

Apple miRNAs and tasiRNAs with novel regulatory networks

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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.	1.2	49
2	Overexpression of microRNA828 reduces anthocyanin accumulation in Arabidopsis. Plant Cell, Tissue and Organ Culture, 2013, 115, 159-167.	1.2	76
3	Trans-acting small interfering RNA4: key to nutraceutical synthesis in grape development?. Trends in Plant Science, 2013, 18, 601-610.	4.3	49
4	A genome-wide identification and characterization of mircoRNAs and their targets in "Suli"™ pear (Pyrus) Tj ETQq1 1 0.784314 rgBT 1.6 19	1.6	19
5	MicroRNAs and Their Cross-Talks in Plant Development. Journal of Genetics and Genomics, 2013, 40, 161-170.	1.7	70
6	Phased, Secondary, Small Interfering RNAs in Posttranscriptional Regulatory Networks. Plant Cell, 2013, 25, 2400-2415.	3.1	543
7	Catalyzing plant science research with RNA-seq. Frontiers in Plant Science, 2013, 4, 66.	1.7	136
8	MicroRNA Superfamilies Descended from miR390 and Their Roles in Secondary Small Interfering RNA Biogenesis in Eudicots. Plant Cell, 2013, 25, 1555-1572.	3.1	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.	13.9	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.	3.8	225
12	Peculiar Evolutionary History of miR390-Guided TAS3-Like Genes in Land Plants. Scientific World Journal, The, 2013, 2013, 1-14.	0.8	18
13	Differential sRNA Regulation in Leaves and Roots of Sugarcane under Water Depletion. PLoS ONE, 2014, 9, e93822.	1.1	37
14	Extending the sRNAome of Apple by Next-Generation Sequencing. PLoS ONE, 2014, 9, e95782.	1.1	17
15	Genome-Wide Discovery and Analysis of Phased Small Interfering RNAs in Chinese Sacred Lotus. PLoS ONE, 2014, 9, e113790.	1.1	28
16	Identification of miRNAs involved in pear fruit development and quality. BMC Genomics, 2014, 15, 953.	1.2	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.	1.5	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.	1.2	60

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19	Identification and profiling of novel and conserved microRNAs during the flower opening process in <i>Prunus mume</i> via deep sequencing. <i>Molecular Genetics and Genomics</i> , 2014, 289, 169-183.	1.0	54
20	Identification and characterization of the microRNA transcriptome of a moth orchid <i>Phalaenopsis aphrodite</i> . <i>Plant Molecular Biology</i> , 2014, 84, 529-548.	2.0	38
21	MicroRNAs as regulators of adventitious root development. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2014, 23, 339-347.	0.9	21
22	miR828 and miR858 regulate homoeologous MYB2 gene functions in <i>Arabidopsis</i> trichome and cotton fibre development. <i>Nature Communications</i> , 2014, 5, 3050.	5.8	215
23	A <i>Medicago truncatula</i> <i>rdr6</i> allele impairs transgene silencing and endogenous phased siRNA production but not development. <i>Plant Biotechnology Journal</i> , 2014, 12, 1308-1318.	4.1	5
24	Binding of miR396 to mRNA of genes encoding growth-regulating transcription factors of plants. <i>Russian Journal of Plant Physiology</i> , 2014, 61, 807-810.	0.5	8
25	High-throughput sequencing reveals small RNAs involved in ASGV infection. <i>BMC Genomics</i> , 2014, 15, 568.	1.2	39
26	Genome-wide comparison of microRNAs and their targeted transcripts among leaf, flower and fruit of sweet orange. <i>BMC Genomics</i> , 2014, 15, 695.	1.2	70
27	Apple ring rot-responsive putative microRNAs revealed by high-throughput sequencing in <i>Malus domestica</i> Borkh.. <i>Molecular Biology Reports</i> , 2014, 41, 5273-5286.	1.0	10
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30	Genome-wide characterization and comparative analysis of R2R3-MYB transcription factors shows the complexity of MYB-associated regulatory networks in <i>Salvia miltiorrhiza</i> . <i>BMC Genomics</i> , 2014, 15, 277.	1.2	92
31	Identification and characterization of microRNAs in the flag leaf and developing seed of wheat (<i>Triticum aestivum</i> L.). <i>BMC Genomics</i> , 2014, 15, 289.	1.2	95
32	A diverse set of miRNAs responsive to begomovirus-associated betasatellite in <i>Nicotiana benthamiana</i> . <i>BMC Plant Biology</i> , 2014, 14, 60.	1.6	19
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34	MicroRNA and mRNA expression profiling analysis revealed the regulation of plant height in <i>Gossypium hirsutum</i> . <i>BMC Genomics</i> , 2015, 16, 886.	1.2	23
35	Identification of miRNAs with potential roles in regulation of anther development and male-sterility in 7B-1 male-sterile tomato mutant. <i>BMC Genomics</i> , 2015, 16, 878.	1.2	58
36	Transition from two to one integument in <i>Prunus</i> species: expression pattern of <i>INNER NO OUTER</i> , <i>INO</i> , <i>ABERRANT TESTA SHAPE</i> and <i>ATS</i> and <i>ETTIN</i> (<i>ETT</i>). <i>New Phytologist</i> , 2015, 208, 584-595.	3.5	26

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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. <i>BMC Genomics</i> , 2015, 16, 945.	1.2	22
39	Genome-wide discovery and validation of Eucalyptus small RNAs reveals variable patterns of conservation and diversity across species of Myrtaceae. <i>BMC Genomics</i> , 2015, 16, 1113.	1.2	13
40	A microRNA allele that emerged prior to apple domestication may underlie fruit size evolution. <i>Plant Journal</i> , 2015, 84, 417-427.	2.8	95
41	Differential mRNA Accumulation upon Early <i>Arabidopsis thaliana</i> Infection with ORMV and TMV-Cg Is Associated with Distinct Endogenous Small RNAs Level. <i>PLoS ONE</i> , 2015, 10, e0134719.	1.1	15
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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. <i>International Journal of Molecular Sciences</i> , 2015, 16, 3377-3390.	1.8	4
52	Identification and characterization of microRNAs from Chinese pollination constant non-astringent persimmon using high-throughput sequencing. <i>BMC Plant Biology</i> , 2015, 15, 11.	1.6	52
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70	Shoot bending promotes flower bud formation by miRNA-mediated regulation in apple (<i>Malus domestica</i> Borkh.). <i>Plant Biotechnology Journal</i> , 2016, 14, 749-770.	4.1	69
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80	Small RNA and PARE sequencing in flower bud reveal the involvement of sRNAs in endodormancy release of Japanese pear (<i>Pyrus pyrifolia</i> 'Kosui'). <i>BMC Genomics</i> , 2016, 17, 230.	1.2	25
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82	An optimized TRV-based virus-induced gene silencing protocol for <i>Malus crabapple</i> . <i>Plant Cell, Tissue and Organ Culture</i> , 2016, 126, 499-509.	1.2	29
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90	Biogenesis of diverse plant phasiRNAs involves an miRNA-trigger and Dicer-processing. <i>Journal of Plant Research</i> , 2017, 130, 17-23.	1.2	75

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92	<i>Malus hupehensis</i> miR168 Targets to ARGONAUTE1 and Contributes to the Resistance against <i>Botryosphaeria dothidea</i> Infection by Altering Defense Responses. <i>Plant and Cell Physiology</i> , 2017, 58, 1541-1557.	1.5	30
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94	Transcriptome analysis reveals differentially expressed small RNAs and genes associated with grapevine leafroll-associated virus 3 infections. <i>Physiological and Molecular Plant Pathology</i> , 2017, 100, 220-236.	1.3	8
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111	Md-miR156ab and Md-miR395 Target WRKY Transcription Factors to Influence Apple Resistance to Leaf Spot Disease. <i>Frontiers in Plant Science</i> , 2017, 8, 526.	1.7	47
112	Small RNA-Sequencing Links Physiological Changes and RdDM Process to Vegetative-to-Floral Transition in Apple. <i>Frontiers in Plant Science</i> , 2017, 8, 873.	1.7	27
113	Allelic Interactions among Pto-MIR475b and Its Four Target Genes Potentially Affect Growth and Wood Properties in Populus. <i>Frontiers in Plant Science</i> , 2017, 8, 1055.	1.7	9
114	microRNAs and Their Targets in Apple (<i>Malus domestica</i> cv. â€œFujiâ€) Involved in Response to Infection of Pathogen <i>Valsa mali</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 2081.	1.7	13
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123	Bioinformatics prediction and annotation of cherry (<i>Prunus avium</i> L.) microRNAs and their targeted proteins. <i>Turkish Journal of Botany</i> , 2018, 42, 382-399.	0.5	4
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140	Genome-wide identification of drought-responsive microRNAs in two sets of <i>Malus</i> from interspecific hybrid progenies. <i>Horticulture Research</i> , 2019, 6, 75.	2.9	43
141	miR828 and miR858 regulate VvMYB114 to promote anthocyanin and flavonol accumulation in grapes. <i>Journal of Experimental Botany</i> , 2019, 70, 4775-4792.	2.4	136
142	Multilocation comparison of fruit composition for "HoneySweet", an RNAi based plum pox virus resistant plum. <i>PLoS ONE</i> , 2019, 14, e0213993.	1.1	6
143	Role of Cytokinin, Strigolactone, and Auxin Export on Outgrowth of Axillary Buds in Apple. <i>Frontiers in Plant Science</i> , 2019, 10, 616.	1.7	38
144	Uncovering anthocyanin biosynthesis related microRNAs and their target genes by small RNA and degradome sequencing in tuberous roots of sweetpotato. <i>BMC Plant Biology</i> , 2019, 19, 232.	1.6	43
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147	Nutritive implications of dietary microRNAs: facts, controversies, and perspectives. <i>Food and Function</i> , 2019, 10, 3044-3056.	2.1	8
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