Apple miRNAs and tasiRNAs with novel regulatory netv

Genome Biology

13, R47

DOI: 10.1186/gb-2012-13-6-r47

Citation Report

#	Article	IF	Citations
1	Small RNA and transcriptome deep sequencing proffers insight into floral gene regulation in Rosa cultivars. BMC Genomics, 2012, 13, 657.	2.8	49
2	Overexpression of microRNA828 reduces anthocyanin accumulation in Arabidopsis. Plant Cell, Tissue and Organ Culture, 2013, 115, 159-167.	2.3	76
3	Trans-acting small interfering RNA4: key to nutraceutical synthesis in grape development?. Trends in Plant Science, 2013, 18, 601-610.	8.8	49
4	A genome-wide identification and characterization of mircoRNAs and their targets in â€˜Suliâ€™ pear (Pyrus) Tj ETQq1 1 0.784314 rg	3.2	19
5	MicroRNAs and Their Cross-Talks in Plant Development. Journal of Genetics and Genomics, 2013, 40, 161-170.	3.9	70
6	Phased, Secondary, Small Interfering RNAs in Posttranscriptional Regulatory Networks. Plant Cell, 2013, 25, 2400-2415.	6.6	543
7	Catalyzing plant science research with RNA-seq. Frontiers in Plant Science, 2013, 4, 66.	3.6	136
8	MicroRNA Superfamilies Descended from miR390 and Their Roles in Secondary Small Interfering RNA Biogenesis in Eudicots. Plant Cell, 2013, 25, 1555-1572.	6.6	141
9	Recent Advances in Temperate Fruit Crops. , 2013, , 251-284.		0
10	Parallel analysis of RNA ends enhances global investigation of microRNAs and target RNAs of Brachypodium distachyon. Genome Biology, 2013, 14, R145.	9.6	67
11	The genome sequence of the most widely cultivated cacao type and its use to identify candidate genes regulating pod color. Genome Biology, 2013, 14, r53.	8.8	225
12	Peculiar Evolutionary History of miR390-Guided TAS3-Like Genes in Land Plants. Scientific World Journal, The, 2013, 2013, 1-14.	2.1	18
13	Differential sRNA Regulation in Leaves and Roots of Sugarcane under Water Depletion. PLoS ONE, 2014, 9, e93822.	2.5	37
14	Extending the sRNAome of Apple by Next-Generation Sequencing. PLoS ONE, 2014, 9, e95782.	2.5	17
15	Genome-Wide Discovery and Analysis of Phased Small Interfering RNAs in Chinese Sacred Lotus. PLoS ONE, 2014, 9, e113790.	2.5	28
16	Identification of miRNAs involved in pear fruit development and quality. BMC Genomics, 2014, 15, 953.	2.8	102
17	Genome-Wide Analysis of leafbladeless1-Regulated and Phased Small RNAs Underscores the Importance of the TAS3 ta-siRNA Pathway to Maize Development. PLoS Genetics, 2014, 10, e1004826.	3.5	49
18	Genome-wide identification of vegetative phase transition-associated microRNAs and target predictions using degradome sequencing in Malus hupehensis. BMC Genomics, 2014, 15, 1125.	2.8	60

#	Article	IF	Citations
19	Identification and profiling of novel and conserved microRNAs during the flower opening process in Prunus mume via deep sequencing. Molecular Genetics and Genomics, 2014, 289, 169-183.	2.1	54
20	Identification and characterization of the microRNA transcriptome of a moth orchid Phalaenopsis aphrodite. Plant Molecular Biology, 2014, 84, 529-548.	3.9	38
21	MicroRNAs as regulators of adventitious root development. Journal of Plant Biochemistry and Biotechnology, 2014, 23, 339-347.	1.7	21
22	miR828 and miR858 regulate homoeologous MYB2 gene functions in Arabidopsis trichome and cotton fibre development. Nature Communications, 2014, 5, 3050.	12.8	215
23	A Medicago truncatula rdr6 allele impairs transgene silencing and endogenous phased si<scp>RNA</scp> production but not development. Plant Biotechnology Journal, 2014, 12, 1308-1318.	8.3	5
24	Binding of miR396 to mRNA of genes encoding growth-regulating transcription factors of plants. Russian Journal of Plant Physiology, 2014, 61, 807-810.	1.1	8
25	High-throughput sequencing reveals small RNAs involved in ASGV infection. BMC Genomics, 2014, 15, 568.	2.8	39
26	Genome-wide comparison of microRNAs and their targeted transcripts among leaf, flower and fruit of sweet orange. BMC Genomics, 2014, 15, 695.	2.8	70
27	Apple ring rot-responsive putative microRNAs revealed by high-throughput sequencing in MalusÂÃ—Âdomestica Borkh.. Molecular Biology Reports, 2014, 41, 5273-5286.	2.3	10
28	High-throughput sequence analysis of small RNAs in skotomorphogenic seedlings of Brassica rapa ssp. rapa. Gene, 2014, 548, 68-74.	2.2	5
29	Micro<scp>RNA</scp>s in fruit trees: discovery, diversity and future research directions. Plant Biology, 2014, 16, 856-865.	3.8	26
30	Genome-wide characterization and comparative analysis of R2R3-MYB transcription factors shows the complexity of MYB-associated regulatory networks in Salvia miltiorrhiza. BMC Genomics, 2014, 15, 277.	2.8	92
31	Identification and characterization of microRNAs in the flag leaf and developing seed of wheat (Triticum aestivum L.). BMC Genomics, 2014, 15, 289.	2.8	95
32	A diverse set of miRNAs responsive to begomovirus-associated betasatellite in Nicotiana benthamiana. BMC Plant Biology, 2014, 14, 60.	3.6	19
33	Polyploidy and small RNA regulation of cotton fiber development. Trends in Plant Science, 2014, 19, 516-528.	8.8	68
34	MicroRNA and mRNA expression profiling analysis revealed the regulation of plant height in Gossypium hirsutum. BMC Genomics, 2015, 16, 886.	2.8	23
35	Identification of miRNAs with potential roles in regulation of anther development and male-sterility in 7B-1 male-sterile tomato mutant. BMC Genomics, 2015, 16, 878.	2.8	58
36	Transition from two to one integument in Prunus species: expression pattern of <scp>INNER NO OUTER</scp> (<scp>INO</scp>), <scp>ABERRANT TESTA SHAPE</scp> (<scp>ATS</scp>) and <scp>ETTIN</scp> (<scp>ETT</scp>). New Phytologist, 2015, 208, 584-595.	7.3	26

#	Article	IF	Citations
37	Secondary si<scp>RNA</scp>s from Medicago <scp>NB</scp>â€<scp>LRR</scp>s modulated via mi<scp>RNA</scp>â€“target interactions and their abundances. Plant Journal, 2015, 83, 451-465.	5.7	67
38	Identification and characterization of microRNAs from in vitro-grown pear shoots infected with Apple stem grooving virus in response to high temperature using small RNA sequencing. BMC Genomics, 2015, 16, 945.	2.8	22
39	Genome-wide discovery and validation of Eucalyptus small RNAs reveals variable patterns of conservation and diversity across species of Myrtaceae. BMC Genomics, 2015, 16, 1113.	2.8	13
40	A micro<scp>RNA</scp> allele that emerged prior to apple domestication may underlie fruit size evolution. Plant Journal, 2015, 84, 417-427.	5.7	95
41	Differential mRNA Accumulation upon Early Arabidopsis thaliana Infection with ORMV and TMV-Cg Is Associated with Distinct Endogenous Small RNAs Level. PLoS ONE, 2015, 10, e0134719.	2.5	15
42	Prunus transcription factors: breeding perspectives. Frontiers in Plant Science, 2015, 6, 443.	3.6	30
43	New opportunities for the regulation of secondary metabolism in plants: focus on microRNAs. Biotechnology Letters, 2015, 37, 1719-1727.	2.2	56
44	Identification and expression profiles of sRNAs and their biogenesis and action-related genes in male and female cones of Pinus tabuliformis. BMC Genomics, 2015, 16, 693.	2.8	40
45	Genome-wide identification of the Phaseolus vulgaris sRNAome using small RNA and degradome sequencing. BMC Genomics, 2015, 16, 423.	2.8	49
46	miRNA expression during prickly pear cactus fruit development. Planta, 2015, 241, 435-448.	3.2	23
47	Food derived microRNAs. Food and Function, 2015, 6, 714-718.	4.6	36
48	Identification of apple miRNAs and their potential role in fire blight resistance. Tree Genetics and Genomes, 2015, 11, 1.	1.6	24
49	Novel and Recently Evolved MicroRNA Clusters Regulate Expansive F-BOX Gene Networks through Phased Small Interfering RNAs in Wild Diploid Strawberry. Plant Physiology, 2015, 169, 594-610.	4.8	73
50	Insights into the Small RNA-Mediated Networks in Response to Abiotic Stress in Plants. , 2015, , 45-91.		6
51	Predicted Trans-Acting siRNAs in the Human Brain. International Journal of Molecular Sciences, 2015, 16, 3377-3390.	4.1	4
52	Identification and characterization of microRNAs from Chinese pollination constant non-astringent persimmon using high-throughput sequencing. BMC Plant Biology, 2015, 15, 11.	3.6	52
53	Small tandem target mimic-mediated blockage of microRNA858 induces anthocyanin accumulation in tomato. Planta, 2015, 242, 283-293.	3.2	152
54	Regulation of the alkaloid biosynthesis by mi<scp>RNA</scp> in opium poppy. Plant Biotechnology Journal, 2015, 13, 409-420.	8.3	97

#	Article	IF	Citations
55	A dynamic evolutionary and functional landscape of plant phased small interfering RNAs. BMC Biology, 2015, 13, 32.	3.8	57
56	Uncovering co-expression gene network modules regulating fruit acidity in diverse apples. BMC Genomics, 2015, 16, 612.	2.8	68
57	Transcription Profiles Reveal Sugar and Hormone Signaling Pathways Mediating Flower Induction in Apple (Malus domesticaBorkh.). Plant and Cell Physiology, 2015, 56, 2052-2068.	3.1	118
58	Extensive Families of miRNAs andPHASLoci in Norway Spruce Demonstrate the Origins of Complex phasiRNA Networks in Seed Plants. Molecular Biology and Evolution, 2015, 32, 2905-2918.	8.9	141
59	Identification of conserved and novel microRNAs in Catharanthus roseus by deep sequencing and computational prediction of their potential targets. Gene, 2015, 554, 181-195.	2.2	33
60	Genomic resources in fruit plants: an assessment of current status. Critical Reviews in Biotechnology, 2015, 35, 438-447.	9.0	16
61	Application of Genomic Technologies to the Breeding of Trees. Frontiers in Genetics, 2016, 7, 198.	2.3	45
62	Identification and Expression Analyses of miRNAs from Two Contrasting Flower Color Cultivars of Canna by Deep Sequencing. PLoS ONE, 2016, 11, e0147499.	2.5	20
63	Identification of MicroRNAs and Their Targets Associated with Fruit-Bagging and Subsequent Sunlight Re-exposure in the â€œGranny Smithâ€•Apple Exocarp Using High-Throughput Sequencing. Frontiers in Plant Science, 2016, 7, 27.	3.6	56
64	Identification and Characterization of Erysiphe necator-Responsive MicroRNAs in Chinese Wild Vitis pseudoreticulata by High-Throughput Sequencing. Frontiers in Plant Science, 2016, 7, 621.	3.6	50
65	The Woody-Preferential Gene EgMYB88 Regulates the Biosynthesis of Phenylpropanoid-Derived Compounds in Wood. Frontiers in Plant Science, 2016, 7, 1422.	3.6	20
66	Involvement of Auxin and Brassinosteroid in Dwarfism of Autotetraploid Apple (Malusâ€‰Ã—â€‰domestica). Scientific Reports, 2016, 6, 26719.	3.3	79
67	Small RNA transcriptomes of mangroves evolve adaptively in extreme environments. Scientific Reports, 2016, 6, 27551.	3.3	18
68	The Legume miR1514a modulates a NAC transcription factor transcript to trigger phasiRNA formation in response to drought. Journal of Experimental Botany, 2017, 68, erw380.	4.8	40
69	A highly specific micro<scp>RNA</scp>â€mediated mechanism silences <scp>LTR</scp> retrotransposons of strawberry. Plant Journal, 2016, 85, 70-82.	5.7	31
70	Shoot bending promotes flower bud formation by mi<scp>RNA</scp>â€mediated regulation in apple (<scp>M</scp>alus domestica <scp>B</scp>orkh.). Plant Biotechnology Journal, 2016, 14, 749-770.	8.3	69
71	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.	2.8	52
72	How microRNA172 affects fruit growth in different species is dependent on fruit type. Plant Signaling and Behavior, 2016, 11, e1156833.	2.4	39

#	Article	IF	Citations
73	Post-transcriptional gene silencing in plants: a double-edged sword. Science China Life Sciences, 2016, 59, 271-276.	4.9	18
74	MicroRNA858 Is a Potential Regulator of Phenylpropanoid Pathway and Plant Development. Plant Physiology, 2016, 171, 944-959.	4.8	163
75	Deep-sequence profiling of miRNAs and their target prediction in Monotropa hypopitys. Plant Molecular Biology, 2016, 91, 441-458.	3.9	5
76	Genome-wide identification of microRNAs in pomegranate (Punica granatum L.) by high-throughput sequencing. BMC Plant Biology, 2016, 16, 122.	3.6	57
77	Identification of phasiRNAs and their droughtâ€•responsiveness in Populus trichocarpa. FEBS Letters, 2016, 590, 3616-3627.	2.8	23
78	Repression of MYBL2 by Both microRNA858a and HY5 Leads to the Activation of Anthocyanin Biosynthetic Pathway in Arabidopsis. Molecular Plant, 2016, 9, 1395-1405.	8.3	146
79	Identification of russet-associated microRNAs in the exocarp of a Dangshansuli pear mutant (Pyrus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.6	4
80	Small RNA and PARE sequencing in flower bud reveal the involvement of sRNAs in endodormancy release of Japanese pear (Pyrus pyrifolia 'Kosui'). BMC Genomics, 2016, 17, 230.	2.8	25
81	Identification of microRNAs, phasiRNAs and Their Targets in Pineapple. Tropical Plant Biology, 2016, 9, 176-186.	1.9	32
82	An optimized TRV-based virus-induced gene silencing protocol for Malus crabapple. Plant Cell, Tissue and Organ Culture, 2016, 126, 499-509.	2.3	29
83	High-resolution identification and abundance profiling of cassava (Manihot esculenta Crantz) microRNAs. BMC Genomics, 2016, 17, 85.	2.8	22
84	Identification and validation of a virus-inducible ta-siRNA-generating TAS4 locus in tomato. Journal of Biosciences, 2016, 41, 109-118.	1.1	9
85	Dormancy-associated MADS-box genes and microRNAs jointly control dormancy transition in pear (Pyrus pyrifoliawhite pear group) flower bud. Journal of Experimental Botany, 2016, 67, 239-257.	4.8	170
86	In silico search and biological validation of microRNAs related to drought response in peach and almond. Functional and Integrative Genomics, 2017, 17, 189-201.	3.5	27
87	Spearmint R2R3â€<scp>MYB</scp> transcription factor Ms<scp>MYB</scp> negatively regulates monoterpene production and suppresses the expression of geranyl diphosphate synthase large subunit (Ms<scp>GPPS</scp>.<scp>LSU</scp>). Plant Biotechnology Journal, 2017, 15, 1105-1119.	8.3	107
88	The Emergence, Evolution, and Diversification of the miR390-TAS3-ARF Pathway in Land Plants. Plant Cell, 2017, 29, 1232-1247.	6.6	149
89	A single miR390 targeting event is sufficient for triggering TAS3-tasiRNA biogenesis in Arabidopsis. Nucleic Acids Research, 2017, 45, 5539-5554.	14.5	48
90	Biogenesis of diverse plant phasiRNAs involves an miRNA-trigger and Dicer-processing. Journal of Plant Research, 2017, 130, 17-23.	2.4	75

#	Article	IF	Citations
91	The small RNA repertoire in phloem tissue of three Vitis vinifera cultivars. Plant Gene, 2017, 10, 60-73.	2.3	15
92	Malus hupehensis miR168 Targets to ARGONAUTE1 and Contributes to the Resistance against Botryosphaeria dothidea Infection by Altering Defense Responses. Plant and Cell Physiology, 2017, 58, 1541-1557.	3.1	30
93	Transcriptome analysis of bagging-treated red Chinese sand pear peels reveals light-responsive pathway functions in anthocyanin accumulation. Scientific Reports, 2017, 7, 63.	3.3	67
94	Transcriptome analysis reveals differentially expressed small RNAs and genes associated with grapevine leafroll-associated virus 3 infections. Physiological and Molecular Plant Pathology, 2017, 100, 220-236.	2.5	8
95	miR156 switches on vegetative phase change under the regulation of redox signals in apple seedlings. Scientific Reports, 2017, 7, 14223.	3.3	48
96	Genome re-sequencing reveals the history of apple and supports a two-stage model for fruit enlargement. Nature Communications, 2017, 8, 249.	12.8	286
97	miR3954 is a trigger of phasi<scp>RNA</scp>s that affects flowering time in citrus. Plant Journal, 2017, 92, 263-275.	5.7	41
98	Biosynthesis and Regulation of Phenylpropanoids in Plants. Critical Reviews in Plant Sciences, 2017, 36, 257-290.	5.7	328
99	De novo assembly and annotation of the Zhe-Maidong (Ophiopogon japonicus (L.f.) Ker-Gawl) transcriptome in different growth stages. Scientific Reports, 2017, 7, 3616.	3.3	14
100	Genome-wide identification and characterization of phased small interfering RNA genes in response to Botrytis cinerea infection in Solanum lycopersicum. Scientific Reports, 2017, 7, 3019.	3.3	13
101	Genome-wide analysis of microRNA targeting impacted by SNPs in cucumber genome. BMC Genomics, 2017, 18, 275.	2.8	12
102	Small RNA sequencing reveals a role for sugarcane miRNAs and their targets in response to Sporisorium scitamineum infection. BMC Genomics, 2017, 18, 325.	2.8	34
103	<scp>SRNAome</scp> and degradome sequencing analysis reveals specific regulation of <scp>sRNA</scp> in response to chilling injury in tomato fruit. Physiologia Plantarum, 2017, 160, 142-154.	5.2	24
105	Role of miRNAs in root development of model plant Arabidopsis thaliana. Indian Journal of Plant Physiology, 2017, 22, 382-392.	0.8	20
106	Artificial MicroRNAs Promote High-Level Production of Biomolecules Through Metabolic Engineering of Phenylpropanoid Pathway. Critical Reviews in Plant Sciences, 2017, 36, 353-366.	5.7	6
107	Response of miR156-SPL Module during the Red Peel Coloration of Bagging-Treated Chinese Sand Pear (Pyrus pyrifolia Nakai). Frontiers in Physiology, 2017, 8, 550.	2.8	71
108	Identification of MicroRNAs and Their Target Genes Related to the Accumulation of Anthocyanins in Litchi chinensis by High-Throughput Sequencing and Degradome Analysis. Frontiers in Plant Science, 2016, 7, 2059.	3.6	69
109	miRNA and Degradome Sequencing Reveal miRNA and Their Target Genes That May Mediate Shoot Growth in Spur Type Mutant â€œYanfu 6â€• Frontiers in Plant Science, 2017, 8, 441.	3.6	22

#	Article	IF	Citations
110	Identification of MicroRNA Targets of Capsicum spp. Using MiRTransâ€"a Trans-Omics Approach. Frontiers in Plant Science, 2017, 8, 495.	3.6	5
111	Md-miR156ab and Md-miR395 Target WRKY Transcription Factors to Influence Apple Resistance to Leaf Spot Disease. Frontiers in Plant Science, 2017, 8, 526.	3.6	47
112	Small RNA-Sequencing Links Physiological Changes and RdDM Process to Vegetative-to-Floral Transition in Apple. Frontiers in Plant Science, 2017, 8, 873.	3.6	27
113	Allelic Interactions among Pto-MIR475b and Its Four Target Genes Potentially Affect Growth and Wood Properties in Populus. Frontiers in Plant Science, 2017, 8, 1055.	3.6	9
114	microRNAs and Their Targets in Apple (Malus domestica cv. â€œFujiâ€) Involved in Response to Infection of Pathogen Valsa mali. Frontiers in Plant Science, 2017, 8, 2081.	3.6	13
115	Genome-wide identification of Hami melon miRNAs with putative roles during fruit development. PLoS ONE, 2017, 12, e0180600.	2.5	11
116	Conservation and divergence of small RNA pathways and microRNAs in land plants. Genome Biology, 2017, 18, 158.	8.8	91
117	Small RNA pathways responsible for non-cell-autonomous regulation of plant reproduction. Plant Reproduction, 2018, 31, 21-29.	2.2	18
118	Biogenesis and regulatory hierarchy of phased small interfering RNAs in plants. Plant Biotechnology Journal, 2018, 16, 965-975.	8.3	68
119	Cisâ€directed cleavage and nonstoichiometric abundances of 21â€nucleotide reproductive phased small interfering <scp>RNA</scp>s in grasses. New Phytologist, 2018, 220, 865-877.	7.3	38
120	Identification and characterization of microRNAs in tree peony during chilling induced dormancy release by high-throughput sequencing. Scientific Reports, 2018, 8, 4537.	3.3	48
121	Maintaining good miRNAs in the body keeps the doctor away?: Perspectives on the relationship between foodâ€derived natural products and microRNAs in relation to exosomes/extracellular vesicles. Molecular Nutrition and Food Research, 2018, 62, 1700080.	3.3	28
122	Coupling of micro<scp>RNA</scp>â€directed phased small interfering <scp>RNA</scp> generation from long noncoding genes with alternative splicing and alternative polyadenylation in small <scp>RNA</scp>â€mediated gene silencing. New Phytologist, 2018, 217, 1535-1550.	7.3	46
123	Bioinformatics prediction and annotation of cherry (Prunus avium L.) microRNAs and their targeted proteins. Turkish Journal of Botany, 2018, 42, 382-399.	1.2	4
124	Potato miR828 Is Associated With Purple Tuber Skin and Flesh Color. Frontiers in Plant Science, 2018, 9, 1742.	3.6	49
125	MicroRNAs, tasiRNAs, phasiRNAs, and Their Potential Functions in Pineapple. Plant Genetics and Genomics: Crops and Models, 2018, , 167-182.	0.3	1
126	Small RNAs, emerging regulators critical for the development of horticultural traits. Horticulture Research, 2018, 5, 63.	6.3	85
127	Comparative phenotype and microRNAome in developing anthers of wild-type and male-sterile Lycium barbarum L.. Plant Science, 2018, 274, 349-359.	3.6	12

#	Article	IF	Citations
128	MYBs Drive Novel Consumer Traits in Fruits and Vegetables. Trends in Plant Science, 2018, 23, 693-705.	8.8	116
129	Genome-wide identification and comprehensive analysis of microRNAs and phased small interfering RNAs in watermelon. BMC Genomics, 2018, 19, 111.	2.8	14
130	Phased secondary small interfering RNAs in Panaxnotoginseng. BMC Genomics, 2018, 19, 41.	2.8	13
131	Spatio-temporal expression of miRNA159 family members and their GAMYB target gene during the modulation of gibberellin-induced grapevine parthenocarpy. Journal of Experimental Botany, 2018, 69, 3639-3650.	4.8	42
132	Identification and Characterization of Stress-Responsive TAS3-Derived TasiRNAs in Melon. Plant and Cell Physiology, 2019, 60, 2382-2393.	3.1	8
133	Cytotoxic and apoptotic effects of different extracts of Moringaï¿½oleifera Lam on lymphoid and monocytoid cells. Experimental and Therapeutic Medicine, 2019, 18, 5-17.	1.8	19
134	Systematic identification of long noncoding <scp>RNA</scp>s expressed during lightâ€induced anthocyanin accumulation in apple fruit. Plant Journal, 2019, 100, 572-590.	5.7	91
135	Molecular Responses to Cold Stress in Temperate Fruit Crops with Focus on Rosaceae Family. Sustainable Development and Biodiversity, 2019, , 105-130.	1.7	6
136	Comparative Analysis of miRNA Abundance Revealed the Function of Vvi-miR828 in Fruit Coloring in Root Restriction Cultivation Grapevine (Vitis vinifera L.). International Journal of Molecular Sciences, 2019, 20, 4058.	4.1	17
137	System Analysis of MIRNAs in Maize Internode Elongation. Biomolecules, 2019, 9, 417.	4.0	11
138	RNAi-Mediated Resistance Against Viruses in Perennial Fruit Plants. Plants, 2019, 8, 359.	3.5	12
139	MicroRNA858-mediated regulation of anthocyanin biosynthesis in kiwifruit (Actinidia arguta) based on small RNA sequencing. PLoS ONE, 2019, 14, e0217480.	2.5	27
140	Genome-wide identification of drought-responsive microRNAs in two sets of Malus from interspecific hybrid progenies. Horticulture Research, 2019, 6, 75.	6.3	43
141	miR828 and miR858 regulate VvMYB114 to promote anthocyanin and flavonol accumulation in grapes. Journal of Experimental Botany, 2019, 70, 4775-4792.	4.8	136
142	Multilocation comparison of fruit composition for â€˜HoneySweetâ€™, an RNAi based plum pox virus resistant plum. PLoS ONE, 2019, 14, e0213993.	2.5	6
143	Role of Cytokinin, Strigolactone, and Auxin Export on Outgrowth of Axillary Buds in Apple. Frontiers in Plant Science, 2019, 10, 616.	3.6	38
144	Uncovering anthocyanin biosynthesis related microRNAs and their target genes by small RNA and degradome sequencing in tuberous roots of sweetpotato. BMC Plant Biology, 2019, 19, 232.	3.6	43
145	Updated annotation of the wild strawberry Fragaria vesca V4 genome. Horticulture Research, 2019, 6, 61.	6.3	102

#	Article	IF	Citations
146	Molecular basis of transitivity in plant RNA silencing. Molecular Biology Reports, 2019, 46, 4645-4660.	2.3	10
147	Nutritive implications of dietary microRNAs: facts, controversies, and perspectives. Food and Function, 2019, 10, 3044-3056.	4.6	8
148	Analysis of microRNAs, phased small interfering RNAs and their potential targets in Rosarugosa Thunb.. BMC Genomics, 2019, 19, 983.	2.8	13
149	Gene Regulation Mediated by microRNA-Triggered Secondary Small RNAs in Plants. Plants, 2019, 8, 112.	3.5	21
150	Sweet cherry fruit miRNAs and effect of high CO2 on the profile associated with ripening. Planta, 2019, 249, 1799-1810.	3.2	14
152	Transcriptome-wide identification of miRNA targets and a TAS3-homologous gene in Populus by degradome sequencing. Genes and Genomics, 2019, 41, 849-861.	1.4	7
153	An integrated analysis of mRNA and sRNA transcriptional profiles in Coffea arabica L. roots: insights on nitrogen starvation responses. Functional and Integrative Genomics, 2019, 19, 151-169.	3.5	28
154	The Role of UV-B light on Small RNA Activity During Grapevine Berry Development. G3: Genes, Genomes, Genetics, 2019, 9, 769-787.	1.8	34
155	Identification and validation of drought-responsive microRNAs from Hevea brasiliensis. Acta Physiologiae Plantarum, 2019, 41, 1.	2.1	6
157	Banana sRNAome and degradome identify microRNAs functioning in differential responses to temperature stress. BMC Genomics, 2019, 20, 33.	2.8	78
158	Introduction to Non-coding RNAs and High Throughput Sequencing. , 2019, , 3-31.		1
159	Identification of TAS and PHAS Loci in Plants. , 2019, , 83-105.		0
161	Identification of microRNAs involved in betalain metabolism in the green and red sectors of amaranth leaves based on Illumina sequencing data. Journal of Horticultural Science and Biotechnology, 2020, 95, 454-469.	1.9	1
162	Cloning and characterization of a homologue of the FLORICAULA/LEAFY gene in Ficus carica L., FcLFY, and its role in flower bud differentiation. Scientia Horticulturae, 2020, 261, 109014.	3.6	11
163	Integrated sRNAome and RNA-Seq analysis reveals miRNA effects on betalain biosynthesis in pitaya. BMC Plant Biology, 2020, 20, 437.	3.6	18
164	Genome wide in-silico miRNA and target network prediction from stress responsive Horsegram (Macrotyloma uniflorum) accessions. Scientific Reports, 2020, 10, 17203.	3.3	12
165	Skin Color in Apple Fruit (Malus Ã— domestica): Genetic and Epigenetic Insights. Epigenomes, 2020, 4, 13.	1.8	8
166	The Apple microR171i-SCARECROW-LIKE PROTEINS26.1 Module Enhances Drought Stress Tolerance by Integrating Ascorbic Acid Metabolism. Plant Physiology, 2020, 184, 194-211.	4.8	40

#	Article	IF	Citations
167	Transcriptional regulation of MdmiR285N microRNA in apple (Malus x domestica) and the heterologous plant system Arabidopsis thaliana. Horticulture Research, 2020, 7, 99.	6.3	6
168	mdm-miR828 Participates in the Feedback Loop to Regulate Anthocyanin Accumulation in Apple Peel. Frontiers in Plant Science, 2020, 11, 608109.	3.6	22
169	Demethylation alters transcriptome profiling of buds and leaves in â€˜Kyohoâ€™ grape. BMC Plant Biology, 2020, 20, 544.	3.6	7
170	The MicroRNA828/MYB12 Module Mediates Bicolor Pattern Development in Asiatic Hybrid Lily (Lilium) Tj ETQq1 1 0.784314 rgBT /Ov	3.6	23
171	miRNA and Degradome Sequencing Identify miRNAs and Their Target Genes Involved in the Browning Inhibition of Fresh-Cut Apples by Hydrogen Sulfide. Journal of Agricultural and Food Chemistry, 2020, 68, 8462-8470.	5.2	23
172	PhasiRNAs in Plants: Their Biogenesis, Genic Sources, and Roles in Stress Responses, Development, and Reproduction. Plant Cell, 2020, 32, 3059-3080.	6.6	139
173	MiR858b Inhibits Proanthocyanidin Accumulation by the Repression of DkMYB19 and DkMYB20 in Persimmon. Frontiers in Plant Science, 2020, 11, 576378.	3.6	17
174	MicroRNA regulation during the tomato fruit development and ripening: A review. Scientia Horticulturae, 2020, 270, 109435.	3.6	17
175	Role of phasiRNAs from two distinct phasing frames of GhMYB2 loci in cis- gene regulation in the cotton genome. BMC Plant Biology, 2020, 20, 219.	3.6	5
176	Research advance in regulation of fruit quality characteristics by microRNAs. Food Quality and Safety, 2020, 4, 1-8.	1.8	15
177	Genome-wide identification and expression profiles of phased siRNAs in a male-sterile somatic cybrid of pummelo (Citrus grandis). Tree Genetics and Genomes, 2020, 16, 1.	1.6	6
178	BrmiR828 Targets BrPAP1, BrMYB82, and BrTAS4 Involved in the Light Induced Anthocyanin Biosynthetic Pathway in Brassica rapa. International Journal of Molecular Sciences, 2020, 21, 4326.	4.1	21
179	Identification of alternatively spliced gene isoforms and novel noncoding RNAs by single-molecule long-read sequencing in Camellia. RNA Biology, 2020, 17, 966-976.	3.1	13
180	Small RNAs With a Big Impact on Horticultural Traits. Critical Reviews in Plant Sciences, 2020, 39, 30-43.	5.7	19
181	Genomic identification of salt induced microRNAs in niger (Guizotia abyssinica Cass.). Plant Gene, 2020, 23, 100242.	2.3	5
182	Transcriptomic and biochemical investigations support the role of rootstock-scion interaction in grapevine berry quality. BMC Genomics, 2020, 21, 468.	2.8	30
183	Apple SERRATE negatively mediates drought resistance by regulating MdMYB88 and MdMYB124 and microRNA biogenesis. Horticulture Research, 2020, 7, 98.	6.3	26
184	A long nonâ€coding apple RNA, MSTRG.85814.11, acts as a transcriptional enhancer of SAUR32 and contributes to the Feâ€deficiency response. Plant Journal, 2020, 103, 53-67.	5.7	42

#	Article	IF	Citations
185	MicroRNA858 negatively regulates anthocyanin biosynthesis by repressing AaMYBC1 expression in kiwifruit (Actinidia arguta). Plant Science, 2020, 296, 110476.	3.6	47
186	Involvement of miRNA-mediated anthocyanin and energy metabolism in the storability of litchi fruit. Postharvest Biology and Technology, 2020, 165, 111200.	6.0	18
187	Identification of miRNA responsive to early flowering in tree peony (Paeonia ostii) by high-throughput sequencing. Journal of Horticultural Science and Biotechnology, 2021, 96, 297-310.	1.9	6
188	R2R3-MYB transcription factors, StmiR858 and sucrose mediate potato flavonol biosynthesis. Horticulture Research, 2021, 8, 25.	6.3	33
189	Genomic analysis uncovers functional variation in the C-terminus of anthocyanin-activating MYB transcription factors. Horticulture Research, 2021, 8, 77.	6.3	28
190	Characterization and Action Mechanism Analysis of VvmiR156b/c/d-VvSPL9 Module Responding to Multiple-Hormone Signals in the Modulation of Grape Berry Color Formation. Foods, 2021, 10, 896.	4.3	16
191	An Atlas of Genomic Resources for Studying Rosaceae Fruits and Ornamentals. Frontiers in Plant Science, 2021, 12, 644881.	3.6	5
192	Noncoding RNAs in Medicinal Plants and their Regulatory Roles in Bioactive Compound Production. Current Pharmaceutical Biotechnology, 2021, 22, 341-359.	1.6	11
193	Repressors of anthocyanin biosynthesis. New Phytologist, 2021, 231, 933-949.	7.3	108
194	Advance in mechanism of plant leaf colour mutation. Notulae Botanicae Horti Agrobotanici Cluj-Napoca, 2021, 49, 12071.	1.1	6
195	Comparative Analysis of miRNA Expression Profiles Provides Insight into Regulation of Biosynthesis of Flavonoids and Terpenoids Between Two Varieties of Toona sinensis Sprouts. Journal of Plant Biology, 2022, 65, 291-310.	2.1	6
196	Identification of microRNAs and their target genes related to needle discoloration of evergreen tree Chinese cedar (Cryptomeria fortunei) in cold winters. Planta, 2021, 254, 31.	3.2	10
197	The long noncoding RNA MdLNC499 bridges MdWRKY1 and MdERF109 function to regulate early-stage light-induced anthocyanin accumulation in apple fruit. Plant Cell, 2021, 33, 3309-3330.	6.6	80
198	MicroRNAs in Woody Plants. Frontiers in Plant Science, 2021, 12, 686831.	3.6	11
199	Small RNAs in Plant Immunity and Virulence of Filamentous Pathogens. Annual Review of Phytopathology, 2021, 59, 265-288.	7.8	27
200	VvMYB114 mediated by miR828 negatively regulates trichome development of Arabidopsis. Plant Science, 2021, 309, 110936.	3.6	4
201	Identification of miRNAs-mediated seed and stone-hardening regulatory networks and their signal pathway of GA-induced seedless berries in grapevine (V. vinifera L.). BMC Plant Biology, 2021, 21, 442.	3.6	4
202	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.	3.6	12

#	Article	IF	Citations
203	Identification of microRNA transcriptome in apple response to Alternaria alternata infection and evidence that miR390 is negative regulator of defense response. Scientia Horticulturae, 2021, 289, 110435.	3.6	6
204	Insight into the regulatory network of miRNA to unravel the ripening physiology of climacteric and non-climacteric fruits. Plant Gene, 2021, 28, 100329.	2.3	2
206	miRNA mediated regulation of NAC transcription factors in plant development and environment stress response. Plant Gene, 2017, 11, 190-198.	2.3	50
209	Integrative Analysis of miRNA and mRNA Profiles in Response to Ethylene in Rose Petals during Flower Opening. PLoS ONE, 2013, 8, e64290.	2.5	70
210	Systems and Evolutionary Characterization of MicroRNAs and Their Underlying Regulatory Networks in Soybean Cotyledons. PLoS ONE, 2014, 9, e86153.	2.5	37
211	Bioinformatics Analysis of Small RNAs in Pima (Gossypium barbadense L.). PLoS ONE, 2015, 10, e0116826.	2.5	7
212	Identification of Novel miRNAs and miRNA Expression Profiling in Wheat Hybrid Necrosis. PLoS ONE, 2015, 10, e0117507.	2.5	26
213	Identification and Characterization of MicroRNAs in Ginkgo biloba var. epiphylla Mak. PLoS ONE, 2015, 10, e0127184.	2.5	37
214	The Complexity of Posttranscriptional Small RNA Regulatory Networks Revealed by In Silico Analysis of Gossypium arboreum L. Leaf, Flower and Boll Small Regulatory RNAs. PLoS ONE, 2015, 10, e0127468.	2.5	11
215	Detection of plant microRNAs in honey. PLoS ONE, 2017, 12, e0172981.	2.5	35
216	Recent advances in fruit crop genomics. Frontiers of Agricultural Science and Engineering, 2014, 1, 21.	1.4	2
217	Identification of MicroRNAs and Their Targets Involved in Paeonia rockii Petal Variegation Using High-throughput Sequencing. Journal of the American Society for Horticultural Science, 2019, 144, 118-129.	1.0	5
221	microRNA Regulation of Fruit Development. Concepts and Strategies in Plant Sciences, 2020, , 75-98.	0.5	1
222	microRNA regulation of fruit development, quality formation and stress response. Fruit Research, 2021, 1, 1-11.	2.0	6
223	microRNA172 targets APETALA2 to regulate flavonoid biosynthesis in apple (Malus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 182	6.3	22
224	Contribution of Omics and Systems Biology to Plant Biotechnology. Advances in Experimental Medicine and Biology, 2021, 1346, 171-188.	1.6	1
225	Comparative Transcriptome Analysis Uncovers the Regulatory Roles of MicroRNAs Involved in Petal Color Change of Pink-Flowered Strawberry. Frontiers in Plant Science, 2022, 13, 854508.	3.6	2
226	Shaping the root system architecture in plants for adaptation to drought stress. Physiologia Plantarum, 2022, 174, e13651.	5.2	39

#	Article	IF	Citations
227	The roles of microRNAs in regulating root formation and growth in plants. Journal of Integrative Agriculture, 2022, 21, 901-916.	3.5	11
228	The Multiverse of Plant Small RNAs: How Can We Explore It?. International Journal of Molecular Sciences, 2022, 23, 3979.	4.1	4
229	MicroRNA-Mediated Gene Regulation of Secondary Metabolism in Plants. Critical Reviews in Plant Sciences, 2021, 40, 459-478.	5.7	7
230	MicroRNA candidate miRcand137 in apple is induced by Botryosphaeria dothidea for impairing host defense. Plant Physiology, 2022, 189, 1814-1832.	4.8	11
236	Heightened miR6024-NLR interactions facilitate necrotrophic pathogenesis in tomato. Plant Molecular Biology, 2022, 109, 717-739.	3.9	17
237	Integrated small RNA profiling and degradome analysis of Anthurium andraeanum cultivars with different-colored spathes. Journal of Plant Research, 2022, 135, 609-626.	2.4	1
238	Identification of anthocyanin-related microRNAs in ornamental kale (Brassica oleracea L. var.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 502	3.6	3
239	MicroRNA828/MYB12 Module Mediated Bicolor Flower Development in <i>Lilium dauricum</i>. Horticulture Journal, 2022, 91, 399-407.	0.8	2
240	Role of phasiRNAs in plant-pathogen interactions: molecular perspectives and bioinformatics tools. Physiology and Molecular Biology of Plants, 2022, 28, 947-961.	3.1	2
241	Cultivar-specific miRNA-mediated RNA silencing in grapes. Planta, 2022, 256, .	3.2	0
242	Identification and characterization of Apple (MalusÂÃ—Âdomestica Borkh.) bud sports mutations in the apple growing Northwestern Himalayan region. Scientia Horticulturae, 2022, 304, 111308.	3.6	1
243	Identification and characterization of miRNAs and PHAS loci related to the early development of the embryo and endosperm in Fragariaâ€‰Ã—â€‰ananassa. BMC Genomics, 2022, 23, .	2.8	3
244	Current insights into posttranscriptional regulation of fleshy fruit ripening. Plant Physiology, 2023, 192, 1785-1798.	4.8	12
245	Heterologous expression of Arabidopsis miR858 modulates biosynthesis of secondary metabolites and affects drought tolerance in tobacco. Plant Cell, Tissue and Organ Culture, 2023, 152, 287-298.	2.3	3
246	MIR390 Is Involved in Regulating Anthracnose Resistance in Apple. Plants, 2022, 11, 3299.	3.5	3
247	Coordinating Diverse Functions of miRNA and lncRNA in Fleshy Fruit. Plants, 2023, 12, 411.	3.5	0
248	The miR156xâ€‰+â€‰p/SPL13-6 module responds to ABA, IAA, and ethylene, and SPL13-6 participates in the juvenileâ€“adult phase transition in Pyrus. Horticulture Environment and Biotechnology, 2023, 64, 437-448.	2.1	1
249	Integrative analysis of microRNAs and mRNAs reveals the regulatory networks of triterpenoid saponin metabolism in Soapberry (Sapindus mukorossi Gaertn.). Frontiers in Plant Science, 0, 13, .	3.6	2

#	Article	IF	Citations
250	Fruit growth and development in apple: a molecular, genomics and epigenetics perspective. Frontiers in Plant Science, 0, 14, .	3.6	1
251	<scp>Mdmâ€miR858</scp> targets MdMYB9 and MdMYBPA1 to participate anthocyanin biosynthesis in redâ€fleshed apple. Plant Journal, 2023, 113, 1295-1309.	5.7	11
252	DNA methylation variation is crucial to restore adventitious rooting ability during in vitro shoot cultureâ€induced rejuvenation in apple rootstock. Plant Journal, 2023, 114, 554-569.	5.7	3
253	Recent Research Advances of Small Regulatory RNA in Fruit Crops. Horticulturae, 2023, 9, 294.	2.8	4
254	Regulation of the regulators: Transcription factors controlling biosynthesis of plant secondary metabolites during biotic stresses and their regulation by miRNAs. Frontiers in Plant Science, 0, 14, .	3.6	9
255	Insights into microRNA regulation of flower coloration in a lily cultivar Vivian petal. Ornamental Plant Research, 2023, 3, 0-0.	0.9	0
256	Plant small RNAs: biogenesis, mechanistic functions and applications. , 2023, , 129-181.		0
257	Grain development and crop productivity: role of small RNA. , 2023, , 385-468.		1
258	A comparative analysis of small RNA sequencing data in tubers of purple potato and its red mutant reveals small RNA regulation in anthocyanin biosynthesis. PeerJ, 0, 11, e15349.	2.0	0
259	Almond miRNA Expression and Horticultural Implications. Compendium of Plant Genomes, 2023, , 33-57.	0.5	0
260	Advances in the endogenous and exogenous regulation of anthocyaninsâ€“the key to color change in eudicots. Critical Reviews in Plant Sciences, 2023, 42, 217-238.	5.7	1
261	Small RNA and Degradome Sequencing Reveal Roles of miRNAs in the Petal Color Fading of Malus Crabapple. International Journal of Molecular Sciences, 2023, 24, 11384.	4.1	3
262	Insights into the molecular mechanisms underlying responses of apple trees to abiotic stresses. Horticulture Research, 2023, 10, .	6.3	1
263	Development, Identification and Validation of a Novel SSR Molecular Marker for Heat Resistance of Grapes Based on miRNA. Horticulturae, 2023, 9, 931.	2.8	2
264	miRNA mediated regulation of nitrogen response and nitrogen use efficiency of plants: the case of wheat. Physiology and Molecular Biology of Plants, 0, , .	3.1	0
265	The potential role of R2R3-MYB gene family in the phenylpropanoid pathway and regulatory mechanism in Fragaria Ã— ananassa. Biologia Plantarum, 0, 67, 249-261.	1.9	0
266	The phased short-interfering RNA siRD29(-) regulates GIBBERELLIN 3-OXIDASE 3 during stolon-to-tuber transitions in potato. Plant Physiology, 0, , .	4.8	1
267	Phased secondary small interfering RNAs in Camellia sinensis var. assamica. NAR Genomics and Bioinformatics, 2023, 5, .	3.2	0

#	Article	IF	Citations
268	Identification of miRNA858 long-loop precursors in seed plants. Plant Cell, 0, , .	6.6	0
269	Emerging roles of plant microRNAs during Colletotrichum spp. infection. Planta, 2024, 259, .	3.2	0
270	MacroLoops for microRNAs: shall we revise the maximum allowed size?. Plant Cell, 2024, 36, 1572-1573.	6.6	0
271	Link between organic nanovescicles from vegetable kingdom and human cell physiology: intracellular calcium signalling. Journal of Nanobiotechnology, 2024, 22, .	9.1	0
272	Genome reannotation of the sweetpotato (<i>Ipomoea batatas</i> (L.) Lam.) using extensive Nanopore and Illumina-based RNA-seq datasets. , 2024, 3, 0-0.		0