family proteins in apple. Tree Genetics and Genomes, 2019, 15, 1.	0.6	16
1087	Construction of Genetic Linkage Maps in Multiparental Populations. Genetics, 2019, 212, 1031-1044.	1.2	11
1088	Genetic characterization of flesh browning trait in apple using the non-browning cultivar â€˜Aori 27â€™. Tree Genetics and Genomes, 2019, 15, 1.	0.6	10
1089	Mutation of a bHLH transcription factor allowed almond domestication. Science, 2019, 364, 1095-1098.	6.0	116

#	ARTICLE	IF	CITATIONS
1090	Changes in DNA methylation pattern of apple long-term in vitro shoot culture and acclimatized plants. Journal of Plant Physiology, 2019, 239, 18-27.	1.6	6
1091	Genotyping apple (Malus x domestica Borkh.) heirloom germplasm collected and maintained by the Regional Administration of Friuli Venezia Giulia (Italy). Scientia Horticulturae, 2019, 252, 229-237.	1.7	15
1092	Transcriptome Analysis of Apple Leaves in Response to Powdery Mildew (Podosphaera leucotricha) Infection. International Journal of Molecular Sciences, 2019, 20, 2326.	1.8	41
1093	Uneven selection pressure accelerating divergence of Populus and Salix. Horticulture Research, 2019, 6, 37.	2.9	15
1094	Advances in genomic, transcriptomic, proteomic, and metabolomic approaches to study biotic stress in fruit crops. Critical Reviews in Biotechnology, 2019, 39, 680-692.	5.1	32
1095	Transcriptome profiling of anthocyanin biosynthesis in the peel of â€˜Granny Smithâ€™ apples (Malus) Tj ETQq1 1 0.784314 rgBT /Over	1.2	28
1096	Triterpenoid-biosynthetic UDP-glycosyltransferases from plants. Biotechnology Advances, 2019, 37, 107394.	6.0	114
1097	Genome-Wide Identification of the Aux/IAA Family Genes (MdIAA) and Functional Analysis of MdIAA18 for Apple Tree Ideotype. Biochemical Genetics, 2019, 57, 709-733.	0.8	6
1098	Genome-wide identification and characterization of UGT family in pigeonpea (Cajanus cajan) and expression analysis in abiotic stress. Trees - Structure and Function, 2019, 33, 987-1002.	0.9	16
1099	Identification of candidate genes responsible for the susceptibility of apple (Malus Ã— domestica) Tj ETQq1 1 0.784314 rgBT /Overlock	1.6	14
1100	Potential use of seed morpho-colourimetric analysis for Sardinian apple cultivar characterisation. Computers and Electronics in Agriculture, 2019, 162, 373-379.	3.7	22
1101	Data mining for apple <i>S</i>-RNase alleles in resequencing datasets. Acta Horticulturae, 2019, , 135-152.	0.1	0
1102	Genome-wide identification, expression and functional analysis of the phosphofructokinase gene family in Chinese white pear (Pyrus bretschneideri). Gene, 2019, 702, 133-142.	1.0	15
1103	Identification of leucoanthocyanidin reductase and anthocyanidin reductase genes involved in proanthocyanidin biosynthesis in Malus crabapple plants. Plant Physiology and Biochemistry, 2019, 139, 141-151.	2.8	39
1104	Phaseolus vulgaris genome possesses CAMTA genes, and phavuCAMTA1 contributes to the drought tolerance. Journal of Genetics, 2019, 98, 1.	0.4	7
1105	Hairy root culture as a valuable tool for allelopathic studies in apple. Tree Physiology, 2019, 39, 888-905.	1.4	17
1106	Validation of SNP markers for fruit quality and disease resistance loci in apple (Malus Ã— domestica) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	2.9	50
1107	Sequencing a Juglans regiaâ€‰Ã—â€‰J. microcarpa hybrid yields high-quality genome assemblies of parental species. Horticulture Research, 2019, 6, 55.	2.9	67

#	ARTICLE	IF	CITATIONS
1108	Insight on Rosaceae Family with Genome Sequencing and Functional Genomics Perspective. BioMed Research International, 2019, 2019, 1-12.	0.9	21
1109	Mapping Gene Markers for Apple Fruit Ring Rot Disease Resistance Using a Multi-omics Approach. G3: Genes, Genomes, Genetics, 2019, 9, 1663-1678.	0.8	27
1110	Identifying Genome-Wide Sequence Variations and Candidate Genes Implicated in Self-Incompatibility by Resequencing Fragaria viridis. International Journal of Molecular Sciences, 2019, 20, 1039.	1.8	6
1111	Evolutionary history and structure of nuclear matrix constituent proteins, the plant analogues of lamins. Journal of Experimental Botany, 2019, 70, 2651-2664.	2.4	20
1112	The Importance of Conserved Serine for C-Terminally Encoded Peptides Function Exertion in Apple. International Journal of Molecular Sciences, 2019, 20, 775.	1.8	9
1114	Construction of a high-density linkage map for bronze loquat using RAD-Seq. Scientia Horticulturae, 2019, 251, 59-64.	1.7	11
1115	A Walkthrough to the Use of GreeNC: The Plant lncRNA Database. Methods in Molecular Biology, 2019, 1933, 397-414.	0.4	7
1116	Apple whole genome sequences: recent advances and new prospects. Horticulture Research, 2019, 6, 59.	2.9	77
1117	Overexpression of Prunus DAM6 inhibits growth, represses bud break competency of dormant buds and delays bud outgrowth in apple plants. PLoS ONE, 2019, 14, e0214788.	1.1	69
1118	The future of walnutâ€“fruit forests in Kyrgyzstan and the status of the iconic Endangered apple Malus niedzwetzkyana. Oryx, 2019, 53, 415-423.	0.5	11
1119	Transcriptome sequencing of Himalayan Raspberry (Rubus ellipticus) and development of simple sequence repeat markers. 3 Biotech, 2019, 9, 161.	1.1	11
1120	A high-quality apple genome assembly reveals the association of a retrotransposon and red fruit colour. Nature Communications, 2019, 10, 1494.	5.8	254
1121	Flowering plant immune repertoires expand under mycorrhizal symbiosis. Plant Direct, 2019, 3, e00125.	0.8	2
1122	Spring Is Coming: Genetic Analyses of the Bud Break Date Locus Reveal Candidate Genes From the Cold Perception Pathway to Dormancy Release in Apple (Malus Ã— domestica Borkh.). Frontiers in Plant Science, 2019, 10, 33.	1.7	28
1123	Hunting for novel disease resistance genes: observations and opportunities from the Rosaceae. Acta Horticulturae, 2019, , 125-134.	0.1	2
1124	Gene duplication and evolution in recurring polyploidizationâ€“diploidization cycles in plants. Genome Biology, 2019, 20, 38.	3.8	542
1125	Genome-Wide Identification and Analysis of High-Copy-Number LTR Retrotransposons in Asian Pears. Genes, 2019, 10, 156.	1.0	4
1126	Origin and evolution of the octoploid strawberry genome. Nature Genetics, 2019, 51, 541-547.	9.4	469

#	ARTICLE	IF	CITATIONS
1127	Family-1 UDP glycosyltransferases in pear (Pyrus bretschneideri): Molecular identification, phylogenomic characterization and expression profiling during stone cell formation. Molecular Biology Reports, 2019, 46, 2153-2175.	1.0	22
1128	Phylogenetic and Expression Analyses of With-No-Lysine Kinase Genes Reveal Novel Gene Family Diversity in Fruit Trees. Horticultural Plant Journal, 2019, 5, 47-58.	2.3	6
1129	Resource allocation trade-offs and the loss of chemical defences during apple domestication. Annals of Botany, 2019, 123, 1029-1041.	1.4	21
1130	The Characterization, Authentication, and Gene Expression Pattern of the MdCER Family in Malus domestica. Horticultural Plant Journal, 2019, 5, 1-9.	2.3	17
1131	Application of High-Throughput Sequencing to Evaluate the Genetic Diversity Among Wild Apple Species Indigenous to Shandong, China, and Introduced Cultivars. Plant Molecular Biology Reporter, 2019, 37, 63-73.	1.0	2
1132	Genomewide analysis of homeobox gene family in apple (Malus domestica Borkh.) and their response to abiotic stress. Journal of Genetics, 2019, 98, 1.	0.4	6
1133	Two large-effect QTLs, Ma and Ma3, determine genetic potential for acidity in apple fruit: breeding insights from a multi-family study. Tree Genetics and Genomes, 2019, 15, 1.	0.6	50
1134	Is the oldest known wild apple tree, at more than 600 years old, associated with the distribution of apple trees in the region of Yili and adjacent areas?. Acta Horticulturae, 2019, , 33-38.	0.1	0
1135	Differential Allelic Richness between Malus sylvestris L. and Malus Ã— domestica Borkh. from Finland as a Measure of Genetic Loss. Sustainability, 2019, 11, 6949.	1.6	5
1136	Genome-Wide Identification and Characterization of ABC Transporters in Nine Rosaceae Species Identifying MdABCG28 as a Possible Cytokinin Transporter linked to Dwarfing. International Journal of Molecular Sciences, 2019, 20, 5783.	1.8	21
1137	The persimmon (Diospyros oleifera Cheng) genome provides new insights into the inheritance of astringency and ancestral evolution. Horticulture Research, 2019, 6, 138.	2.9	39
1138	Pseudo-chromosomeâ€"length genome assembly of a double haploid â€œBartlettâ€• pear (Pyrus communis L.). GigaScience, 2019, 8, .	3.3	76
1139	Comparative Proteomic Analysis Reveals Key Proteins Linked to the Accumulation of Soluble Sugars and Organic Acids in the Mature Fruits of the Wild Malus Species. Plants, 2019, 8, 488.	1.6	13
1140	Regulation of the Central Carbon Metabolism in Apple Fruit Exposed to Postharvest Low-Oxygen Stress. Frontiers in Plant Science, 2019, 10, 1384.	1.7	26
1142	Evidence for pre-climacteric activation of AOX transcription during cold-induced conditioning to ripen in European pear (Pyrus communis L.). PLoS ONE, 2019, 14, e0225886.	1.1	9
1143	A <i>Ma10</i> gene encoding Pâ€type <scp>ATP</scp>ase is involved in fruit organic acid accumulation in apple. Plant Biotechnology Journal, 2019, 17, 674-686.	4.1	62
1144	Genome-wide annotation and expression responses to biotic stresses of the WALL-ASSOCIATED KINASE - RECEPTOR-LIKE KINASE (WAK-RLK) gene family in Apple (Malus domestica). European Journal of Plant Pathology, 2019, 153, 771-785.	0.8	20
1145	Decoding systems biology of plant stress for sustainable agriculture development and optimized food production. Progress in Biophysics and Molecular Biology, 2019, 145, 19-39.	1.4	15

#	ARTICLE	IF	CITATIONS
1146	Genome-wide identification of the HKT genes in five Rosaceae species and expression analysis of HKT genes in response to salt-stress in Fragaria vesca. Genes and Genomics, 2019, 41, 325-336.	0.5	18
1147	Co-expression networks provide insights into molecular mechanisms of postharvest temperature modulation of apple fruit to reduce superficial scald. Postharvest Biology and Technology, 2019, 149, 27-41.	2.9	18
1148	Responses of Fuji (Malus domestica) and Shandingzi (Malus baccata) apples to Marssonina coronaria infection revealed by comparative transcriptome analysis. Physiological and Molecular Plant Pathology, 2019, 106, 87-95.	1.3	9
1149	An AP2/ERF gene, IbRAP2-12, from sweetpotato is involved in salt and drought tolerance in transgenic Arabidopsis. Plant Science, 2019, 281, 19-30.	1.7	58
1150	15 years of GDR: New data and functionality in the Genome Database for Rosaceae. Nucleic Acids Research, 2019, 47, D1137-D1145.	6.5	285
1151	Effect of fermentation time on nutritional components of red-fleshed apple cider. Food and Bioproducts Processing, 2019, 114, 276-285.	1.8	11
1152	Genome-wide identification and biochemical characterization of the UGT88F subfamily in Malus x domestica Borkh. Phytochemistry, 2019, 157, 135-144.	1.4	10
1153	Molecular cloning and functional analysis of a biphenyl phytoalexin-specific O-methyltransferase from apple cell suspension cultures. Planta, 2019, 249, 677-691.	1.6	11
1154	Isolation of two novel promoters from ramie (Boehmeria nivea L. Gaudich) and its functional characterization in Arabidopsis thaliana. Plant Cell, Tissue and Organ Culture, 2019, 136, 467-478.	1.2	6
1155	Pathogen-induced changes in floral scent may increase honeybee-mediated dispersal of <i>Erwinia amylovora</i>. ISME Journal, 2019, 13, 847-859.	4.4	45
1156	Proteomic fingerprinting of apple fruit, juice, and cider via combinatorial peptide ligand libraries and MS analysis. Electrophoresis, 2019, 40, 266-271.	1.3	7
1157	Application of sodium silicate retards apple softening by suppressing the activity of enzymes related to cell wall degradation. Journal of the Science of Food and Agriculture, 2019, 99, 1828-1833.	1.7	30
1158	Chloroplast sequence data differentiate Maleae, and specifically Pyrus, species in the USDA-ARS National Plant Germplasm System. Genetic Resources and Crop Evolution, 2019, 66, 5-15.	0.8	4
1159	The regulatory module Md<scp>PUB</scp>29â€Mdb<scp>HLH</scp>3 connects ethylene biosynthesis with fruit quality in apple. New Phytologist, 2019, 221, 1966-1982.	3.5	88
1160	Highly Accurate and Efficient Data-Driven Methods for Genotype Imputation. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1107-1116.	1.9	6
1161	Sun injury on apple fruit: Physiological, biochemical and molecular advances, and future challenges. Scientia Horticulturae, 2020, 260, 108866.	1.7	24
1162	Differential gene expression and epigenetic analyses between striped and blushed skinned sports of â€˜Fujiâ€™ apple. Scientia Horticulturae, 2020, 261, 108944.	1.7	20
1163	New Insights on â€˜GALAâ€™ Apple Fruit Development: Sugar and Acid Accumulation: A Transcriptomic Approach. Journal of Plant Growth Regulation, 2020, 39, 680-702.	2.8	12

#	Article	IF	Citations
1164	Immunological characterization of recombinant Mal d 1, the main allergen from apple (Malus x) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 74	1.7	2
1165	Genomeâ€wide analysis of coding and nonâ€coding RNA reveals a conserved miR164â€<i>NAC</i> regulatory pathway for fruit ripening. New Phytologist, 2020, 225, 1618-1634.	3.5	86
1166	Complete nucleotide sequence of loquat virus A, a member of the family Betaflexiviridae with a novel genome organization. Archives of Virology, 2020, 165, 223-226.	0.9	6
1167	A Braitenberg Vehicle Based on Memristive Neuromorphic Circuits. Advanced Intelligent Systems, 2020, 2, 1900103.	3.3	16
1168	Analysis of sorbitol content variation in wild and cultivated apples. Journal of the Science of Food and Agriculture, 2020, 100, 139-144.	1.7	20
1169	Genome wide identification and functional characterization of strawberry pectin methylesterases related to fruit softening. BMC Plant Biology, 2020, 20, 13.	1.6	41
1170	Analysis of MADS-box genes revealed modified flowering gene network and diurnal expression in pineapple. BMC Genomics, 2020, 21, 8.	1.2	21
1171	The Long Ashton Legacy: Characterising United Kingdom West Country cider apples using a genotyping by targeted sequencing approach. Plants People Planet, 2020, 2, 167-175.	1.6	4
1172	Genetic mapping of a locus controlling the intergeneric hybridization barrier between apple and pear. Tree Genetics and Genomes, 2020, 16, 1.	0.6	7
1173	A genome-wide association study for the detection of genes related to apple Marssonina Blotch disease resistance in apples. Scientia Horticulturae, 2020, 262, 108986.	1.7	6
1174	Transcriptome Analysis of Apple Leaves Infected by the Rust Fungus<i>Gymnosporangium yamadae</i>at Two Sporulation Stages. Molecular Plant-Microbe Interactions, 2020, 33, 444-461.	1.4	17
1175	Genome-wide identification and expression analysis of major latex protein (MLP) family genes in the apple (Malus domestica Borkh.) genome. Gene, 2020, 733, 144275.	1.0	15
1176	Characterization of Fe deficiency induced RING finger family members in apple species. Plant Gene, 2020, 21, 100209.	1.4	0
1177	Genome-wide identification and characterization of Respiratory Burst Oxidase Homolog genes in six Rosaceae species and an analysis of their effects on adventitious rooting in apple. PLoS ONE, 2020, 15, e0239705.	1.1	10
1178	Characteristics and Expression Analyses of Trehalose-6-Phosphate Synthase Family in Prunus mume Reveal Genes Involved in Trehalose Biosynthesis and Drought Response. Biomolecules, 2020, 10, 1358.	1.8	9
1179	Identification and validation of early genetic biomarkers for apple replant disease. PLoS ONE, 2020, 15, e0238876.	1.1	13
1180	The genome of Chinese flowering cherry (Cerasus serrulata) provides new insights into Cerasus species. Horticulture Research, 2020, 7, 165.	2.9	22
1181	Identification of two QTLs associated with high fruit acidity in apple using pooled genome sequencing analysis. Horticulture Research, 2020, 7, 171.	2.9	15

#	ARTICLE	IF	CITATIONS
1182	Threat to Asian wild apple trees posed by gene flow from domesticated apple trees and their â€œpestifiedâ€• pathogens. Molecular Ecology, 2020, 29, 4925-4941.	2.0	9
1183	Genome-Wide Identification of the TCP Gene Family in Broussonetia papyrifera and Functional Analysis of BpTCP8, 14 and 19 in Shoot Branching. Plants, 2020, 9, 1301.	1.6	5
1184	Effectiveness of Conventional Crop Improvement Strategies vs. Omics. , 2020, , 253-284.		5
1185	Genome-wide identification and expression analysis of the MYB transcription factor in Japanese plum (Prunus salicina). Genomics, 2020, 112, 4875-4886.	1.3	25
1186	Fruit Breeding in Regard to Color and Seed Hardness: A Genomic View from Pomegranate. Agronomy, 2020, 10, 991.	1.3	9
1187	Skin Color in Apple Fruit (Malus Ã— domestica): Genetic and Epigenetic Insights. Epigenomes, 2020, 4, 13.	0.8	8
1188	Characterization of FLOWERING LOCUS C Homologs in Apple as a Model for Fruit Trees. International Journal of Molecular Sciences, 2020, 21, 4562.	1.8	12
1189	Genome-Scale Characterization of Predicted Plastid-Targeted Proteomes in Higher Plants. Scientific Reports, 2020, 10, 8281.	1.6	7
1190	Defining the QTL associated with chill requirement during endodormancy in Malusâ€‰Ã—â€‰domestica Borkh. Euphytica, 2020, 216, 1.	0.6	2
1191	A Rosaceae Family-Level Approach To Identify Loci Influencing Soluble Solids Content in Blackberry for DNA-Informed Breeding. G3: Genes, Genomes, Genetics, 2020, 10, 3729-3740.	0.8	6
1192	Portuguese wild grapevine genome re-sequencing (Vitis vinifera sylvestris). Scientific Reports, 2020, 10, 18993.	1.6	4
1193	The Peptide PbrPSK2 From Phytosulfokine Family Induces Reactive Oxygen Species (ROS) Production to Regulate Pear Pollen Tube Growth. Frontiers in Plant Science, 2020, 11, 601993.	1.7	9
1194	Advances in Genomic, Transcriptomic, and Metabolomic Analyses of Fruit Quality in Fruit Crops. Horticultural Plant Journal, 2020, 6, 361-371.	2.3	33
1195	Genome-wide survey of sucrose non-fermenting 1-related protein kinase 2 in Rosaceae and expression analysis of PbrSnRK2 in response to ABA stress. BMC Genomics, 2020, 21, 781.	1.2	11
1196	An efficient protocol for functional studies of apple transcription factors using a glucocorticoid receptor fusion system. Applications in Plant Sciences, 2020, 8, e11396.	0.8	3
1197	Characterization and Comparison of Two Complete Plastomes of Rosaceae Species (Potentilla dickinsii) Tj ETQq1 1 0.784314 rgBT /Ove Molecular Sciences, 2020, 21, 4933.	1.8	14
1198	Comprehensive genomic analysis of the RNase T2 gene family in Rosaceae and expression analysis in Pyrus bretschneideri. Plant Systematics and Evolution, 2020, 306, 1.	0.3	7
1199	Genome-Wide Identification of Apple Ubiquitin SINA E3 Ligase and Functional Characterization of MdSINA2. Frontiers in Plant Science, 2020, 11, 1109.	1.7	21

#	ARTICLE	IF	CITATIONS
1200	The MADS-Box Gene MdDAM1 Controls Growth Cessation and Bud Dormancy in Apple. Frontiers in Plant Science, 2020, 11, 1003.	1.7	38
1201	Biosynthesis of the Dihydrochalcone Sweetener Trilobatin Requires <i>Phloretin Glycosyltransferase2</i>. Plant Physiology, 2020, 184, 738-752.	2.3	15
1202	Advances in Biosynthesis, Regulation, and Function of Apple Cuticular Wax. Frontiers in Plant Science, 2020, 11, 1165.	1.7	30
1203	Phased diploid genome assemblies and pan-genomes provide insights into the genetic history of apple domestication. Nature Genetics, 2020, 52, 1423-1432.	9.4	168
1204	Identification, characterisation and expression analysis of MADS-box genes in sweetpotato wild relative Ipomoea trifida. Acta Physiologiae Plantarum, 2020, 42, 1.	1.0	10
1205	Construction of a dense genetic map of the Malus fusca fire blight resistant accession MAL0045 using tunable genotyping-by-sequencing SNPs and microsatellites. Scientific Reports, 2020, 10, 16358.	1.6	17
1206	CRISPR-Cas9 enrichment and long read sequencing for fine mapping in plants. Plant Methods, 2020, 16, 121.	1.9	31
1207	A high-quality chromosome-level genome assembly reveals genetics for important traits in eggplant. Horticulture Research, 2020, 7, 153.	2.9	85
1208	Type-B cytokinin response regulators link hormonal stimuli and molecular responses during the transition from endo- to ecodormancy in apple buds. Plant Cell Reports, 2020, 39, 1687-1703.	2.8	8
1209	Detection of QTL for apple fruit acidity and sweetness using sensorial evaluation in multiple pedigreed full-sib families. Tree Genetics and Genomes, 2020, 16, 1.	0.6	15
1210	Genome wide annotation and characterization of young, intact long terminal repeat retrotransposons (In-LTR-RTs) of seven legume species. Genetica, 2020, 148, 253-268.	0.5	0
1211	Genome-wide identification of lysin motif containing protein family genes in eight rosaceae species, and expression analysis in response to pathogenic fungus Botryosphaeria dothidea in Chinese white pear. BMC Genomics, 2020, 21, 612.	1.2	9
1212	Myo-inositol mediates reactive oxygen species-induced programmed cell death via salicylic acid-dependent and ethylene-dependent pathways in apple. Horticulture Research, 2020, 7, 138.	2.9	23
1213	Advances in cultivar and rootstock breeding: a case study in peach. Acta Horticulturae, 2020, , 1-8.	0.1	0
1214	Light: An Alternative Method for Physical Control of Postharvest Rotting Caused by Fungi of Citrus Fruit. Journal of Food Quality, 2020, 2020, 1-12.	1.4	19
1215	RosBREED: bridging the chasm between discovery and application to enable DNA-informed breeding in rosaceous crops. Horticulture Research, 2020, 7, 177.	2.9	34
1216	Fox Hunting in Wild Apples: Searching for Novel Genes in Malus Sieversii. International Journal of Molecular Sciences, 2020, 21, 9516.	1.8	4
1217	Chromosome-level draft genome of a diploid plum (<i>Prunus salicina</i>). GigaScience, 2020, 9, .	3.3	39

#	ARTICLE	IF	CITATIONS
1218	Genomeâ€wide analysis of the soybean DREB gene family: Identification, genomic organization and expression profiles in response to drought stress. Plant Breeding, 2020, 139, 1158-1167.	1.0	13
1219	Application of genome-wide insertion/deletion markers on genetic structure analysis and identity signature of Malus accessions. BMC Plant Biology, 2020, 20, 540.	1.6	7
1220	Transcriptional regulation of bark freezing tolerance in apple (Malus domestica Borkh.). Horticulture Research, 2020, 7, 205.	2.9	12
1221	Identification of Phytochrome-Interacting Factor Family Members and Functional Analysis of MdPIF4 in Malus domestica. International Journal of Molecular Sciences, 2020, 21, 7350.	1.8	17
1222	Genome-Wide Characterization of the HSP20 Gene Family Identifies Potential Members Involved in Temperature Stress Response in Apple. Frontiers in Genetics, 2020, 11, 609184.	1.1	27
1223	Genetic integrity is still maintained in natural populations of the indigenous wild apple species <i>Malus sylvestris</i> (Mill.) in Saxony as demonstrated with nuclear SSR and chloroplast DNA markers. Ecology and Evolution, 2020, 10, 11798-11809.	0.8	9
1224	The sucrose transporter MdSUT4.1 participates in the regulation of fruit sugar accumulation in apple. BMC Plant Biology, 2020, 20, 191.	1.6	33
1225	Genome-wide identification and comparative analysis of GST gene family in apple (Malus domestica) and their expressions under ALA treatment. 3 Biotech, 2020, 10, 307.	1.1	13
1226	Genome-wide identification and comparative analysis of the ADH gene family in Chinese white pear (Pyrus bretschneideri) and other Rosaceae species. Genomics, 2020, 112, 3484-3496.	1.3	20
1227	Genome-wide identification and characterization of UDP-glucose dehydrogenase family genes in moso bamboo and functional analysis of PeUGDH4 in hemicellulose synthesis. Scientific Reports, 2020, 10, 10124.	1.6	11
1228	Genome-Wide Identification and Characterization of Vacuolar Processing Enzyme Gene Family and Diverse Expression Under Stress in Apple (Malus Ã— Domestic). Frontiers in Plant Science, 2020, 11, 626.	1.7	11
1229	Recommendations for Choosing the Genotyping Method and Best Practices for Quality Control in Crop Genome-Wide Association Studies. Frontiers in Genetics, 2020, 11, 447.	1.1	48
1230	Molecular characterisation of apple accessions with respect to aminocyclopropane-1-carboxylic acid synthase gene (ACS1) polymorphism. Zahradnictvi (Prague, Czech Republic: 1992), 2020, 47, 69-79.	0.3	1
1231	The Citrus Genome. Compendium of Plant Genomes, 2020, , .	0.3	16
1232	Transcriptome Analysis Identifies Two Ethylene Response Factors That Regulate Proanthocyanidin Biosynthesis During Malus Crabapple Fruit Development. Frontiers in Plant Science, 2020, 11, 76.	1.7	14
1233	Phylogenetic analyses of key developmental genes provide insight into the complex evolution of seeds. Molecular Phylogenetics and Evolution, 2020, 147, 106778.	1.2	8
1234	Characterization and pathogenicity of six <i>Cytospora</i> strains causing stem canker of wild apple in the Tianshan Forest, China. Forest Pathology, 2020, 50, e12587.	0.5	17
1235	Genomeâ€wide identification and characterization of the <i>BES1</i> gene family in apple (<i>Malus) Tj ETQq1 1 0.784314 rgBT /Ov	1.8	24

#	ARTICLE	IF	CITATIONS
1236	Molecular karyotypes of loquat (Eriobotrya japonica) aneuploids can be detected by using SSR markers combined with quantitative PCR irrespective of heterozygosity. Plant Methods, 2020, 16, 22.	1.9	9
1237	Manipulation of ZDS in tomato exposes carotenoidâ€•and ABAâ€specific effects on fruit development and ripening. Plant Biotechnology Journal, 2020, 18, 2210-2224.	4.1	44
1238	Genome-Wide Identification of the MdKNOX Gene Family and Characterization of Its Transcriptional Regulation in Malus domestica. Frontiers in Plant Science, 2020, 11, 128.	1.7	24
1239	Traditional breeding. , 2020, , 129-148.		15
1240	Regulation of phenylpropanoid biosynthesis by MdMYB88 and MdMYB124 contributes to pathogen and drought resistance in apple. Horticulture Research, 2020, 7, 102.	2.9	64
1241	Identification of CDF family members in apple and their expression in response to sucrose during floral induction. Journal of Plant Interactions, 2020, 15, 241-256.	1.0	6
1242	The importance and prevalence of allopolyploidy in Aotearoa New Zealand. Journal of the Royal Society of New Zealand, 2020, 50, 189-210.	1.0	5
1243	EjFRI, FRIGIDA (FRI) Ortholog from Eriobotrya japonica, Delays Flowering in Arabidopsis. International Journal of Molecular Sciences, 2020, 21, 1087.	1.8	8
1244	Introgressing blue mold resistance into elite apple germplasm by rapid cycle breeding and foreground and background DNA-informed selection. Tree Genetics and Genomes, 2020, 16, 1.	0.6	16
1245	ChIP-seq and RNA-seq for complex and low-abundance tree buds reveal chromatin and expression co-dynamics during sweet cherry bud dormancy. Tree Genetics and Genomes, 2020, 16, 1.	0.6	20
1246	The genome sequence of celery (Apium graveolens L.), an important leaf vegetable crop rich in apigenin in the Apiaceae family. Horticulture Research, 2020, 7, 9.	2.9	61
1247	Crop Origins and Phylo Food: A database and a phylogenetic tree to stimulate comparative analyses on the origins of food crops. Global Ecology and Biogeography, 2020, 29, 606-614.	2.7	29
1248	Prospects for achieving durable disease resistance with elite fruit quality in apple breeding. Tree Genetics and Genomes, 2020, 16, 1.	0.6	22
1249	Latent postharvest pathogens of pome fruit and their management: from single measures to a systems intervention approach. European Journal of Plant Pathology, 2020, 156, 663-681.	0.8	61
1250	Report on a complete chloroplast genome sequence of wild apple tree, Malus sieversii (Lebed.) M. Roem. Mitochondrial DNA Part B: Resources, 2020, 5, 1504-1505.	0.2	0
1251	Identification and expression analysis of the small auxin-up RNA (SAUR) gene family in apple by inducing of auxin. Gene, 2020, 750, 144725.	1.0	20
1252	A systematic analysis of apple root resistance traits to Pythium ultimum infection and the underpinned molecular regulations of defense activation. Horticulture Research, 2020, 7, 62.	2.9	24
1253	Genome-wide DNA polymorphisms in four Actinidia arguta genotypes based on whole-genome re-sequencing. PLoS ONE, 2020, 15, e0219884.	1.1	3

#	ARTICLE	IF	CITATIONS
1254	The role of conventional plant breeding in ensuring safe levels of naturally occurring toxins in food crops. Trends in Food Science and Technology, 2020, 100, 51-66.	7.8	58
1255	Turbocharging introgression breeding of perennial fruit crops: a case study on apple. Horticulture Research, 2020, 7, 47.	2.9	22
1256	Functional characterisation and in silico modelling of MdPSY2 variants and MdPSY5 phytoene synthases from Malus domestica. Journal of Plant Physiology, 2020, 249, 153166.	1.6	8
1257	Genome-wide identification and expression analysis of asparagine synthetase family in apple. Journal of Integrative Agriculture, 2020, 19, 1261-1273.	1.7	5
1258	The Rubber Tree Genome. Compendium of Plant Genomes, 2020, , .	0.3	3
1259	Identification of early fruit development reference genes in plum. PLoS ONE, 2020, 15, e0230920.	1.1	8
1260	Genome-wide analysis of auxin response factor (ARF) genes and functional identification of <i>MdARF2</i> reveals the involvement in the regulation of anthocyanin accumulation in apple. New Zealand Journal of Crop and Horticultural Science, 2021, 49, 78-91.	0.7	15
1261	Insights into the aridification history of Central Asian Mountains and international conservation strategy from the endangered wild apple tree. Journal of Biogeography, 2021, 48, 332-344.	1.4	11
1262	Ethnobotany of the crab apple tree (Malus sylvestris (L.) Mill., Rosaceae) in Spain. Genetic Resources and Crop Evolution, 2021, 68, 795-808.	0.8	7
1263	Identification and characterization of NRT gene family reveals their critical response to nitrate regulation during adventitious root formation and development in apple rootstock. Scientia Horticulturae, 2021, 275, 109642.	1.7	23
1264	Effects of sodium selenite spray on apple production, quality, and sucrose metabolism-related enzyme activity. Food Chemistry, 2021, 339, 127883.	4.2	26
1265	Abscisic acid homeostasis is mediated by feedback regulation of <i>MdMYB88</i> and <i>MdMYB124</i>. Journal of Experimental Botany, 2021, 72, 592-607.	2.4	27
1266	Genome-Wide Analysis of Heat Shock Transcription Factors in Ziziphus jujuba Identifies Potential Candidates for Crop Improvement Under Abiotic Stress. Applied Biochemistry and Biotechnology, 2021, 193, 1023-1041.	1.4	6
1269	Chromosomeâ€level reference genome assembly provides insights into aroma biosynthesis in passion fruit (<i>Passiflora edulis</i>). Molecular Ecology Resources, 2021, 21, 955-968.	2.2	31
1270	Genome-wide analysis of the MADS-Box gene family in Chrysanthemum. Computational Biology and Chemistry, 2021, 90, 107424.	1.1	26
1271	Transcriptome analysis Malus domestica â€˜M9T337â€™ root molecular responses to Fusarium solani infection. Physiological and Molecular Plant Pathology, 2021, 113, 101567.	1.3	18
1272	Effectors, chaperones, and harpins of the Type III secretion system in the fire blight pathogen Erwinia amylovora: a review. Journal of Plant Pathology, 2021, 103, 25-39.	0.6	23
1273	CaPSY1 gene plays likely the key role in carotenoid metabolism of pepper (Capsicum annuum) at ripening. Functional Plant Biology, 2021, 48, 141.	1.1	14

#	Article	IF	Citations
1274	Apples before the fall: Does shape stability coincide with maturity?. Quantitative Plant Biology, 2021, 2, .	0.8	0
1275	Agri/Bioinformatics: Shaping Next-Generation Agriculture. , 2021, , 111-134.		1
1276	Citrus Tristeza Virus Genotype Detection Using High-Throughput Sequencing. Viruses, 2021, 13, 168.	1.5	12
1277	Apple Genetic Resources: Diversity and Conservation. Compendium of Plant Genomes, 2021, , 33-45.	0.3	0
1278	The Apple Microbiome: Structure, Function, and Manipulation for Improved Plant Health. Compendium of Plant Genomes, 2021, , 341-382.	0.3	8
1279	Genetics and Genomics of Fruit Color Development in Apple. Compendium of Plant Genomes, 2021, , 271-295.	0.3	2
1280	Genetic and Physical Mapping of the Apple Genome. Compendium of Plant Genomes, 2021, , 131-168.	0.3	4
1281	GIS- and AHP-based land suitability analysis of Malus domestica Borkh. (apple) in West Kameng district of Arunachal Pradesh, India. Applied Geomatics, 2021, 13, 349-360.	1.2	8
1282	RECENT ADVANCES IN THE REGULATION OF CLIMACTERIC FRUIT RIPENING: HORMONE, TRANSCRIPTION FACTOR AND EPIGENETIC MODIFICATIONS. Frontiers of Agricultural Science and Engineering, 2021, .	0.9	2
1283	Genome-wide identification of the 14â€“3-3 gene family and its participation in floral transition by interacting with TFL1/FT in apple. BMC Genomics, 2021, 22, 41.	1.2	25
1284	Genome Editing in Apple. Compendium of Plant Genomes, 2021, , 213-225.	0.3	2
1285	Genetics and Breeding of Apple Scions. Compendium of Plant Genomes, 2021, , 73-103.	0.3	6
1286	The Genome Sequence and Transcriptome Studies in Mango (Mangifera indica L.). Compendium of Plant Genomes, 2021, , 165-186.	0.3	2
1287	Genomic-assisted breeding for abiotic stress tolerance in horticultural crops. , 2021, , 91-118.		0
1288	Ploidy, Genome Size, and Cytogenetics of Apple. Compendium of Plant Genomes, 2021, , 47-71.	0.3	5
1289	The CONSTANS-LIKE (COL) Genes in Brassica Plants. Compendium of Plant Genomes, 2021, , 91-99.	0.3	0
1290	Genetic Admixture in the Population of Wild Apple (Malus sieversii) from the Tien Shan Mountains, Kazakhstan. Genes, 2021, 12, 104.	1.0	13
1291	DNA Markers and Molecular Breeding in Pear and Other Rosaceae Fruit Trees. Horticulture Journal, 2021, 90, 1-13.	0.3	6

#	Article	IF	Citations
1292	Diverse Evolution in 111 Plant Genomes Reveals Purifying and Dosage Balancing Selection Models for F-Box Genes. International Journal of Molecular Sciences, 2021, 22, 871.	1.8	7
1293	Regulatory Sequences in Apple. Compendium of Plant Genomes, 2021, , 189-211.	0.3	0
1294	The Apple Genome and Epigenome. Compendium of Plant Genomes, 2021, , 169-187.	0.3	3
1295	Future Prospects of â€˜Omicsâ€™ and of Other Technologies for Genetic Improvement of Apple. Compendium of Plant Genomes, 2021, , 395-412.	0.3	3
1296	Genome-wide identification and comprehensive analysis of NAC family genes involved in fruit development in kiwifruit (Actinidia). BMC Plant Biology, 2021, 21, 44.	1.6	23
1297	Genome survey sequencing and genetic diversity of cultivated Akebia trifoliata assessed via phenotypes and SSR markers. Molecular Biology Reports, 2021, 48, 241-250.	1.0	15
1298	Chromosome-level genome assembly of Ophiorrhiza pumila reveals the evolution of camptothecin biosynthesis. Nature Communications, 2021, 12, 405.	5.8	77
1299	Genome-wide bioinformatics analysis revealed putative substrate specificities of SABATH and MES family members in silver birch (<i>Betula pendula</i>). Silvae Genetica, 2021, 70, 57-74.	0.4	3
1300	Genetic mechanisms associated with floral initiation and the repressive effect of fruit on flowering in apple (Malus x domestica Borkh). PLoS ONE, 2021, 16, e0245487.	1.1	9
1302	A Review of Strawberry Photobiology and Fruit Flavonoids in Controlled Environments. Frontiers in Plant Science, 2021, 12, 611893.	1.7	43
1303	Chromosome-scale genome assembly of Japanese pear (<i>Pyrus pyrifolia</i>) variety â€˜Nijisseikiâ€™. DNA Research, 2021, 28, .	1.5	26
1304	Genome-wide analysis of the apple CaCA superfamily reveals that MdCAX proteins are involved in the abiotic stress response as calcium transporters. BMC Plant Biology, 2021, 21, 81.	1.6	23
1305	Genome-wide association study for apple flesh browning: detection, validation, and physiological roles of QTLs. Tree Genetics and Genomes, 2021, 17, 1.	0.6	4
1306	Two Korean Endemic Clematis Chloroplast Genomes: Inversion, Reposition, Expansion of the Inverted Repeat Region, Phylogenetic Analysis, and Nucleotide Substitution Rates. Plants, 2021, 10, 397.	1.6	14
1307	Adaptive evolution driving the young duplications in six Rosaceae species. BMC Genomics, 2021, 22, 112.	1.2	5
1308	Transcriptomic Profiling of Apple Calli With a Focus on the Key Genes for ALA-Induced Anthocyanin Accumulation. Frontiers in Plant Science, 2021, 12, 640606.	1.7	14
1309	Tracing founder haplotypes of Japanese apple varieties: application in genomic prediction and genome-wide association study. Horticulture Research, 2021, 8, 49.	2.9	21
1310	Determination of sugar content in Lingwu jujube by NIRâ€“hyperspectral imaging. Journal of Food Science, 2021, 86, 1201-1214.	1.5	11

#	Article	IF	Citations
1311	Expression and Characterization of MdERFs with Roles in Apple Softening. Russian Journal of Plant Physiology, 2021, 68, 238-245.	0.5	0
1312	Functional Analysis of the Blackberry Sucrose Transporter Gene RuSUT2. Russian Journal of Plant Physiology, 2021, 68, 246-253.	0.5	4
1313	Genomeâ€wide association mapping identifies novel loci underlying fire blight resistance in apple. Plant Genome, 2021, 14, e20087.	1.6	11
1314	Identification and functional characterization of a new flavonoid synthase gene MdFLS1 from apple. Planta, 2021, 253, 105.	1.6	4
1315	Candidate genes and signatures of directional selection on fruit quality traits during apple domestication. American Journal of Botany, 2021, 108, 616-627.	0.8	6
1316	Genome-wide analysis of zinc finger motif-associated homeodomain (ZF-HD) family genes and their expression profiles under abiotic stresses and phytohormones stimuli in tea plants (Camellia) Tj ETQq1 1 0.784314 rg BT /Overlock 10 Tf	1.7	13
1317	Genomic analysis uncovers functional variation in the C-terminus of anthocyanin-activating MYB transcription factors. Horticulture Research, 2021, 8, 77.	2.9	28
1318	Rosa Romana apple: A heritage of the apple germoplasm of the Tuscan-Emilian Apennines to be recovered and promoted. Scientia Horticulturae, 2021, 280, 109955.	1.7	0
1320	Comparative Analysis of the Apple Root Transcriptome as Affected by Rootstock Genotype and Brassicaceae Seed Meal Soil Amendment: Implications for Plant Health. Microorganisms, 2021, 9, 763.	1.6	2
1321	An Atlas of Genomic Resources for Studying Rosaceae Fruits and Ornamentals. Frontiers in Plant Science, 2021, 12, 644881.	1.7	5
1322	Transcriptional profile of AvrRpt2EA-mediated resistance and susceptibility response to Erwinia amylovora in apple. Scientific Reports, 2021, 11, 8685.	1.6	4
1323	Integration of Infinium and Axiom SNP array data in the outcrossing species Malus Ã— domestica and causes for seemingly incompatible calls. BMC Genomics, 2021, 22, 246.	1.2	15
1324	Genome-wide analysis of SET-domain group histone methyltransferases in apple reveals their role in development and stress responses. BMC Genomics, 2021, 22, 283.	1.2	8
1325	Identification and Characterization of the CCoAOMT Gene Family in Apple, Chinese White Pear, and Peach. Journal of the American Society for Horticultural Science, 2021, 146, 184-195.	0.5	2
1326	Genome size estimation of Cotoneaster species (Rosaceae) from the Western Carpathians. Biologia (Poland), 2021, 76, 2067-2078.	0.8	3
1327	Rose without prickle: genomic insights linked to moisture adaptation. National Science Review, 2021, 8, nwab092.	4.6	15
1328	Research progress of fruit color development in apple (Malus domestica Borkh.). Plant Physiology and Biochemistry, 2021, 162, 267-279.	2.8	50
1329	An accumulation of genetic variation and selection across the disease-related genes during apple domestication. Tree Genetics and Genomes, 2021, 17, 1.	0.6	10

#	Article	IF	Citations
1330	Polyploidy underlies co-option and diversification of biosynthetic triterpene pathways in the apple tribe. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	37
1331	Genome-Wide Identification of PRP Genes in Apple Genome and the Role of MdPRP6 in Response to Heat Stress. International Journal of Molecular Sciences, 2021, 22, 5942.	1.8	15
1333	Fruit Development and Primary Metabolism in Apple. Agronomy, 2021, 11, 1160.	1.3	14
1334	Transcriptome Characterization and Expression Profiles of Disease Defense-Related Genes of Table Grapes in Response to Pichia anomala Induced with Chitosan. Foods, 2021, 10, 1451.	1.9	9
1335	Genome-wide comparison of the GRAS protein family in eight Rosaceae species and <i>GRAS</i> gene expression analysis in Chinese white pear (<i>Pyrus bretschneideri</i> Rehder). New Zealand Journal of Crop and Horticultural Science, 2022, 50, 303-325.	0.7	5
1336	Study on the differences of gene expression between pear and apple wild cultivation materials based on RNA-seq technique. BMC Plant Biology, 2021, 21, 256.	1.6	3
1337	Quantifying apple diversity: A phenomic characterization of Canadaâ€™s Apple Biodiversity Collection. Plants People Planet, 2021, 3, 747-760.	1.6	20
1338	The Origins of the Apple in Central Asia. Journal of World Prehistory, 2021, 34, 159-193.	1.1	8
1339	Construction of a High-Density Genetic Map and Identification of Leaf Trait-Related QTLs in Chinese Bayberry (Myrica rubra). Frontiers in Plant Science, 2021, 12, 675855.	1.7	6
1340	The TAZ domain-containing proteins play important role in the heavy metals stress biology in plants. Environmental Research, 2021, 197, 111030.	3.7	15
1344	Behavior of<i>Prunus persica</i>as Green and Friendly Corrosion Inhibitor for Corrosion Protection. , 0, , .		2
1345	Advanced genebank management of genetic resources of European wild apple, Malus sylvestris, using genome-wide SNP array data. Tree Genetics and Genomes, 2021, 17, 1.	0.6	6
1346	LjaFGD: <i>Lonicera japonica</i> functional genomics database. Journal of Integrative Plant Biology, 2021, 63, 1422-1436.	4.1	12
1347	Identification of GH17 gene family in Vitis vinifera and expression analysis of GH17 under various adversities. Physiology and Molecular Biology of Plants, 2021, 27, 1423-1436.	1.4	3
1348	Full-Length Transcriptome-Wide Characteristic and Functional Identification of WRKY Family in Malus sieversii during the Valsa Canker Disease Response. Forests, 2021, 12, 790.	0.9	3
1349	The transcriptomes of healthy and bitter pit-affected â€˜Honeycrispâ€™ fruit reveal genes associated with disorder development and progression. Tree Genetics and Genomes, 2021, 17, 1.	0.6	5
1351	Genome-wide identification and expression analysis of glycosyltransferase gene family 1 in Quercus robur L.. Journal of Applied Genetics, 2021, 62, 559-570.	1.0	5
1352	Relative performance of customized and universal probe sets in target enrichment: A case study in subtribe Malinae. Applications in Plant Sciences, 2021, 9, e11442.	0.8	20

#	Article	IF	Citations
1353	Regulation of Flowering Time by Improving Leaf Health Markers and Expansion by Salicylic Acid Treatment: A New Approach to Induce Flowering in Malus domestica. Frontiers in Plant Science, 2021, 12, 655974.	1.7	6
1354	Identification, through transcriptome analysis, of transcription factors that regulate anthocyanin biosynthesis in different parts of red-fleshed apple â€˜Mayâ€™ fruit. Horticultural Plant Journal, 2022, 8, 11-21.	2.3	6
1355	Reconstructing 50,000 years of human history from our DNA: lessons from modern genomics. Comptes Rendus - Biologies, 2021, 344, 177-187.	0.1	2
1356	Insights into the effect of human civilization on <i>Malus</i> evolution and domestication. Plant Biotechnology Journal, 2021, 19, 2206-2220.	4.1	23
1357	Random mutagenesis in vegetatively propagated crops: opportunities, challenges and genome editing prospects. Molecular Biology Reports, 2022, 49, 5729-5749.	1.0	7
1358	No Evidence of Unexpected Transgenic Insertions in T1190 â€“ A Transgenic Apple Used in Rapid Cycle Breeding â€“ Following Whole Genome Sequencing. Frontiers in Plant Science, 2021, 12, 715737.	1.7	2
1359	Split-root approach reveals localized root responses towards apple replant disease (ARD) in terms of ARD biomarker gene expression and content of phenolic compounds. Scientia Horticulturae, 2021, 286, 110117.	1.7	8
1360	Genomeâ€wide investigation and comparative analysis of <scp>MATE</scp> gene family in Rosaceae species and their regulatory role in abiotic stress responses in Chinese pear (<i>Pyrus) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 45	2.6	17
1361	Genome-wide identification, molecular evolution, and expression divergence of the hexokinase gene family in apple. Journal of Integrative Agriculture, 2021, 20, 2112-2125.	1.7	9
1362	Plastome characterization and comparative analyses of wild crabapples (Malus baccata and M.) Tj ETQq1 1 0.784314 rgBT /Overlock 10 and Genomes, 2021, 17, 1.	0.6	11
1363	The chromosomeâ€scale reference genome of <i>Rubus chingii</i> Hu provides insight into the biosynthetic pathway of hydrolyzable tannins. Plant Journal, 2021, 107, 1466-1477.	2.8	26
1364	Crucial Cell Signaling Compounds Crosstalk and Integrative Multi-Omics Techniques for Salinity Stress Tolerance in Plants. Frontiers in Plant Science, 2021, 12, 670369.	1.7	47
1365	Unraveling a genetic roadmap for improved taste in the domesticated apple. Molecular Plant, 2021, 14, 1454-1471.	3.9	47
1366	Chromosomeâ€scale genome assembly and population genomics provide insights into the adaptation, domestication, and flavonoid metabolism of Chinese plum. Plant Journal, 2021, 108, 1174-1192.	2.8	16
1367	Linkage map and QTL mapping of red flesh locus in apple using a R1R1â€¯Ã—â€¯R6R6 population. Horticultural Plant Journal, 2021, 7, 393-400.	2.3	13
1368	Niche differentiation between Malus sylvestris and its hybrid with Malus domestica indicated by plant community, soil and light. Journal of Vegetation Science, 2021, 32, e13078.	1.1	2
1369	Mobile forms of carbon in trees: metabolism and transport. Tree Physiology, 2022, 42, 458-487.	1.4	11
1370	Analysis of PRX Gene Family and Its Function on Cell Lignification in Pears (Pyrus bretschneideri). Plants, 2021, 10, 1874.	1.6	4

#	Article	IF	Citations
1371	Early Response to Dehydration Six-Like Transporter Family: Early Origin in Streptophytes and Evolution in Land Plants. Frontiers in Plant Science, 2021, 12, 681929.	1.7	11
1373	Genomic-Wide Identification and Characterization of the Uridine Diphosphate Glycosyltransferase Family in Eucommia ulmoides Oliver. Plants, 2021, 10, 1934.	1.6	7
1374	Development of Genome-Wide Functional Markers Using Draft Genome Assembly of Guava (Psidium) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 708332.	1.7	8
1375	Construction of a high-density genetic linkage map and QTL analysis of morphological traits in an F1 Malusdomesticaâ€‰Ã—â€‰Malus baccata hybrid. Physiology and Molecular Biology of Plants, 2021, 27, 1997-2007.	1.4	1
1376	Rambutan genome revealed gene networks for spine formation and aril development. Plant Journal, 2021, 108, 1037-1052.	2.8	7
1377	Genome-wide investigation of Hydroxycinnamoyl CoA: Shikimate Hydroxycinnamoyl Transferase (HCT) gene family in Carthamus tinctorius L.. Notulae Botanicae Horti Agrobotanici Cluj-Napoca, 2021, 49, 12489.	0.5	4
1378	Laccase Directed Lignification Is One of the Major Processes Associated With the Defense Response Against Pythium ultimum Infection in Apple Roots. Frontiers in Plant Science, 2021, 12, 629776.	1.7	12
1379	Transcriptome analysis of postharvest pear (Pyrus pyrifolia Nakai) in response to Penicillium expansum infection. Scientia Horticulturae, 2021, 288, 110361.	1.7	7
1380	Transcriptomic analysis of the effects of Î³-aminobutyric acid treatment on browning and induced disease resistance in fresh-cut apples. Postharvest Biology and Technology, 2021, 181, 111686.	2.9	20
1381	Genome-wide analysis reveals widespread roles for RcREM genes in floral organ development in Rosa chinensis. Genomics, 2021, 113, 3881-3894.	1.3	7
1382	Genome-Wide Identification, Expression Profiling and Protein-Protein Interaction Properties of the BEL-Like Homeodomain Gene Family in Apple. Phyton, 2022, 91, 315-331.	0.4	2
1383	Origin of the Domesticated Apples. Compendium of Plant Genomes, 2021, , 383-394.	0.3	3
1384	Genomics of Fruit Acidity and Sugar Content in Apple. Compendium of Plant Genomes, 2021, , 297-309.	0.3	1
1385	Genetics and Genomics of Cold Hardiness and Dormancy. Compendium of Plant Genomes, 2021, , 247-270.	0.3	0
1386	Determination of Post-Harvest Biochemical Composition, Enzymatic Activities, and Oxidative Browning in 14 Apple Cultivars. Foods, 2021, 10, 186.	1.9	18
1387	Genome-wide identification and expression analysis of the pear autophagy-related gene PbrATG8 and functional verification of PbrATG8c in Pyrus bretschneideri Rehd. Planta, 2021, 253, 32.	1.6	10
1388	Current approaches in horticultural crops to mitigate the effect of drought stress. , 2021, , 213-240.		0
1389	Genomic consequences of apple improvement. Horticulture Research, 2021, 8, 9.	2.9	53

#	ARTICLE	IF	CITATIONS
1390	Botany, Taxonomy, and Origins of the Apple. Compendium of Plant Genomes, 2021, , 19-32.	0.3	5
1391	Long noncoding RNAs in fruit crops. , 2021, , 225-242.		0
1392	Flowering and Juvenility in Apple. Compendium of Plant Genomes, 2021, , 227-246.	0.3	1
1394	Methods for the Design, Implementation, and Analysis of Illumina Infiniumâ„¢ SNP Assays in Plants. Methods in Molecular Biology, 2015, 1245, 281-298.	0.4	7
1395	Citrus Genomes: From Sequence Variations to Epigenetic Modifications. Compendium of Plant Genomes, 2020, , 141-165.	0.3	1
1396	Nicotiana benthamiana, A Popular Model for Genome Evolution and Plantâ€"Pathogen Interactions. Compendium of Plant Genomes, 2020, , 231-247.	0.3	6
1397	The RRIM 600 Rubber Tree Genome: Sequencing and Analysis Strategies of a Premier Pedigree Clone. Compendium of Plant Genomes, 2020, , 41-54.	0.3	1
1398	Clonal Cultivars from Multistage Multitrait Selection. , 2016, , 343-386.		2
1399	The Kiwifruit Genome. Compendium of Plant Genomes, 2016, , 101-114.	0.3	1
1400	Bioinformatics Tools to Assist Breeding for Climate Change. , 2013, , 391-414.		3
1402	Sexual incompatibility in Rosaceae fruit tree species: molecular interactions and evolutionary dynamics. Biologia Plantarum, 0, , .	1.9	1
1403	Genome-wide annotation and expression responses to biotic stresses of the WALL-ASSOCIATED KINASE - RECEPTOR-LIKE KINASE (WAK-RLK) gene family in Apple (Malus domestica). , 2019, 153, 771.		1
1404	Genome wide identification of superoxide dismutase (SOD) genes and their expression profiles under 1-methylcyclopropene (1-MCP) treatment during ripening of apple fruit. Scientia Horticulturae, 2020, 271, 109471.	1.7	18
1406	Pre-harvest climate and post-harvest acclimation to cold prevent from superficial scald development in Granny Smith apples. Scientific Reports, 2020, 10, 6180.	1.6	12
1415	Demographically idiosyncratic responses to climate change and rapid Pleistocene diversification of the walnut genus <i>Juglans</i> (Juglandaceae) revealed by wholeâ€genome sequences. New Phytologist, 2018, 217, 1726-1736.	3.5	98
1416	Developmental Mechanisms of Fleshy Fruit Diversity in Rosaceae. Annual Review of Plant Biology, 2020, 71, 547-573.	8.6	38
1418	Comparative Genetics and Genomics Initiatives. , 2012, , 270-291.		3
1419	Functional Genomics. , 2012, , 292-322.		2

#	ARTICLE	IF	CITATIONS
1420	Physical mapping of black spot disease resistance/susceptibility-related genome regions in Japanese pear (<i>Pyrus pyrifolia</i>) by BAC-FISH. Breeding Science, 2016, 66, 444-449.	0.9	6
1421	Efficient isolation of chloroplasts from in vitro shoots of Malus and Prunus. Zemdirbyste, 2018, 105, 171-176.	0.3	1
1423	A Genome-Wide Analysis of the LBD (LATERAL ORGAN BOUNDARIES Domain) Gene Family in Malus domestica with a Functional Characterization of MdLBD11. PLoS ONE, 2013, 8, e57044.	1.1	49
1424	Genome-Wide Characterization and Linkage Mapping of Simple Sequence Repeats in Mei (Prunus mume) Tj ETQq1 1 0.784314 rgBT /O	1.1	41
1425	Transcript Assembly and Quantification by RNA-Seq Reveals Differentially Expressed Genes between Soft-Endocarp and Hard-Endocarp Hawthorns. PLoS ONE, 2013, 8, e72910.	1.1	30
1426	Plastid Genome Sequence of a Wild Woody Oil Species, Prinsepia utilis, Provides Insights into Evolutionary and Mutational Patterns of Rosaceae Chloroplast Genomes. PLoS ONE, 2013, 8, e73946.	1.1	60
1427	A Multidisciplinary Approach Providing New Insight into Fruit Flesh Browning Physiology in Apple (Malus x domestica Borkh.). PLoS ONE, 2013, 8, e78004.	1.1	63
1428	Characterization of Resistance Gene Analogues (RGAs) in Apple (Malus Ã— domestica Borkh.) and Their Evolutionary History of the Rosaceae Family. PLoS ONE, 2014, 9, e83844.	1.1	71
1429	Genome-Wide Analysis of the MADS-Box Gene Family in Brachypodium distachyon. PLoS ONE, 2014, 9, e84781.	1.1	72
1430	Genome-Wide Identification and Evolutionary Analysis of the SBP-Box Gene Family in Castor Bean. PLoS ONE, 2014, 9, e86688.	1.1	37
1431	The Draft Genome Sequence of European Pear (Pyrus communis L. â€˜Bartlettâ€™). PLoS ONE, 2014, 9, e92644.	1.1	241
1432	Genome-Wide Analysis of Repeat Diversity across the Family Musaceae. PLoS ONE, 2014, 9, e98918.	1.1	54
1433	Genome-Wide Identification and Expression Analysis of NBS-Encoding Genes in Malus x domestica and Expansion of NBS Genes Family in Rosaceae. PLoS ONE, 2014, 9, e107987.	1.1	80
1434	Comparative Analysis of Predicted Plastid-Targeted Proteomes of Sequenced Higher Plant Genomes. PLoS ONE, 2014, 9, e112870.	1.1	8
1435	Transcriptomic Signatures in Seeds of Apple (Malus domestica L. Borkh) during Fruitlet Abscission. PLoS ONE, 2015, 10, e0120503.	1.1	19
1436	Proteome Analysis of Pathogen-Responsive Proteins from Apple Leaves Induced by the Alternaria Blotch Alternaria alternata. PLoS ONE, 2015, 10, e0122233.	1.1	37
1437	How Did Host Domestication Modify Life History Traits of Its Pathogens?. PLoS ONE, 2015, 10, e0122909.	1.1	6
1438	Genome Survey Sequencing for the Characterization of the Genetic Background of Rosa roxburghii Tratt and Leaf Ascorbate Metabolism Genes. PLoS ONE, 2016, 11, e0147530.	1.1	60

#	ARTICLE	IF	CITATIONS
1439	Mapping the sensory perception of apple using descriptive sensory evaluation in a genome wide association study. PLoS ONE, 2017, 12, e0171710.	1.1	47
1440	Genotyping-by-sequencing markers facilitate the identification of quantitative trait loci controlling resistance to Penicillium expansum in Malus sieversii. PLoS ONE, 2017, 12, e0172949.	1.1	47
1441	Functional analysis of the GmESR1 gene associated with soybean regeneration. PLoS ONE, 2017, 12, e0175656.	1.1	3
1442	Is biotechnology (more) acceptable when it enables a reduction in phytosanitary treatments? A European comparison of the acceptability of transgenesis and cisgenesis. PLoS ONE, 2017, 12, e0183213.	1.1	16
1443	Genome-wide expression analysis of salt-stressed diploid and autotetraploid Paulownia tomentosa. PLoS ONE, 2017, 12, e0185455.	1.1	22
1444	e-RGA: enhanced Reference Guided Assembly of Complex Genomes. EMBnet Journal, 2011, 17, 46.	0.2	17
1445	Hybridization and Genetic Diversity in Wild Apple (Malus sylvestris (L.) MILL.) from Various Regions in Germany and from Luxembourg. Silvae Genetica, 2014, 63, 81-93.	0.4	27
1446	Recent advances in fruit crop genomics. Frontiers of Agricultural Science and Engineering, 2014, 1, 21.	0.9	2
1447	Pre-isolation, isolation and regeneration protoplasts from leaf mesophyll of in vivo Malus domestica â€˜Annaâ€™ cv.. Revista Brasileira De Fruticultura, 2019, 41, .	0.2	2
1448	Development of new genomic resources and tools for molecular breeding in blackberry. Acta Horticulturae, 2020, , 39-46.	0.1	5
1449	Ensuring the genetic diversity of apples. Burleigh Dodds Series in Agricultural Science, 2017, , 3-22.	0.1	2
1450	Characterizing Water Use Efficiency and Water Deficit Responses in Apple (Malus Ã—domestica Borkh.) Tj ETQq1 1 0.784314 rgBT /Ove Hortcultural Science, 2011, 46, 1079-1084.	0.5	24
1451	Malus sieversii: A Diverse Central Asian Apple Species in the USDA-ARS National Plant Germplasm System. Hortscience: A Publication of the American Society for Hortcultural Science, 2013, 48, 1440-1444.	0.5	17
1452	Genetic Mapping of PcDw Determining Pear Dwarf Trait. Journal of the American Society for Horticultural Science, 2011, 136, 48-53.	0.5	22
1453	Reflective Films and Expression of Light-regulated Genes in Field-grown Apple. Journal of the American Society for Horticultural Science, 2014, 139, 487-494.	0.5	5
1454	The effects of Î²-lactam antibiotics and hygromycin B on de novo shoot organogenesis in apple cv. Golden Delicious. Archives of Biological Sciences, 2018, 70, 179-190.	0.2	8
1455	Recent Progress on Studies of Chromosome Observation in Deciduous Fruit Trees. Japanese Society for Horticultural Science, 2012, 81, 305-313.	0.8	9
1456	Current trends in apple tree breeding (Malus Mill.). Horticulture and Viticulture, 2020, , 5-11.	0.0	3

#	ARTICLE	IF	CITATIONS
1457	Morphological, biochemical and male-meiotic characterization of apple (<i>Malus</i> Ã—) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.4	10
1458	New Strategies to Overcome Present CRISPR/Cas9 Limitations in Apple and Pear: Efficient Dechimerization and Base Editing. International Journal of Molecular Sciences, 2021, 22, 319.	1.8	53
1459	Genomic Organization, Phylogenetic Comparison, and Differential Expression of the Nuclear Factor-Y Gene Family in Apple (Malus Domestica). Plants, 2021, 10, 16.	1.6	11
1461	Plant microRNAs: new players in functional genomics. Turk Tarim Ve Ormancilik Dergisi/Turkish Journal of Agriculture and Forestry, 0, , .	0.8	13
1462	Genomics of crop plant genetic resources. Advances in Bioscience and Biotechnology (Print), 2012, 03, 378-385.	0.3	10
1463	Transcript Profiles of Auxin Efflux Carrier and IAA-Amido Synthetase Genes Suggest the Role of Auxin on Apple (&lt;i&gt;Malus&lt;/i&gt; &#215;) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 542 Td (&lt;i&a Sciences, 2015, 06, 620-632.	0.3	6
1464	A Phenotyping Protocol for Detailed Evaluation of Apple Root Resistance Responses Utilizing Tissue Culture Micropropagated Apple Plants. American Journal of Plant Sciences, 2018, 09, 2183-2204.	0.3	6
1465	Evaluation of five protocols for DNA extraction from leaves of Malus sieversii, Vitis vinifera, and Armeniaca vulgaris. Genetics and Molecular Research, 2014, 13, 1278-1287.	0.3	9
1466	Identification of functional SNPs in genes and their effects on plant phenotypes. Journal of Plant Biotechnology, 2016, 43, 1-11.	0.1	43
1467	Genetic and Physical Mapping of QTLs for Fruit Juice Browning and Fruit Acidity on Linkage Group 16 in Apple. Tree Genetics and Molecular Breeding, 0, , .	0.0	2
1468	The complete chloroplast genome sequence of strawberry (<i>Fragaria</i>ÂÃ—Â<i>ananassa</i>Duch.) and comparison with related species of Rosaceae. PeerJ, 2017, 5, e3919.	0.9	68
1469	Identification and comparative analysis of the <i>CIPK</i> gene family and characterization of the cold stress response in the woody plant <i>Prunus mume</i>. PeerJ, 2019, 7, e6847.	0.9	20
1470	Cloning, sequencing, and expression analysis of 32 NAC transcription factors (MdNAC) in apple. PeerJ, 2020, 8, e8249.	0.9	8
1471	Isolation, sequencing, and expression analysis of 30 AP2/ERF transcription factors in apple. PeerJ, 2020, 8, e8391.	0.9	5
1472	Development of an Apple F₁Segregating Population Genetic Linkage Map Using Genotyping-By-Sequencing. Plant Breeding and Biotechnology, 2018, 6, 434-443.	0.3	4
1473	The Streptochaeta Genome and the Evolution of the Grasses. Frontiers in Plant Science, 2021, 12, 710383.	1.7	8
1474	Chromosomeâ€scale genome assembly of <i>Castanopsis tibetana</i> provides a powerful comparative framework to study the evolution and adaptation of Fagaceae trees. Molecular Ecology Resources, 2022, 22, 1178-1189.	2.2	6
1476	Genome-Wide Identification and Expression Analysis of MADS-Box Family Genes in Litchi (Litchi) Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.6	13

#	Article	IF	Citations
1477	Combining novel technologies with interdisciplinary basic research to enhance horticultural crops. Plant Journal, 2022, 109, 35-46.	2.8	17
1478	Phylogeny of<i>Crataegus</i>(Rosaceae) based on 257 nuclear loci and chloroplast genomes: evaluating the impact of hybridization. PeerJ, 2021, 9, e12418.	0.9	6
1479	Niche Shifts, Hybridization, Polyploidy and Geographic Parthenogenesis in Western North American Hawthorns (Crataegus subg. Sanguineae, Rosaceae). Agronomy, 2021, 11, 2133.	1.3	3
1480	Frequent germplasm exchanges drive the high genetic diversity of Chinese-cultivated common apricot germplasm. Horticulture Research, 2021, 8, 215.	2.9	16
1481	Genome-wide survey of GÎ³ subunit gene family in eight Rosaceae and expression analysis of PbrGGs in pear (Pyrus bretschneideri). BMC Plant Biology, 2021, 21, 471.	1.6	1
1483	Advances in Sugarcane Genomics and Genetics. Sugar Tech, 2022, 24, 354-368.	0.9	9
1484	The bayberry database: a multiomic database for Myrica rubra, an important fruit tree with medicinal value. BMC Plant Biology, 2021, 21, 452.	1.6	7
1485	Study Of Genetic Diversity And Resistance Of Fruit Crops To Main Pathogens Using DNA Markers. Eurasian Journal of Applied Biotechnology, 2021, , .	0.0	0
1486	Analysis of genetic diversity and structure across a wide range of germplasm reveals genetic relationships among seventeen species of Malus Mill. native to China. Journal of Integrative Agriculture, 2021, 20, 3186-3198.	1.7	6
1488	The Evolution Analysis of Resistance Genes in Sorghum. Communications in Computer and Information Science, 2011, , 171-177.	0.4	1
1489	Genomic and Functional Genomic Resources of Melon. , 2011, , 286-308.		0
1490	Analyzing the Papaya Genome. Advances in Microbial Ecology, 2012, , 297-308.	0.1	0
1492	Illusion or reality, abstract or concrete art? Models in health: do they answer the questions?. Revista Da AssociaÃ§Ã£o MÃ©dica Brasileira, 2012, 58, 269-271.	0.3	0
1493	Development of an SNP Identification Pipeline for Highly Heterozygous Crops. , 2013, , 131-139.		0
1494	Bioinformatics as a Tool for Stone Fruit Research. , 2012, , 355-377.		1
1495	Adapting Apple Ideotypes to Low-Input Fruit Production Agro-Ecosystems. , 2014, , 131-148.		3
1496	Molecular Tools for Exploring Polyploid Genomes in Plants. , 2014, , 73-97.		0
1497	DNA Markers in Tree Improvement of Tropical Plantation Species. , 2014, , 568-592.		0

#	ARTICLE	IF	CITATIONS
1498	Identification of Four New Est-Based Markers on the Apple <i>(MALUS â‹‰ DOMESTICA)</i> Genetic Map. Journal of Horticultural Research, 2014, 22, 93-100.	0.4	0
1499	Polyol Metabolism and Stress Tolerance in Horticultural Plants. , 2015, , 59-73.		5
1500	Watercore in Fruits. , 2015, , 127-145.		4
1501	Agriculture: From a Development Perspective to Plant Resource Domestication. Journal of Agriculture and Forestry (New York, N Y), 2015, 3, 127.	0.2	1
1502	The Representatives of Amelanchier Medik. Genus in Ukraine. Vestnik Volgogradskogo Gosudarstvennogo Universiteta SeriÃ¢ 11 Estestvennye Nauki, 2015, , 15-33.	0.0	1
1504	Current status of peach genomics and transcriptomics research. Journal of Plant Biotechnology, 2015, 42, 312-325.	0.1	1
1505	Plant functional genomics: Approaches and applications. , 2016, , 157-186.		2
1506	Rediscovery of haploid breeding in the genomics era. Journal of Plant Biotechnology, 2016, 43, 12-20.	0.1	1
1507	Salinity Stress: â€œOmicsâ€•Approaches. , 2017, , 295-310.		1
1508	Analysis of Tissue Specific Expression of <i>SOT</i> Gene Family in White Pear. Botanical Research, 2018, 07, 496-506.	0.0	0
1509	Morphological characterization of apple varieties found in yasin valley, gilgit-baltistan, Pakistan. Forestry Research and Engineering International Journal, 2018, 2, .	0.1	1
1512	The Genome of Prunus mume. Compendium of Plant Genomes, 2019, , 31-52.	0.3	0
1513	Progress in plant genome sequencing: research directions. Vavilovskii Zhurnal Genetiki I Selektsii, 2019, 23, 38-48.	0.4	4
1517	In Silico Prediction of Cell Wall Remodeling Genes in Tomato, Banana, Melon and Grape. International Journal of Life Sciences and Biotechnology, 2019, 2, 108-121.	0.2	2
1524	Enhance Fruit Ripening Uniformity and Accelerate the Rutab Stage by Using ATP in â€˜Zaghloulâ€™ Dates during the Shelf Life. Foods, 2021, 10, 2641.	1.9	8
1525	A draft genome, resequencing, and metabolomes reveal the genetic background and molecular basis of the nutritional and medicinal properties of loquat (Eriobotrya japonica (Thunb.) Lindl). Horticulture Research, 2021, 8, 231.	2.9	14
1526	The Gillenia trifoliata genome reveals dynamics correlated with growth and reproduction in Rosaceae. Horticulture Research, 2021, 8, 233.	2.9	4
1527	Essential Oils in Citrus. Compendium of Plant Genomes, 2020, , 211-223.	0.3	1

#	ARTICLE	IF	CITATIONS
1529	Transcriptional Profiles of Mdwrky33 in Apple Root in Response to Infection by Pythium Ultimum, Abiotic Stresses and Chemical Treatments. International Journal of Phytopathology, 2019, 8, ACCEPTED.	0.1	1
1530	Genetic Diversity in Rosaceous Fruits of Jammu and Kashmir State: Apple, Apricot, and Almond. Topics in Biodiversity and Conservation, 2020, , 227-246.	0.3	2
1531	Genomic Bioinformatics Analysis of Cordyceps militaris. Advances in Microbiology, 2020, 09, 51-59.	0.0	0
1533	Genome-Wide Identification and Characterization of Apple P3A-Type ATPase Genes, with Implications for Alkaline Stress Responses. Forests, 2020, 11, 292.	0.9	2
1535	Elucidation of the Origin of the Monumental Olive Tree of Vouves in Crete, Greece. Plants, 2021, 10, 2374.	1.6	7
1538	High-throughput whole genome sequencing of apricot (Prunus armeniaca) cultivar â€˜HacÄ±haliloÄŸluâ€™. Acta Horticulturae, 2020, , 53-58.	0.1	0
1539	Identification and characterization of phenylalanine ammonia lyase involved in biosynthesis of floral scents in<i>Prunus mume</i>. Acta Horticulturae, 2020, , 103-116.	0.1	0
1540	Identification of zygotic and nucellar seedlings in<i>Citrus limon</i>: the search for molecular markers. Acta Horticulturae, 2018, , 35-42.	0.1	0
1541	Identification of zygotic and nucellar seedlings in<i>Citrus limon</i>: the search for molecular markers. Acta Horticulturae, 2018, , 35-42.	0.1	0
1542	Genome-wide analysis of the family of light-harvesting chlorophyll a/b-binding proteins in pomegranate (<i>Punica granatum</i> L.). Acta Horticulturae, 2020, , 647-652.	0.1	1
1543	Validation of Reference Genes for Quantifying Changes in Physiological Gene Expression in Apple Tree under Cold Stress and Virus Infection. Research in Plant Disease, 2020, 26, 144-158.	0.3	0
1545	Sequencing Crop Genomes: A Gateway to Improve Tropical Agriculture. Tropical Life Sciences Research, 2016, 27, 93-114.	0.5	15
1546	Effects of two apple tonoplast sugar transporters, MdTST1 and MdTST2, on the accumulation of sugar. Scientia Horticulturae, 2022, 293, 110719.	1.7	5
1547	Expression Analysis of AUX/IAA Family Genes in Apple Under Salt Stress. Biochemical Genetics, 2022, 60, 1205-1221.	0.8	5
1549	The draft chromosome-level genome assembly of tetraploid ground cherry (Prunus fruticosa Pall.) from long reads. Genomics, 2021, 113, 4173-4183.	1.3	14
1550	Genome-Wide Analysis of the Apple CBL Family Reveals That Mdcbl10.1 Functions Positively in Modulating Apple Salt Tolerance. International Journal of Molecular Sciences, 2021, 22, 12430.	1.8	11
1551	A Novel Pear Scab (Venturia nashicola) Resistance Gene, Rvn3, from Interspecific Hybrid Pear (Pyrus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.6	3
1553	Analysis of CcGASA family members in Citrus clementina (Hort. ex Tan.) by a genome-wide approach. BMC Plant Biology, 2021, 21, 565.	1.6	9

#	ARTICLE	IF	CITATIONS
1554	Anticipated Polymorphic SSRs and Their Application Based on Next Generation Sequencing of Prunus Persica. Han'guk Yukchong Hakhoe Chi, 2021, 53, 350-360.	0.2	1
1556	Two divergent haplotypes from a highly heterozygous lychee genome suggest independent domestication events for early and late-maturing cultivars. Nature Genetics, 2022, 54, 73-83.	9.4	88
1557	Genetic characterization of elite tropical, subtropical and temperate maize germplasm based on genome-wide SNP markers. Cereal Research Communications, 0, , 1.	0.8	0
1558	Genomics of Plant Gene Banks: Prospects for Managing and Delivering Diversity in the Digital Age. Population Genomics, 2021, , 1.	0.2	0
1559	Significant improvement of apple (Malus domestica Borkh.) transgenic plant production by pre-transformation with a Baby boom transcription factor.. Horticulture Research, 2022, 9, .	2.9	18
1560	Pear genetics: Recent advances, new prospects, and a roadmap for the future. Horticulture Research, 2022, 9, .	2.9	12
1561	Ethylene response factor MdERF4 and histone deacetylase MdHDA19 suppress apple fruit ripening through histone deacetylation of ripening-related genes. Plant Physiology, 2022, 188, 2166-2181.	2.3	29
1562	The Roles of Floral Organ Genes in Regulating Rosaceae Fruit Development. Frontiers in Plant Science, 2021, 12, 644424.	1.7	7
1563	Perspectives and recent progress of genome-wide association studies (GWAS) in fruits. Molecular Biology Reports, 2022, 49, 5341-5352.	1.0	12
1564	Identification of Novel Candidate Genes Involved in Apple Cuticle Integrity and Russeting-Associated Triterpene Synthesis Using Metabolomic, Proteomic, and Transcriptomic Data. Plants, 2022, 11, 289.	1.6	8
1565	MYB transcription factor family in sweet cherry (Prunus avium L.): genome-wide investigation, evolution, structure, characterization and expression patterns. BMC Plant Biology, 2022, 22, 2.	1.6	28
1566	Function and transcriptional regulation of <i>CsKCS20</i> in the elongation of very-long-chain fatty acids and wax biosynthesis in <i>Citrus sinensis</i> flavedo. Horticulture Research, 2022, 9, .	2.9	11
1567	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. Horticulture Research, 2022, 9, .	2.9	10
1568	Whole genome re-sequencing and transcriptome reveal an alteration in hormone signal transduction in a more-branching mutant of apple. Gene, 2022, 818, 146214.	1.0	2
1569	A MdMa13 gene encoding tonoplast P3B-type ATPase regulates organic acid accumulation in apple. Scientia Horticulturae, 2022, 296, 110916.	1.7	3
1570	Phosphorylation of MdERF17 by MdMPK4 promotes apple fruit peel degreening during light/dark transitions. Plant Cell, 2022, 34, 1980-2000.	3.1	16
1571	Pigmentation and Flavonoid Metabolite Diversity in Immature â€˜Fujiâ€™ Apple Fruits in Response to Lights and Methyl Jasmonate. International Journal of Molecular Sciences, 2022, 23, 1722.	1.8	13
1572	Genome-wide identification of the NLR gene family in Haynaldia villosa by SMRT-RenSeq. BMC Genomics, 2022, 23, 118.	1.2	11

#	ARTICLE	IF	CITATIONS
1573	Genome Wide Identification and Characterization of Apple WD40 Proteins and Expression Analysis in Response to ABA, Drought, and Low Temperature. Horticulturae, 2022, 8, 141.	1.2	4
1574	Genome-wide identification and characterization of AINTEGUMENTA-LIKE (AIL) family genes in apple (Malus domestica Borkh.). Genomics, 2022, 114, 110313.	1.3	7
1575	Bulk segregation analysis in the <scp>NGS</scp> era: a review of its teenage years. Plant Journal, 2022, 109, 1355-1374.	2.8	58
1576	genome possesses genes, and contributes to the drought tolerance. Journal of Genetics, 2019, 98, .	0.4	2
1577	Scion Traits Related to Nutrient Distribution, Hormone Status, and Antioxidative Stress Tolerance Affect Rootstock Activity in Apple. SSRN Electronic Journal, 0, , .	0.4	0
1579	Identification of Mdmed Family, Key Role of Mdmed81, and Salicylic Acid at the Right Time of Year Triggers Mdmed81 to Induce Flowering in Malus Domestica. SSRN Electronic Journal, 0, , .	0.4	0
1580	Chromosome-Scale Cerasus Humilis Genome Assembly Reveals Gene Family Evolution and Possible Genomic Basis of Calcium Accumulation in Fruits. SSRN Electronic Journal, 0, , .	0.4	0
1581	Chromosome-scale assembly and population diversity analyses provide insights into the evolution of <i>Sapindus mukorossi</i>. Horticulture Research, 2022, 9, .	2.9	4
1582	Genetic architecture and genomic predictive ability of apple quantitative traits across environments. Horticulture Research, 2022, 9, .	2.9	20
1583	Genome-Wide Identification, Classification, and Expression Analysis of the HD-Zip Transcription Factor Family in Apple (Malus domestica Borkh.). International Journal of Molecular Sciences, 2022, 23, 2632.	1.8	3
1584	Genome-Wide Analysis of the Gene Structure, Expression and Protein Interactions of the Peach (Prunus persica) TIFY Gene Family. Frontiers in Plant Science, 2022, 13, 792802.	1.7	11
1585	The Chromosome-Scale Reference Genome of Macadamia tetraphylla Provides Insights Into Fatty Acid Biosynthesis. Frontiers in Genetics, 2022, 13, 835363.	1.1	4
1586	Complete chloroplast genome studies of different apple varieties indicated the origin of modern cultivated apples from <i>Malus sieversii</i> and <i>Malus sylvestris</i>. PeerJ, 2022, 10, e13107.	0.9	5
1587	Genome-wide analysis of the GRF gene family and their expression profiling in peach (<i>Prunus) Tj ETQq1 1 0.784314 rgBT /Overlock	1.0	8
1588	Phylogenomic conflict analyses in the apple genus <i>Malus</i> s.l. reveal widespread hybridization and allopolyploidy driving diversification, with insights into the complex biogeographic history in the Northern Hemisphere. Journal of Integrative Plant Biology, 2022, 64, 1020-1043.	4.1	31
1589	Genome-wide identification and comparative analysis of the PYL gene family in eight Rosaceae species and expression analysis of seeds germination in pear. BMC Genomics, 2022, 23, 233.	1.2	8
1590	Pan-Genome Analysis Reveals the Abundant Gene Presence/Absence Variations Among Different Varieties of Melon and Their Influence on Traits. Frontiers in Plant Science, 2022, 13, 835496.	1.7	8
1591	Genome sequence and population genomics provide insights into chromosomal evolution and phytochemical innovation of <i>Hippophae rhamnoides</i>. Plant Biotechnology Journal, 2022, 20, 1257-1273.	4.1	17

#	ARTICLE	IF	CITATIONS
1592	A chromosome-level genome sequence assembly of the red raspberry (Rubus idaeus L.). PLoS ONE, 2022, 17, e0265096.	1.1	11
1593	Phenotypic divergence between the cultivated apple (Malus domestica) and its primary wild progenitor (Malus sieversii). PLoS ONE, 2022, 17, e0250751.	1.1	7
1594	Transposon insertions regulate genomeâ€wide alleleâ€specific expression and underpin flower colour variations in apple (<i>Malus</i> spp.). Plant Biotechnology Journal, 2022, 20, 1285-1297.	4.1	21
1595	Comprehensive insights on Apple (MalusÂÃ—Âdomestica Borkh.) bud sport mutations and epigenetic regulations. Scientia Horticulturae, 2022, 297, 110979.	1.7	9
1596	Genome-wide TCP transcription factors analysis provides insight into their new functions in seasonal and diurnal growth rhythm in Pinus tabuliformis. BMC Plant Biology, 2022, 22, 167.	1.6	9
1597	Genome-wide identification of WOX gene family in apple and a functional analysis of MdWOX4b during adventitious root formation. Journal of Integrative Agriculture, 2022, 21, 1332-1345.	1.7	7
1598	Chromosome-scale Cerasus humilis genome assembly reveals gene family evolution and possible genomic basis of calcium accumulation in fruits. Scientia Horticulturae, 2022, 299, 111012.	1.7	5
1599	Variation in the promoter of the sorbitol dehydrogenase gene <i>MdSDH2</i> affects binding of the transcription factor MdABI3 and alters fructose content in apple fruit. Plant Journal, 2022, 109, 1183-1198.	2.8	15
1600	Comparative transcriptomic analysis of apple and peach fruits: insights into fruit type specification. Plant Journal, 2022, 109, 1614-1629.	2.8	4
1601	Deciphering Evolutionary Dynamics of WRKY I Genes in Rosaceae Species. Frontiers in Ecology and Evolution, 2021, 9, .	1.1	0
1602	Comprehensive Genome-Wide Identification and Transcript Profiling of GABA Pathway Gene Family in Apple (Malus domestica). Genes, 2021, 12, 1973.	1.0	2
1604	Celebrating Mendel, McClintock, and Darlington: On end-to-end chromosome fusions and nested chromosome fusions. Plant Cell, 2022, 34, 2475-2491.	3.1	7
1605	Elevating fruit carotenoid content in apple (Malus x domestica Borkh). Methods in Enzymology, 2022, , 63-98.	0.4	0
1606	Expression Characteristics in Roots, Phloem, Leaves, Flowers and Fruits of Apple circRNA. Genes, 2022, 13, 712.	1.0	5
1607	Malice at the Gates of Eden: current and future distribution of <i>Agrilus mali</i> threatening wild and domestic apples. Bulletin of Entomological Research, 2022, 112, 745-757.	0.5	2
1699	Study on Supergenus Rubus L.: Edible, Medicinal, and Phylogenetic Characterization. Plants, 2022, 11, 1211.	1.6	9
1700	Infrageneric Plastid Genomes of Cotoneaster (Rosaceae): Implications for the Plastome Evolution and Origin of C. wilsonii on Ulleung Island. Genes, 2022, 13, 728.	1.0	5
1701	Parental origins of the cultivated tetraploid sour cherry (<scp><i>Prunus cerasus</i></scp> L.). Plants People Planet, 2022, 4, 444-450.	1.6	5

#	ARTICLE	IF	CITATIONS
1702	The East Asian wild apples, <i>Malus baccata</i> (L.) Borkh and <i>Malus hupehensis</i> (Pamp.) Rehder., are additional contributors to the genomes of cultivated European and Chinese varieties. Molecular Ecology, 2023, 32, 5125-5139.	2.0	3
1703	Genetic characterization of cultivated apple (Malus x domestica Borkh.) in Morocco using microsatellite (SSR) markers. Ecological Genetics and Genomics, 2022, 23, 100122.	0.3	2
1704	Genome-wide Identification and Comparative Analysis of Genes Encoding AAPs in Apple (Malus Ã—) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.0	0
1705	Mapping of quantitative trait loci for scab resistance in apple (Malusâ€‰Ã—â€‰domestica) variety, Shireen. Molecular Biology Reports, 2022, 49, 5555-5566.	1.0	2
1706	HDACs Gene Family Analysis of Eight Rosaceae Genomes Reveals the Genomic Marker of Cold Stress in Prunus mume. International Journal of Molecular Sciences, 2022, 23, 5957.	1.8	7
1707	Root Breeding in the Post-Genomics Era: From Concept to Practice in Apple. Plants, 2022, 11, 1408.	1.6	4
1708	Taxonomic Uncertainty and Its Conservation Implications in Management, a Case from Pyrus hopeiensis (Rosaceae). Diversity, 2022, 14, 417.	0.7	4
1709	Genome-wide analyses of metal tolerance protein genes in apple (Malus domestica): Identification, characterization, expression and response to various metal ion stresses. Environmental and Experimental Botany, 2022, 201, 104948.	2.0	5
1710	MdGRF11, a growth-regulating factor, participates in the regulation of flowering time and interacts with MdTFL1/MdFT1 in apple. Plant Science, 2022, 321, 111339.	1.7	5
1711	Comprehensive identification of sugar transporters in the Malus spp. genomes reveals their potential functions in sugar accumulation in apple fruits. Scientia Horticulturae, 2022, 303, 111232.	1.7	4
1712	Next-Generation Sequencing Technologies: Approaches and Applications for Crop Improvement. Springer Protocols, 2022, , 31-94.	0.1	3
1713	An Update on Progress and Challenges of Crop Genomes. Springer Protocols, 2022, , 1-11.	0.1	1
1714	A Comprehensive Study of the WRKY Transcription Factor Family in Strawberry. Plants, 2022, 11, 1585.	1.6	5
1715	Wild Apples Are Not That Wild: Conservation Status and Potential Threats of Malus sieversii in the Mountains of Central Asia Biodiversity Hotspot. Diversity, 2022, 14, 489.	0.7	6
1716	Cultivated hawthorn (<i>Crataegus pinnatifida</i> var. major) genome sheds light on the evolution of Maleae (apple tribe). Journal of Integrative Plant Biology, 2022, 64, 1487-1501.	4.1	12
1717	Versatile roles of sorbitol in higher plants: luxury resource, effective defender or something else?. Planta, 2022, 256, .	1.6	10
1718	Multi-omics Approaches for Strategic Improvements of Crops Under Changing Climatic Conditions. , 2022, , 57-92.		1
1719	Evolution of Chromosome Number in Wild Onions (<i>Allium</i>, Amaryllidaceae). Systematic Botany, 2022, 47, 335-346.	0.2	0

#	Article	IF	Citations
1720	Research Progress on Genetic Basis of Fruit Quality Traits in Apple (Malus Ã— domestica). Frontiers in Plant Science, 0, 13, .	1.7	5
1721	A chromosomeâ€level genome of <i>Syringa oblata</i> provides new insights into chromosome formation in Oleaceae and evolutionary history of lilacs. Plant Journal, 2022, 111, 836-848.	2.8	9
1722	Genome-wide identification and comparative evolutionary analysis of sorbitol metabolism pathway genes in four Rosaceae species and three model plants. BMC Plant Biology, 2022, 22, .	1.6	5
1723	Morphological and olfactory tree traits influence the susceptibility and suitability of the apple species <i>Malus domestica</i> and <i>M. sylvestris</i> to the florivorous weevil <i>Anthonomus pomorum</i> (Coleoptera: Curculionidae). PeerJ, 0, 10, e13566.	0.9	0
1724	Genome-wide identification and characterization of the abiotic-stress-responsive lipoxygenase gene family in diploid woodland strawberry (Fragaria vesca). Journal of Integrative Agriculture, 2022, 21, 1982-1996.	1.7	2
1725	Molecular Mechanisms Regulating the Columnar Tree Architecture in Apple. Forests, 2022, 13, 1084.	0.9	3
1726	Computational analysis of potential candidate genes involved in the cold stress response of ten Rosaceae members. BMC Genomics, 2022, 23, .	1.2	1
1727	Utilizing paralogues for phylogenetic reconstruction has the potential to increase species tree support and reduce gene tree discordance in target enrichment data. Molecular Ecology Resources, 2022, 22, 3018-3034.	2.2	8
1728	The inhibitory effects of Ulva prolifera extracts on early growth of Spartina alterniflora and the underlying mechanisms. Journal of Environmental Management, 2022, 319, 115639.	3.8	4
1729	Identification of MdMED family, key role of MdMED81, and salicylic acid at the right time of year triggers MdMED81 to induce flowering in Malus domestica. Scientia Horticulturae, 2022, 304, 111341.	1.7	3
1730	An apple somatic mutation of delayed fruit maturation date is primarily caused by a retrotransposon insertionâ€associated large deletion. Plant Journal, 2022, 111, 1609-1625.	2.8	4
1731	Genetic Resources, Breeding, and Molecular Genetic Markers for Orchard Improvement and Management. Impact of Meat Consumption on Health and Environmental Sustainability, 2022, , 70-115.	0.4	0
1732	Methylation of a MITE insertion in the <i>MdRFNR1-1</i> promoter is positively associated with its allelic expression in apple in response to drought stress. Plant Cell, 2022, 34, 3983-4006.	3.1	20
1734	Characterization of CBL-Interacting Protein Kinasesâ€™ Gene Family and Expression Pattern Reveal Their Important Roles in Response to Salt Stress in Poplar. Forests, 2022, 13, 1353.	0.9	5
1735	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. Journal of Horticultural Science and Biotechnology, 2023, 98, 178-193.	0.9	1
1736	A Ca2+-sensor switch for tolerance to elevated salt stress in Arabidopsis. Developmental Cell, 2022, 57, 2081-2094.e7.	3.1	30
1737	Multi-omics analyses reveal <i>MdMYB10</i> hypermethylation being responsible for a bud sport of apple fruit color. Horticulture Research, 2022, 9, .	2.9	4
1738	High hydrostatic pressure assisted by food-grade enzymes as a sustainable approach for the development of an antioxidant ingredient. LWT - Food Science and Technology, 2022, 169, 113968.	2.5	3

#	ARTICLE	IF	CITATIONS
1739	Genomic Approaches to Improve Abiotic Stress Tolerance in Apple (Malusâ€‰Ã—â€‰ domestica). , 2022, , 1-17.		1
1740	State of the art of omics technologies in horticultural crops. , 2022, , 1-14.		1
1741	Salicylic acid treatment inhibits ethylene synthesis and starch-sugar conversion to maintain apple fruit quality during shelf life. Scientia Horticulturae, 2023, 308, 111586.	1.7	7
1742	Chasing Consistency: An Update of the TCP Gene Family of Malus Ã— Domestica. Genes, 2022, 13, 1696.	1.0	2
1743	The role of invasive plant species in drought resilience in agriculture: the case of sweet briar (<i>Rosa rubiginosa</i> L.). Journal of Experimental Botany, 2023, 74, 2799-2810.	2.4	3
1744	Overexpression of PSY1 increases fruit skin and flesh carotenoid content and reveals associated transcription factors in apple (Malus Ã— domestica). Frontiers in Plant Science, 0, 13, .	1.7	7
1745	Transcriptome analysis reveals candidate genes involved in nitrogen deficiency stress in apples. Journal of Plant Physiology, 2022, 279, 153822.	1.6	11
1746	A phased, chromosome-scale genome of â€˜Honeycrispâ€™ apple (Malus domestica). GigaByte, 0, 2022, 1-15.	0.0	6
1747	How plants conquered land: evolution of terrestrial adaptation. Journal of Evolutionary Biology, 2023, 36, 5-14.	0.8	6
1748	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.	2.3	2
1749	MdMYB52 regulates lignin biosynthesis upon the suberization process in apple. Frontiers in Plant Science, 0, 13, .	1.7	2
1750	The Apricot Genome. Compendium of Plant Genomes, 2022, , 41-67.	0.3	0
1751	The Longan (Dimocarpus longan) Genome. Compendium of Plant Genomes, 2022, , 87-109.	0.3	0
1752	Chinese Jujube: Crop Background and Genome Sequencing. Compendium of Plant Genomes, 2022, , 69-86.	0.3	0
1753	Molecular characterization of intergeneric hybrids between <i>Malus</i> and <i>Pyrus</i>. Horticulture Research, 2023, 10, .	2.9	2
1756	DNA profiling with the 20K apple SNP array reveals Malus domestica hybridization and admixture in M. sieversii, M.Âorientalis, and M. sylvestris genebank accessions. Frontiers in Plant Science, 0, 13, .	1.7	2
1757	Genome-wide analysis of MADS-box families and their expressions in flower organs development of pineapple (Ananas comosus (L.) Merr.). Frontiers in Plant Science, 0, 13, .	1.7	3
1758	<scp>MPK6â€mediated HY5</scp> phosphorylation regulates <scp>lightâ€induced</scp> anthocyanin accumulation in apple fruit. Plant Biotechnology Journal, 2023, 21, 283-301.	4.1	18

#	ARTICLE	IF	CITATIONS
1759	Genome-wide identification and expression analysis of the MADS-box gene family during female and male flower development in Juglans mandshurica. Frontiers in Plant Science, 0, 13, .	1.7	2
1760	Building a foundation for gene family analysis in Rosaceae genomes with a novel workflow: A case study in Pyrus architecture genes. Frontiers in Plant Science, 0, 13, .	1.7	6
1761	Identification of the HAK gene family reveals their critical response to potassium regulation during adventitious root formation in apple rootstock. Horticultural Plant Journal, 2023, 9, 45-59.	2.3	3
1762	Analysis of the Small Auxin-Up RNA (SAUR) Genes Regulating Root Growth Angle (RGA) in Apple. Genes, 2022, 13, 2121.	1.0	2
1763	A chromosome-length genome assembly and annotation of blackberry (<i>Rubus argutus</i>, cv.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.8	9
1764	Zinc Fingerâ€"homeodomain Gene Family in Apple and Their Expression Analysis in Apple Rootstock Malus hupehensis Under Abiotic Stress. Journal of the American Society for Horticultural Science, 2022, 147, 312-321.	0.5	0
1765	The Feasibility of Using Autofluorescence to Detect Lignin Deposition Pattern during Defense Response in Apple Roots to Pythium ultimum Infection. Horticulturae, 2022, 8, 1085.	1.2	1
1767	Genome-wide identification and characterization of SPX domain-containing proteins and their responses to phosphorus and/or nitrogen deficiency in apple (Malus domestica Borkh.). Scientia Horticulturae, 2023, 310, 111767.	1.7	2
1768	Identification and functional analysis of glycosyltransferase catalyzing the synthesis of phlorizin and trilobatin in Lithocarpus polystachyus Rehd.. Industrial Crops and Products, 2023, 192, 116056.	2.5	3
1769	MdPP2C24/37, Protein Phosphatase Type 2Cs from Apple, Interact with MdPYL2/12 to Negatively Regulate ABA Signaling in Transgenic Arabidopsis. International Journal of Molecular Sciences, 2022, 23, 14375.	1.8	4
1770	Assessment of fire blight introduction in the wild apple forests of Kazakhstan. Biodiversity, 0, , 1-6.	0.5	1
1771	Analyses of Cullin1 homologs reveal functional redundancy in S-RNase-based self-incompatibility and evolutionary relationships in eudicots. Plant Cell, 2023, 35, 673-699.	3.1	2
1772	SSRâ€based DNA fingerprinting of fruit crops. Crop Science, 2023, 63, 390-459.	0.8	5
1773	The genome sequence of the apple, MalusÂdomesticaÂ(Suckow) Borkh., 1803. Wellcome Open Research, 0, 7, 297.	0.9	1
1774	The genome sequence of the European crab apple, Malus sylvestrisÂ(L.) Mill., 1768. Wellcome Open Research, 0, 7, 296.	0.9	2
1775	Deciphering the Plant Hormones Cross-Talk during Fruit Development: A Review. , 0, , .		0
1776	Regionally Adapted Model of an Ideal MalusÃ—domestica Borkh Apple Variety for Industrial-Scale Cultivation in European Russia. Agriculture (Switzerland), 2022, 12, 2124.	1.4	2
1777	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, .	2.9	12

#	Article	IF	Citations
1778	Genome-wide identification and stress response analysis of cyclophilin gene family in apple (Malus Ã—) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.2	4
1779	De novo transcriptome assembly and functional analysis reveal a dihydrochalcone 3-hydroxylase(DHC3H) of wild Malus species that produces sieboldin in vivo. Frontiers in Plant Science, 0, 13, .	1.7	3
1781	Phenotypic and transcriptomic analyses reveal major differences between apple and pear scab nonhost resistance. , 0, 3, .		0
1782	The Role of Italy in the Use of Advanced Plant Genomic Techniques on Fruit Trees: State of the Art and Future Perspectives. International Journal of Molecular Sciences, 2023, 24, 977.	1.8	5
1783	Genome-wide characterization of Ficus carica MADS-box transcription factors with a focus on their roles during fruit development. Horticulture Environment and Biotechnology, 0, , .	0.7	0
1784	Bearing Fruit: Miocene Apes and Rosaceous Fruit Evolution. Biological Theory, 0, , .	0.8	0
1785	Genome-wide identification and expression profile analysis of SWEET genes in Chinese jujube. PeerJ, 0, 11, e14704.	0.9	5
1786	Genome-wide identification, characterization and evolutionary dynamic of invertase gene family in apple, and revealing its roles in cold tolerance. International Journal of Biological Macromolecules, 2023, 229, 766-777.	3.6	7
1787	Biotechnological Interventions for Reducing the Juvenility in Perennials. Horticulturae, 2023, 9, 33.	1.2	2
1788	Production and assortment of apple in Serbia. Biljni Lekar, 2022, 50, 411-426.	0.0	1
1789	Mfu16 is an unstable fire blight resistance QTL on linkage group 16 of Malus fusca MAL0045. , 0, , .		1
1790	Genetic linkage maps and QTLs associated with fruit skin color and acidity in apple (Malus Ã—) Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.7	2
1791	Advances in genomics for diversity studies and trait improvement in temperate fruit and nut crops under changing climatic scenarios. Frontiers in Plant Science, 0, 13, .	1.7	0
1792	The rhizosphere Microbiome of Malus sieversii (Ldb.) Roem. in the geographic and environmental gradients of China's Xinjiang. BMC Microbiology, 2023, 23, .	1.3	1
1793	Other Sources of Sugar. , 2012, , 323-539.		0
1794	Genome structure-based Juglandaceae phylogenies contradict alignment-based phylogenies and substitution rates vary with DNA repair genes. Nature Communications, 2023, 14, .	5.8	13
1795	Fruit growth and development in apple: a molecular, genomics and epigenetics perspective. Frontiers in Plant Science, 0, 14, .	1.7	1
1797	Time-course RNA-sequencing and Co-expression Modules Revealed a Critical Salt Response Regulatory Network in Apple. Journal of the American Society for Horticultural Science, 2023, 148, 53-63.	0.5	0

#	Article	IF	Citations
1798	Chromosome-Level Assembly of Flowering Cherry (Prunus campanulata) Provides Insight into Anthocyanin Accumulation. Genes, 2023, 14, 389.	1.0	1
1799	Genome-wide identification of apple auxin receptor family genes and functional characterization of MdAFB1. Horticultural Plant Journal, 2023, , .	2.3	0
1801	Malus Species with Diverse Bloom Times Exhibit Variable Rates of Floral Development. Journal of the American Society for Horticultural Science, 2023, 148, 64-73.	0.5	2
1802	Genome assembly, resequencing and genomeâ€wide association analyses provide novel insights into the origin, evolution and flower colour variations of flowering cherry. Plant Journal, 2023, 114, 519-533.	2.8	4
1803	Comparative transcriptome analysis of apple cultivars reveals key genes and pathways in response to Alternaria alternata apple pathotype infection. Horticultural Plant Journal, 2023, , .	2.3	4
1804	Comprehensive genomic analysis of the Rho GTPases regulators in seven Rosaceae species revealed that PbrGDI1 controls pollen tube growth in Pyrus via mediating cellulose deposition. International Journal of Biological Macromolecules, 2023, 235, 123860.	3.6	0
1805	Population Structure and Association Mapping for Agronomical and Biochemical Traits of a Large Spanish Apple Germplasm. Plants, 2023, 12, 1249.	1.6	2
1806	Genome-Wide Analysis of MIKCC-Type MADS-Box Genes Reveals Their Involvement in Flower Development in Malus Lineage. Horticulturae, 2023, 9, 373.	1.2	0
1809	Genetic information from phased SNP array data can improve assemblies of whole genome sequences. Acta Horticulturae, 2023, , 81-88.	0.1	0
1810	Marker-assisted breeding (MAB) on apple and pear and new approaches for QTLs and major gene genotyping involved in disease resistance. Acta Horticulturae, 2023, , 221-230.	0.1	1
1811	Genomic selection in apple: lessons from preliminary studies. Acta Horticulturae, 2023, , 113-122.	0.1	0
1812	Genome-Wide Identification and Expression Analysis of CAMTA Gene Family Implies PbrCAMTA2 Involved in Fruit Softening in Pear. Horticulturae, 2023, 9, 467.	1.2	3
1813	A chromosome-scale genome assembly of Malus domestica, a multi-stress resistant apple variety. Genomics, 2023, 115, 110627.	1.3	6
1814	SnRK1 kinase-mediated phosphorylation of transcription factor bZIP39 regulates sorbitol metabolism in apple. Plant Physiology, 2023, 192, 2123-2142.	2.3	5
1815	Genome-wide analysis of UDP-glycosyltransferasesÂfamily and identification of UGT genes involved in abiotic stress and flavonol biosynthesis in NicotianaÂtabacum. BMC Plant Biology, 2023, 23, .	1.6	8
1816	Apples: Role of Nutraceutical Compounds. , 2023, , 1-56.		0
1822	Role of integrative omics and bioinformatics approaches in berries research and genetic improvement. , 2023, , 159-192.		0
1866	Malus Species: Germplasm Conservation and Utilization. , 2023, , 1-36.		0

#	Article	IF	Citations
1868	Conservation and Use of Temperate Fruit and Nut Genetic Resources. , 2023, , 1-25.		0
1870	Targeted Gene Editing in Pome Fruit Genetics and Breeding: State-of-the-Art, Application Potential and Perspectives. , 2024, , 309-345.		0
1872	Apples: Role of Nutraceutical Compounds. , 2023, , 843-897.		0
1883	Water Loss: A Postharvest Quality Marker in Apple Storage. Food and Bioprocess Technology, 0, , .	2.6	0
1886	Burning questions for fire blight research: I. Genomics and evolution of Erwinia amylovora and analyses of host-pathogen interactions. , 0, , .		0
1891	Editing of banana, apple, and grapevine genomes using the CRISPR-Cas9 system. , 2024, , 349-364.		0