

High-quality de novo assembly of the apple genome and development

Nature Genetics

49, 1099-1106

DOI: [10.1038/ng.3886](https://doi.org/10.1038/ng.3886)

Citation Report

#	ARTICLE	IF	CITATIONS
1	Genetic diversity, population structure, and linkage disequilibrium of elite and local apple accessions from Belgium using the IRSC array. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	31
2	Global DNA Methylation Patterns Can Play a Role in Defining Terroir in Grapevine (<i>Vitis vinifera</i> cv.) <i>Tj ETQq1 1 0.784314 rgBT /Overlook</i>	1.7	58
3	Multiple Copies of a Simple MYB-Binding Site Confers Trans-regulation by Specific Flavonoid-Related R2R3 MYBs in Diverse Species. <i>Frontiers in Plant Science</i> , 2017, 8, 1864.	1.7	38
4	Genome-Wide Association Mapping of Flowering and Ripening Periods in Apple. <i>Frontiers in Plant Science</i> , 2017, 8, 1923.	1.7	73
5	Strategies for optimizing BioNano and Dovetail explored through a second reference quality assembly for the legume model, <i>Medicago truncatula</i> . <i>BMC Genomics</i> , 2017, 18, 578.	1.2	54
6	Draft Sequencing of the Heterozygous Diploid Genome of Satsuma (<i>Citrus unshiu</i> Marc.) Using a Hybrid Assembly Approach. <i>Frontiers in Genetics</i> , 2017, 8, 180.	1.1	49
7	An integrated approach for increasing breeding efficiency in apple and peach in Europe. <i>Horticulture Research</i> , 2018, 5, 11.	2.9	98
8	Meta-analysis of chromosome-scale crossover rate variation in eukaryotes and its significance to evolutionary genomics. <i>Molecular Ecology</i> , 2018, 27, 2477-2497.	2.0	144
9	Chromosome-scale scaffolding of the black raspberry (<i>Rubus occidentalis</i> L.) genome based on chromatin interaction data. <i>Horticulture Research</i> , 2018, 5, 8.	2.9	50
10	QTLs for susceptibility to <i>Stemphylium vesicarium</i> in pear. <i>Molecular Breeding</i> , 2018, 38, 1.	1.0	7
11	Genetics of resistance in apple against <i>Venturia inaequalis</i> (Wint.) Cke. <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	0.6	43
12	Evolutionary diversification of galactinol synthases in Rosaceae: adaptive roles of galactinol and raffinose during apple bud dormancy. <i>Journal of Experimental Botany</i> , 2018, 69, 1247-1259.	2.4	33
13	From genes to networks. <i>Nature Plants</i> , 2018, 4, 55-55.	4.7	2
14	Identification of candidate genes at the Dp-fl locus conferring resistance against the rosy apple aphid <i>Dysaphis plantaginea</i> . <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	0.6	3
15	Exploring DNA variant segregation types in pooled genome sequencing enables effective mapping of weeping trait in <i>Malus</i> . <i>Journal of Experimental Botany</i> , 2018, 69, 1499-1516.	2.4	33
16	Epistatic fire blight resistance QTL alleles in the apple cultivar "Enterprise"™ and selection X-6398 discovered and characterized through pedigree-informed analysis. <i>Molecular Breeding</i> , 2018, 38, 1.	1.0	51
17	Two QTL characterized for soft scald and soggy breakdown in apple (<i>Malus domestica</i>) through pedigree-based analysis of a large population of interconnected families. <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	0.6	26
18	Comparative epigenomics reveals evolution of duplicated genes in potato and tomato. <i>Plant Journal</i> , 2018, 93, 460-471.	2.8	33

#	ARTICLE	IF	CITATIONS
19	Exploiting natural variation for accelerating discoveries in plant specialized metabolism. <i>Phytochemistry Reviews</i> , 2018, 17, 17-36.	3.1	9
20	Acibenzolar-S-Methyl Reprograms Apple Transcriptome Toward Resistance to Rosy Apple Aphid. <i>Frontiers in Plant Science</i> , 2018, 9, 1795.	1.7	17
21	Empirical Research on Domestic Violence in Contemporary China: Continuity and Advances. <i>International Journal of Offender Therapy and Comparative Criminology</i> , 2018, 62, 4879-4887.	0.8	18
22	Transposable Elements as Tool for Crop Improvement. <i>Advances in Botanical Research</i> , 2018, , 165-202.	0.5	11
23	Chromosome level high-density integrated genetic maps improve the <i>Pyrus bretschneideri</i> "DangshanSuli" v1.0 genome. <i>BMC Genomics</i> , 2018, 19, 833.	1.2	34
24	Leveraging Transcriptome Data for Enhanced Gene Expression Analysis in Apple. <i>Journal of the American Society for Horticultural Science</i> , 2018, 143, 333-346.	0.5	4
25	Comprehensive genomic analysis of the TYROSINE AMINOTRANSFERASE (TAT) genes in apple (<i>Malus domestica</i>) reveals stresses in plants. <i>Plant Physiology and Biochemistry</i> , 2018, 133, 81-91.	2.8	16
26	Anthocyanin accumulation correlates with hormones in the fruit skin of "Red Delicious" and its four generation bud sport mutants. <i>BMC Plant Biology</i> , 2018, 18, 363.	1.6	55
27	Evaluation and Recommendations for Routine Genotyping Using Skim Whole Genome Re-sequencing in Canola. <i>Frontiers in Plant Science</i> , 2018, 9, 1809.	1.7	24
28	Epigenetic Regulations of Fleshy Fruit Development and Ripening and Their Potential Applications to Breeding Strategies. <i>Advances in Botanical Research</i> , 2018, 88, 327-360.	0.5	7
29	Purge Haplotigs: allelic contig reassignment for third-gen diploid genome assemblies. <i>BMC Bioinformatics</i> , 2018, 19, 460.	1.2	706
30	Genome-wide analyses of genes encoding FK506-binding proteins reveal their involvement in abiotic stress responses in apple. <i>BMC Genomics</i> , 2018, 19, 707.	1.2	16
31	Genome-Wide Identification, Molecular Evolution, and Expression Divergence of Aluminum-Activated Malate Transporters in Apples. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2807.	1.8	22
32	RNA sequencing analysis provides new insights into dynamic molecular responses to <i>Valsa mali</i> pathogenicity in apple "Changfu No. 2". <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	0.6	6
33	Genome-Wide Characterization of DNA Demethylase Genes and Their Association with Salt Response in <i>Pyrus</i> . <i>Genes</i> , 2018, 9, 398.	1.0	14
34	Ten steps to get started in Genome Assembly and Annotation. <i>F1000Research</i> , 2018, 7, 148.	0.8	85
35	Genome-wide identification and characterization of apple long-chain Acyl-CoA synthetases and expression analysis under different stresses. <i>Plant Physiology and Biochemistry</i> , 2018, 132, 320-332.	2.8	41
36	Genomic approaches for studying crop evolution. <i>Genome Biology</i> , 2018, 19, 140.	3.8	54

#	ARTICLE	IF	CITATIONS
37	Bioinformatic characterisation of the effector repertoire of the strawberry pathogen <i>Phytophthora cactorum</i> . <i>PLoS ONE</i> , 2018, 13, e0202305.	1.1	40
38	Retrospective and perspective of plant epigenetics in China. <i>Journal of Genetics and Genomics</i> , 2018, 45, 621-638.	1.7	45
39	Genome-wide identification and expression analysis of brassinosteroid biosynthesis and metabolism genes regulating apple tree shoot and lateral root growth. <i>Journal of Plant Physiology</i> , 2018, 231, 68-85.	1.6	16
40	Towards map-based cloning of FB_Mfu10: identification of a receptor-like kinase candidate gene underlying the <i>Malus fusca</i> fire blight resistance locus on linkage group 10. <i>Molecular Breeding</i> , 2018, 38, 106.	1.0	28
41	Novo&Stitch: accurate reconciliation of genome assemblies via optical maps. <i>Bioinformatics</i> , 2018, 34, i43-i51.	1.8	16
42	Identification of QTLs Associated with Conversion of Sucrose to Hexose in Mature Fruit of Japanese Pear. <i>Plant Molecular Biology Reporter</i> , 2018, 36, 643-652.	1.0	12
43	Dynamics and function of DNA methylation in plants. <i>Nature Reviews Molecular Cell Biology</i> , 2018, 19, 489-506.	16.1	1,145
44	Identification of a leucine-rich repeat receptor-like serine/threonine-protein kinase as a candidate gene for Rvi12 (Vb)-based apple scab resistance. <i>Molecular Breeding</i> , 2018, 38, 1.	1.0	8
45	Characterization of 25 full-length S-RNase alleles, including flanking regions, from a pool of resequenced apple cultivars. <i>Plant Molecular Biology</i> , 2018, 97, 279-296.	2.0	17
46	A Single-Nucleotide Polymorphism in the Promoter of a Hairpin RNA Contributes to <i>Alternaria alternata</i> Leaf Spot Resistance in Apple (<i>Malus domestica</i>). <i>Plant Cell</i> , 2018, 30, 1924-1942.	3.1	54
47	Genome-wide analysis and identification of the SMXL gene family in apple (<i>Malus domestica</i>). <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	0.6	12
48	Woody Ornamentals of the Temperate Zone. <i>Handbook of Plant Breeding</i> , 2018, , 803-887.	0.1	9
49	Cherry Breeding: Sweet Cherry (<i>Prunus avium</i> L.) and Sour Cherry (<i>Prunus cerasus</i> L.). , 2018, , 31-88.		2
50	RNA-sequencing Analysis Identifies Genes Associated with Chilling-mediated Endodormancy Release in Apple. <i>Journal of the American Society for Horticultural Science</i> , 2018, 143, 194-206.	0.5	21
51	A transcriptome analysis of two apple (<i>Malus domestica</i>) cultivars with different flowering abilities reveals a gene network module associated with floral transitions. <i>Scientia Horticulturae</i> , 2018, 239, 269-281.	1.7	20
52	Genome-wide identification, characterization and expression analysis of long non-coding RNAs in different tissues of apple. <i>Gene</i> , 2018, 666, 44-57.	1.0	28
53	Developing gene-tagged molecular markers for evaluation of genetic association of apple SWEET genes with fruit sugar accumulation. <i>Horticulture Research</i> , 2018, 5, 14.	2.9	73
54	Structural and functional analyses of genes encoding VQ proteins in apple. <i>Plant Science</i> , 2018, 272, 208-219.	1.7	46

#	ARTICLE	IF	CITATIONS
55	Apple fruit acidity is genetically diversified by natural variations in three hierarchical epistatic genes: <i>MdSAUR37</i> , <i>MdPP2CH</i> and <i>MdALMTII</i> . <i>Plant Journal</i> , 2018, 95, 427-443.	2.8	71
56	Transposable elements: all mobile, all different, some stress responsive, some adaptive?. <i>Current Opinion in Genetics and Development</i> , 2018, 49, 106-114.	1.5	81
57	A near complete, chromosome-scale assembly of the black raspberry (<i>Rubus occidentalis</i>) genome. <i>GigaScience</i> , 2018, 7, .	3.3	86
58	Mediation of Flower Induction by Gibberellin and its Inhibitor Paclobutrazol: mRNA and miRNA Integration Comprises Complex Regulatory Cross-Talk in Apple. <i>Plant and Cell Physiology</i> , 2018, 59, 2288-2307.	1.5	21
59	Genome-Wide Analysis and Cloning of the Apple Stress-Associated Protein Gene Family Reveals <i>MdSAP15</i> , Which Confers Tolerance to Drought and Osmotic Stresses in Transgenic Arabidopsis. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2478.	1.8	40
60	Improved <i>Brassica rapa</i> reference genome by single-molecule sequencing and chromosome conformation capture technologies. <i>Horticulture Research</i> , 2018, 5, 50.	2.9	224
61	Ethylene receptors and related proteins in climacteric and non-climacteric fruits. <i>Plant Science</i> , 2018, 276, 63-72.	1.7	79
62	Ethylene â€œdependent and â€œindependent superficial scald resistance mechanisms in â€œGranny Smithâ€™ apple fruit. <i>Scientific Reports</i> , 2018, 8, 11436.	1.6	65
63	Identification and characterization of histone modification gene family reveal their critical responses to flower induction in apple. <i>BMC Plant Biology</i> , 2018, 18, 173.	1.6	21
64	Expansion and evolutionary patterns of GDSL-type esterases/lipases in Rosaceae genomes. <i>Functional and Integrative Genomics</i> , 2018, 18, 673-684.	1.4	37
65	A high-quality genome sequence of <i>Rosa chinensis</i> to elucidate ornamental traits. <i>Nature Plants</i> , 2018, 4, 473-484.	4.7	224
66	The red bayberry genome and genetic basis of sex determination. <i>Plant Biotechnology Journal</i> , 2019, 17, 397-409.	4.1	61
67	Natural variation in cytokinin maintenance improves salt tolerance in apple rootstocks. <i>Plant, Cell and Environment</i> , 2019, 42, 424-436.	2.8	32
68	The use of a fertile doubled haploid apple line for QTL analysis of fruit traits. <i>Breeding Science</i> , 2019, 69, 410-419.	0.9	7
69	A novel miRNA negatively regulates resistance to <i>Glomerella</i> leaf spot by suppressing expression of an NBS gene in apple. <i>Horticulture Research</i> , 2019, 6, 93.	2.9	30
70	Differential Chloroplast Proteomics of Temperature Adaptation in Apple (<i>Malus x domestica</i> Borkh.) Microshoots. <i>Proteomics</i> , 2019, 19, e1800142.	1.3	2
71	Genome-wide identification and analysis of the MADS-box gene family and its potential role in fruit development and ripening in red bayberry (<i>Morella rubra</i>). <i>Gene</i> , 2019, 717, 144045.	1.0	13
72	Cell type-specific gene expression underpins remodelling of cell wall pectin in exocarp and cortex during apple fruit development. <i>Journal of Experimental Botany</i> , 2019, 70, 6085-6099.	2.4	5

#	ARTICLE	IF	CITATIONS
73	Transcriptome Analysis Reveals New Insights into <i>MdBAK1</i> -Mediated Plant Growth in <i>Malus domestica</i> . <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 9757-9771.	2.4	9
74	A Multifaceted Overview of Apple Tree Domestication. <i>Trends in Plant Science</i> , 2019, 24, 770-782.	4.3	46
75	High-quality, genome-wide SNP genotypic data for pedigreed germplasm of the diploid outbreeding species apple, peach, and sweet cherry through a common workflow. <i>PLoS ONE</i> , 2019, 14, e0210928.	1.1	67
76	Systematic identification of long noncoding <i>scnRNA</i> s expressed during light-induced anthocyanin accumulation in apple fruit. <i>Plant Journal</i> , 2019, 100, 572-590.	2.8	91
77	Common and specific responses to iron and phosphorus deficiencies in roots of apple tree (<i>Malus domestica</i>). <i>Journal of Experimental Botany</i> , 2019, 60, 1515-1526.	2.9	15
78	Whole-Genome Duplications in Pear and Apple. <i>Compendium of Plant Genomes</i> , 2019, , 279-299.	0.3	11
79	A high-quality <i>Actinidia chinensis</i> (kiwifruit) genome. <i>Horticulture Research</i> , 2019, 6, 117.	2.9	109
80	Genetic mechanisms in the repression of flowering by gibberellins in apple (<i>Malus x domestica</i> Borkh.). <i>BMC Genomics</i> , 2019, 20, 747.	1.2	56
81	Genome sequences of horticultural plants: past, present, and future. <i>Horticulture Research</i> , 2019, 6, 112.	2.9	108
82	Identification of DNA methyltransferases and demethylases in <i>Solanum melongena</i> L., and their transcription dynamics during fruit development and after salt and drought stresses. <i>PLoS ONE</i> , 2019, 14, e0223581.	1.1	20
83	AppleMDO: A Multi-Dimensional Omics Database for Apple Co-Expression Networks and Chromatin States. <i>Frontiers in Plant Science</i> , 2019, 10, 1333.	1.7	44
84	Single-pollen-cell sequencing for gamete-based phased diploid genome assembly in plants. <i>Genome Research</i> , 2019, 29, 1889-1899.	2.4	28
85	Genome-wide association studies in apple reveal loci of large effect controlling apple polyphenols. <i>Horticulture Research</i> , 2019, 6, 107.	2.9	50
86	Whole-genome DNA methylation patterns and complex associations with gene expression associated with anthocyanin biosynthesis in apple fruit skin. <i>Planta</i> , 2019, 250, 1833-1847.	1.6	53
87	Transcriptome Sequencing and Expression Analysis of Genes Related to Anthocyanin Biosynthesis in Leaves of <i>Malus domestica</i> Profusion™ Infected by Japanese Apple Rust. <i>Forests</i> , 2019, 10, 665.	0.9	8
88	The population genetics of structural variants in grapevine domestication. <i>Nature Plants</i> , 2019, 5, 965-979.	4.7	229
89	An artificial miRNA as a new tool to silence and explore gene functions in apple. <i>Transgenic Research</i> , 2019, 28, 611-626.	1.3	9
90	Haplotype-resolved genomes of geminivirus-resistant and geminivirus-susceptible African cassava cultivars. <i>BMC Biology</i> , 2019, 17, 75.	1.7	42

#	ARTICLE	IF	CITATIONS
91	Development of an integrated 200K <sc>SNP</sc> genotyping array and application for genetic mapping, genome assembly improvement and genome wide association studies in pear (<i>Pyrus</i>). Plant Biotechnology Journal, 2019, 17, 1582-1594.	4.1	46
92	Aligning optical maps to de Bruijn graphs. Bioinformatics, 2019, 35, 3250-3256.	1.8	4
93	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
94	Comparative RNA-Sequencing and DNA Methylation Analyses of Apple (<i>Malus domestica</i> Borkh.) Buds with Diverse Flowering Capabilities Reveal Novel Insights into the Regulatory Mechanisms of Flower Bud Formation. Plant and Cell Physiology, 2019, 60, 1702-1721.	1.5	27
95	A chromosome-scale genome assembly of cucumber (<i>Cucumis sativus</i> L.). GigaScience, 2019, 8, .	3.3	138
96	Transcriptome Changes during Major Developmental Transitions Accompanied with Little Alteration of DNA Methylome in Two Pleurotus Species. Genes, 2019, 10, 465.	1.0	8
97	Contribution of methylation regulation of MpDREB2A promoter to drought resistance of Mauls prunifolia. Plant and Soil, 2019, 441, 15-32.	1.8	16
98	The complete chloroplast genome of <i>Malus sieversii</i> (Rosaceae), a wild apple tree in Xinjiang, China. Mitochondrial DNA Part B: Resources, 2019, 4, 983-984.	0.2	3
99	Genome-Wide Association Studies in Apple Reveal Loci for Aroma Volatiles, Sugar Composition, and Harvest Date. Plant Genome, 2019, 12, 180104.	1.6	70
100	Genome-Wide Distribution of Novel Ta-3A1 Mini-Satellite Repeats and Its Use for Chromosome Identification in Wheat and Related Species. Agronomy, 2019, 9, 60.	1.3	8
101	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
102	Role of Cytokinin, Strigolactone, and Auxin Export on Outgrowth of Axillary Buds in Apple. Frontiers in Plant Science, 2019, 10, 616.	1.7	38
103	Genetic characterization of flesh browning trait in apple using the non-browning cultivar 'Aori 27'™. Tree Genetics and Genomes, 2019, 15, 1.	0.6	10
104	Tools and Strategies for Long-Read Sequencing and De Novo Assembly of Plant Genomes. Trends in Plant Science, 2019, 24, 700-724.	4.3	80
105	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
106	Diversity and dynamics of DNA methylation: epigenomic resources and tools for crop breeding. Breeding Science, 2019, 69, 191-204.	0.9	30
107	OMGS: Optical Map-Based Genome Scaffolding. Lecture Notes in Computer Science, 2019, , 190-207.	1.0	1
108	Dynamic Cytosine DNA Methylation Patterns Associated with mRNA and siRNA Expression Profiles in Alternate Bearing Apple Trees. Journal of Agricultural and Food Chemistry, 2019, 67, 5250-5264.	2.4	14

#	ARTICLE	IF	CITATIONS
109	Gibberellic acid induced parthenocarpic "Honeycrisp" apples (<i>Malus domestica</i>) exhibit reduced ovary width and lower acidity. <i>Horticulture Research</i> , 2019, 6, 41.	2.9	29
110	Identification of candidate genes responsible for the susceptibility of apple (<i>Malus domestica</i>) to overloading. <i>Horticulture Research</i> , 2019, 6, 41.	1.6	14
111	Genome of <i>Crucihimalaya himalaica</i> , a close relative of <i>Arabidopsis</i> , shows ecological adaptation to high altitude. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 7137-7146.	3.3	108
112	Genetic mapping of the European canker (<i>Neonectria ditissima</i>) resistance locus Rnd1 from <i>Malus robusta</i> . <i>Tree Genetics and Genomes</i> , 2019, 15, 1.	0.6	23
113	Transcriptomic analysis reveals the regulatory module of apple (<i>Malus domestica</i>) floral transition in response to 6-BA. <i>BMC Plant Biology</i> , 2019, 19, 93.	1.6	25
114	Sequencing a <i>Juglans regia</i> × <i>J. microcarpa</i> hybrid yields high-quality genome assemblies of parental species. <i>Horticulture Research</i> , 2019, 6, 55.	2.9	67
115	Insight on Rosaceae Family with Genome Sequencing and Functional Genomics Perspective. <i>BioMed Research International</i> , 2019, 2019, 1-12.	0.9	21
116	Mapping Gene Markers for Apple Fruit Ring Rot Disease Resistance Using a Multi-omics Approach. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1663-1678.	0.8	27
117	Comparative Transcriptome Analysis between Ornamental Apple Species Provides Insights into Mechanism of Double Flowering. <i>Agronomy</i> , 2019, 9, 112.	1.3	3
118	Genetics of zonal leaf chlorosis and genetic linkage to a major gene regulating skin anthocyanin production (MdMYB1) in the apple (<i>Malus domestica</i>) cultivar Honeycrisp. <i>PLoS ONE</i> , 2019, 14, e0210611.	1.1	11
119	RdDM-independent de novo and heterochromatin DNA methylation by plant CMT and DNMT3 orthologs. <i>Nature Communications</i> , 2019, 10, 1613.	5.8	46
120	Improved laser capture microdissection (LCM)-based method for isolation of RNA, including miRNA and expression analysis in woody apple bud meristem. <i>Planta</i> , 2019, 249, 2015-2020.	1.6	3
121	Apple whole genome sequences: recent advances and new prospects. <i>Horticulture Research</i> , 2019, 6, 59.	2.9	77
122	A hybrid de novo genome assembly of the honeybee, <i>Apis mellifera</i> , with chromosome-length scaffolds. <i>BMC Genomics</i> , 2019, 20, 275.	1.2	171
123	Agroinfiltration is a key factor to improve the efficiency of apple and pear transformation. <i>Scientia Horticulturae</i> , 2019, 251, 150-154.	1.7	14
124	A high-quality apple genome assembly reveals the association of a retrotransposon and red fruit colour. <i>Nature Communications</i> , 2019, 10, 1494.	5.8	254
125	Spring Is Coming: Genetic Analyses of the Bud Break Date Locus Reveal Candidate Genes From the Cold Perception Pathway to Dormancy Release in Apple (<i>Malus domestica</i> Borkh.). <i>Frontiers in Plant Science</i> , 2019, 10, 33.	1.7	28
126	Differential gene regulatory pathways and co-expression networks associated with fire blight infection in apple (<i>Malus domestica</i>). <i>Horticulture Research</i> , 2019, 6, 35.	2.9	20

#	ARTICLE	IF	CITATIONS
127	Metacaspase gene family in Rosaceae genomes: Comparative genomic analysis and their expression during pear pollen tube and fruit development. PLoS ONE, 2019, 14, e0211635.	1.1	9
128	Resource allocation trade-offs and the loss of chemical defences during apple domestication. Annals of Botany, 2019, 123, 1029-1041.	1.4	21
129	Methylome and transcriptome analyses of apple fruit somatic mutations reveal the difference of red phenotype. BMC Genomics, 2019, 20, 117.	1.2	41
130	Elucidating the genetic background of the early-flowering transgenic genetic stock T1190 with a high-density SNP array. Molecular Breeding, 2019, 39, 1.	1.0	7
131	MdGSTF6, activated by MdMYB1, plays an essential role in anthocyanin accumulation in apple. Horticulture Research, 2019, 6, 40.	2.9	105
132	In vitro tissue culture of apple and other Malus species: recent advances and applications. Planta, 2019, 249, 975-1006.	1.6	42
133	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
134	Transcriptomes collide: simultaneous expression analysis of apple (<i>Malus domestica</i>) Tj ETQq1 1 0.784314 rgBT / Over 399-406.	0.1	0
135	Identification of <i>Venturia inaequalis</i> Races in Morioka, Japan and Identification of a Quantitative Trait Locus Associated with Resistance to Apple Scab in 'Akane' Apples. Horticultural Research (Japan), 2019, 18, 349-361.	0.1	5
136	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
137	Photodamage repair pathways contribute to the accurate maintenance of the DNA methylome landscape upon UV exposure. PLoS Genetics, 2019, 15, e1008476.	1.5	16
138	Genome sequence of the model rice variety KitaakeX. BMC Genomics, 2019, 20, 905.	1.2	59
139	Pseudo-chromosome length genome assembly of a double haploid 'Bartlett' pear (<i>Pyrus communis</i> L.). GigaScience, 2019, 8, .	3.3	76
140	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
141	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
142	A de novo genome assembly of the dwarfing pear rootstock Zhongai 1. Scientific Data, 2019, 6, 281.	2.4	28
143	Parallel Bud Mutation Sequencing Reveals that Fruit Sugar and Acid Metabolism Potentially Influence Stress in Malus. International Journal of Molecular Sciences, 2019, 20, 5988.	1.8	11
144	Functional identification of lncRNAs in sweet cherry (<i>Prunus avium</i>) pollen tubes via transcriptome analysis using single-molecule long-read sequencing. Horticulture Research, 2019, 6, 135.	2.9	8

#	ARTICLE	IF	CITATIONS
145	Best Foot Forward: Nanopore Long Reads, Hybrid Meta-Assembly, and Haplotig Purging Optimizes the First Genome Assembly for the Southern Hemisphere Blacklip Abalone (<i>Haliotis rubra</i>). <i>Frontiers in Genetics</i> , 2019, 10, 889.	1.1	25
146	Evolutionary and ecological functional genomics, from lab to the wild. <i>Plant Journal</i> , 2019, 97, 40-55.	2.8	39
147	<i>De novo</i> genome assembly of the stress tolerant forest species <i>Casuarina equisetifolia</i> provides insight into secondary growth. <i>Plant Journal</i> , 2019, 97, 779-794.	2.8	44
148	Co-expression networks provide insights into molecular mechanisms of postharvest temperature modulation of apple fruit to reduce superficial scald. <i>Postharvest Biology and Technology</i> , 2019, 149, 27-41.	2.9	18
149	Biotic Stress-Induced Priming and De-Priming of Transcriptional Memory in Arabidopsis and Apple. <i>Epigenomes</i> , 2019, 3, 3.	0.8	13
150	15 years of GDR: New data and functionality in the Genome Database for Rosaceae. <i>Nucleic Acids Research</i> , 2019, 47, D1137-D1145.	6.5	285
151	The Versatility of SMRT Sequencing. <i>Genes</i> , 2019, 10, 24.	1.0	16
152	Genome-wide identification and biochemical characterization of the UGT88F subfamily in <i>Malus x domestica</i> Borkh. <i>Phytochemistry</i> , 2019, 157, 135-144.	1.4	10
153	<i>De novo</i> assembly of a wild pear (<i>Pyrus betuleafolia</i>) genome. <i>Plant Biotechnology Journal</i> , 2020, 18, 581-595.	4.1	72
154	Fast and accurate correction of optical mapping data via spaced seeds. <i>Bioinformatics</i> , 2020, 36, 682-689.	1.8	5
155	Reduced fire blight susceptibility in apple cultivars using a high efficiency CRISPR/Cas9-FLP/FRT-based gene editing system. <i>Plant Biotechnology Journal</i> , 2020, 18, 845-858.	4.1	98
156	Using whole-genome SNP data to reconstruct a large multi-generation pedigree in apple germplasm. <i>BMC Plant Biology</i> , 2020, 20, 2.	1.6	65
158	Genetic mapping of a locus controlling the intergeneric hybridization barrier between apple and pear. <i>Tree Genetics and Genomes</i> , 2020, 16, 1.	0.6	7
159	Epigenetic patterns within the haplotype phased fig (<i>Ficus carica</i> L.) genome. <i>Plant Journal</i> , 2020, 102, 600-614.	2.8	43
160	A genome-wide association study for the detection of genes related to apple Marssonina Blotch disease resistance in apples. <i>Scientia Horticulturae</i> , 2020, 262, 108986.	1.7	6
161	Genome-wide identification and expression analysis of major latex protein (MLP) family genes in the apple (<i>Malus domestica</i> Borkh.) genome. <i>Gene</i> , 2020, 733, 144275.	1.0	15
162	Genome-Wide Analysis of the Apple (<i>Malus domestica</i>) Cysteine-Rich Receptor-Like Kinase (CRK) Family: Annotation, Genomic Organization, and Expression Profiles in Response to Fungal Infection. <i>Plant Molecular Biology Reporter</i> , 2020, 38, 14-24.	1.0	20
163	Characterization of Fe deficiency induced RING finger family members in apple species. <i>Plant Gene</i> , 2020, 21, 100209.	1.4	0

#	ARTICLE	IF	CITATIONS
164	Identification of Candidate Genes Involved in Fruit Ripening and Crispness Retention Through Transcriptome Analyses of a "Honeycrisp" Population. <i>Plants</i> , 2020, 9, 1335.	1.6	11
165	Identification of two QTLs associated with high fruit acidity in apple using pooled genome sequencing analysis. <i>Horticulture Research</i> , 2020, 7, 171.	2.9	15
166	Transcriptional and physiological analyses of reduced density in apple provide insight into the regulation involved in photosynthesis. <i>PLoS ONE</i> , 2020, 15, e0239737.	1.1	4
167	A new species of <i>Malus</i> in China, <i>Malus shizongensis</i> Liu sp. nov. <i>Journal of Integrative Agriculture</i> , 2020, 19, 2451-2457.	1.7	2
168	The high-quality genome of diploid strawberry (<i>Fragaria nilgerrensis</i>) provides new insights into anthocyanin accumulation. <i>Plant Biotechnology Journal</i> , 2020, 18, 1908-1924.	4.1	51
169	Skin Color in Apple Fruit (<i>Malus domestica</i>): Genetic and Epigenetic Insights. <i>Epigenomes</i> , 2020, 4, 13.	0.8	8
170	MdINT1 enhances apple salinity tolerance by regulating the antioxidant system, homeostasis of ions, and osmosis. <i>Plant Physiology and Biochemistry</i> , 2020, 154, 689-698.	2.8	9
171	Defining the QTL associated with chill requirement during endodormancy in <i>Malus domestica</i> Borkh. <i>Euphytica</i> , 2020, 216, 1.	0.6	2
172	Beyond Ethylene: New Insights Regarding the Role of Alternative Oxidase in the Respiratory Climacteric. <i>Frontiers in Plant Science</i> , 2020, 11, 543958.	1.7	19
173	A Rosaceae Family-Level Approach To Identify Loci Influencing Soluble Solids Content in Blackberry for DNA-Informed Breeding. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3729-3740.	0.8	6
174	A high-quality reference genome sequence of <i>Salvia miltiorrhiza</i> provides insights into tanshinone synthesis in its red rhizomes. <i>Plant Genome</i> , 2020, 13, e20041.	1.6	45
175	Assembly and Annotation of the Nuclear and Organellar Genomes of a Dwarf Coconut (Chowghat) Tj ETQq1 1 0.784314 rgBT /Overlock 24, 726-742.	1.0	25
176	Intricate genetic variation networks control the adventitious root growth angle in apple. <i>BMC Genomics</i> , 2020, 21, 852.	1.2	6
177	Endogenous Auxin Content Contributes to Larger Size of Apple Fruit. <i>Frontiers in Plant Science</i> , 2020, 11, 592540.	1.7	23
178	The apple REFPOP" a reference population for genomics-assisted breeding in apple. <i>Horticulture Research</i> , 2020, 7, 189.	2.9	37
179	An efficient protocol for functional studies of apple transcription factors using a glucocorticoid receptor fusion system. <i>Applications in Plant Sciences</i> , 2020, 8, e11396.	0.8	3
180	DNA methylation and its effects on gene expression during primary to secondary growth in poplar stems. <i>BMC Genomics</i> , 2020, 21, 498.	1.2	23
181	Comprehensive genomic analysis of the RNase T2 gene family in Rosaceae and expression analysis in <i>Pyrus bretschneideri</i> . <i>Plant Systematics and Evolution</i> , 2020, 306, 1.	0.3	7

#	ARTICLE	IF	CITATIONS
182	Genome-Wide Identification of Apple Ubiquitin SINA E3 Ligase and Functional Characterization of MdSINA2. <i>Frontiers in Plant Science</i> , 2020, 11, 1109.	1.7	21
183	Biosynthesis of the Dihydrochalcone Sweetener Trilobatin Requires <i>Phloretin Glycosyltransferase2</i>. <i>Plant Physiology</i> , 2020, 184, 738-752.	2.3	15
184	Genomics-assisted prediction of salt and alkali tolerances and functional marker development in apple rootstocks. <i>BMC Genomics</i> , 2020, 21, 550.	1.2	17
185	Dormant but Active: Chilling Accumulation Modulates the Epigenome and Transcriptome of <i>Prunus avium</i> During Bud Dormancy. <i>Frontiers in Plant Science</i> , 2020, 11, 1115.	1.7	27
186	Phased diploid genome assemblies and pan-genomes provide insights into the genetic history of apple domestication. <i>Nature Genetics</i> , 2020, 52, 1423-1432.	9.4	168
187	Construction of a dense genetic map of the <i>Malus fusca</i> fire blight resistant accession MAL0045 using tunable genotyping-by-sequencing SNPs and microsatellites. <i>Scientific Reports</i> , 2020, 10, 16358.	1.6	17
188	Raw transcriptomics data to gene specific SSRs: a validated free bioinformatics workflow for biologists. <i>Scientific Reports</i> , 2020, 10, 18236.	1.6	8
189	Candidate gene mapping identifies genomic variations in the fire blight susceptibility genes HIPM and DIPM across the <i>Malus</i> germplasm. <i>Scientific Reports</i> , 2020, 10, 16317.	1.6	10
190	CRISPR-Cas9 enrichment and long read sequencing for fine mapping in plants. <i>Plant Methods</i> , 2020, 16, 121.	1.9	31
191	HEAT SHOCK FACTOR A8a Modulates Flavonoid Synthesis and Drought Tolerance. <i>Plant Physiology</i> , 2020, 184, 1273-1290.	2.3	92
192	Type-B cytokinin response regulators link hormonal stimuli and molecular responses during the transition from endo- to ecodormancy in apple buds. <i>Plant Cell Reports</i> , 2020, 39, 1687-1703.	2.8	8
193	Quantitative trait loci-based genomics-assisted prediction for the degree of apple fruit cover color. <i>Plant Genome</i> , 2020, 13, e20047.	1.6	12
194	Auxin and Its Interaction With Ethylene Control Adventitious Root Formation and Development in Apple Rootstock. <i>Frontiers in Plant Science</i> , 2020, 11, 574881.	1.7	19
195	Detection of QTL for apple fruit acidity and sweetness using sensorial evaluation in multiple pedigreed full-sib families. <i>Tree Genetics and Genomes</i> , 2020, 16, 1.	0.6	15
196	Epigenetic silencing of clustered tRNA genes in <i>Arabidopsis</i> . <i>Nucleic Acids Research</i> , 2020, 48, 10297-10312.	6.5	12
197	Decoding altitude-activated regulatory mechanisms occurring during apple peel ripening. <i>Horticulture Research</i> , 2020, 7, 120.	2.9	30
198	Advances in genomics of cashew tree: molecular tools and strategies for accelerated breeding. <i>Tree Genetics and Genomes</i> , 2020, 16, 1.	0.6	13
199	Fox Hunting in Wild Apples: Searching for Novel Genes in <i>Malus Sieversii</i> . <i>International Journal of Molecular Sciences</i> , 2020, 21, 9516.	1.8	4

#	ARTICLE	IF	CITATIONS
200	Screening of <i>Helicoverpa armigera</i> Mobilome Revealed Transposable Element Insertions in Insecticide Resistance Genes. <i>Insects</i> , 2020, 11, 879.	1.0	25
201	Chromosome-level draft genome of a diploid plum (<i>Prunus salicina</i>). <i>GigaScience</i> , 2020, 9, .	3.3	39
202	Application of genome-wide insertion/deletion markers on genetic structure analysis and identity signature of <i>Malus</i> accessions. <i>BMC Plant Biology</i> , 2020, 20, 540.	1.6	7
203	Genome-Wide Identification and Coexpression Network Analysis of DNA Methylation Pathway Genes and Their Differentiated Functions in <i>Ginkgo biloba</i> L.. <i>Forests</i> , 2020, 11, 1076.	0.9	6
204	Identification of Phytochrome-Interacting Factor Family Members and Functional Analysis of MdPIF4 in <i>Malus domestica</i> . <i>International Journal of Molecular Sciences</i> , 2020, 21, 7350.	1.8	17
205	Genome-Wide Characterization of the HSP20 Gene Family Identifies Potential Members Involved in Temperature Stress Response in Apple. <i>Frontiers in Genetics</i> , 2020, 11, 609184.	1.1	27
206	The sucrose transporter MdSUT4.1 participates in the regulation of fruit sugar accumulation in apple. <i>BMC Plant Biology</i> , 2020, 20, 191.	1.6	33
207	High-quality chromosome-scale assembly of the walnut (<i>Juglans regia</i> L.) reference genome. <i>GigaScience</i> , 2020, 9, .	3.3	83
208	Exploring DNA Variant Segregation Types Enables Mapping Loci for Recessive Phenotypic Suppression of Columnar Growth in Apple. <i>Frontiers in Plant Science</i> , 2020, 11, 692.	1.7	5
209	The Citrus Genome. <i>Compendium of Plant Genomes</i> , 2020, , .	0.3	16
210	Molecular karyotypes of loquat (<i>Eriobotrya japonica</i>) aneuploids can be detected by using SSR markers combined with quantitative PCR irrespective of heterozygosity. <i>Plant Methods</i> , 2020, 16, 22.	1.9	9
211	Prospects for the Study and Improvement of Abiotic Stress Tolerance in Date Palms in the Post-genomics Era. <i>Frontiers in Plant Science</i> , 2020, 11, 293.	1.7	34
212	A high-quality genome provides insights into the new taxonomic status and genomic characteristics of <i>Cladopus chinensis</i> (Podostemaceae). <i>Horticulture Research</i> , 2020, 7, 46.	2.9	11
213	Genome-Wide Identification of the VQ Protein Gene Family of Tobacco (<i>Nicotiana tabacum</i> L.) and Analysis of Its Expression in Response to Phytohormones and Abiotic and Biotic Stresses. <i>Genes</i> , 2020, 11, 284.	1.0	21
214	Major Latex Protein MdMLP423 Negatively Regulates Defense against Fungal Infections in Apple. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1879.	1.8	25
215	Systems-Based Approaches to Unravel Networks and Individual Elements Involved in Apple Superficial Scald. <i>Frontiers in Plant Science</i> , 2020, 11, 8.	1.7	24
216	Divergent DNA Methylation Signatures of Juvenile Seedlings, Grafts and Adult Apple Trees. <i>Epigenomes</i> , 2020, 4, 4.	0.8	12
217	Genome-wide analysis of the light-harvesting chlorophyll <i>a/b</i> -binding gene family in apple (<i>Malus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 1 osmotic stress. <i>Plant Physiology and Biochemistry</i> , 2020, 154, 517-529.	2.8	33

#	ARTICLE	IF	CITATIONS
218	Optical map guided genome assembly. <i>BMC Bioinformatics</i> , 2020, 21, 285.	1.2	10
219	Integrative Analyses of Widely Targeted Metabolic Profiling and Transcriptome Data Reveals Molecular Insight into Metabolomic Variations during Apple (<i>Malus domestica</i>) Fruit Development and Ripening. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4797.	1.8	52
220	The assessment of epigenetic diversity, differentiation, and structure in the "Fuji"™ mutation line implicates roles of epigenetic modification in the occurrence of different mutant groups as well as spontaneous mutants. <i>PLoS ONE</i> , 2020, 15, e0235073.	1.1	9
221	Overexpression of chalcone isomerase in apple reduces phloridzin accumulation and increases susceptibility to herbivory by two-spotted mites. <i>Plant Journal</i> , 2020, 103, 293-307.	2.8	13
222	Transcriptomic and Metabolic Analyses Provide New Insights into the Apple Fruit Quality Decline during Long-Term Cold Storage. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 4699-4716.	2.4	32
223	Introgressing blue mold resistance into elite apple germplasm by rapid cycle breeding and foreground and background DNA-informed selection. <i>Tree Genetics and Genomes</i> , 2020, 16, 1.	0.6	16
224	Methylation of <i>MdMYB1</i> locus mediated by RdDM pathway regulates anthocyanin biosynthesis in apple. <i>Plant Biotechnology Journal</i> , 2020, 18, 1736-1748.	4.1	42
225	Analysis of Fruit Lignin Content, Composition, and Linkage Types in Pear Cultivars and Related Species. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 2493-2505.	2.4	13
226	Genomic analyses of a "living fossil" The endangered dove tree. <i>Molecular Ecology Resources</i> , 2020, 20, 756-769.	2.2	26
227	A long non-coding apple RNA, MSTRG.85814.11, acts as a transcriptional enhancer of <i>SAUR32</i> and contributes to the Fe-deficiency response. <i>Plant Journal</i> , 2020, 103, 53-67.	2.8	42
228	<i>MdMYB8</i> is associated with flavonol biosynthesis via the activation of the <i>MdFLS</i> promoter in the fruits of <i>Malus crabapple</i> . <i>Horticulture Research</i> , 2020, 7, 19.	2.9	39
229	Analysis of the <i>Rdr1</i> gene family in different Rosaceae genomes reveals an origin of an R-gene cluster after the split of Rubiaceae within the Rosoideae subfamily. <i>PLoS ONE</i> , 2020, 15, e0227428.	1.1	5
230	A bushel of viruses: Identification of seventeen novel putative viruses by RNA-seq in six apple trees. <i>PLoS ONE</i> , 2020, 15, e0227669.	1.1	36
231	A systematic analysis of apple root resistance traits to <i>Pythium ultimum</i> infection and the underpinned molecular regulations of defense activation. <i>Horticulture Research</i> , 2020, 7, 62.	2.9	24
232	Genome wide analysis and functional identification of <i>MdKCS</i> genes in apple. <i>Plant Physiology and Biochemistry</i> , 2020, 151, 299-312.	2.8	32
233	Identification of early fruit development reference genes in plum. <i>PLoS ONE</i> , 2020, 15, e0230920.	1.1	8
234	Identification of gene co-expression networks and key genes regulating flavonoid accumulation in apple (<i>Malus domestica</i>) fruit skin. <i>Plant Science</i> , 2021, 304, 110747.	1.7	23
235	The <i>MdXTHB</i> gene is involved in fruit softening in "Golden Del. Reinders"™ (<i>Malus pumila</i>). <i>Journal of the Science of Food and Agriculture</i> , 2021, 101, 564-572.	1.7	12

#	ARTICLE	IF	CITATIONS
236	Abscisic acid homeostasis is mediated by feedback regulation of <i>MdMYB88</i> and <i>MdMYB124</i> . <i>Journal of Experimental Botany</i> , 2021, 72, 592-607.	2.4	27
237	MYB_SH[AL]QKY[RF] transcription factors <i>MdLUX</i> and <i>MdPCL-like</i> promote anthocyanin accumulation through DNA hypomethylation and <i>MdF3H</i> activation in apple. <i>Tree Physiology</i> , 2021, 41, 836-848.	1.4	7
238	The genome of Shanputao (<i>Vitis amurensis</i>) provides a new insight into cold tolerance of grapevine. <i>Plant Journal</i> , 2021, 105, 1495-1506.	2.8	52
239	Role of <i>MdERF3</i> and <i>MdERF118</i> natural variations in apple flesh firmness/crispness retainability and development of QTL-based genomics-assisted prediction. <i>Plant Biotechnology Journal</i> , 2021, 19, 1022-1037.	4.1	24
240	Effectors, chaperones, and harpins of the Type III secretion system in the fire blight pathogen <i>Erwinia amylovora</i> : a review. <i>Journal of Plant Pathology</i> , 2021, 103, 25-39.	0.6	23
241	Genomic analyses of diverse wild and cultivated accessions provide insights into the evolutionary history of jujube. <i>Plant Biotechnology Journal</i> , 2021, 19, 517-531.	4.1	41
242	Tracing the Diploid Ancestry of the Cultivated Octoploid Strawberry. <i>Molecular Biology and Evolution</i> , 2021, 38, 478-485.	3.5	50
243	Functional and expressional analyses of apple <i>FLC</i> -like in relation to dormancy progress and flower bud development. <i>Tree Physiology</i> , 2021, 41, 562-570.	1.4	19
244	The Apple Microbiome: Structure, Function, and Manipulation for Improved Plant Health. <i>Compendium of Plant Genomes</i> , 2021, , 341-382.	0.3	8
245	Genetics and Genomics of Fruit Color Development in Apple. <i>Compendium of Plant Genomes</i> , 2021, , 271-295.	0.3	2
246	Genetic and Physical Mapping of the Apple Genome. <i>Compendium of Plant Genomes</i> , 2021, , 131-168.	0.3	4
247	Date Palm Genetic Identification and Improvement Utilizing Molecular Markers and DNA Barcoding. <i>Compendium of Plant Genomes</i> , 2021, , 101-134.	0.3	1
248	Genome Editing in Apple. <i>Compendium of Plant Genomes</i> , 2021, , 213-225.	0.3	2
249	Genetics and Breeding of Apple Scions. <i>Compendium of Plant Genomes</i> , 2021, , 73-103.	0.3	6
250	Advancements in High-Throughput Omics-Technologies for Understanding the Biology of Neglected and Underutilized Crops. , 2021, , 203-236.		0
251	Expression Analysis of Endodormancy and Flowering-related Genes in Greenhouse-cultivated Flowering Disorder Trees of Japanese pear (<i>Pyrus pyrifolia</i> Nakai) 'Kosui'™. <i>Horticulture Journal</i> , 2021, 90, 38-47.	0.3	1
252	Regulatory Sequences in Apple. <i>Compendium of Plant Genomes</i> , 2021, , 189-211.	0.3	0
253	The Apple Genome and Epigenome. <i>Compendium of Plant Genomes</i> , 2021, , 169-187.	0.3	3

#	ARTICLE	IF	CITATIONS
254	Future Prospects of "Omics" and of Other Technologies for Genetic Improvement of Apple. Compendium of Plant Genomes, 2021, , 395-412.	0.3	3
255	Genetic mechanisms associated with floral initiation and the repressive effect of fruit on flowering in apple (<i>Malus x domestica</i> Borkh). PLoS ONE, 2021, 16, e0245487.	1.1	9
256	Natural variations in a pectin acetyltransferase gene, <i>MdPAE10</i> , contribute to prolonged apple fruit shelf life. Plant Genome, 2021, 14, e20084.	1.6	14
257	Chromosome-scale genome assembly of Japanese pear (<i>Pyrus pyrifolia</i>) variety "Nijisseiki". DNA Research, 2021, 28, .	1.5	26
258	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
259	Contributions of Reduced Susceptibility Alleles in Breeding Apple Cultivars with Durable Resistance to Fire Blight. Plants, 2021, 10, 409.	1.6	5
260	Genome-Wide Analysis of Somatic Embryogenesis-Related Transcription Factors in Cultivated Strawberry (<i>Fragaria Å— ananassa</i>) and Evolutionary Relationships among Rosaceae Species. Agronomy, 2021, 11, 356.	1.3	1
261	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
263	De novo assembly and characterization of the first draft genome of quince (<i>Cydonia oblonga</i> Mill.). Scientific Reports, 2021, 11, 3818.	1.6	10
265	There is more to flowering than those DAM genes: the biology behind bloom in rosaceous fruit trees. Current Opinion in Plant Biology, 2021, 59, 101995.	3.5	16
266	Fire blight QTL analysis in a multi-family apple population identifies a reduced-susceptibility allele in "Honeycrisp". Horticulture Research, 2021, 8, 28.	2.9	20
267	Genetic variation in the promoter of an R2R3-MYB transcription factor determines fruit malate content in apple (<i>Malus domestica</i> Borkh.). Plant Physiology, 2021, 186, 549-568.	2.3	31
268	Genome-wide characterization of PEBP family genes in nine Rosaceae tree species and their expression analysis in <i>P. mume</i> . BMC Ecology and Evolution, 2021, 21, 32.	0.7	10
270	Tracing founder haplotypes of Japanese apple varieties: application in genomic prediction and genome-wide association study. Horticulture Research, 2021, 8, 49.	2.9	21
272	Cross-Species Comparison of Metabolomics to Decipher the Metabolic Diversity in Ten Fruits. Metabolites, 2021, 11, 164.	1.3	12
273	Preliminary genetic mapping of fire blight and European canker resistances in two apple breeding families. Acta Horticulturae, 2021, , 199-204.	0.1	1
274	Genome-wide association mapping identifies novel loci underlying fire blight resistance in apple. Plant Genome, 2021, 14, e20087.	1.6	11
275	Toward Systematic Understanding of Flower Bud Induction in Apple: A Multi-Omics Approach. Frontiers in Plant Science, 2021, 12, 604810.	1.7	12

#	ARTICLE	IF	CITATIONS
276	Using RNA-seq to characterize pollen-stigma interactions for pollination studies. <i>Scientific Reports</i> , 2021, 11, 6635.	1.6	2
277	High-Quality Nursing Care for the Elderly in the Department of Otolaryngology. <i>Journal of Healthcare Engineering</i> , 2021, 2021, 1-10.	1.1	1
278	Candidate genes and signatures of directional selection on fruit quality traits during apple domestication. <i>American Journal of Botany</i> , 2021, 108, 616-627.	0.8	6
279	Genomic analysis uncovers functional variation in the C-terminus of anthocyanin-activating MYB transcription factors. <i>Horticulture Research</i> , 2021, 8, 77.	2.9	28
280	QTL analysis of crown gall disease resistance in apple: first plant R gene candidates effective against <i>Rhizobium rhizogenes</i> (Ti). <i>Tree Genetics and Genomes</i> , 2021, 17, 1.	0.6	5
281	Differential regulation of triterpene biosynthesis induced by an early failure in cuticle formation in apple. <i>Horticulture Research</i> , 2021, 8, 75.	2.9	23
282	Genetic Analysis and Fine Mapping of the Fire Blight Resistance Locus of <i>Malus × arnoldiana</i> on Linkage Group 12 Reveal First Candidate Genes. <i>Frontiers in Plant Science</i> , 2021, 12, 667133.	1.7	12
283	An Atlas of Genomic Resources for Studying Rosaceae Fruits and Ornamentals. <i>Frontiers in Plant Science</i> , 2021, 12, 644881.	1.7	5
284	Integration of Infinium and Axiom SNP array data in the outcrossing species <i>Malus × domestica</i> and causes for seemingly incompatible calls. <i>BMC Genomics</i> , 2021, 22, 246.	1.2	15
285	Genome-wide analysis of SET-domain group histone methyltransferases in apple reveals their role in development and stress responses. <i>BMC Genomics</i> , 2021, 22, 283.	1.2	8
286	Dynamics of DNA Methylation and Its Functions in Plant Growth and Development. <i>Frontiers in Plant Science</i> , 2021, 12, 596236.	1.7	84
287	Identification and Characterization of the CCoAOMT Gene Family in Apple, Chinese White Pear, and Peach. <i>Journal of the American Society for Horticultural Science</i> , 2021, 146, 184-195.	0.5	2
288	Extensive variation within the pan-genome of cultivated and wild sorghum. <i>Nature Plants</i> , 2021, 7, 766-773.	4.7	94
289	Research progress of fruit color development in apple (<i>Malus domestica</i> Borkh.). <i>Plant Physiology and Biochemistry</i> , 2021, 162, 267-279.	2.8	50
290	The MdMYB16/MdMYB1-miR7125-MdCCR module regulates the homeostasis between anthocyanin and lignin biosynthesis during light induction in apple. <i>New Phytologist</i> , 2021, 231, 1105-1122.	3.5	50
291	LTR-retrotransposon dynamics in common fig (<i>Ficus carica</i> L.) genome. <i>BMC Plant Biology</i> , 2021, 21, 221.	1.6	5
292	Apple MPK4 mediates phosphorylation of MYB1 to enhance light-induced anthocyanin accumulation. <i>Plant Journal</i> , 2021, 106, 1728-1745.	2.8	38
293	Pests, diseases, and aridity have shaped the genome of <i>Corymbia citriodora</i> . <i>Communications Biology</i> , 2021, 4, 537.	2.0	21

#	ARTICLE	IF	CITATIONS
294	An accumulation of genetic variation and selection across the disease-related genes during apple domestication. <i>Tree Genetics and Genomes</i> , 2021, 17, 1.	0.6	10
295	Polyploidy underlies co-option and diversification of biosynthetic triterpene pathways in the apple tribe. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	37
296	Characterization of the pectin methylesterase inhibitor gene family in Rosaceae and role of PbrPMEI23/39/41 in methylesterified pectin distribution in pear pollen tube. <i>Planta</i> , 2021, 253, 118.	1.6	13
298	Stories that can't be told by SNPs; DNA methylation variation in plant populations. <i>Current Opinion in Plant Biology</i> , 2021, 61, 101989.	3.5	17
299	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). <i>New Zealand Journal of Crop and Horticultural Science</i> , 2022, 50, 303-325.	0.7	5
300	Study on the differences of gene expression between pear and apple wild cultivation materials based on RNA-seq technique. <i>BMC Plant Biology</i> , 2021, 21, 256.	1.6	3
301	Identification of DNA Methylation and Transcriptomic Profiles Associated With Fruit Mealiness in <i>Prunus persica</i> (L.) Batsch. <i>Frontiers in Plant Science</i> , 2021, 12, 684130.	1.7	12
303	Advanced genebank management of genetic resources of European wild apple, <i>Malus sylvestris</i> , using genome-wide SNP array data. <i>Tree Genetics and Genomes</i> , 2021, 17, 1.	0.6	6
304	Apple Ripening Is Controlled by a NAC Transcription Factor. <i>Frontiers in Genetics</i> , 2021, 12, 671300.	1.1	29
305	Full-Length Transcriptome-Wide Characteristic and Functional Identification of WRKY Family in <i>Malus sieversii</i> during the Valsa Canker Disease Response. <i>Forests</i> , 2021, 12, 790.	0.9	3
306	The transcriptomes of healthy and bitter pit-affected "Honeycrisp" fruit reveal genes associated with disorder development and progression. <i>Tree Genetics and Genomes</i> , 2021, 17, 1.	0.6	5
307	Classifying Cider Apple Germplasm Using Genetic Markers for Fruit Acidity. <i>Journal of the American Society for Horticultural Science</i> , 2021, 146, 267-275.	0.5	4
308	Chromosome Level Assembly of Homozygous Inbred Line "Wongyo 3115" Facilitates the Construction of a High-Density Linkage Map and Identification of QTLs Associated With Fruit Firmness in Octoploid Strawberry (<i>Fragaria × ananassa</i>). <i>Frontiers in Plant Science</i> , 2021, 12, 696229.	1.7	14
309	Characterization of genomic DNA sequence of the candidate gene for FB_Mfu10 associated with fire blight resistance in <i>Malus</i> species. <i>BMC Research Notes</i> , 2021, 14, 291.	0.6	5
310	Relative performance of customized and universal probe sets in target enrichment: A case study in subtribe Malinae. <i>Applications in Plant Sciences</i> , 2021, 9, e11442.	0.8	20
311	Multi-omics analyses on <i>Kandelia obovata</i> reveal its response to transplanting and genetic differentiation among populations. <i>BMC Plant Biology</i> , 2021, 21, 341.	1.6	4
312	The long noncoding RNA MdLNC499 bridges MdWRKY1 and MdERF109 function to regulate early-stage light-induced anthocyanin accumulation in apple fruit. <i>Plant Cell</i> , 2021, 33, 3309-3330.	3.1	80
313	Insights into the effect of human civilization on <i>Malus</i> evolution and domestication. <i>Plant Biotechnology Journal</i> , 2021, 19, 2206-2220.	4.1	23

#	ARTICLE	IF	CITATIONS
314	Advances in production and structural derivatization of the promising molecule ursolic acid. <i>Biotechnology Journal</i> , 2021, 16, e2000657.	1.8	9
315	No Evidence of Unexpected Transgenic Insertions in T1190 “A Transgenic Apple Used in Rapid Cycle Breeding” Following Whole Genome Sequencing. <i>Frontiers in Plant Science</i> , 2021, 12, 715737.	1.7	2
316	Genome-wide identification, characterization and expression analysis of MATE family genes in apple (<i>Malus domestica</i> Borkh). <i>BMC Genomics</i> , 2021, 22, 632.	1.2	12
317	Genome-wide investigation and comparative analysis of MATE gene family in Rosaceae species and their regulatory role in abiotic stress responses in Chinese pear (<i>Pyrus</i>). <i>Journal of Integrative Agriculture</i> , 2021, 20, 2112-2125.	1.7	9
319	Genome-wide identification, molecular evolution, and expression divergence of the hexokinase gene family in apple. <i>Journal of Integrative Agriculture</i> , 2021, 20, 2112-2125.	1.7	9
320	Genome-wide association study of individual sugar content in fruit of Japanese pear (<i>Pyrus</i> spp.). <i>BMC Plant Biology</i> , 2021, 21, 378.	1.6	14
321	New high-quality peach (<i>Prunus persica</i> L. Batsch) genome assembly to analyze the molecular evolutionary mechanism of volatile compounds in peach fruits. <i>Plant Journal</i> , 2021, 108, 281-295.	2.8	31
322	The chromosome-scale reference genome of <i>Rubus chingii</i> Hu provides insight into the biosynthetic pathway of hydrolyzable tannins. <i>Plant Journal</i> , 2021, 107, 1466-1477.	2.8	26
323	Transcriptomics of Improved Fruit Retention by Hexanal in “Honeycrisp” Reveals Hormonal Crosstalk and Reduced Cell Wall Degradation in the Fruit Abscission Zone. <i>International Journal of Molecular Sciences</i> , 2021, 22, 8830.	1.8	11
324	Biosynthetic Pathway of Proanthocyanidins in Major Cash Crops. <i>Plants</i> , 2021, 10, 1792.	1.6	7
326	Pan-genome of <i>Raphanus</i> highlights genetic variation and introgression among domesticated, wild, and weedy radishes. <i>Molecular Plant</i> , 2021, 14, 2032-2055.	3.9	56
327	Unraveling a genetic roadmap for improved taste in the domesticated apple. <i>Molecular Plant</i> , 2021, 14, 1454-1471.	3.9	47
328	A DNA test for high incidence of soft scald and soggy breakdown postharvest disorders in <i>Malus domestica</i> Borkh. <i>Molecular Breeding</i> , 2021, 41, 1.	1.0	0
329	High quality haplotype-resolved genome assemblies of <i>Populus tomentosa</i> Carr., a stabilized interspecific hybrid species widespread in Asia. <i>Molecular Ecology Resources</i> , 2022, 22, 786-802.	2.2	19
330	Linkage map and QTL mapping of red flesh locus in apple using a R1R1 × R6R6 population. <i>Horticultural Plant Journal</i> , 2021, 7, 393-400.	2.3	13
331	Genome-Wide Characterization of HSP90 Gene Family in <i>Malus sieversii</i> and Their Potential Roles in Response to <i>Valsa mali</i> Infection. <i>Forests</i> , 2021, 12, 1232.	0.9	2
332	Cyclic nucleotide gated channel genes (CNGCs) in Rosaceae: genome-wide annotation, evolution and the roles on <i>Valsa</i> canker resistance. <i>Plant Cell Reports</i> , 2021, 40, 2369-2382.	2.8	10
333	K-mer counting and curated libraries drive efficient annotation of repeats in plant genomes. <i>Plant Genome</i> , 2021, 14, e20143.	1.6	5

#	ARTICLE	IF	CITATIONS
334	A high-quality chromosome-level genome of wild <i>Rosa rugosa</i> . DNA Research, 2021, 28, .	1.5	10
335	Integrating genomics and multiplatform metabolomics enables metabolite quantitative trait loci detection in breeding-relevant apple germplasm. New Phytologist, 2021, 232, 1944-1958.	3.5	7
338	Combined Profiling of Transcriptome and DNA Methylome Reveal Genes Involved in Accumulation of Soluble Sugars and Organic Acid in Apple Fruits. Foods, 2021, 10, 2198.	1.9	11
339	Field Evaluation of CRISPR-Driven Jointless Pedicel Fresh-Market Tomatoes. Agronomy, 2021, 11, 1957.	1.3	4
340	Genomic basis of high-altitude adaptation in Tibetan Prunus fruit trees. Current Biology, 2021, 31, 3848-3860.e8.	1.8	41
341	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
342	Melatonin: Biosynthesis, content, and function in horticultural plants and potential application. Scientia Horticulturae, 2021, 288, 110392.	1.7	40
343	Advances in genomics and genome editing for breeding next generation of fruit and nut crops. Genomics, 2021, 113, 3718-3734.	1.3	19
344	Genome-wide identification of microRNAs involved in the regulation of fruit ripening in apple (<i>Malus</i>) Tj ETQq0 0 0 rBT /Overlock 10 Tf	1.7	6
345	Genome-Wide Identification, Expression Profiling and Protein-Protein Interaction Properties of the BEL-Like Homeodomain Gene Family in Apple. Phytom, 2022, 91, 315-331.	0.4	2
346	Origin of the Domesticated Apples. Compendium of Plant Genomes, 2021, , 383-394.	0.3	3
347	Genomics of Fruit Acidity and Sugar Content in Apple. Compendium of Plant Genomes, 2021, , 297-309.	0.3	1
348	Genetics and Genomics of Cold Hardiness and Dormancy. Compendium of Plant Genomes, 2021, , 247-270.	0.3	0
349	Current approaches in horticultural crops to mitigate the effect of drought stress. , 2021, , 213-240.		0
350	Genomic consequences of apple improvement. Horticulture Research, 2021, 8, 9.	2.9	53
351	Botany, Taxonomy, and Origins of the Apple. Compendium of Plant Genomes, 2021, , 19-32.	0.3	5
352	Genome Wide Transcriptomic Analysis of <i>WRKY</i> Gene Family Response to Biotic Stresses in <i>Malus</i> ×<i>domestica</i>. American Journal of Plant Sciences, 2021, 12, 858-885.	0.3	4
353	HapSolo: an optimization approach for removing secondary haplotigs during diploid genome assembly and scaffolding. BMC Bioinformatics, 2021, 22, 9.	1.2	9

#	ARTICLE	IF	CITATIONS
354	Flowering and Juvenility in Apple. <i>Compendium of Plant Genomes</i> , 2021, , 227-246.	0.3	1
355	Ploidy Manipulation for Citrus Breeding, Genetics, and Genomics. <i>Compendium of Plant Genomes</i> , 2020, , 75-105.	0.3	10
356	Citrus Genomes: From Sequence Variations to Epigenetic Modifications. <i>Compendium of Plant Genomes</i> , 2020, , 141-165.	0.3	1
357	Systematic analysis of the OFP genes in six Rosaceae genomes and their roles in stress response in Chinese pear (<i>Pyrus bretschneideri</i>). <i>Physiology and Molecular Biology of Plants</i> , 2020, 26, 2085-2094.	1.4	8
358	Genome-wide identification of genes involved in heterotrimeric G-protein signaling in Tartary buckwheat (<i>Fagopyrum tataricum</i>) and their potential roles in regulating fruit development. <i>International Journal of Biological Macromolecules</i> , 2021, 171, 435-447.	3.6	4
359	The current revolution in transposable element biology enabled by long reads. <i>Current Opinion in Plant Biology</i> , 2020, 54, 49-56.	3.5	36
360	Pre-harvest climate and post-harvest acclimation to cold prevent from superficial scald development in Granny Smith apples. <i>Scientific Reports</i> , 2020, 10, 6180.	1.6	12
361	Establishment, maintenance, and biological roles of non-CG methylation in plants. <i>Essays in Biochemistry</i> , 2019, 63, 743-755.	2.1	49
362	MdERDL6-mediated glucose efflux to the cytosol promotes sugar accumulation in the vacuole through up-regulating TSTs in apple and tomato. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	74
363	Exploiting epigenetic variation for plant breeding.. <i>CAB Reviews: Perspectives in Agriculture, Veterinary Science, Nutrition and Natural Resources</i> , 0, , 1-11.	0.6	1
371	Developmental Mechanisms of Fleshy Fruit Diversity in Rosaceae. <i>Annual Review of Plant Biology</i> , 2020, 71, 547-573.	8.6	38
372	Development of new genomic resources and tools for molecular breeding in blackberry. <i>Acta Horticulturae</i> , 2020, , 39-46.	0.1	5
373	Current trends in apple tree breeding (<i>Malus Mill.</i>). <i>Horticulture and Viticulture</i> , 2020, , 5-11.	0.0	3
374	Recent Development on Plant Aldehyde Dehydrogenase Enzymes and Their Functions in Plant Development and Stress Signaling. <i>Genes</i> , 2021, 12, 51.	1.0	41
375	New Strategies to Overcome Present CRISPR/Cas9 Limitations in Apple and Pear: Efficient Dechimerization and Base Editing. <i>International Journal of Molecular Sciences</i> , 2021, 22, 319.	1.8	53
376	A Phenotyping Protocol for Detailed Evaluation of Apple Root Resistance Responses Utilizing Tissue Culture Micropropagated Apple Plants. <i>American Journal of Plant Sciences</i> , 2018, 09, 2183-2204.	0.3	6
377	A de novo assembly of the sweet cherry (<i>Prunus avium</i> cv. Tieton) genome using linked-read sequencing technology. <i>PeerJ</i> , 2020, 8, e9114.	0.9	8
378	Genome-wide analysis of the C3H zinc finger family reveals its functions in salt stress responses of <i>Pyrus betulaefolia</i> . <i>PeerJ</i> , 2020, 8, e9328.	0.9	16

#	ARTICLE	IF	CITATIONS
379	A high-throughput <i>S-RNase</i> genotyping method for apple. <i>Fruit Research</i> , 2021, 1, 1-9.	0.9	2
380	Phylogeny of <i>Crataegus</i> (Rosaceae) based on 257 nuclear loci and chloroplast genomes: evaluating the impact of hybridization. <i>PeerJ</i> , 2021, 9, e12418.	0.9	6
384	Epigenetic Regulation in Fleshy Fruit: Perspective for Grape Berry Development and Ripening. <i>Compendium of Plant Genomes</i> , 2019, , 167-197.	0.3	1
392	Genome-Wide Identification, Characterization and Expression Profiling of Aluminum-Activated Malate Transporters in <i>Eriobotrya japonica</i> Lindl.. <i>Horticulturae</i> , 2021, 7, 441.	1.2	13
393	The <i>Gillenia trifoliata</i> genome reveals dynamics correlated with growth and reproduction in Rosaceae. <i>Horticulture Research</i> , 2021, 8, 233.	2.9	4
395	Epigenetic modification for horticultural plant improvement comes of age. <i>Scientia Horticulturae</i> , 2022, 292, 110633.	1.7	10
396	Genome-wide identification and expression analysis of the ASMT gene family reveals their role in abiotic stress tolerance in apple. <i>Scientia Horticulturae</i> , 2022, 293, 110683.	1.7	15
397	Transcriptional Profiles of <i>Mdwrky33</i> in Apple Root in Response to Infection by <i>Pythium Ultimum</i> , Abiotic Stresses and Chemical Treatments. <i>International Journal of Phytopathology</i> , 2019, 8, ACCEPTED.	0.1	1
398	Genome-Wide Identification and Characterization of Apple P3A-Type ATPase Genes, with Implications for Alkaline Stress Responses. <i>Forests</i> , 2020, 11, 292.	0.9	2
399	Genome-Wide Identification of ARF Gene Family Suggests a Functional Expression Pattern during Fruitlet Abscission in <i>Prunus avium</i> L.. <i>International Journal of Molecular Sciences</i> , 2021, 22, 11968.	1.8	10
401	High-throughput whole genome sequencing of apricot (<i>Prunus armeniaca</i>) cultivar 'Hacihalilo'™. <i>Acta Horticulturae</i> , 2020, , 53-58.	0.1	0
402	Validation of Reference Genes for Quantifying Changes in Physiological Gene Expression in Apple Tree under Cold Stress and Virus Infection. <i>Research in Plant Disease</i> , 2020, 26, 144-158.	0.3	0
403	The genotype-specific laccase gene expression and lignin deposition patterns in apple root during <i>Pythium ultimum</i> infection. <i>Fruit Research</i> , 2021, 1, 1-9.	0.9	4
404	Effects of two apple tonoplast sugar transporters, <i>MdTST1</i> and <i>MdTST2</i> , on the accumulation of sugar. <i>Scientia Horticulturae</i> , 2022, 293, 110719.	1.7	5
405	Harnessing epigenetic variability for crop improvement: current status and future prospects. <i>Genes and Genomics</i> , 2022, 44, 259-266.	0.5	4
406	Elucidating the genetic mechanisms underlying tolerance to apple replant disease (ARD). <i>Acta Horticulturae</i> , 2021, , 49-56.	0.1	0
407	<i>MdBBX21</i> , a B-Box Protein, Positively Regulates Light-Induced Anthocyanin Accumulation in Apple Peel. <i>Frontiers in Plant Science</i> , 2021, 12, 774446.	1.7	14
408	The draft chromosome-level genome assembly of tetraploid ground cherry (<i>Prunus fruticosa</i> Pall.) from long reads. <i>Genomics</i> , 2021, 113, 4173-4183.	1.3	14

#	ARTICLE	IF	CITATIONS
410	Anticipated Polymorphic SSRs and Their Application Based on Next Generation Sequencing of <i>Prunus Persica</i> . <i>Han'guk Yukchong Hakhoe Chi</i> , 2021, 53, 350-360.	0.2	1
411	Coreless apples generated by the suppression of carpel genes and hormone-induced fruit set. <i>Fruit Research</i> , 2021, 1, 1-9.	0.9	4
412	Allele-aware chromosome-scale assembly of the allopolyploid genome of hexaploid Ma bamboo (<i>Dendrocalamus latiflorus</i> Munro). <i>Journal of Integrative Plant Biology</i> , 2022, 64, 649-670.	4.1	24
413	Proteomic differences in apple spur buds from high and non-cropping trees during floral initiation. <i>Journal of Proteomics</i> , 2022, 253, 104459.	1.2	4
414	Significant improvement of apple (<i>Malus domestica</i> Borkh.) transgenic plant production by pre-transformation with a Baby boom transcription factor.. <i>Horticulture Research</i> , 2022, 9, .	2.9	18
415	Pear genetics: Recent advances, new prospects, and a roadmap for the future. <i>Horticulture Research</i> , 2022, 9, .	2.9	12
416	Tree architecture, light interception and water-use related traits are controlled by different genomic regions in an apple tree core collection. <i>New Phytologist</i> , 2022, 234, 209-226.	3.5	5
417	Ethylene response factor MdERF4 and histone deacetylase MdHDA19 suppress apple fruit ripening through histone deacetylation of ripening-related genes. <i>Plant Physiology</i> , 2022, 188, 2166-2181.	2.3	29
418	Chromosome restructuring and number change during the evolution of <i>Morus notabilis</i> and <i>Morus alba</i> . <i>Horticulture Research</i> , 2022, 9, .	2.9	16
419	Duplication and Specialization of <i>NUDX1</i> in <i>Rosaceae</i> Led to Geraniol Production in Rose Petals. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	13
420	The Roles of Floral Organ Genes in Regulating <i>Rosaceae</i> Fruit Development. <i>Frontiers in Plant Science</i> , 2021, 12, 644424.	1.7	7
421	Gramene: A Resource for Comparative Analysis of Plants Genomes and Pathways. <i>Methods in Molecular Biology</i> , 2022, 2443, 101-131.	0.4	23
422	microRNA172 targets <i>APETALA2</i> to regulate flavonoid biosynthesis in apple (<i>Malus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 262	2.9	22
423	Time-Resolved Analysis of Candidate Gene Expression and Ambient Temperature During Bud Dormancy in Apple. <i>Frontiers in Plant Science</i> , 2021, 12, 803341.	1.7	4
424	Overexpression of apple <i>Ma12</i> , a mitochondrial pyrophosphatase pump gene, leads to malic acid accumulation and the upregulation of malate dehydrogenase in tomato and apple calli. <i>Horticulture Research</i> , 2022, 9, .	2.9	10
425	Genome-Wide Investigation of the Zinc Finger-Homeodomain Family Genes Reveals Potential Roles in Apple Fruit Ripening. <i>Frontiers in Genetics</i> , 2021, 12, 783482.	1.1	3
426	Epigenome guided crop improvement: current progress and future opportunities. <i>Emerging Topics in Life Sciences</i> , 2022, 6, 141-151.	1.1	5
427	Genome-wide identification and characterization of long noncoding RNAs involved in apple fruit development and ripening. <i>Scientia Horticulturae</i> , 2022, 295, 110898.	1.7	4

#	ARTICLE	IF	CITATIONS
428	Whole genome re-sequencing and transcriptome reveal an alteration in hormone signal transduction in a more-branching mutant of apple. <i>Gene</i> , 2022, 818, 146214.	1.0	2
429	Genome Wide Identification and Characterization of Apple WD40 Proteins and Expression Analysis in Response to ABA, Drought, and Low Temperature. <i>Horticulturae</i> , 2022, 8, 141.	1.2	4
430	Genome-wide identification and characterization of AINTEGUMENTA-LIKE (AIL) family genes in apple (<i>Malus domestica</i> Borkh.). <i>Genomics</i> , 2022, 114, 110313.	1.3	7
431	Genome-Wide In Silico Analysis and Expression Profiling of Phosphoenolpyruvate Carboxylase Genes in Loquat, Apple, Peach, Strawberry and Pear. <i>Agronomy</i> , 2022, 12, 25.	1.3	7
432	Bulk segregation analysis in the <sc>NGS</sc> era: a review of its teenage years. <i>Plant Journal</i> , 2022, 109, 1355-1374.	2.8	58
433	Genetic architecture and genomic predictive ability of apple quantitative traits across environments. <i>Horticulture Research</i> , 2022, 9, .	2.9	20
434	Identification of Putative Markers of Non-infectious Bud Failure in Almond [<i>Prunus dulcis</i> (Mill.) D.A. Webb] Through Genome Wide DNA Methylation Profiling and Gene Expression Analysis in an Almond Ã—Peach Hybrid Population. <i>Frontiers in Plant Science</i> , 2022, 13, 804145.	1.7	5
435	Genome-wide Identification, Expression, and Functional Analysis of MdMSI Genes in Apples (<i>Malus</i>) Tj ETQq1 1 0.784314 rgBJ /Overlo	1.1	2
436	Genome-Wide Identification of Apple Atypical bHLH Subfamily PRE Members and Functional Characterization of MdPRE4.3 in Response to Abiotic Stress. <i>Frontiers in Genetics</i> , 2022, 13, 846559.	1.1	6
437	Can Epigenetics Guide the Production of Better Adapted Cultivars?. <i>Agronomy</i> , 2022, 12, 838.	1.3	6
438	An efficient chromatin immunoprecipitation (ChIP) protocol for studying histone modifications in peach reproductive tissues. <i>Plant Methods</i> , 2022, 18, 43.	1.9	5
439	A chromosome-level genome sequence assembly of the red raspberry (<i>Rubus idaeus</i> L.). <i>PLoS ONE</i> , 2022, 17, e0265096.	1.1	11
440	Transposon insertions regulate genome-wide allele-specific expression and underpin flower colour variations in apple (<i>Malus</i> spp.). <i>Plant Biotechnology Journal</i> , 2022, 20, 1285-1297.	4.1	21
441	An <i>Erwinia amylovora</i> inducible promoter for improvement of apple fire blight resistance. <i>Plant Cell Reports</i> , 2022, 41, 1499-1513.	2.8	4
442	Genome-wide identification of WOX gene family in apple and a functional analysis of MdWOX4b during adventitious root formation. <i>Journal of Integrative Agriculture</i> , 2022, 21, 1332-1345.	1.7	7
443	Genome assembly, annotation, and comparative analysis of the cattail <i>Typha latifolia</i> . <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	6
444	Development of SSR Databases Available for Both NGS and Capillary Electrophoresis in Apple, Pear and Tea. <i>Plants</i> , 2021, 10, 2796.	1.6	5
445	Comparative transcriptomic analysis of apple and peach fruits: insights into fruit type specification. <i>Plant Journal</i> , 2022, 109, 1614-1629.	2.8	4

#	ARTICLE	IF	CITATIONS
446	Profiling of N6-Methyladenosine (m6A) Modification Landscape in Response to Drought Stress in Apple (<i>Malus prunifolia</i> (Willd.) Borkh). <i>Plants</i> , 2022, 11, 103.	1.6	20
447	Comprehensive Genome-Wide Identification and Transcript Profiling of GABA Pathway Gene Family in Apple (<i>Malus domestica</i>). <i>Genes</i> , 2021, 12, 1973.	1.0	2
448	Transcriptomic Insights on the Preventive Action of Apple (cv Granny Smith) Skin Wounding on Superficial Scald Development. <i>International Journal of Molecular Sciences</i> , 2021, 22, 13425.	1.8	1
450	Identification of Genes Associated with Nitrogen Stress Responses in Apple Leaves. <i>Plants</i> , 2021, 10, 2649.	1.6	2
451	The Identification of Small RNAs Differentially Expressed in Apple Buds Reveals a Potential Role of the Mir159-MYB Regulatory Module during Dormancy. <i>Plants</i> , 2021, 10, 2665.	1.6	9
452	Transcriptome analysis of transgenic apple fruit overexpressing microRNA172 reveals candidate transcription factors regulating apple fruit development at early stages. <i>PeerJ</i> , 2021, 9, e12675.	0.9	3
453	Elevating fruit carotenoid content in apple (<i>Malus x domestica</i> Borkh). <i>Methods in Enzymology</i> , 2022, , 63-98.	0.4	0
454	Expression Characteristics in Roots, Phloem, Leaves, Flowers and Fruits of Apple circRNA. <i>Genes</i> , 2022, 13, 712.	1.0	5
498	Genomic and Bioinformatic Resources for Perennial Fruit Species. <i>Current Genomics</i> , 2022, 23, .	0.7	0
499	RSNET: inferring gene regulatory networks by a redundancy silencing and network enhancement technique. <i>BMC Bioinformatics</i> , 2022, 23, 165.	1.2	6
500	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. <i>Molecular Ecology</i> , 2023, 32, 5125-5139.	2.0	3
501	Time Is of the Essence—Early Activation of the Mevalonate Pathway in Apple Challenged With Gray Mold Correlates With Reduced Susceptibility During Postharvest Storage. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	4
502	Genome-wide identification of the <i>SWEET</i> gene family mediating the cold stress response in <i>Prunus mume</i> . <i>PeerJ</i> , 2022, 10, e13273.	0.9	4
503	Identification of Candidate Genes Associated With Tolerance to Apple Replant Disease by Genome-Wide Transcriptome Analysis. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	5
504	MdARF8: An Auxin Response Factor Involved in Jasmonate Signaling Pathway in <i>Malus domestica</i> . <i>Journal of Plant Growth Regulation</i> , 2023, 42, 1738-1749.	2.8	2
505	Genome-wide analysis of MdABF Subfamily and functional identification of MdABF1 in drought tolerance in apple. <i>Environmental and Experimental Botany</i> , 2022, 199, 104904.	2.0	1
506	Genome-wide Identification and Comparative Analysis of Genes Encoding AAPs in Apple (<i>Malus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.0	0
507	Unravelling the Role of Epigenetic Modifications in Development and Reproduction of Angiosperms: A Critical Appraisal. <i>Frontiers in Genetics</i> , 2022, 13, .	1.1	7

#	ARTICLE	IF	CITATIONS
508	Apple Fruit Size QTLs on Chromosomes 8 and 16 Characterized in "Honeycrisp"™-Derived Germplasm. <i>Agronomy</i> , 2022, 12, 1279.	1.3	6
509	Unexpected Low DNA Methylation in Transposable Elements at the 5'CCGG Sites in Three Fruit Tree Cultivars. <i>Agronomy</i> , 2022, 12, 1347.	1.3	0
510	New insights into the role of melatonin in photosynthesis. <i>Journal of Experimental Botany</i> , 2022, 73, 5918-5927.	2.4	20
511	MdGRF11, a growth-regulating factor, participates in the regulation of flowering time and interacts with MdTFL1/MdFT1 in apple. <i>Plant Science</i> , 2022, 321, 111339.	1.7	5
512	Comprehensive identification of sugar transporters in the <i>Malus</i> spp. genomes reveals their potential functions in sugar accumulation in apple fruits. <i>Scientia Horticulturae</i> , 2022, 303, 111232.	1.7	4
513	<sc>H3K4me3</sc> plays a key role in establishing permissive chromatin states during bud dormancy and bud break in apple. <i>Plant Journal</i> , 2022, 111, 1015-1031.	2.8	13
514	Flexible and digestible wood caused by viral-induced alteration of cell wall composition. <i>Current Biology</i> , 2022, , .	1.8	0
515	Target of rapamycin (TOR) regulates the response to low nitrogen stress via autophagy and hormone pathways in <i>Malus hupehensis</i> . <i>Horticulture Research</i> , 2022, 9, .	2.9	5
516	Research Progress on Genetic Basis of Fruit Quality Traits in Apple (<i>Malus domestica</i>). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	5
517	MdNRT2.4 interacts with rhizosphere bacteria to enhance nitrate uptake in apple rootstocks. <i>Journal of Experimental Botany</i> , 0, , .	2.4	6
518	Identification and Comprehensive Genome-Wide Analysis of Glutathione S-Transferase Gene Family in Sweet Cherry (<i>Prunus avium</i>) and Their Expression Profiling Reveals a Likely Role in Anthocyanin Accumulation. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	5
519	Integrative Analysis of the DICER-like (DCL) Genes From Peach (<i>Prunus persica</i>): A Critical Role in Response to Drought Stress. <i>Frontiers in Ecology and Evolution</i> , 0, 10, .	1.1	4
520	Utilizing paralogues for phylogenetic reconstruction has the potential to increase species tree support and reduce gene tree discordance in target enrichment data. <i>Molecular Ecology Resources</i> , 2022, 22, 3018-3034.	2.2	8
521	Genome-Wide Identification and Expression Profiling Reveal the Potential Functions of the SWEET Gene Family during the Sink Organ Development Period in Apple (<i>Malus domestica</i> Borkh.). <i>Agronomy</i> , 2022, 12, 1747.	1.3	6
522	Large-Effect QTLs for Titratable Acidity and Soluble Solids Content Validated in "Honeycrisp"™-Derived Apple Germplasm. <i>Agronomy</i> , 2022, 12, 1703.	1.3	3
523	An apple somatic mutation of delayed fruit maturation date is primarily caused by a retrotransposon insertion-associated large deletion. <i>Plant Journal</i> , 2022, 111, 1609-1625.	2.8	4
524	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. <i>Plant Cell</i> , 2022, 34, 3983-4006.	3.1	20
526	Environmentally driven transcriptomic and metabolic changes leading to color differences in "Golden Reinders" apples. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1

#	ARTICLE	IF	CITATIONS
529	Genomic signatures and evolutionary history of the endangered blue-crowned laughingthrush and other Garrulax species. BMC Biology, 2022, 20, .	1.7	1
530	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
531	Genotyping-by-sequencing of Canada's apple biodiversity collection. Frontiers in Genetics, 0, 13, .	1.1	2
532	Integrated multi-omic analysis of fruit maturity identifies biomarkers with drastic abundance shifts spanning the harvest period in 'Royal Gala' apple. Postharvest Biology and Technology, 2022, 193, 112059.	2.9	12
533	Genome-wide identification of apple PPI genes and a functional analysis of the response of MxPPI1 to Fe deficiency stress. Plant Physiology and Biochemistry, 2022, 189, 94-103.	2.8	3
534	The role of gene duplication in the divergence of the sweet cherry. Plant Gene, 2022, 32, 100379.	1.4	0
535	Genomic Approaches to Improve Abiotic Stress Tolerance in Apple (<i>Malus domestica</i>). , 2022, , 1-17.		1
536	Genome-wide identification of MAPK family genes and their response to abiotic stresses in tea plant (<i>Camellia sinensis</i>). Open Life Sciences, 2022, 17, 1064-1074.	0.6	5
537	Genome-Wide Identification, In Silico Analysis and Expression Profiling of SWEET Gene Family in Loquat (<i>Eriobotrya japonica</i> Lindl.). Agriculture (Switzerland), 2022, 12, 1312.	1.4	6
538	Chasing Consistency: An Update of the TCP Gene Family of <i>Malus Domestica</i> . Genes, 2022, 13, 1696.	1.0	2
539	GWAS provides new insights into the genetic mechanisms of phytochemicals production and red skin colour in apple. Horticulture Research, 0, , .	2.9	6
540	Exploring epigenetic variation for breeding climate resilient apple crops. Physiologia Plantarum, 2022, 174, .	2.6	2
541	Integrating ATAC-seq and RNA-seq Reveals the Dynamics of Chromatin Accessibility and Gene Expression in Apple Response to Drought. International Journal of Molecular Sciences, 2022, 23, 11191.	1.8	12
542	A genome-wide association study provides insights into fatty acid synthesis and metabolism in <i>Malus</i> fruits. Journal of Experimental Botany, 2022, 73, 7467-7476.	2.4	1
543	Overexpression of PSY1 increases fruit skin and flesh carotenoid content and reveals associated transcription factors in apple (<i>Malus Domestica</i>). Frontiers in Plant Science, 0, 13, .	1.7	7
544	Genetic structure and gene flow of <i>Malus</i> across the Korean Peninsula using genotyping-by-sequencing. Scientific Reports, 2022, 12, .	1.6	1
545	Transcriptome analysis reveals candidate genes involved in nitrogen deficiency stress in apples. Journal of Plant Physiology, 2022, 279, 153822.	1.6	11
546	A phased, chromosome-scale genome of 'Honeycrisp' apple (<i>Malus domestica</i>). GigaByte, 0, 2022, 1-15.	0.0	6

#	ARTICLE	IF	CITATIONS
547	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
548	MdMYB52 regulates lignin biosynthesis upon the suberization process in apple. Frontiers in Plant Science, 0, 13, .	1.7	2
549	Chinese Jujube: Crop Background and Genome Sequencing. Compendium of Plant Genomes, 2022, , 69-86.	0.3	0
550	Identification and evolutionary characterization of SFBB genes in 'Yali' and its spontaneous self-compatible mutant 'Jinzhui' (Pyrus bretschneideri). Horticultural Plant Journal, 2023, 9, 909-919.	2.3	1
551	Comparative Transcriptome Analysis to Identify Candidate Genes Related to Chlorogenic Acid and Flavonoids Biosynthesis in Iridaceae. Forests, 2022, 13, 1632.	0.9	5
552	Determination of physiological, biochemical and molecular interactions between Fraser's Photinia (Photinia fraseri Dress.) and its endophytic bacterium PCB_invit. Plant Cell, Tissue and Organ Culture, 2022, 151, 631-649.	1.2	2
553	Methylation in the CHH Context Allows to Predict Recombination in Rice. International Journal of Molecular Sciences, 2022, 23, 12505.	1.8	3
554	Anthocyanin Accumulation Provides Protection against High Light Stress While Reducing Photosynthesis in Apple Leaves. International Journal of Molecular Sciences, 2022, 23, 12616.	1.8	8
555	The dynamics of lncRNAs transcription in interspecific F1 allotriploid hybrids between Brassica species. Genomics, 2022, 114, 110505.	1.3	3
556	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
557	Characterization of the genetic and regulatory networks associated with sugar and acid metabolism in apples via an integrated strategy. Frontiers in Plant Science, 0, 13, .	1.7	0
558	Analysis of the Small Auxin-Up RNA (SAUR) Genes Regulating Root Growth Angle (RGA) in Apple. Genes, 2022, 13, 2121.	1.0	2
559	Genome-wide characterization of the chitinase gene family in wild apple (Malus sieversii) and domesticated apple (Malus domestica) reveals its role in resistance to Valsa mali. Frontiers in Plant Science, 0, 13, .	1.7	8
560	A chromosome-length genome assembly and annotation of blackberry (<i>Rubus argutus</i> , cv. Tj ETQq1 1 0.784314 rgBT _g /Overlook	0.8	0
562	CRISPR/Cas9 genome editing applied to MdPGT1 in apple results in reduced foliar phloridzin without impacting plant growth. Plant Journal, 2023, 113, 92-105.	2.8	9
563	A transcriptomic study of 'Granny Smith' apple fruit response to x-ray irradiation using RNA-Seq. Scientia Horticulturae, 2023, 311, 111777.	1.7	2
564	Multi-omics analysis reveals the mechanism of bHLH130 responding to low-nitrogen stress of apple rootstock. Plant Physiology, 2023, 191, 1305-1323.	2.3	5
565	The 'Candidatus Phytoplasma mali' effector protein SAP11CaPm interacts with MdTCP16, a class II CYC/TB1 transcription factor that is highly expressed during phytoplasma infection. PLoS ONE, 2022, 17, e0272467.	1.1	2

#	ARTICLE	IF	CITATIONS
566	Elucidation and characterization of QTLs for Russet formation on apple fruit in "Honeycrisp"™-derived breeding germplasm. <i>Tree Genetics and Genomes</i> , 2023, 19, .	0.6	0
567	The Current Developments in Medicinal Plant Genomics Enabled the Diversification of Secondary Metabolites™ Biosynthesis. <i>International Journal of Molecular Sciences</i> , 2022, 23, 15932.	1.8	15
568	Genome-wide identification and characterization of the IPT family members in nine Rosaceae species and a functional analysis of MdIPT5b in cold resistance. <i>Horticultural Plant Journal</i> , 2023, 9, 616-630.	2.3	1
569	Transcriptional Effects of Rootstock on Scion after Drought: A Case Study of Using MdGH3 RNAi as the Rootstock. <i>Horticulturae</i> , 2022, 8, 1212.	1.2	0
570	Genome-wide identification and stress response analysis of cyclophilin gene family in apple (<i>Malus domestica</i>) cv. 'Overlock 10'. <i>Frontiers in Plant Science</i> , 2023, 14, 1157232.	1.2	4
571	Systematic genome-wide and expression analysis of RNA-directed DNA methylation pathway genes in grapes predicts their involvement in multiple biological processes. <i>Frontiers in Plant Science</i> , 2023, 14, 1157232.	1.7	1
572	Plasma Membrane-Localized Transporter MdSWEET12 Is Involved in Sucrose Unloading in Apple Fruit. <i>Journal of Agricultural and Food Chemistry</i> , 2022, 70, 15517-15530.	2.4	3
573	De novo transcriptome assembly and functional analysis reveal a dihydrochalcone 3-hydroxylase(DHC3H) of wild <i>Malus</i> species that produces sieboldin in vivo. <i>Frontiers in Plant Science</i> , 2023, 14, 1157232.	1.7	3
575	Transcriptome Analysis of the Effects of Grafting Interstocks on Apple Rootstocks and Scions. <i>International Journal of Molecular Sciences</i> , 2023, 24, 807.	1.8	3
576	Transcriptome analyses reveal the effects of mixed saline-alkali stress on indoleacetic acid and cytokinins in <i>Malus hupehensis</i> Rehd. leaves. <i>Physiology and Molecular Biology of Plants</i> , 2023, 29, 11-22.	1.4	1
577	The Role of Italy in the Use of Advanced Plant Genomic Techniques on Fruit Trees: State of the Art and Future Perspectives. <i>International Journal of Molecular Sciences</i> , 2023, 24, 977.	1.8	5
578	Genome-wide identification, characterization and evolutionary dynamic of invertase gene family in apple, and revealing its roles in cold tolerance. <i>International Journal of Biological Macromolecules</i> , 2023, 229, 766-777.	3.6	7
579	Genome-wide analysis of the 6B-INTERACTING PROTEIN1 gene family with functional characterization of MdSIP1-2 in <i>Malus domestica</i> . <i>Plant Physiology and Biochemistry</i> , 2023, 195, 89-100.	2.8	4
580	Genetic linkage maps and QTLs associated with fruit skin color and acidity in apple (<i>Malus domestica</i>) cv. 'Overlock 10'. <i>Frontiers in Plant Science</i> , 2023, 14, 1157232.	0.7	2
581	PlantTribes2: Tools for comparative gene family analysis in plant genomics. <i>Frontiers in Plant Science</i> , 2023, 14, 1157232.	1.7	5
582	Characterization of the REVEILLE family in Rosaceae and role of PpLHY in flowering time regulation. <i>BMC Genomics</i> , 2023, 24, .	1.2	7
584	Genome-wide characterization and functional identification of MYB genes in <i>Malus sieversii</i> infected by <i>Valsa mali</i> . <i>Frontiers in Plant Science</i> , 2023, 14, .	1.7	2
585	Fruit growth and development in apple: a molecular, genomics and epigenetics perspective. <i>Frontiers in Plant Science</i> , 2023, 14, .	1.7	1

#	ARTICLE	IF	CITATIONS
586	Metabolomic and transcriptomic analysis reveals the molecular mechanism by which blue light promotes lutein synthesis in strawberry. <i>Journal of Integrative Agriculture</i> , 2023, 22, 1695-1703.	1.7	0
587	MdbZIP74 negatively regulates osmotic tolerance and adaptability to moderate drought conditions of apple plants. <i>Journal of Plant Physiology</i> , 2023, 283, 153965.	1.6	0
589	Characterization of a pollen-part self-compatible apple (<i>Malus domestica</i> Borkh.) mutant induced by γ -ray mutagenesis. <i>Scientia Horticulturae</i> , 2023, 312, 111867.	1.7	2
590	Insights on the stem elongation of spur-type bud sport mutant of "Red Delicious" apple. <i>Planta</i> , 2023, 257, .	1.6	3
591	Deducing genotypes for loci of interest from SNP array data via haplotype sharing, demonstrated for apple and cherry. <i>PLoS ONE</i> , 2023, 18, e0272888.	1.1	1
592	Parametric mapping of QTL for resistance to European canker in apple in "Aroma" and "Discovery". <i>Tree Genetics and Genomes</i> , 2023, 19, .	0.6	0
593	Transcriptome and Metabolome Analysis Reveals Salt-Tolerance Pathways in the Leaves and Roots of ZM-4 (<i>Malus zumi</i>) in the Early Stages of Salt Stress. <i>International Journal of Molecular Sciences</i> , 2023, 24, 3638.	1.8	2
594	Red-TE Homozygous Alleles of MdMYB10 Confer Full-Red Apple Fruit Skin in a High-Temperature Region. <i>Horticulturae</i> , 2023, 9, 270.	1.2	2
595	Genome-wide analysis of MdGeBP family and functional identification of MdGeBP3 in <i>Malus domestica</i> . <i>Environmental and Experimental Botany</i> , 2023, 208, 105262.	2.0	1
596	Elucidation of the GAUT gene family in eight Rosaceae species and function analysis of PbrGAUT22 in pear pollen tube growth. <i>Planta</i> , 2023, 257, .	1.6	1
597	Autochthonous Apple Cultivars from the Campania Region (Southern Italy): Bio-Agronomic and Qualitative Traits. <i>Plants</i> , 2023, 12, 1160.	1.6	0
598	Integrated ATAC-Seq and RNA-Seq Data Analysis to Reveal OsbZIP14 Function in Rice in Response to Heat Stress. <i>International Journal of Molecular Sciences</i> , 2023, 24, 5619.	1.8	5
599	The Identification of SQS/SQE/OSC Gene Families in Regulating the Biosynthesis of Triterpenes in <i>Potentilla anserina</i> . <i>Molecules</i> , 2023, 28, 2782.	1.7	1
600	Genetic analysis and QTL mapping of aroma volatile compounds in the apple progeny "Fuji" and "Cripps Pink". <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	0
601	Sufficient coumarin accumulation improves apple resistance to <i>Cytospora mali</i> under high-potassium status. <i>Plant Physiology</i> , 0, , .	2.3	3
602	Promoter Variation of the Key Apple Fruit Texture Related Gene MdPG1 and the Upstream Regulation Analysis. <i>Plants</i> , 2023, 12, 1452.	1.6	1
603	Genetic information from phased SNP array data can improve assemblies of whole genome sequences. <i>Acta Horticulturae</i> , 2023, , 81-88.	0.1	0
604	Deciphering the Mechanism of Tolerance to Apple Replant Disease Using a Genetic Mapping Approach in a Malling 9 M. robusta 5 Population Identifies SNP Markers Linked to Candidate Genes. <i>International Journal of Molecular Sciences</i> , 2023, 24, 6307.	1.8	1

#	ARTICLE	IF	CITATIONS
605	Marker-assisted breeding (MAB) on apple and pear and new approaches for QTLs and major gene genotyping involved in disease resistance. <i>Acta Horticulturae</i> , 2023, , 221-230.	0.1	1
606	Genomic selection in apple: lessons from preliminary studies. <i>Acta Horticulturae</i> , 2023, , 113-122.	0.1	0
607	A strategy for aggregating multi-source historical phenotypic and genotypic data sets containing homonyms for global genomic prediction in apple (<i>Malus domestica</i>). <i>Acta Horticulturae</i> , 2023, , 123-130.	0.1	0
608	A chromosome-scale genome assembly of <i>Malus domestica</i> , a multi-stress resistant apple variety. <i>Genomics</i> , 2023, 115, 110627.	1.3	6
609	DNA methylation signatures of duplicate gene evolution in angiosperms. <i>Plant Physiology</i> , 2023, 192, 2883-2901.	2.3	1
610	Extreme-phenotype GWAS unravels a complex nexus between apple (<i>Malus domestica</i>) red-flesh colour and internal flesh browning. <i>Fruit Research</i> , 2022, 2, 1-14.	0.9	1
625	Epigenetic Regulation in Almond. <i>Compendium of Plant Genomes</i> , 2023, , 59-75.	0.3	0
662	<i>Malus Species: Germplasm Conservation and Utilization.</i> , 2023, , 1-36.		0
691	Deep learning for genomics and epi-genomics in horticulture crops improvement. , 2024, , 217-232.		0