## Criteria for Annotation of Plant MicroRNAs

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Citation Report

#	Article	IF	CITATIONS
1	AGO1 Homeostasis Involves Differential Production of 21-nt and 22-nt miR168 Species by MIR168a and MIR168b. PLoS ONE, 2009, 4, e6442.	1.1	88
2	Clusters and superclusters of phased small RNAs in the developing inflorescence of rice. Genome Research, 2009, 19, 1429-1440.	2.4	283
3	Uncovering Small RNA-Mediated Responses to Phosphate Deficiency in Arabidopsis by Deep Sequencing. Plant Physiology, 2009, 151, 2120-2132.	2.3	631
4	Review of Current Methodological Approaches for Characterizing MicroRNAs in Plants. International Journal of Plant Genomics, 2009, 2009, 1-11.	2.2	62
5	Genome-Wide <i>Medicago truncatula</i> Small RNA Analysis Revealed Novel MicroRNAs and Isoforms Differentially Regulated in Roots and Nodules. Plant Cell, 2009, 21, 2780-2796.	3.1	270
6	Identification of Nutrient-Responsive Arabidopsis and Rapeseed MicroRNAs by Comprehensive Real-Time Polymerase Chain Reaction Profiling and Small RNA Sequencing   Â. Plant Physiology, 2009, 150, 1541-1555.	2.3	414
7	Computational and analytical framework for small RNA profiling by high-throughput sequencing. Rna, 2009, 15, 992-1002.	1.6	112
8	MicroPC (μPC): A comprehensive resource for predicting and comparing plant microRNAs. BMC Genomics, 2009, 10, 366.	1.2	32
9	Deep sequencing of Brachypodium small RNAs at the global genome level identifies microRNAs involved in cold stress response. BMC Genomics, 2009, 10, 449.	1.2	287
10	Enrichment of a set of microRNAs during the cotton fiber development. BMC Genomics, 2009, 10, 457.	1.2	113
11	High throughput approaches reveal splicing of primary microRNA transcripts and tissue specific expression of mature microRNAs in Vitis vinifera. BMC Genomics, 2009, 10, 558.	1.2	62
12	Genome-wide profiling of Populus small RNAs. BMC Genomics, 2009, 10, 620.	1.2	90
13	MicroRNA and tasiRNA diversity in mature pollen of Arabidopsis thaliana. BMC Genomics, 2009, 10, 643.	1.2	112
14	Deep-sequencing of plant viral small RNAs reveals effective and widespread targeting of viral genomes. Virology, 2009, 392, 203-214.	1.1	274
15	Cloning and validation of novel miRNA from basmati rice indicates cross talk between abiotic and biotic stresses. Molecular Genetics and Genomics, 2009, 282, 463-74.	1.0	77
16	Novel microRNAs uncovered by deep sequencing of small RNA transcriptomes in bread wheat (Triticum) Tj ETQq1 499-511.	1 0.7843 1.4	14 rgBT /C 153
17	Conserved and novel miRNAs in the legume Phaseolus vulgaris in response to stress. Plant Molecular Biology, 2009, 70, 385-401.	2.0	235
18	Computational identification of microRNAs and their targets in wheat (Triticum aestivum L.). Science in China Series C: Life Sciences, 2009, 52, 1091-1100.	1.3	34

	CITATION	CITATION REPORT	
#	Article	lF	CITATIONS
19	Cloning and characterization of small non oding RNAs from grape. Plant Journal, 2009, 59, 750-763.	2.8	133
20	A loop-to-base processing mechanism underlies the biogenesis of plant microRNAs miR319 and miR159. EMBO Journal, 2009, 28, 3646-3656.	3.5	191
21	Cloning and characterization of small RNAs from <i>Medicago truncatula</i> reveals four novel legumeâ€specific microRNA families. New Phytologist, 2009, 184, 85-98.	3.5	162
22	MicroRNAs in the Rhizobia Legume Symbiosis. Plant Physiology, 2009, 151, 1002-1008.	2.3	63
23	Origin, Biogenesis, and Activity of Plant MicroRNAs. Cell, 2009, 136, 669-687.	13.5	2,004
24	Identification of conserved Aquilegia coerulea microRNAs and their targets. Gene, 2009, 448, 46-56.	1.0	21
25	Conserved miRNA analysis in Gossypium hirsutum through small RNA sequencing. Genomics, 2009, 94, 263-268.	1.3	79
26	Plant polycistronic precursors containing non-homologous microRNAs target transcripts encoding functionally related proteins. Genome Biology, 2009, 10, R136.	13.9	80
27	Genome-wide analysis reveals rapid and dynamic changes in miRNA and siRNA sequence and expression during ovule and fiber development in allotetraploid cotton (Gossypium hirsutum L.). Genome Biology, 2009, 10, R122.	13.9	128
28	Rice MicroRNA Effector Complexes and Targets Â. Plant Cell, 2009, 21, 3421-3435.	3.1	316
29	Retrotransposons and non-protein coding RNAs. Briefings in Functional Genomics & Proteomics, 2009, 8, 493-501.	3.8	18
30	Prediction of novel miRNAs and associated target genes in Glycine max. BMC Bioinformatics, 2010, 11, S14.	1.2	108
32	Discovery and comparative profiling of microRNAs in a sweet orange red-flesh mutant and its wild type. BMC Genomics, 2010, 11, 246.	1.2	120
33	Deep sequencing discovery of novel and conserved microRNAs in trifoliate orange (Citrus trifoliata). BMC Genomics, 2010, 11, 431.	1.2	195
34	A computational-based update on microRNAs and their targets in barley (Hordeum vulgare L.). BMC Genomics, 2010, 11, 595.	1.2	57
35	Diverse set of microRNAs are responsive to powdery mildew infection and heat stress in wheat (Triticum aestivum L.). BMC Plant Biology, 2010, 10, 123.	1.6	459
36	Phloem small RNAs, nutrient stress responses, and systemic mobility. BMC Plant Biology, 2010, 10, 64.	1.6	265
37	Naturally occurring variations in sequence length creates microRNA isoforms that differ in argonaute effector complex specificity. Silence: A Journal of RNA Regulation, 2010, 1, 12.	8.0	55

#	Article	IF	CITATIONS
38	Short RNAs in Tomato. Journal of Integrative Plant Biology, 2010, 52, 388-392.	4.1	25
39	Transcriptome-wide identification of microRNA targets in rice. Plant Journal, 2010, 62, 742-759.	2.8	370
40	Unique functionality of 22-nt miRNAs in triggering RDR6-dependent siRNA biogenesis from target transcripts in Arabidopsis. Nature Structural and Molecular Biology, 2010, 17, 997-1003.	3.6	448
41	RNA-based antiviral immunity. Nature Reviews Immunology, 2010, 10, 632-644.	10.6	764
42	A set of miRNAs from Brassica napus in response to sulphate deficiency and cadmium stress. Plant Biotechnology Journal, 2010, 8, 887-899.	4.1	179
43	Computational identification of citrus microRNAs and target analysis in citrus expressed sequence tags. Plant Biology, 2010, 12, 927-934.	1.8	55
44	Analysis of Antisense Expression by Whole Genome Tiling Microarrays and siRNAs Suggests Mis-Annotation of Arabidopsis Orphan Protein-Coding Genes. PLoS ONE, 2010, 5, e10710.	1.1	4
45	siRNAs from miRNA sites mediate DNA methylation of target genes. Nucleic Acids Research, 2010, 38, 6883-6894.	6.5	153
46	Conservation and divergence of microRNAs and their functions in Euphorbiaceous plants. Nucleic Acids Research, 2010, 38, 981-995.	6.5	110
47	Methodological framework for functional characterization of plant microRNAs. Journal of Experimental Botany, 2010, 61, 2271-2280.	2.4	9
48	MicroRNA Gene Evolution in <i>Arabidopsis lyrata</i> and <i>Arabidopsis thaliana</i> Â Â. Plant Cell, 2010, 22, 1074-1089.	3.1	234
49	<i>Arabidopsis</i> RNA-Dependent RNA Polymerases and Dicer-Like Proteins in Antiviral Defense and Small Interfering RNA Biogenesis during <i>Turnip Mosaic Virus</i> Infection Â. Plant Cell, 2010, 22, 481-496.	3.1	454
50	Arabidopsis lyrata Small RNAs: Transient MIRNA and Small Interfering RNA Loci within the Arabidopsis Genus. Plant Cell, 2010, 22, 1090-1103.	3.1	221
51	miRBase: microRNA Sequences and Annotation. Current Protocols in Bioinformatics, 2010, 29, Unit 12.9.1-10.	25.8	171
52	Identification of microRNAs and their targets in switchgrass, a model biofuel plant species. Journal of Plant Physiology, 2010, 167, 896-904.	1.6	66
53	High throughput DNA sequencing: The new sequencing revolution. Plant Science, 2010, 179, 407-422.	1.7	76
54	The biosynthetic pathways and biological scopes of plant small RNAs. Trends in Plant Science, 2010, 15, 337-345.	4.3	141
55	Virus-derived small interfering RNAs at the core of plant–virus interactions. Trends in Plant Science, 2010, 15, 701-707.	4.3	180

#	Article	IF	CITATIONS
56	miRNAs in the biogenesis of trans-acting siRNAs in higher plants. Seminars in Cell and Developmental Biology, 2010, 21, 798-804.	2.3	145
57	Identification of novel stress-regulated microRNAs from Oryza sativa L Genomics, 2010, 95, 47-55.	1.3	105
58	Small RNA Diversity in Plants and its Impact in Development. Current Genomics, 2010, 11, 14-23.	0.7	88
59	Plant MicroRNAs. Methods in Molecular Biology, 2010, , .	0.4	7
60	Bioinformatics approaches for genomics and post genomics applications of next-generation sequencing. Briefings in Bioinformatics, 2010, 11, 181-197.	3.2	141
61	Multiple distinct small RNAs originate from the same microRNA precursors. Genome Biology, 2010, 11, R81.	13.9	118
62	Vive la différence: biogenesis and evolution of microRNAs in plants and animals. Genome Biology, 2011, 12, 221.	13.9	393
63	Function and Evolution of a MicroRNA That Regulates a Ca2+-ATPase and Triggers the Formation of Phased Small Interfering RNAs in Tomato Reproductive Growth Â. Plant Cell, 2011, 23, 3185-3203.	3.1	88
64	Plant siRNAs from introns mediate DNA methylation of host genes. Rna, 2011, 17, 1012-1024.	1.6	35
65	miRBase: integrating microRNA annotation and deep-sequencing data. Nucleic Acids Research, 2011, 39, D152-D157.	6.5	3,263
66	Differential expression of the microRNAs in superior and inferior spikelets in rice (Oryza sativa). Journal of Experimental Botany, 2011, 62, 4943-4954.	2.4	95
67	Overview of Plant RNAi. Methods in Molecular Biology, 2011, 744, 1-11.	0.4	12
69	Biogenesis of Plant MicroRNAs. , 2011, , 251-268.		4
72	Computational dissection of Arabidopsis smRNAome leads to discovery of novel microRNAs and short interfering RNAs associated with transcription start sites. Genomics, 2011, 97, 235-243.	1.3	8
73	Implementation of a de novo genome-wide computational approach for updating Brachypodium miRNAs. Genomics, 2011, 97, 282-293.	1.3	17
74	Global analysis of gene-level microRNA expression in Arabidopsis using deep sequencing data. Genomics, 2011, 98, 40-46.	1.3	40
75	Identification and temporal expression analysis of conserved and novel microRNAs in Sorghum. Genomics, 2011, 98, 460-468.	1.3	88
76	In silico Detection of Novel MicroRNAs Genes in Soybean Genome. Agricultural Sciences in China, 2011, 10, 1336-1345.	0.6	15

	CITATION	Report	
#	Article	IF	Citations
77	Deep sequencing on genome-wide scale reveals the unique composition and expression patterns of microRNAs in developing pollen of Oryza sativa. Genome Biology, 2011, 12, R53.	3.8	148
78	Response, Tolerance and Adaptation to Abiotic Stress of Olive, Grapevine and Chestnut in the Mediterranean Region: Role of Abscisic Acid, Nitric Oxide and MicroRNAs. , 2011, , .		3
79	Overview of the potential of microRNAs and their target gene detection for cassava (Manihot) Tj ETQq0 0 0 rgl	3T /Overloc	k 10 Tf 50 66
80	High-Throughput Sequencing, Characterization and Detection of New and Conserved Cucumber miRNAs. PLoS ONE, 2011, 6, e19523.	1.1	98
81	Specific Impact of Tobamovirus Infection on the Arabidopsis Small RNA Profile. PLoS ONE, 2011, 6, e19549.	1.1	70
82	Evolution of MicroRNA Genes in Oryza sativa and Arabidopsis thaliana: An Update of the Inverted Duplication Model. PLoS ONE, 2011, 6, e28073.	1.1	31
83	Differential Expression of miRNAs in Response to Topping in Flue-Cured Tobacco (Nicotiana tabacum) Roots. PLoS ONE, 2011, 6, e28565.	1.1	32
84	Genetic Mapping in Conifers. , 2011, , 224-266.		10
85	Deep sequencing of grapevine flower and berry short RNA library for discovery of novel microRNAs and validation of precise sequences of grapevine microRNAs deposited in miRBase. Physiologia Plantarum, 2011, 143, 64-81.	2.6	81
86	Deep sequencing of small RNAs specifically associated with Arabidopsis AGO1 and AGO4 uncovers new AGO functions. Plant Journal, 2011, 67, 292-304.	2.8	114
87	Small RNAs from MITEâ€derived stemâ€loop precursors regulate abscisic acid signaling and abiotic stress responses in rice. Plant Journal, 2011, 65, 820-828.	2.8	82
88	Plant Small RNAs: Biogenesis, Mode of Action and Their Roles in Abiotic Stresses. Genomics, Proteomics and Bioinformatics, 2011, 9, 183-199.	3.0	127
89	Identification of Novel and Conserved microRNAs in Rehmannia glutinosa L. by Solexa Sequencing. Plant Molecular Biology Reporter, 2011, 29, 986-996.	1.0	16
90	Identification and validation of conserved microRNAs along with their differential expression in roots of Vigna unguiculata grown under salt stress. Plant Cell, Tissue and Organ Culture, 2011, 105, 233-242.	1.2	75
91	Identification and characterization of microRNAs from citrus expressed sequence tags. Tree Genetics and Genomes, 2011, 7, 117-133.	0.6	16
92	Identification of Potential microRNAs and Their Targets in Brassica rapa L Molecules and Cells, 2011, 32, 21-38.	1.0	43
93	Cell-to-cell trafficking of RNA and RNA silencing through plasmodesmata. Protoplasma, 2011, 248, 101-116.	1.0	51
94	Identification and comparative analysis of drought-associated microRNAs in two cowpea genotypes. BMC Plant Biology, 2011, 11, 127.	1.6	187

#	Article	IF	CITATIONS
95	Identification of novel maize miRNAs by measuring the precision of precursor processing. BMC Plant Biology, 2011, 11, 141.	1.6	39
96	Differential miRNA expression in Rehmannia glutinosaplants subjected to continuous cropping. BMC Plant Biology, 2011, 11, 53.	1.6	53
97	Interspecific discovery and expression profiling of Eucalyptusmicro RNAs by deep sequencing. BMC Proceedings, 2011, 5, .	1.8	2
98	Evolution of MIR159/319 microRNA genes and their post-transcriptional regulatory link to siRNA pathways. BMC Evolutionary Biology, 2011, 11, 122.	3.2	61
99	Characterization of statistical features for plant microRNA prediction. BMC Genomics, 2011, 12, 108.	1.2	63
100	Discovery of barley miRNAs through deep sequencing of short reads. BMC Genomics, 2011, 12, 129.	1.2	118
101	Identification and characterization of maize microRNAs involved in the very early stage of seed germination. BMC Genomics, 2011, 12, 154.	1.2	129
102	Identification of novel soybean microRNAs involved in abiotic and biotic stresses. BMC Genomics, 2011, 12, 307.	1.2	313
103	Identification and characterization of microRNAs from Phaeodactylum tricornutum by high-throughput sequencing and bioinformatics analysis. BMC Genomics, 2011, 12, 337.	1.2	55
104	Characterization of the small RNA component of the transcriptome from grain and sweet sorghum stems. BMC Genomics, 2011, 12, 356.	1.2	52
105	Identification of drought-responsive microRNAs in Medicago truncatula by genome-wide high-throughput sequencing. BMC Genomics, 2011, 12, 367.	1.2	291
106	Analysis of the melon (Cucumis melo) small RNAome by high-throughput pyrosequencing. BMC Genomics, 2011, 12, 393.	1.2	58
107	Genetically engineered resistance to <i>Plum pox virus</i> infection in herbaceous and stone fruit hosts. GM Crops, 2011, 2, 24-33.	1.8	27
108	Genome-wide characterization of new and drought stress responsive microRNAs in Populus euphratica. Journal of Experimental Botany, 2011, 62, 3765-3779.	2.4	291
109	miRDeep-P: a computational tool for analyzing the microRNA transcriptome in plants. Bioinformatics, 2011, 27, 2614-2615.	1.8	257
110	Evolution and Functional Diversification of <i>MIRNA</i> Genes. Plant Cell, 2011, 23, 431-442.	3.1	645
111	Efficient Silencing of Endogenous MicroRNAs Using Artificial MicroRNAs in Arabidopsis thaliana. Molecular Plant, 2011, 4, 157-170.	3.9	72
113	Enhancing miRNA annotation confidence in miRBase by continuous cross dataset analysis. RNA Biology, 2011, 8, 378-383.	1.5	32

#	Article	IF	CITATIONS
114	Stars and Symbiosis: MicroRNA- and MicroRNA*-Mediated Transcript Cleavage Involved in Arbuscular Mycorrhizal Symbiosis  Â. Plant Physiology, 2011, 156, 1990-2010.	2.3	235
115	MicroRNAs in the shoot apical meristem of soybean. Journal of Experimental Botany, 2011, 62, 2495-2506.	2.4	80
116	Massive Analysis of Rice Small RNAs: Mechanistic Implications of Regulated MicroRNAs and Variants for Differential Target RNA Cleavage Â. Plant Cell, 2011, 23, 4185-4207.	3.1	341
117	Non Coding RNAs and Gene Silencing in Grape. , 2011, , 67-78.		2
118	SplamiR—prediction of spliced miRNAs in plants. Bioinformatics, 2011, 27, 1215-1223.	1.8	15
119	Identification and analysis of seven H2O2-responsive miRNAs and 32 new miRNAs in the seedlings of rice (Oryza sativa L. ssp. indica). Nucleic Acids Research, 2011, 39, 2821-2833.	6.5	218
120	Gene Expression and Stress Response Mediated by the Epigenetic Regulation of a Transposable Element Small RNA. PLoS Genetics, 2012, 8, e1002474.	1.5	191
121	Identification and Characterization of MicroRNAs from Barley (Hordeum vulgare L.) by High-Throughput Sequencing. International Journal of Molecular Sciences, 2012, 13, 2973-2984.	1.8	80
122	Give It AGO: The Search for miRNA-Argonaute Sorting Signals in Arabidopsis thaliana Indicates a Relevance of Sequence Positions Other than the 5′-Position Alone. Frontiers in Plant Science, 2012, 3, 272.	1.7	25
123	Role of Transposon-Derived Small RNAs in the Interplay between Genomes and Parasitic DNA in Rice. PLoS Genetics, 2012, 8, e1002953.	1.5	79
124	Deep Annotation of Populus trichocarpa microRNAs from Diverse Tissue Sets. PLoS ONE, 2012, 7, e33034.	1.1	63
125	Origins and Evolution of MicroRNA Genes in Plant Species. Genome Biology and Evolution, 2012, 4, 230-239.	1.1	231
126	Uncovering Small RNA-Mediated Responses to Cold Stress in a Wheat Thermosensitive Genic Male-Sterile Line by Deep Sequencing  Â. Plant Physiology, 2012, 159, 721-738.	2.3	166
127	Small RNA Profiling in Two <i>Brassica napus</i> Cultivars Identifies MicroRNAs with Oil Production- and Development-Correlated Expression and New Small RNA Classes  Â. Plant Physiology, 2012, 158, 813-823.	2.3	111
128	Grass MicroRNA Gene Paleohistory Unveils New Insights into Gene Dosage Balance in Subgenome Partitioning after Whole-Genome Duplication. Plant Cell, 2012, 24, 1776-1792.	3.1	53
129	Identification of miRNAs in sorghum by using bioinformatics approach. Plant Signaling and Behavior, 2012, 7, 246-259.	1.2	38
130	Genome-wide identification of Brassica napus microRNAs and their targets in response to cadmium. Journal of Experimental Botany, 2012, 63, 4597-4613.	2.4	181
131	MicroRNAs in Amoebozoa: Deep sequencing of the small RNA population in the social amoeba <i>Dictyostelium discoideum</i> reveals developmentally regulated microRNAs. Rna, 2012, 18, 1771-1782.	1.6	42

ARTICLE IF CITATIONS # MicroRNAs: Potentially important regulators for schistosome development and therapeutic targets 132 0.7 27 against schistosomiasis. Parasitology, 2012, 139, 669-679. PsRobot: a web-based plant small RNA meta-analysis toolbox. Nucleic Acids Research, 2012, 40, 133 6.5 448 W22-W28. A Comparative miRNAome Analysis Reveals Seven Fiber Initiation-Related and 36 Novel miRNAs in 134 3.9 58 Developing Cotton Ovules. Molecular Plant, 2012, 5, 889-900. A MicroRNA Superfamily Regulates Nucleotide Binding Site–Leucine-Rich Repeats and Other mRNAs. 3.1 Plant Cell, 2012, 24, 859-874. Genomic dissection of small <scp>RNA</scp>s in wild rice (<i>Oryza rufipogon</i>): lessons for rice 136 3.5 33 domestication. New Phytologist, 2012, 196, 914-925. Are all the miRBase-registered microRNAs true?. RNA Biology, 2012, 9, 249-253. 1.5 56 138 Apple miRNAs and tasiRNAs with novel regulatory networks. Genome Biology, 2012, 13, R47. 13.9 272 Do miRNAs have a deep evolutionary history?. BioEssays, 2012, 34, 857-866. 1.2 96 Genome-wide analysis of microRNAs in rubber tree (Hevea brasiliensis L.) using high-throughput 140 1.6 41 sequencing. Planta, 2012, 236, 437-445. Discovery and profiling of novel and conserved microRNAs during flower development in Carya 141 1.6 cathayensis via deep sequencing. Planta, 2012, 236, 613-621. Subgenomic analysis of microRNAs in polyploid wheat. Functional and Integrative Genomics, 2012, 12, 142 1.4 43 465-479. Small RNA profiling of virus-infected grapevines: evidences for virus infection-associated and 1.4 variety-specific miRNAs. Functional and Integrative Genomics, 2012, 12, 659-669. MicroRNAs in trees. Plant Molecular Biology, 2012, 80, 37-53. 144 2.0 23 miRDeepFinder: a miRNA analysis tool for deep sequencing of plant small RNAs. Plant Molecular 145 1,159 Biology, 2012, 80, 75-84. Identification and comparative profiling of microRNAs in wild-type Xanthoceras sorbifolia and its 146 0.514 double flower mutant. Genes and Genomics, 2012, 34, 561-568. Identification of conserved and novel microRNAs that are responsive to heat stress in Brassica rapa. 147 2.4 229 Journal of Experimental Botany, 2012, 63, 1025-1038. Miniature Inverted-Repeat Transposable Elements (MITEs) Have Been Accumulated through 148 Amplification Bursts and Play Important Roles in Gene Expression and Species Diversity in Oryza sativa. 3.5 191 Molecular Biology and Evolution, 2012, 29, 1005-1017. Ethylene-responsive miRNAs in roots of Medicago truncatula identified by high-throughput sequencing at whole genome level. Plant Science, 2012, 184, 14-19.

ARTICLE IF CITATIONS # Exploration of small non coding RNAs in wheat (Triticum aestivum L.). Plant Molecular Biology, 2012, 151 2.0 20 80, 67-73. MicroRNAs and their diverse functions in plants. Plant Molecular Biology, 2012, 80, 17-36. 272 153 Conservation and divergence in plant microRNAs. Plant Molecular Biology, 2012, 80, 3-16. 2.0 143 Genome-wide identification of microRNAs in larch and stage-specific modulation of 11 conserved 154 microRNAs and their targets during somatic embryogenesis. Planta, 2012, 236, 647-657. Identification and Analyses of miRNA Genes in Allotetraploid Gossypium hirsutum Fiber Cells Based on 155 1.7 31 the Sequenced Diploid G.Âraimondii Genome. Journal of Genetics and Genomics, 2012, 39, 351-360. Identification and developmental profiling of conserved and novel microRNAs in Manduca sexta. Insect Biochemistry and Molecular Biology, 2012, 42, 381-395. 1.2 Genome-wide identification of cold-responsive and new microRNAs in Populus tomentosa by 157 high-throughput sequencing. Biochemical and Biophysical Research Communications, 2012, 417, 1.0 98 892-896. Identification and validation of Asteraceae miRNAs by the expressed sequence tag analysis. Gene, 2012, 158 1.0 493, 253-259. Identification and characterization of miRNAome in tobacco (Nicotiana tabacum) by deep sequencing 159 1.0 15 combined with microarray. Gene, 2012, 501, 24-32. Genome-wide identification and expression analysis of heat-responsive and novel microRNAs in 1.0 Populus tomentosa. Gene, 2012, 504, 160-165. Two MicroRNAs Linked to Nodule Infection and Nitrogen-Fixing Ability in the Legume <i>Lotus 161 2.3 116 japonicus</i> Â Â. Plant Physiology, 2012, 160, 2137-2154. miREvo: an integrative microRNA evolutionary analysis platform for next-generation sequencing 1.2 468 experiments. BMC Bioinformatics, 2012, 13, 140. Identification of microRNAs from Amur grape (vitis amurensis Rupr.) by deep sequencing and analysis 163 1.2 98 of microRNA variations with bioinformatics. BMC Genomics, 2012, 13, 122. Transcriptome-wide identification and characterization of miRNAs from Pinus densata. BMC Genomics, 164 1.2 2012, 13, 132. Genome organization and characteristics of soybean microRNAs. BMC Genomics, 2012, 13, 169. 165 1.2 77 Identification of novel MiRNAs and MiRNA expression profiling during grain development in indica 1.2 rice. BMC Genomics, 2012, 13, 264. Computational identification and analysis of novel sugarcane microRNAs. BMC Genomics, 2012, 13, 290. 167 1.2 63 Characterization of the small RNA component of leaves and fruits from four different cucurbit 1.2 species. BMC Genomics, 2012, 13, 329.

#	Article	IF	CITATIONS
169	High-throughput sequencing of small RNAs and analysis of differentially expressed microRNAs associated with pistil development in Japanese apricot. BMC Genomics, 2012, 13, 371.	1.2	64
170	The miRNAome of globe artichoke: conserved and novel micro RNAs and target analysis. BMC Genomics, 2012, 13, 41.	1.2	44
171	Genome wide identification of chilling responsive microRNAs in Prunus persica. BMC Genomics, 2012, 13, 481.	1.2	126
172	Small RNA and transcriptome deep sequencing proffers insight into floral gene regulation in Rosa cultivars. BMC Genomics, 2012, 13, 657.	1.2	49
173	Sculpting the maturation, softening and ethylene pathway: The influences of microRNAs on tomato fruits. BMC Genomics, 2012, 13, 7.	1.2	99
174	miRNA regulation in the early development of barley seed. BMC Plant Biology, 2012, 12, 120.	1.6	68
175	High throughput sequencing reveals novel and abiotic stress-regulated microRNAs in the inflorescences of rice. BMC Plant Biology, 2012, 12, 132.	1.6	157
176	Identification and characterization of small non-coding RNAs from Chinese fir by high throughput sequencing. BMC Plant Biology, 2012, 12, 146.	1.6	95
177	Unique expression, processing regulation, and regulatory network of peach (Prunus persica) miRNAs. BMC Plant Biology, 2012, 12, 149.	1.6	112
178	Identification of wild soybean miRNAs and their target genes responsive to aluminum stress. BMC Plant Biology, 2012, 12, 182.	1.6	137
179	smRNAome profiling to identify conserved and novel microRNAs in Stevia rebaudiana Bertoni. BMC Plant Biology, 2012, 12, 197.	1.6	18
180	Bioinformatic identification of cassava miRNAs differentially expressed in response to infection by Xanthomonas axonopodis pv. manihotis. BMC Plant Biology, 2012, 12, 29.	1.6	57
181	The Ectocarpus Genome and Brown Algal Genomics. Advances in Botanical Research, 2012, 64, 141-184.	0.5	18
182	Functional Specialization of the Plant miR396 Regulatory Network through Distinct MicroRNA–Target Interactions. PLoS Genetics, 2012, 8, e1002419.	1.5	192
183	Small RNA-Regulated Networks and the Evolution of Novel Structures in Plants. Cold Spring Harbor Symposia on Quantitative Biology, 2012, 77, 221-233.	2.0	11
184	Noncanonical MicroRNAs and Endogenous siRNAs in Lytic Infection of Murine Gammaherpesvirus. PLoS ONE, 2012, 7, e47863.	1.1	20
185	Generation of PVY Coat Protein siRNAs in Transgenic Potatoes Resistant to PVY. American Journal of Potato Research, 2012, 89, 374-383.	0.5	11
186	MiR1511 co-regulates with miR1511* to cleave the GmRPL4a gene in soybean. Science Bulletin, 2012, 57, 3804-3810.	1.7	7

#	Article	IF	CITATIONS
187	C-mii: a tool for plant miRNA and target identification. BMC Genomics, 2012, 13, S16.	1.2	51
188	Cloning and Characterization of Maize miRNAs Involved in Responses to Nitrogen Deficiency. PLoS ONE, 2012, 7, e29669.	1.1	142
189	A Combined Approach of High-Throughput Sequencing and Degradome Analysis Reveals Tissue Specific Expression of MicroRNAs and Their Targets in Cucumber. PLoS ONE, 2012, 7, e33040.	1.1	113
190	Identification of Soybean MicroRNAs Involved in Soybean Cyst Nematode Infection by Deep Sequencing. PLoS ONE, 2012, 7, e39650.	1.1	116
191	Identification and Comparative Profiling of miRNAs in an Early Flowering Mutant of Trifoliate Orange and Its Wild Type by Genome-Wide Deep Sequencing. PLoS ONE, 2012, 7, e43760.	1.1	38
192	High-Throughput Sequencing and Characterization of the Small RNA Transcriptome Reveal Features of Novel and Conserved MicroRNAs in Panax ginseng. PLoS ONE, 2012, 7, e44385.	1.1	59
193	microRNAs Associated with Drought Response in the Bioenergy Crop Sugarcane (Saccharum spp.). PLoS ONE, 2012, 7, e46703.	1.1	127
194	Genome-Wide Identification of Reverse Complementary microRNA Genes in Plants. PLoS ONE, 2012, 7, e46991.	1.1	21
195	Phylogenetic Analysis and Molecular Evolution Patterns in the MIR482-MIR1448 Polycistron of Populus L. PLoS ONE, 2012, 7, e47811.	1.1	13
196	Identification of Nitrogen Starvation-Responsive MicroRNAs in Arabidopsis thaliana. PLoS ONE, 2012, 7, e48951.	1.1	242
197	TriAnnot: A Versatile and High Performance Pipeline for the Automated Annotation of Plant Genomes. Frontiers in Plant Science, 2012, 3, 5.	1.7	73
198	Manipulation of Plant Host Susceptibility: An Emerging Role for Viral Movement Proteins?. Frontiers in Plant Science, 2012, 3, 10.	1.7	24
199	Genome-Wide Profiling of miRNAs and Other Small Non-Coding RNAs in the Verticillium dahliae–Inoculated Cotton Roots. PLoS ONE, 2012, 7, e35765.	1.1	115
200	Computational prediction of candidate miRNAs and their targets from the completed Linum ussitatissimum genome and EST database. Journal of Nucleic Acids Investigation, 2012, 3, 2.	0.5	3
201	Analyzing the microRNA Transcriptome in Plants Using Deep Sequencing Data. Biology, 2012, 1, 297-310.	1.3	15
202	MicroRNAs and Their Role in Plants During Abiotic Stresses. , 2012, , 265-278.		3
203	MicroRNA profiles and their control of male gametophyte development in rice. Plant Molecular Biology, 2012, 80, 85-102.	2.0	40
204	High-resolution experimental and computational profiling of tissue-specific known and novel miRNAs in <i>Arabidopsis</i> . Genome Research, 2012, 22, 163-176.	2.4	140

#	Article	IF	CITATIONS
205	Small RNAs in Plants. Signaling and Communication in Plants, 2012, , 1-28.	0.5	4
206	Role of MicroRNA miR319 in Plant Development. Signaling and Communication in Plants, 2012, , 29-47.	0.5	46
207	Cloning and Expression Studies of Novel Small RNAs in Tetraploid Cotton. Plant Molecular Biology Reporter, 2012, 30, 710-718.	1.0	5
208	Identification of miRNAs and Their Target Genes Using Deep Sequencing and Degradome Analysis in Trifoliate Orange [Poncirus trifoliate (L.) Raf]. Molecular Biotechnology, 2012, 51, 44-57.	1.3	49
209	Genome-wide profiling of novel and conserved Populus microRNAs involved in pathogen stress response by deep sequencing. Planta, 2012, 235, 873-883.	1.6	90
210	Identification of novel and conserved Populus tomentosa microRNA as components of a response to water stress. Functional and Integrative Genomics, 2012, 12, 327-339.	1.4	75
211	Genomeâ€wide identification of <i>Medicago truncatula</i> microRNAs and their targets reveals their differential regulation by heavy metal. Plant, Cell and Environment, 2012, 35, 86-99.	2.8	182
212	Roles of DCL4 and DCL3b in rice phased small RNA biogenesis. Plant Journal, 2012, 69, 462-474.	2.8	289
213	MAJOR DEVELOPMENTAL REGULATORS AND THEIR EXPRESSION IN TWO CLOSELY RELATED SPECIES OF <i>PORPHYRA</i> (RHODOPHYTA) <sup>1</sup> . Journal of Phycology, 2012, 48, 883-896.	1.0	19
214	Comprehensive analysis of differential genes and miRNA profiles for discovery of toppingâ€responsive genes in flueâ€cured tobacco roots. FEBS Journal, 2012, 279, 1054-1070.	2.2	28
215	Global Analysis of Nonâ€coding Small RNAs in <i>Arabidopsis</i> in Response to Jasmonate Treatment by Deep Sequencing Technology. Journal of Integrative Plant Biology, 2012, 54, 73-86.	4.1	18
216	Highâ€ŧhroughput sequence analysis of small <scp>RNA</scp> s in grapevine ( <i><scp>V</scp>itis) Tj ETQq1 1 ( 1060-1076.</i>	).784314 2.0	rgBT /Overlo 74
217	SoMART: a web server for plant miRNA, tasiRNA and target gene analysis. Plant Journal, 2012, 70, 891-901.	2.8	71
218	Mining of miRNAs and potential targets from gene oriented clusters of transcripts sequences of the anti-malarial plant, Artemisia annua. Biotechnology Letters, 2012, 34, 737-745.	1.1	23
219	Isolation and cloning of microRNAs from recalcitrant plant tissues with small amounts of total RNA: a step-by step approach. Molecular Biology Reports, 2012, 39, 1783-1790.	1.0	3
220	Identification of aluminum-responsive microRNAs in Medicago truncatula by genome-wide high-throughput sequencing. Planta, 2012, 235, 375-386.	1.6	156
221	Computational identification of microRNAs and their targets in apple. Genes and Genomics, 2013, 35, 377-385.	0.5	14
222	Structural and functional based identification of the bean (Phaseolus) microRNAs and their targets from expressed sequence tags. Journal of Structural and Functional Genomics, 2013, 14, 11-18.	1.2	15

## # ARTICLE

In silico Characterisation and Phylogenetic Analysis of Two Evolutionarily Conserved miRNAs (miR166) Tj ETQq0 0 Q rgBT /Overlock 10 T

224	Identification of microRNAs potentially involved in male sterility of Brassica campestris ssp. chinensis using microRNA array and quantitative RT-PCR assays. Cellular and Molecular Biology Letters, 2013, 18, 416-32.	2.7	11
225	Identification of drought-responsive and novel Populus trichocarpamicroRNAs by high-throughput sequencing and their targets using degradome analysis. BMC Genomics, 2013, 14, 233.	1.2	148
226	MicroRNAs and their putative targets in Brassica napusseed maturation. BMC Genomics, 2013, 14, 140.	1.2	99
227	Genome-wide identification of alternate bearing-associated microRNAs (miRNAs) in olive (Olea) Tj ETQq0 0 0 rgB	Г /Qyerlocl 1.9	₹ 10 Tf 50
228	Abiotic stress-associated microRNAs in plants: discovery, expression analysis, and evolution. Frontiers in Biology, 2013, 8, 189-197.	0.7	16
229	Computational Identification of MicroRNAs and Their Targets in Cassava (Manihot esculenta Crantz.). Molecular Biotechnology, 2013, 53, 257-269.	1.3	76
230	Genome-Wide Analysis of MicroRNAs in Sacred Lotus, Nelumbo nucifera (Gaertn). Tropical Plant Biology, 2013, 6, 117-130.	1.0	25
231	Identification of miRNAs and miRNA-mediated regulatory pathways in Carica papaya. Planta, 2013, 238, 739-752.	1.6	40
232	Effects of drought on the microtranscriptome of field-grown sugarcane plants. Planta, 2013, 237, 783-798.	1.6	59
233	Genetics and Genomics of Rice. , 2013, , .		8
234	The role of rice microRNAs in abiotic stress responses. Journal of Plant Biology, 2013, 56, 187-197.	0.9	83
235	Multiple RNA recognition patterns during microRNA biogenesis in plants. Genome Research, 2013, 23, 1675-1689.	2.4	110
236	Identification of novel microRNA-like-coding sites on the long-stem microRNA precursors in Arabidopsis. Gene, 2013, 527, 477-483.	1.0	9
237	MicroRNA expression analysis of rosette and folding leaves in Chinese cabbage using high-throughput Solexa sequencing. Gene, 2013, 532, 222-229.	1.0	20
238	"A draft Musa balbisiana genome sequence for molecular genetics in polyploid, inter- and intra-specific Musa hybridsâ€: BMC Genomics, 2013, 14, 683.	1.2	159
239	Development-associated microRNAs in grains of wheat (Triticum aestivumL.). BMC Plant Biology, 2013, 13, 140.	1.6	88
240	Integrating microRNA and mRNA expression profiling in Symbiodinium microadriaticum, a dinoflagellate symbiont of reef-building corals. BMC Genomics, 2013, 14, 704.	1.2	109

#	Article	IF	CITATIONS
241	Genome-wide analysis of small RNAs reveals eight fiber elongation-related and 257 novel microRNAs in elongating cotton fiber cells. BMC Genomics, 2013, 14, 629.	1.2	52
242	Genome-wide identification, molecular cloning, expression profiling and posttranscriptional regulation analysis of the Argonaute gene family in Salvia miltiorrhiza, an emerging model medicinal plant. BMC Genomics, 2013, 14, 512.	1.2	37
243	Genome-wide characterization of microRNA in foxtail millet (Setaria italica). BMC Plant Biology, 2013, 13, 212.	1.6	47
244	Genome-wide identification of Thellungiella salsuginea microRNAs with putative roles in the salt stress response. BMC Plant Biology, 2013, 13, 180.	1.6	66
245	High-throughput sequencing identification of novel and conserved miRNAs in the Brassica oleracea leaves. BMC Genomics, 2013, 14, 801.	1.2	42
246	Genome-Wide Identification of MicroRNAs in Medicago truncatula by High-Throughput Sequencing. Methods in Molecular Biology, 2013, 1069, 67-80.	0.4	1
247	Changes to DNA methylation and homologous recombination frequency in the progeny of stressed plants. Biochemistry and Cell Biology, 2013, 91, 1-5.	0.9	30
248	ShortStack: Comprehensive annotation and quantification of small RNA genes. Rna, 2013, 19, 740-751.	1.6	413
249	Small RNA and degradome sequencing reveal complex miRNA regulation during cotton somatic embryogenesis. Journal of Experimental Botany, 2013, 64, 1521-1536.	2.4	179
250	Conserved microRNAs and their targets in rubber tree and the related Euphorbiaceous species. Journal of Plant Biochemistry and Biotechnology, 2013, 22, 52-61.	0.9	3
251	Classification and Comparison of Small RNAs from Plants. Annual Review of Plant Biology, 2013, 64, 137-159.	8.6	832
252	Addressing the Role of microRNAs in Reprogramming Leaf Growth during Drought Stress in Brachypodium distachyon. Molecular Plant, 2013, 6, 423-443.	3.9	75
253	Ecological and evolutionary genomics of marine photosynthetic organisms. Molecular Ecology, 2013, 22, 867-907.	2.0	29
254	Processing of plant microRNA precursors. Briefings in Functional Genomics, 2013, 12, 37-45.	1.3	57
255	MicroRNA prediction and its function in regulating drought-related genes in cowpea. Plant Science, 2013, 210, 25-35.	1.7	35
256	Identification and comparative analysis of low phosphate tolerance-associated microRNAs in two maize genotypes. Plant Physiology and Biochemistry, 2013, 70, 221-234.	2.8	40
257	Discovery of MicroRNAs Associated with the S Type Cytoplasmic Male Sterility in Maize. Journal of Integrative Agriculture, 2013, 12, 229-238.	1.7	14
259	Biogenesis and function of rice small RNAs from non-coding RNA precursors. Current Opinion in Plant Biology, 2013, 16, 170-179.	3.5	83

#	Article	IF	CITATIONS
260	ldentification and characterization of novel and conserved microRNAs in radish (Raphanus sativus L.) using high-throughput sequencing. Plant Science, 2013, 201-202, 108-114.	1.7	30
261	Detection and evolutionary analysis of soybean miRNAs responsive to soybean mosaic virus. Planta, 2013, 237, 1213-1225.	1.6	48

263	miRNA–transcription factor interactions: a combinatorial regulation of gene expression. Molecular Genetics and Genomics, 2013, 288, 77-87.	1.0	145
264	Deep sequencing discovery of novel and conserved <scp>microRNAs</scp> in strawberry ( <i>Fragaria</i> A— <i>ananassa</i> ). Physiologia Plantarum, 2013, 148, 387-396.	2.6	45
265	Global identification of miRNAs and targets in Populus euphratica under salt stress. Plant Molecular Biology, 2013, 81, 525-539.	2.0	138
266	Identification and characterization of salt-responsive microRNAs in Populus tomentosa by high-throughput sequencing. Biochimie, 2013, 95, 743-750.	1.3	48
267	Interaction of small <scp>RNA</scp> –8105 and the intron of <i>lbMYB1 </i> <scp>RNA</scp> regulates <i>lbMYB1</i> family genes through secondary siRNAs and <scp>DNA</scp> methylation after wounding. Plant Journal, 2013, 75, 781-794.	2.8	23
268	Deep sequencing discovery of novel and conserved microRNAs in wild type and a white-flesh mutant strawberry. Planta, 2013, 238, 695-713.	1.6	40
269	Manipulation of microRNA expression to improve nitrogen use efficiency. Plant Science, 2013, 210, 70-81.	1.7	83
270	<i>Rice yellow stunt rhabdovirus</i> Protein 6 Suppresses Systemic RNA Silencing by Blocking RDR6-Mediated Secondary siRNA Synthesis. Molecular Plant-Microbe Interactions, 2013, 26, 927-936.	1.4	92
271	Identification of microRNAs in Caragana intermedia by high-throughput sequencing and expression analysis of 12 microRNAs and their targets under salt stress. Plant Cell Reports, 2013, 32, 1339-1349.	2.8	49
272	Identification of a novel micro <scp>RNA</scp> (mi <scp>RNA</scp> ) from rice that targets an alternatively spliced transcript of the <i><scp>N</scp>ramp6</i> ( <i><scp>N</scp>atural) Tj ETQq0 0 0 rgBT /O Phytologist, 2013, 199, 212-227.</i>	verlock 10	) Tf 50 262 1 221

273	Comprehensive Investigation of MicroRNAs Enhanced by Analysis of Sequence Variants, Expression Patterns, ARGONAUTE Loading, and Target Cleavage. Plant Physiology, 2013, 162, 1225-1245.	2.3	61
274	Small RNA pathways and diversity in model legumes: lessons from genomics. Frontiers in Plant Science, 2013, 4, 236.	1.7	30
275	Comparative profiling of miRNA expression in developing seeds of high linoleic and high oleic safflower (Carthamus tinctorius L.) plants. Frontiers in Plant Science, 2013, 4, 489.	1.7	31
276	Identification and Dynamic Regulation of microRNAs Involved in Salt Stress Responses in Functional Soybean Nodules by High-Throughput Sequencing. International Journal of Molecular Sciences, 2013, 14, 2717-2738.	1.8	73
277	Composition and Expression of Conserved MicroRNA Genes in Diploid Cotton (Gossypium) Species. Genome Biology and Evolution, 2013, 5, 2449-2459.	1.1	35

#	Article	IF	CITATIONS
278	Phased, Secondary, Small Interfering RNAs in Posttranscriptional Regulatory Networks. Plant Cell, 2013, 25, 2400-2415.	3.1	543
279	miRNAs: Small Genes with Big Potential in Metazoan Phylogenetics. Molecular Biology and Evolution, 2013, 30, 2369-2382.	3.5	118
280	Discovery of MicroRNA169 Gene Copies in Genomes of Flowering Plants through Positional Information. Genome Biology and Evolution, 2013, 5, 402-417.	1.1	20
281	Identification of Cassava MicroRNAs under Abiotic Stress. International Journal of Genomics, 2013, 2013, 1-10.	0.8	57
282	Genome-wide identification and characterization of cadmium-responsive microRNAs and their target genes in radish (Raphanus sativus L.) roots. Journal of Experimental Botany, 2013, 64, 4271-4287.	2.4	117
283	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
284	Expression of the rice microRNA <i>miR820</i> is associated with epigenetic modifications at its own locus. Genes and Genetic Systems, 2013, 88, 105-112.	0.2	10
285	Parallel analysis of RNA ends enhances global investigation of microRNAs and target RNAs of Brachypodium distachyon. Genome Biology, 2013, 14, R145.	13.9	67
286	Comparative expression profiling of miRNA during anther development in genetic male sterile and wild type cotton. BMC Plant Biology, 2013, 13, 66.	1.6	65
287	MicroRNAs may solve the mystery of chronic hepatitis B virus infection. World Journal of Gastroenterology, 2013, 19, 4867.	1.4	25
288	Genome-Wide Identification and Comparative Analysis of Conserved and Novel MicroRNAs in Grafted Watermelon by High-Throughput Sequencing. PLoS ONE, 2013, 8, e57359.	1.1	55
289	Sexual Dimorphism Floral MicroRNA Profiling and Target Gene Expression in Andromonoecious Poplar (Populus tomentosa). PLoS ONE, 2013, 8, e62681.	1.1	31
290	Genome-Wide Analysis Reveals Diversity of Rice Intronic miRNAs in Sequence Structure, Biogenesis and Function. PLoS ONE, 2013, 8, e63938.	1.1	11
291	The Hot Pepper (Capsicum annuum) MicroRNA Transcriptome Reveals Novel and Conserved Targets: A Foundation for Understanding MicroRNA Functional Roles in Hot Pepper. PLoS ONE, 2013, 8, e64238.	1.1	55
292	Transcriptome/Degradome-Wide Identification of R. glutinosa miRNAs and Their Targets: The Role of miRNA Activity in the Replanting Disease. PLoS ONE, 2013, 8, e68531.	1.1	23
293	Genome-Wide Analysis of Small RNA and Novel MicroRNA Discovery during Fiber and Seed Initial Development in Gossypium hirsutum. L. PLoS ONE, 2013, 8, e69743.	1.1	17
294	Unique and Conserved MicroRNAs in Wheat Chromosome 5D Revealed by Next-Generation Sequencing. PLoS ONE, 2013, 8, e69801.	1.1	41
295	Characterization and Evolution of Conserved MicroRNA through Duplication Events in Date Palm (Phoenix dactylifera). PLoS ONE, 2013, 8, e71435.	1.1	22

#	Article	IF	CITATIONS
296	Identification of miRNAs and Their Target Genes in Peach (Prunus persica L.) Using High-Throughput Sequencing and Degradome Analysis. PLoS ONE, 2013, 8, e79090.	1.1	33
297	Identification and Functional Analysis of Flowering Related microRNAs in Common Wild Rice (Oryza) Tj ETQq1 1	0.784314 1.1	rgBT /Over
298	Microarray and Degradome Sequencing Reveal MicroRNA Differential Expression Profiles and Their Targets in Pinellia pedatisecta. PLoS ONE, 2013, 8, e75978.	1.1	8
299	Identification and Expression Analysis of microRNAs at the Grain Filling Stage in Rice(Oryza sativa) Tj ETQq1 1 0.7	784314 rg 1.1	BT_/Overloci 75
300	Novel MicroRNAs and Microsatellite-like Small RNAs in Sexual and Apomictic Boechera Species. MicroRNA (Shariqah, United Arab Emirates), 2013, 2, 46-63.	0.6	11
301	Mammalian miRNA curation through next-generation sequencing. Frontiers in Genetics, 2013, 4, 145.	1.1	36
302	Molecular Signatures in Arabidopsis thaliana in Response to Insect Attack and Bacterial Infection. PLoS ONE, 2013, 8, e58987.	1.1	67
303	Extending the sRNAome of Apple by Next-Generation Sequencing. PLoS ONE, 2014, 9, e95782.	1.1	17
304	A Comprehensive Genome-Wide Study on Tissue-Specific and Abiotic Stress-Specific miRNAs in Triticum aestivum. PLoS ONE, 2014, 9, e95800.	1.1	76
305	Identification and Characterization of MicroRNAs in Small Brown Planthopper (Laodephax) Tj ETQq1 1 0.784314	rgBT /Ove	rlock 10 Tf
306	Identification and Characterization of Wilt and Salt Stress-Responsive MicroRNAs in Chickpea through High-Throughput Sequencing. PLoS ONE, 2014, 9, e108851.	1.1	101
307	De Novo Transcriptome and Small RNA Analysis of Two Chinese Willow Cultivars Reveals Stress Response Genes in Salix matsudana. PLoS ONE, 2014, 9, e109122.	1.1	23
308	Novel MiRNA and PhasiRNA Biogenesis Networks in Soybean Roots from Two Sister Lines That Are Resistant and Susceptible to SCN Race 4. PLoS ONE, 2014, 9, e110051.	1.1	25
309	Discovery of Novel Leaf Rust Responsive microRNAs in Wheat and Prediction of Their Target Genes. Journal of Nucleic Acids, 2014, 2014, 1-12.	0.8	28
310	Identification of novel and conserved microRNAs in Coffea canephora and Coffea arabica. Genetics and Molecular Biology, 2014, 37, 671-682.	0.6	15
311	Identification of miRNAs involved in pear fruit development and quality. BMC Genomics, 2014, 15, 953.	1.2	102
312	The diversity of small non-coding RNAs in the diatom Phaeodactylum tricornutum. BMC Genomics, 2014, 15, 698.	1.2	40
313	Small RNA profiling reveals regulation of Arabidopsis miR168 and heterochromatic siRNA415 in response to fungal elicitors. BMC Genomics, 2014, 15, 1083.	1.2	39

#	Article	IF	CITATIONS
314	Global and local perturbation of the tomato microRNA pathway by atrans-activatedDICER-LIKE 1mutant. Journal of Experimental Botany, 2014, 65, 725-739.	2.4	27
315	Automated Update, Revision, and Quality Control of the Maize Genome Annotations Using MAKER-P Improves the B73 RefGen_v3 Gene Models and Identifies New Genes Â. Plant Physiology, 2014, 167, 25-39.	2.3	53
316	A survey of the small RNA population during far-red light-induced apical hook opening. Frontiers in Plant Science, 2014, 5, 156.	1.7	18
317	MicroRNAs Suppress NB Domain Genes in Tomato That Confer Resistance to Fusarium oxysporum. PLoS Pathogens, 2014, 10, e1004464.	2.1	187
318	The miR9863 Family Regulates Distinct Mla Alleles in Barley to Attenuate NLR Receptor-Triggered Disease Resistance and Cell-Death Signaling. PLoS Genetics, 2014, 10, e1004755.	1.5	121
319	Genome-wide identification of non-coding RNAs interacted with microRNAs in soybean. Frontiers in Plant Science, 2014, 5, 743.	1.7	53
320	Sex specific expression and distribution of small RNAs in papaya. BMC Genomics, 2014, 15, 20.	1.2	28
321	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
322	Genome-wide discovery and differential regulation of conserved and novel microRNAs in chickpea via deep sequencing. Journal of Experimental Botany, 2014, 65, 5945-5958.	2.4	71
323	An Atlas of Soybean Small RNAs Identifies Phased siRNAs from Hundreds of Coding Genes. Plant Cell, 2014, 26, 4584-4601.	3.1	163
324	Dominance hierarchy arising from the evolution of a complex small RNA regulatory network. Science, 2014, 346, 1200-1205.	6.0	61
325	miRNEST 2.0: a database of plant and animal microRNAs. Nucleic Acids Research, 2014, 42, D74-D77.	6.5	68
326	Identification of chilling stress-responsive tomato microRNAs and their target genes by high-throughput sequencing and degradome analysis. BMC Genomics, 2014, 15, 1130.	1.2	93
327	Genome-wide identification of microRNA and siRNA responsive to endophytic beneficial diazotrophic bacteria in maize. BMC Genomics, 2014, 15, 766.	1.2	56
328	Identification and characterization of miRNAome in root, stem, leaf and tuber developmental stages of potato (Solanum tuberosum L.) by high-throughput sequencing. BMC Plant Biology, 2014, 14, 6.	1.6	105
329	Identification of novel microRNAs in the Verticillium wilt-resistant upland cotton variety KV-1 by high-throughput sequencing. SpringerPlus, 2014, 3, 564.	1.2	24
330	Deep sequencing on a genome-wide scale reveals diverse stage-specific microRNAs in cambium during dormancy-release induced by chilling in poplar. BMC Plant Biology, 2014, 14, 267.	1.6	37
331	Identification and characterization of cold-responsive microRNAs in tea plant (Camellia sinensis) and their targets using high-throughput sequencing and degradome analysis. BMC Plant Biology, 2014, 14, 271.	1.6	147

#	Article	IF	CITATIONS
332	The small RNA diversity from Medicago truncatularoots under biotic interactions evidences the environmental plasticity of the miRNAome. Genome Biology, 2014, 15, 457.	3.8	78
333	Novel insights from non-conserved microRNAs in plants. Frontiers in Plant Science, 2014, 5, 586.	1.7	44
334	sRNAbench: profiling of small RNAs and its sequence variants in single or multi-species high-throughput experiments. Methods in Next Generation Sequencing, 2014, 1, .	1.5	44
335	The I2 resistance gene homologues in Solanum have complex evolutionary patterns and are targeted by miRNAs. BMC Genomics, 2014, 15, 743.	1.2	33
336	sPARTA: a parallelized pipeline for integrated analysis of plant miRNA and cleaved mRNA data sets, including new miRNA target-identification software. Nucleic Acids Research, 2014, 42, e139-e139.	6.5	69
337	Identification of Conserved and Novel Cold-Responsive MicroRNAs in Trifoliate Orange (Poncirus) Tj ETQq1 1 0 328-341.	.784314 rgE 1.0	BT /Overlock 68
338	Exploring the interaction between small RNAs and R genes during Brachypodium response to Fusarium culmorum infection. Gene, 2014, 536, 254-264.	1.0	21
339	Morphogenesis of simple leaves: regulation of leaf size and shape. Wiley Interdisciplinary Reviews: Developmental Biology, 2014, 3, 41-57.	5.9	97
340	New wheat microRNA using whole-genome sequence. Functional and Integrative Genomics, 2014, 14, 363-379.	1.4	36
341	Transcriptome-wide analysis of dynamic variations in regulation modes of grapevine microRNAs on their target genes during grapevine development. Plant Molecular Biology, 2014, 84, 269-285.	2.0	54
342	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.	1.0	54
343	GC content fluctuation around plant small RNAâ€generating sites. FEBS Letters, 2014, 588, 764-769.	1.3	4
344	Dynamic expression of novel and conserved microRNAs and their targets in diploid and tetraploid of Paulownia tomentosa. Biochimie, 2014, 102, 68-77.	1.3	24
345	Identification of novel and conserved miRNAs involved in pollen development in Brassica campestris ssp. chinensi s by high-throughput sequencing and degradome analysis. BMC Genomics, 2014, 15, 146.	1.2	85
346	Grapevine microRNAs responsive to exogenous gibberellin. BMC Genomics, 2014, 15, 111.	1.2	58
347	Computational Identification and Comparative Analysis of miRNAs in Wheat Group 7 Chromosomes. Plant Molecular Biology Reporter, 2014, 32, 487-500.	1.0	10
348	Genome-Wide Identification of Embryogenesis-Associated microRNAs in Radish (Raphanus sativus L.) by High-Throughput Sequencing. Plant Molecular Biology Reporter, 2014, 32, 900-915.	1.0	30
349	Identification and characterization of the microRNA transcriptome of a moth orchid Phalaenopsis aphrodite. Plant Molecular Biology, 2014, 84, 529-548.	2.0	38

#	Article	IF	CITATIONS
350	Identification of miRNAs and their target genes in developing maize ears by combined small RNA and degradome sequencing. BMC Genomics, 2014, 15, 25.	1.2	94
351	miRNA profiling in leaf and cork tissues of Quercus suber reveals novel miRNAs and tissue-specific expression patterns. Tree Genetics and Genomes, 2014, 10, 721-737.	0.6	20
352	Seeing the forest for the trees: annotating small RNA producing genes in plants. Current Opinion in Plant Biology, 2014, 18, 87-95.	3.5	38
353	Endogenous Small RNA Clusters in Plants. Genomics, Proteomics and Bioinformatics, 2014, 12, 64-71.	3.0	24
354	High-throughput analysis of small RNAs and characterization of novel microRNAs affected by abiotic stress in a local celery cultivar. Scientia Horticulturae, 2014, 169, 36-43.	1.7	20
355	Synthesis and characterization of a highly stable poly (3,4-ethylenedioxythiophene)-gold nanoparticles composite film and its application to electrochemical dopamine sensors. RSC Advances, 2014, 4, 8415-8420.	1.7	13
356	Evolutionary history of plant microRNAs. Trends in Plant Science, 2014, 19, 175-182.	4.3	182
358	Identification of microRNAs and their targets in tomato infected with Cucumber mosaic virus based on deep sequencing. Planta, 2014, 240, 1335-1352.	1.6	66
359	Analysis of small RNAs derived from Chinese wheat mosaic virus. Archives of Virology, 2014, 159, 3077-3082.	0.9	22
360	Identification and Profiling of Known and Novel Fiber MicroRNAs during the Secondary Wall Thickening Stage in Cotton (Cossypium hirsutum) via High-Throughput Sequencing. Journal of Genetics and Genomics, 2014, 41, 553-556.	1.7	3
361	In silico identification and characterization of conserved plant microRNAs in barley. Open Life Sciences, 2014, 9, 841-852.	0.6	1
362	Insight into small RNA abundance and expression in high- and low-temperature stress response using deep sequencing in Arabidopsis. Plant Physiology and Biochemistry, 2014, 84, 105-114.	2.8	34
363	Natural genetic variation in MIR172 isolated from Brassica species. Biologia Plantarum, 2014, 58, 627-640.	1.9	12
364	Small <scp>RNA</scp> and degradome profiling reveals a role for mi <scp>RNA</scp> s and their targets in the developing fibers of <i><scp>G</scp>ossypium barbadense</i> . Plant Journal, 2014, 80, 331-344.	2.8	81
365	Identification of 23 novel conserved microRNAs in three rice cultivars. Gene, 2014, 548, 285-293.	1.0	6
366	miRPlant: an integrated tool for identification of plant miRNA from RNA sequencing data. BMC Bioinformatics, 2014, 15, 275.	1.2	114
367	Genome-wide comparison of microRNAs and their targeted transcripts among leaf, flower and fruit of sweet orange. BMC Genomics, 2014, 15, 695.	1.2	70
368	Differentially expressed microRNA cohorts in seed development may contribute to poor grain filling of inferior spikelets in rice. BMC Plant Biology, 2014, 14, 196.	1.6	64

ARTICLE IF CITATIONS # Computational identification of novel microRNAs and targets in Glycine max. Molecular Biology 369 1.0 7 Reports, 2014, 41, 4965-4975. Apple ring rot-responsive putative microRNAs revealed by high-throughput sequencing in 370 1.0 MalusÂ×Âdomestica Borkh.. Molecular Biology Reports, 2014, 41, 5273-5286. System analysis of micro<scp>RNA</scp>s in the development and aluminium stress responses of the 371 4.1 47 maize root system. Plant Biotechnology Journal, 2014, 12, 1108-1121. High-throughput sequencing and degradome analysis reveal microRNA differential expression profiles 1.2 and their targets in Paulownia fortunei. Plant Cell, Tissue and Organ Culture, 2014, 119, 457-468. Comprehensive genome-wide identification and expression profiling of foxtail millet [Setaria italica (L.)] miRNAs in response to abiotic stress and development of miRNA database. Plant Cell, Tissue and 373 1.2 56 Organ Culture, 2014, 118, 279-292. Computational Identification of MicroRNAs and Their Targets in Perennial Ryegrass (Lolium perenne). Applied Biochemistry and Biotechnology, 2014, 173, 1011-1022. 374 1.4 High throughput sequencing of two celery varieties small RNAs identifies microRNAs involved in 375 1.2 56 temperature stress response. BMC Genomics, 2014, 15, 242. Identification and characterization of microRNAs in the flag leaf and developing seed of wheat 1.2 95 (Triticum aestivum L.). BMC Genomics, 2014, 15, 289. Identification of boron-deficiency-responsive microRNAs in Citrus sinensis roots by Illumina 377 1.6 57 sequencing. BMC Plant Biology, 2014, 14, 123. Whole-genome discovery of miRNAs and their targets in wheat (Triticum aestivum L.). BMC Plant 378 1.6 Biology, 2014, 14, 142. A diverse set of miRNAs responsive to begomovirus-associated betasatellite in Nicotiana benthamiana. 379 1.6 19 BMC Plant Biology, 2014, 14, 60. Roles of small <scp>RNA</scp>s in soybean defense against <i><scp>P</scp>hytophthora sojae</i> 380 2.8 infection. Plant Journal, 2014, 79, 928-940. miR-PREFeR: an accurate, fast and easy-to-use plant miRNA prediction tool using small RNA-Seq data. 381 1.8 118 Bioinformatics, 2014, 30, 2837-2839. Prediction of potential novel microRNAs in soybean when in symbiosis. Genetics and Molecular Research, 2014, 13, 8519-8529. 0.3 Genome-wide analysis of salt-responsive and novel microRNAs in Populus euphratica by deep 383 2.7 43 sequencing. BMC Genetics, 2014, 15, S6. Small RNAs from the wheat stripe rust fungus (Puccinia striiformis f.sp. tritici). BMC Genomics, 2015, 384 An approach to identify the novel miRNA encoded from H. Annuus EST sequences. Genomics Data, 2015, 385 1.315 6, 139-144. Identification and characterization of microRNA expression in Ginkgo biloba L. leaves. Tree Genetics and Genomes, 2015, 11, 1.

#	Article	IF	CITATIONS
387	MicroRNA and mRNA expression profiling analysis revealed the regulation of plant height in Gossypium hirsutum. BMC Genomics, 2015, 16, 886.	1.2	23
388	Comparative miRNAs analysis of Two contrasting broccoli inbred lines with divergent head-forming capacity under temperature stress. BMC Genomics, 2015, 16, 1026.	1.2	22
389	Identification of bolting-related microRNAs and their targets reveals complex miRNA-mediated flowering-time regulatory networks in radish (Raphanus sativus L.). Scientific Reports, 2015, 5, 14034.	1.6	63
390	Transcriptome-wide analysis of chromium-stress responsive microRNAs to explore miRNA-mediated regulatory networks in radish (Raphanus sativus L.). Scientific Reports, 2015, 5, 14024.	1.6	76
392	Identification of miRNAs and their targets in transgenic Brassica napus and its acceptor (Westar) by high-throughput sequencing and degradome analysis. RSC Advances, 2015, 5, 85383-85394.	1.7	11
393	Impacts of Whole-Genome Triplication on <i>MIRNA</i> Evolution in <i>Brassica rapa</i> . Genome Biology and Evolution, 2015, 7, 3085-3096.	1.1	18
394	Identification of novel and conserved microRNAs in Panax notoginseng roots by high-throughput sequencing. BMC Genomics, 2015, 16, 835.	1.2	38
395	Secondary si <scp>RNA</scp> s from <i>Medicago <scp>NB</scp>â€<scp>LRR</scp>s</i> modulated via mi <scp>RNA</scp> –target interactions and their abundances. Plant Journal, 2015, 83, 451-465.	2.8	67
396	Identification of four functionally important microRNA families with contrasting differential expression profiles between drought-tolerant and susceptible rice leaf at vegetative stage. BMC Genomics, 2015, 16, 692.	1.2	85
397	Identification of novel small ncRNAs in pollen of tomato. BMC Genomics, 2015, 16, 714.	1.2	27
398	Pathogen-regulated genes in wheat isogenic lines differing in resistance to brown rust Puccinia triticina. BMC Genomics, 2015, 16, 742.	1.2	27
399	Identification of miRNAs involved in fruit ripening in Cavendish bananas by deep sequencing. BMC Genomics, 2015, 16, 776.	1.2	61
400	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.	1.2	13
401	Boron-deficiency-responsive microRNAs and their targets in Citrus sinensis leaves. BMC Plant Biology, 2015, 15, 271.	1.6	34
402	Novel and conserved miRNAs in the halophyte Suaeda maritima identified by deep sequencing and computational predictions using the ESTs of two mangrove plants. BMC Plant Biology, 2015, 15, 301.	1.6	20
403	Genomeâ€wide identification of chromium stressâ€responsive micro RNAs and their target genes in tobacco ( <i>Nicotiana tabacum</i> ) roots. Environmental Toxicology and Chemistry, 2015, 34, 2573-2582.	2.2	50
404	Identification of miRNAs and Their Targets in Cotton Inoculated with Verticillium dahliae by High-Throughput Sequencing and Degradome Analysis. International Journal of Molecular Sciences, 2015, 16, 14749-14768.	1.8	46
405	Small RNAs in Plant Responses to Abiotic Stresses: Regulatory Roles and Study Methods. International Journal of Molecular Sciences, 2015, 16, 24532-24554.	1.8	42

#	Article	IF	CITATIONS
406	Coordination of MicroRNAs, PhasiRNAs, and NB‣RR Genes in Response to a Plant Pathogen: Insights from Analyses of a Set of Soybean Rps Gene Nearâ€ŀsogenic Lines. Plant Genome, 2015, 8, eplantgenome2014.09.0044.	1.6	31
407	Identification of MicroRNAs and Target Genes in the Fruit and Shoot Tip of Lycium chinense: A Traditional Chinese Medicinal Plant. PLoS ONE, 2015, 10, e0116334.	1.1	27
408	Transcriptome-Wide Identification of miRNAs and Their Targets from Typha angustifolia by RNA-Seq and Their Response to Cadmium Stress. PLoS ONE, 2015, 10, e0125462.	1.1	20
409	High-Throughput Sequencing Identifies Novel and Conserved Cucumber (Cucumis sativus L.) microRNAs in Response to Cucumber Green Mottle Mosaic Virus Infection. PLoS ONE, 2015, 10, e0129002.	1.1	26
410	Global Identification of MicroRNAs and Their Targets in Barley under Salinity Stress. PLoS ONE, 2015, 10, e0137990.	1.1	71
411	Small RNA and Degradome Sequencing Reveal Complex Roles of miRNAs and Their Targets in Developing Wheat Grains. PLoS ONE, 2015, 10, e0139658.	1.1	64
412	Identification of Novel and Conserved miRNAs from Extreme Halophyte, Oryza coarctata, a Wild Relative of Rice. PLoS ONE, 2015, 10, e0140675.	1.1	42
413	Role of bioinformatics in establishing microRNAs as modulators of abiotic stress responses: the new revolution. Frontiers in Physiology, 2015, 6, 286.	1.3	37
414	Identification of novel drought-responsive microRNAs and trans-acting siRNAs from Sorghum bicolor (L.) Moench by high-throughput sequencing analysis. Frontiers in Plant Science, 2015, 6, 506.	1.7	76
415	Identification of cold-inducible microRNAs in grapevine. Frontiers in Plant Science, 2015, 6, 595.	1.7	80
416	A genome-wide identification of the miRNAome in response to salinity stress in date palm (Phoenix) Tj ETQq0 0 C	) rgBT /Ove	erlggk 10 Tf 5
417	Identification and Characterization of Novel Maize Mirnas Involved in Different Genetic Background. International Journal of Biological Sciences, 2015, 11, 781-793.	2.6	19
418	High-Throughput Sequencing Reveals Diverse Sets of Conserved, Nonconserved, and Species-Specific miRNAs in Jute. International Journal of Genomics, 2015, 2015, 1-14.	0.8	14
419	Small <scp>RNA</scp> deep sequencing reveals the important role of micro <scp>RNA</scp> s in the halophyte <i>Halostachys caspica</i> . Plant Biotechnology Journal, 2015, 13, 395-408.	4.1	37
420	The use of high-throughput sequencing methods for plant microRNA research. RNA Biology, 2015, 12, 709-719.	1.5	50
422	Small RNA and degradome sequencing reveals microRNAs and their targets involved in tomato pedicel abscission. Planta, 2015, 242, 963-984.	1.6	22
423	Identification and characterization of microRNAs at different flowering developmental stages in moso bamboo (Phyllostachys edulis) by high-throughput sequencing. Molecular Genetics and Genomics, 2015, 290, 2335-2353.	1.0	25
424	Identification of Radish (Raphanus sativus L.) miRNAs and Their Target Genes to Explore miRNA-Mediated Regulatory Networks in Lead (Pb) Stress Responses by High-Throughput Sequencing and Degradome Analysis. Plant Molecular Biology Reporter, 2015, 33, 358-376.	1.0	27

		REPORT	
#	Article	IF	CITATIONS
425	Genome-Wide Identification of microRNAs and Their Targets in Cold-Stored Potato Tubers by Deep Sequencing and Degradome Analysis. Plant Molecular Biology Reporter, 2015, 33, 584-597.	1.0	17
426	Comparative analysis of the Dicer-like gene family reveals loss of miR162 target site in SmDCL1 from Salvia miltiorrhiza. Scientific Reports, 2015, 5, 9891.	1.6	26
427	Systematic discovery and characterization of stress-related microRNA genes in Oryza sativa. Biologia (Poland), 2015, 70, 75-84.	0.8	1
428	Genome-wide identification of microRNAs associated with taproot development in radish (Raphanus) Tj ETQq1	1 0.784314 1.0	4 rgBT /Oved
429	Genome-wide identification of the Phaseolus vulgaris sRNAome using small RNA and degradome sequencing. BMC Genomics, 2015, 16, 423.	1.2	49
430	Transcriptome, microRNA, and degradome analyses of the gene expression of Paulownia with phytoplamsa. BMC Genomics, 2015, 16, 896.	1.2	29
431	micro <scp>RNA</scp> evolution and expression analysis in polyploidized cotton genome. Plant Biotechnology Journal, 2015, 13, 421-434.	4.1	44
432	Small RNA and Degradome Deep Sequencing Reveals Peanut MicroRNA Roles in Response to Pathogen Infection. Plant Molecular Biology Reporter, 2015, 33, 1013-1029.	1.0	49
433	Transcriptome-Wide Characterization of Novel and Heat-Stress-Responsive microRNAs in Radish (Raphanus Sativus L.) Using Next-Generation Sequencing. Plant Molecular Biology Reporter, 2015, 33, 867-880.	1.0	35
434	Genomeâ€Wide Identification of Micro <scp>RNA</scp> s Responsive to High Temperature in Rice ( <i><scp>O</scp>ryza sativa</i> ) by Highâ€Throughput Deep Sequencing. Journal of Agronomy and Crop Science, 2015, 201, 379-388.	1.7	28
435	Micro <scp>RNA</scp> 156 as a promising tool for alfalfa improvement. Plant Biotechnology Journal, 2015, 13, 779-790.	4.1	131
436	A Novel Arabidopsis MicroRNA Promotes IAA Biosynthesis via the Indole-3-acetaldoxime Pathway by Suppressing SUPERROOT1. Plant and Cell Physiology, 2015, 56, 715-726.	1.5	44
437	Conserved and novel heat stressâ€responsive micro <scp>RNAs</scp> were identified by deep sequencing in <scp><i>S</i></scp> <i>accharina japonica</i> ( <scp>L</scp> aminariales, <scp>P</scp> haeophyta). Plant, Cell and Environment, 2015, 38, 1357-1367.	2.8	52
438	Genome-wide development of novel miRNA-based microsatellite markers of rice (Oryza sativa) for genotyping applications. Molecular Breeding, 2015, 35, 1.	1.0	50
439	Genomewide analysis of small <scp>RNA</scp> s in nonembryogenic and embryogenic tissues of citrus: micro <scp>RNA</scp> â€and si <scp>RNA</scp> â€mediated transcript cleavage involved in somatic embryogenesis. Plant Biotechnology Journal, 2015, 13, 383-394.	4.1	88
440	Identification and characterization of mRNA-like noncoding RNAs in Salvia miltiorrhiza. Planta, 2015, 241, 1131-1143.	1.6	21
441	Identification and characterization of conserved and novel microRNAs in Xanthoceras sorbifolium via deep sequencing. Genes and Genomics, 2015, 37, 281-286.	0.5	2
442	Identification of microRNAs in two species of tomato, Solanum lycopersicum and Solanum habrochaites, by deep sequencing. Journal of Integrative Agriculture, 2015, 14, 42-49.	1.7	7

#	Article	IF	CITATIONS
443	Small RNA sequencing identifies miRNA roles in ovule and fibre development. Plant Biotechnology Journal, 2015, 13, 355-369.	4.1	98
444	Identification of microRNAs differentially expressed involved in male flower development. Functional and Integrative Genomics, 2015, 15, 225-232.	1.4	14
445	MicroRNA expression profiles in conventional and micropropagated Dendrobium officinale. Genes and Genomics, 2015, 37, 315-325.	0.5	6
446	miRNAome analysis associated with anatomic and transcriptomic investigations reveal the polar exhibition of corky split vein in boron deficient Citrus sinensis. Molecular Genetics and Genomics, 2015, 290, 1639-1657.	1.0	8
447	Identification and comparative analysis of differentially expressed miRNAs in leaves of two wheat (Triticum aestivum L.) genotypes during dehydration stress. BMC Plant Biology, 2015, 15, 21.	1.6	76
448	MicroRNA-mediated regulation of gene expression in the response of rice plants to fungal elicitors. RNA Biology, 2015, 12, 847-863.	1.5	116
449	Novel and Recently Evolved MicroRNA Clusters Regulate Expansive <i>F-BOX</i> Gene Networks through Phased Small Interfering RNAs in Wild Diploid Strawberry. Plant Physiology, 2015, 169, 594-610.	2.3	73
450	MicroRNA nomenclature and the need for a revised naming prescription. Briefings in Functional Genomics, 2016, 15, elv026.	1.3	53
451	Silencing of active transposable elements in plants. Current Opinion in Plant Biology, 2015, 27, 67-76.	3.5	124
452	Identification and characterization of cucumber microRNAs in response to Pseudoperonospora cubensis infection. Gene, 2015, 569, 225-232.	1.0	30
453	Genome-wide identification of turnip mosaic virus-responsive microRNAs in non-heading Chinese cabbage by high-throughput sequencing. Gene, 2015, 571, 178-187.	1.0	26
454	Identification and Functional Analysis of MicroRNAs and Their Targets in Platanus acerifolia under Lead (Pb) Stress. International Journal of Molecular Sciences, 2015, 16, 7098-7111.	1.8	25
455	Identification and Characterization of High Temperature Stress Responsive Novel miRNAs in French Bean (Phaseolus vulgaris). Applied Biochemistry and Biotechnology, 2015, 176, 835-849.	1.4	8
457	Genome-wide analysis of small RNAs in the wheat pathogenic fungus Zymoseptoria tritici. Fungal Biology, 2015, 119, 631-640.	1.1	17
458	Evolutionary Patterns and Coevolutionary Consequences of <i>MIRNA</i> Genes and MicroRNA Targets Triggered by Multiple Mechanisms of Genomic Duplications in Soybean. Plant Cell, 2015, 27, 546-562.	3.1	89
459	Comparative expression profiling of miRNAs between the cytoplasmic male sterile line MeixiangA and its maintainer line MeixiangB during rice anther development. Planta, 2015, 241, 109-123.	1.6	55
460	Unique miRNome during anthesis in drought-tolerant indica rice var. Nagina 22. Planta, 2015, 241, 1543-1559.	1.6	35
461	NERF encodes a RING E3 ligase important for drought resistance and enhances the expression of its antisense gene NFYA5 in Arabidopsis. Nucleic Acids Research, 2015, 43, 607-617.	6.5	41

#	Article	IF	CITATIONS
462	Identification of novel and salt-responsive miRNAs to explore miRNA-mediated regulatory network of salt stress response in radish (Raphanus sativus L.). BMC Genomics, 2015, 16, 197.	1.2	110
463	Identification and characterization of microRNAs from Chinese pollination constant non-astringent persimmon using high-throughput sequencing. BMC Plant Biology, 2015, 15, 11.	1.6	52
464	Characterization of miRNAs associated with Botrytis cinerea infection of tomato leaves. BMC Plant Biology, 2015, 15, 1.	1.6	441
465	Transcriptome profiling of root microRNAs reveals novel insights into taproot thickening in radish (Raphanus sativus L.). BMC Plant Biology, 2015, 15, 30.	1.6	24
466	miRVine: a microRNA expression atlas of grapevine based on small RNA sequencing. BMC Genomics, 2015, 16, 393.	1.2	73
467	Stress-induced endogenous siRNAs targeting regulatory intron sequences in <i>Brachypodium</i> . Rna, 2015, 21, 145-163.	1.6	19
468	High throughput sequencing of small RNA component of leaves and inflorescence revealed conserved and novel miRNAs as well as phasiRNA loci in chickpea. Plant Science, 2015, 235, 46-57.	1.7	53
469	Genome-wide analysis reveals dynamic changes in expression of microRNAs during vascular cambium development in Chinese fir, Cunninghamia lanceolata. Journal of Experimental Botany, 2015, 66, 3041-3054.	2.4	37
470	Identification by deep sequencing and profiling of conserved and novel hickory microRNAs involved in the graft process. Plant Biotechnology Reports, 2015, 9, 115-124.	0.9	13
472	Overexpression of potato miR482e enhanced plant sensitivity to <i>Verticillium dahliae</i> infection. Journal of Integrative Plant Biology, 2015, 57, 1078-1088.	4.1	124
473	High-throughput sequencing-based genome-wide identification of microRNAs expressed in developing cotton seeds. Science China Life Sciences, 2015, 58, 778-786.	2.3	10
474	Identification, evolution, and expression partitioning of miRNAs in allopolyploid <i>Brassica napus</i> . Journal of Experimental Botany, 2015, 66, 7241-7253.	2.4	44
475	The microRNAs of Brachypodium. Plant Genetics and Genomics: Crops and Models, 2015, , 129-145.	0.3	0
476	An integrative approach to identify hexaploid wheat miRNAome associated with development and tolerance to abiotic stress. BMC Genomics, 2015, 16, 339.	1.2	25
477	Functional marker development of miR1511-InDel and allelic diversity within the genus Glycine. BMC Genomics, 2015, 16, 467.	1.2	8
478	The liverwort <i><scp>P</scp>ellia endiviifolia</i> shares microtranscriptomic traits that are common to green algae and land plants. New Phytologist, 2015, 206, 352-367.	3.5	84
479	Extensive Families of miRNAs and <i>PHAS</i> Loci in Norway Spruce Demonstrate the Origins of Complex phasiRNA Networks in Seed Plants. Molecular Biology and Evolution, 2015, 32, 2905-2918.	3.5	141
480	MicroRNAs and targets in senescent litchi fruit during ambient storage and post-cold storage shelf life. BMC Plant Biology, 2015, 15, 181.	1.6	37

	CHAIGH	INEPORT	
#	Article	IF	CITATIONS
481	Discovering MicroRNAs and Their Targets in Plants. Critical Reviews in Plant Sciences, 2015, 34, 553-571.	2.7	12
482	Ectopic expression of LjmiR156 delays flowering, enhances shoot branching, and improves forage quality in alfalfa. Plant Biotechnology Reports, 2015, 9, 379-393.	0.9	41
483	Novel and conserved heat-responsive microRNAs in wheat (Triticum aestivum L.). Functional and Integrative Genomics, 2015, 15, 323-348.	1.4	121
484	Genome-Wide Characterization of Rice Black Streaked Dwarf Virus-Responsive MicroRNAs in Rice Leaves and Roots by Small RNA and Degradome Sequencing. Plant and Cell Physiology, 2015, 56, 688-699.	1.5	44
485	A system biology approach for understanding the miRNA regulatory network in colon rectal cancer. International Journal of Data Mining and Bioinformatics, 2015, 11, 1.	0.1	2
486	Differential expression of <scp>miRNAs</scp> and their target genes in senescing leaves and siliques: insights from deep sequencing of small <scp>RNAs</scp> and cleaved target <scp>RNAs</scp> . Plant, Cell and Environment, 2015, 38, 188-200.	2.8	69
487	De novo transcriptome assembly, gene annotation, marker development, and miRNA potential target genes validation under abiotic stresses in Oenanthe javanica. Molecular Genetics and Genomics, 2015, 290, 671-683.	1.0	48
488	Prediction and characterization of Tomato leaf curl New Delhi virus (ToLCNDV) responsive novel microRNAs in Solanum lycopersicum. Virus Research, 2015, 195, 183-195.	1.1	40
489	Identification of conserved and novel microRNAs in Catharanthus roseus by deep sequencing and computational prediction of their potential targets. Gene, 2015, 554, 181-195.	1.0	33
490	Differential profiling analysis of miRNAs reveals a regulatory role in low N stress response of Populus. Functional and Integrative Genomics, 2015, 15, 93-105.	1.4	30
491	Genome-wide DNA Methylation Profiles and Their Relationships with mRNA and the microRNA Transcriptome in Bovine Muscle Tissue (Bos taurine). Scientific Reports, 2015, 4, 6546.	1.6	97
492	Genome-wide identification of novel long non-coding RNAs in Populus tomentosa tension wood, opposite wood and normal wood xylem by RNA-seq. Planta, 2015, 241, 125-143.	1.6	109
493	Analysis of phytoplasma-responsive sRNAs provide insight into the pathogenic mechanisms of mulberry yellow dwarf disease. Scientific Reports, 2014, 4, 5378.	1.6	54
494	Small <scp>RNA</scp> deep sequencing identifies novel and saltâ€stressâ€regulated <scp>microRNAs</scp> from roots of <i>Medicago sativa</i> and <i>Medicago truncatula</i> . Physiologia Plantarum, 2015, 154, 13-27.	2.6	46
495	Efficient transformation and artificial mi <scp>RNA</scp> gene silencing in <i><scp>L</scp>emna minor</i> . Plant Biology, 2015, 17, 59-65.	1.8	53
496	MicroRNAs Sequencing for Understanding the Genetic Regulation of Plant Genomes. , 2016, , .		3
497	Characterization and comparison of flower bud microRNAs from yellow-horn species. Genetics and Molecular Research, 2016, 15, .	0.3	4
498	[Letter to the Editor] Comparison of small RNA next-generation sequencing with and without isolation of small RNA fraction. BioTechniques, 2016, 60, 273-8.	0.8	5

#	Article	IF	CITATIONS
499	Computational prediction and experimental validation of a novel miRNA in Suaeda maritima, a halophyte. Genetics and Molecular Research, 2016, 15, .	0.3	2
500	Assessing the Gene Content of the Megagenome: Sugar Pine ( <i>Pinus lambertiana</i> ). G3: Genes, Genomes, Genetics, 2016, 6, 3787-3802.	0.8	51
501	Identification and Target Prediction of MicroRNAs in Ulmus pumila L. Seedling Roots under Salt Stress by High-Throughput Sequencing. Forests, 2016, 7, 318.	0.9	3
502	Identification and Functional Analysis of microRNAs Involved in the Anther Development in Cotton Genic Male Sterile Line Yu98-8A. International Journal of Molecular Sciences, 2016, 17, 1677.	1.8	14
503	Identification and characterization of miRNAs and targets in flax (Linum usitatissimum) under saline, alkaline, and saline-alkaline stresses. BMC Plant Biology, 2016, 16, 124.	1.6	57
504	MicroRNA from Moringa oleifera: Identification by High Throughput Sequencing and Their Potential Contribution to Plant Medicinal Value. PLoS ONE, 2016, 11, e0149495.	1.1	47
505	Unveiling the Micronome of Cassava (Manihot esculenta Crantz). PLoS ONE, 2016, 11, e0147251.	1.1	20
506	Identification and Expression Analyses of miRNAs from Two Contrasting Flower Color Cultivars of Canna by Deep Sequencing. PLoS ONE, 2016, 11, e0147499.	1.1	20
507	Identification of Novel and Conserved miRNAs in Leaves of In vitro Grown Citrus reticulata "Lugan― Plantlets by Solexa Sequencing. Frontiers in Plant Science, 2015, 6, 1212.	1.7	20
508	Genome-Wide Small RNA Analysis of Soybean Reveals Auxin-Responsive microRNAs that are Differentially Expressed in Response to Salt Stress in Root Apex. Frontiers in Plant Science, 2015, 6, 1273.	1.7	57
509	MicroRNA Regulatory Mechanisms on Citrus sinensis leaves to Magnesium-Deficiency. Frontiers in Plant Science, 2016, 7, 201.	1.7	35
510	Small RNA Profiles of the Rice PTGMS Line Wuxiang S Reveal miRNAs Involved in Fertility Transition. Frontiers in Plant Science, 2016, 7, 514.	1.7	24
511	Identification of microRNAs Involved in Regeneration of the Secondary Vascular System in Populus tomentosa Carr. Frontiers in Plant Science, 2016, 7, 724.	1.7	29
512	Identification of microRNAs and Their Target Genes Explores miRNA-Mediated Regulatory Network of Cytoplasmic Male Sterility Occurrence during Anther Development in Radish (Raphanus sativus L.). Frontiers in Plant Science, 2016, 7, 1054.	1.7	40
513	Identification of Ice Plant (Mesembryanthemum crystallinum L.) MicroRNAs Using RNA-Seq and Their Putative Roles in High Salinity Responses in Seedlings. Frontiers in Plant Science, 2016, 7, 1143.	1.7	47
514	High-Throughput MicroRNA and mRNA Sequencing Reveals That MicroRNAs May Be Involved in Melatonin-Mediated Cold Tolerance in Citrullus lanatus L Frontiers in Plant Science, 2016, 7, 1231.	1.7	46
515	Genome-Wide Identification, Characterization and Expression Analysis of the TCP Gene Family in Prunus mume. Frontiers in Plant Science, 2016, 7, 1301.	1.7	41
516	Identification and Comparative Analysis of microRNA in Wheat (Triticum aestivum L.) Callus Derived from Mature and Immature Embryos during In vitro Culture. Frontiers in Plant Science, 2016, 7, 1302.	1.7	27

#	Article	IF	CITATIONS
517	Comparative Analysis of miRNAs and Their Target Transcripts between a Spontaneous Late-Ripening Sweet Orange Mutant and Its Wild-Type Using Small RNA and Degradome Sequencing. Frontiers in Plant Science, 2016, 7, 1416.	1.7	23
518	The Influence of Genotype and Environment on Small RNA Profiles in Grapevine Berry. Frontiers in Plant Science, 2016, 7, 1459.	1.7	40
519	Comparative Profiling of miRNAs and Target Gene Identification in Distant-Grafting between Tomato and Lycium (Goji Berry). Frontiers in Plant Science, 2016, 7, 1475.	1.7	29
520	High-Throughput Sequencing Reveals H2O2 Stress-Associated MicroRNAs and a Potential Regulatory Network in Brachypodium distachyon Seedlings. Frontiers in Plant Science, 2016, 7, 1567.	1.7	16
521	Identification and Profiling of microRNAs Expressed in Elongating Cotton Fibers Using Small RNA Deep Sequencing. Frontiers in Plant Science, 2016, 7, 1722.	1.7	12
522	Identification of miRNAs Affecting the Establishment of Brassica Alboglabra Seedling. Frontiers in Plant Science, 2016, 7, 1760.	1.7	10
523	Identification of miRNAs and their targets involved in the secondary metabolic pathways of Mentha spp Computational Biology and Chemistry, 2016, 64, 154-162.	1.1	58
524	Genomeâ€wide identification of <scp>microRNAs</scp> responding to early stages of phosphate deficiency in maize. Physiologia Plantarum, 2016, 157, 161-174.	2.6	18
525	Small <scp>RNA</scp> and degradome profiling reveals important roles for <scp>microRNAs</scp> and their targets in tea plant response to drought stress. Physiologia Plantarum, 2016, 158, 435-451.	2.6	51
526	Genomeâ€wide identification and characterization of <i>Eutrema salsugineum</i> <scp>microRNAs</scp> for salt tolerance. Physiologia Plantarum, 2016, 157, 453-468.	2.6	13
527	A naìve Bayesian classifier for identifying plant micro <scp>RNA</scp> s. Plant Journal, 2016, 86, 481-492.	2.8	13
528	miRNA863-3p sequentially targets negative immune regulator ARLPKs and positive regulator SERRATE upon bacterial infection. Nature Communications, 2016, 7, 11324.	5.8	66
529	Deep sequencing of wheat sRNA transcriptome reveals distinct temporal expression pattern of miRNAs in response to heat, light and UV. Scientific Reports, 2016, 6, 39373.	1.6	51
530	The miRNAome of durum wheat: isolation and characterisation of conserved and novel microRNAs and their target genes. BMC Genomics, 2016, 17, 505.	1.2	44
531	A novel comprehensive wheat miRNA database, including related bioinformatics software. Current Plant Biology, 2016, 7-8, 31-33.	2.3	19
532	Genome-wide Investigation of microRNAs and Their Targets in Brassica rapa ssp. pekinensis Root with Plasmodiophora brassicae Infection. Horticultural Plant Journal, 2016, 2, 209-216.	2.3	16
533	A transcriptome-wide, organ-specific regulatory map of Dendrobium officinale, an important traditional Chinese orchid herb. Scientific Reports, 2016, 6, 18864.	1.6	44
534	Identification of novel miRNAs from drought tolerant rice variety Nagina 22. Scientific Reports, 2016, 6, 30786.	1.6	82

#	Article	IF	CITATIONS
535	Small RNA profiles in soybean primary root tips under water deficit. BMC Systems Biology, 2016, 10, 126.	3.0	33
536	High-throughput sequencing and degradome analysis reveal altered expression of miRNAs and their targets in a male-sterile cybrid pummelo (Citrus grandis). BMC Genomics, 2016, 17, 591.	1.2	36
537	A highly specific micro <scp>RNA</scp> â€mediated mechanism silences <scp>LTR</scp> retrotransposons of strawberry. Plant Journal, 2016, 85, 70-82.	2.8	31
538	Identification and functional characterization of soybean root hair micro <scp>RNA</scp> s expressed in response to <i><scp>B</scp>radyrhizobium japonicum</i> infection. Plant Biotechnology Journal, 2016, 14, 332-341.	4.1	40
539	Shoot bending promotes flower bud formation by mi <scp>RNA</scp> â€mediated regulation in apple ( <i><scp>M</scp>alus domestica </i> <scp>B</scp> orkh.). Plant Biotechnology Journal, 2016, 14, 749-770.	4.1	69
540	RNA-seq analysis in forest tree species: bioinformatic problems and solutions. Tree Genetics and Genomes, 2016, 12, 1.	0.6	25
541	Characterization and expression analysis of conserved miRNAs and their targets in Pinus densata. Biologia Plantarum, 2016, 60, 427-434.	1.9	6
542	Microsynteny and phylogenetic analysis of tandemly organised miRNA families across five members of Brassicaceae reveals complex retention and loss history. Plant Science, 2016, 247, 35-48.	1.7	19
543	Differential miRNA expression in maize ear subjected to shading tolerance. Acta Physiologiae Plantarum, 2016, 38, 1.	1.0	5
544	Dissection of allelic interactions among Pto-miR257 and its targets and their effects on growth and wood properties in Populus. Heredity, 2016, 117, 73-83.	1.2	7
545	Genome-wide identification and characterization of novel lncRNAs in Populus under nitrogen deficiency. Molecular Genetics and Genomics, 2016, 291, 1663-1680.	1.0	117
546	Deep-sequence profiling of miRNAs and their target prediction in Monotropa hypopitys. Plant Molecular Biology, 2016, 91, 441-458.	2.0	5
547	Small RNA sequencing and degradome analysis of developing fibers of short fiber mutants Ligon-lintles-1 (Li 1 ) and â^2 (Li 2 ) revealed a role for miRNAs and their targets in cotton fiber elongation. BMC Genomics, 2016, 17, 360.	1.2	22
548	Analysis of high iron rice lines reveals new miRNAs that target iron transporters in roots. Journal of Experimental Botany, 2016, 67, 5811-5824.	2.4	35
549	Identification and differential regulation of microRNAs in response to methyl jasmonate treatment in Lycoris aurea by deep sequencing. BMC Genomics, 2016, 17, 789.	1.2	25
550	Genome-wide identification of microRNAs in pomegranate (Punica granatum L.) by high-throughput sequencing. BMC Plant Biology, 2016, 16, 122.	1.6	57
551	Differential micro ribonucleic acid expression profiling in ovarian endometrioma with leuprolide acetate treatment. Journal of Obstetrics and Gynaecology Research, 2016, 42, 1734-1743.	0.6	7
552	Comparative analysis of microRNAs and putative target genes in hybrid clone Paulownia â€~yuza 1' under drought stress. Acta Physiologiae Plantarum, 2016, 38, 1.	1.0	3

#	Article	IF	CITATIONS
553	Genome-wide mining for microRNAs and their targets in Betula luminifera using high-throughput sequencing and degradome analyses. Tree Genetics and Genomes, 2016, 12, 1.	0.6	10
554	Genome-Wide Investigation of MicroRNAs and Their Targets in Response to Freezing Stress in <i>Medicago sativa</i> L., Based on High-Throughput Sequencing. G3: Genes, Genomes, Genetics, 2016, 6, 755-765.	0.8	48
555	Identification of microRNAs and their targets in Paulownia fortunei plants free from phytoplasma pathogen after methyl methane sulfonate treatment. Biochimie, 2016, 127, 271-280.	1.3	12
556	Systems Biology Approaches to Improve Drought Stress Tolerance in Plants: State of the Art and Future Challenges. , 2016, , 433-471.		1
557	Comparative analysis of microRNA profiles of rice anthers between cool-sensitive and cool-tolerant cultivars under cool-temperature stress. Genes and Genetic Systems, 2016, 91, 97-109.	0.2	9
558	Genome-scale mRNA and small RNA transcriptomic insights into initiation of citrus apomixis. Journal of Experimental Botany, 2016, 67, 5743-5756.	2.4	36
559	Identification and characterization of microRNAs in Humulus lupulus using high-throughput sequencing and their response to Citrus bark cracking viroid (CBCVd) infection. BMC Genomics, 2016, 17, 919.	1.2	26
560	Expression Variations of miRNAs and mRNAs in Rice ( <i>Oryza sativa</i> ). Genome Biology and Evolution, 2016, 8, 3529-3544.	1.1	32
561	<i>In silico</i> analysis of microRNA binding to the genome of <i>Beet curly top Iran virus</i> in tomato. Archives of Phytopathology and Plant Protection, 2016, 49, 434-444.	0.6	3
562	Illumina microRNA profiles reveal the involvement of miR397a in Citrus adaptation to long-term boron toxicity via modulating secondary cell-wall biosynthesis. Scientific Reports, 2016, 6, 22900.	1.6	41
563	Identification of chilling-responsive microRNAs and their targets in vegetable soybean (Glycine max L.). Scientific Reports, 2016, 6, 26619.	1.6	44
564	Transcriptome-Wide Comparative Analysis of microRNA Profiles in the Telogen Skins of Liaoning Cashmere Goats ( <i>Capra hircus</i> ) and Fine-Wool Sheep ( <i>Ovis aries</i> ) by Solexa Deep Sequencing. DNA and Cell Biology, 2016, 35, 696-705.	0.9	16
565	Identification and characterization of microRNAs in maize endosperm response to exogenous sucrose using small RNA sequencing. Genomics, 2016, 108, 216-223.	1.3	12
566	Identification of drought-responsive microRNAs and their targets in Ammopiptanthus mongolicus by using high-throughput sequencing. Scientific Reports, 2016, 6, 34601.	1.6	38
567	Control of cell proliferation by microRNAs in plants. Current Opinion in Plant Biology, 2016, 34, 68-76.	3.5	60
568	Novel functional microRNAs from virus-free and infected Vitis vinifera plants under water stress. Scientific Reports, 2016, 6, 20167.	1.6	81
569	Transposon-derived small RNA is responsible for modified function of WRKY45 locus. Nature Plants, 2016, 2, 16016.	4.7	79
570	Identification of miRNAs and their targets in wild tomato at moderately and acutely elevated temperatures by high-throughput sequencing and degradome analysis. Scientific Reports, 2016, 6, 33777.	1.6	43

#	Article	IF	CITATIONS
571	Exploring miRNAs involved in blue/UV-A light response in Brassica rapa reveals special regulatory mode during seedling development. BMC Plant Biology, 2016, 16, 111.	1.6	28
572	Genome-Wide Analysis of NBS-LRR Genes in Sorghum Genome Revealed Several Events Contributing to NBS-LRR Gene Evolution in Grass Species. Evolutionary Bioinformatics, 2016, 12, EBO.S36433.	0.6	34
573	The walnut ( <i>Juglans regia</i> ) genome sequence reveals diversity in genes coding for the biosynthesis of nonâ€structural polyphenols. Plant Journal, 2016, 87, 507-532.	2.8	233
574	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.	1.2	25
575	Transcriptome deep sequencing, identification of novel microRNAs and validation under drought stress in turmeric (Curcuma longa L.). Plant Biotechnology Reports, 2016, 10, 227-240.	0.9	10
576	Identification of microRNAs, phasiRNAs and Their Targets in Pineapple. Tropical Plant Biology, 2016, 9, 176-186.	1.0	32
577	Tight regulation of the interaction between Brassica napus and Sclerotinia sclerotiorum at the microRNA level. Plant Molecular Biology, 2016, 92, 39-55.	2.0	52
578	Discovery and profiling of microRNAs and their targets in Paulownia â€~Yuza 1' plants via high-throughput sequencing and degradome analysis. Genes and Genomics, 2016, 38, 757-766.	0.5	4
579	Combined small RNA and degradome sequencing to identify miRNAs and their targets in response to drought in foxtail millet. BMC Genetics, 2016, 17, 57.	2.7	56
580	Identification of miRNAs and their targets by high-throughput sequencing and degradome analysis in cytoplasmic male-sterile line NJCMS1A and its maintainer NJCMS1B of soybean. BMC Genomics, 2016, 17, 24.	1.2	43
581	Genomic profiling of exogenous abscisic acid-responsive microRNAs in tomato (Solanum) Tj ETQq0 0 0 rgBT /Ove	erlock 10 T 1.2	f 50 342 Td
582	Identification of miRNAs and their targets through high-throughput sequencing and degradome analysis in male and female Asparagus officinalis. BMC Plant Biology, 2016, 16, 80.	1.6	31
583	Novel drought-responsive regulatory coding and non-coding transcripts from Oryza Sativa L Genes and Genomics, 2016, 38, 949-960.	0.5	9
584	High-resolution identification and abundance profiling of cassava (Manihot esculenta Crantz) microRNAs. BMC Genomics, 2016, 17, 85.	1.2	22
585	Small RNA changes in synthetic Brassica napus. Planta, 2016, 244, 607-622.	1.6	13
586	The genome of the seagrass Zostera marina reveals angiosperm adaptation to the sea. Nature, 2016, 530, 331-335.	13.7	460
587	Association genetics in Populus reveals the interactions between Pto-miR160a and its target Pto-ARF16. Molecular Genetics and Genomics, 2016, 291, 1069-1082.	1.0	22
588	The Naming of Names: Guidelines for Gene Nomenclature in <i>Marchantia</i> . Plant and Cell Physiology, 2016, 57, 257-261.	1.5	60

#	Article	IF	CITATIONS
589	PlanTE-MIR DB: a database for transposable element-related microRNAs in plant genomes. Functional and Integrative Genomics, 2016, 16, 235-242.	1.4	29
590	Genetics and Genomics of Brachypodium. Plant Genetics and Genomics: Crops and Models, 2016, , .	0.3	22
591	Identification and characterization of microRNAs in turmeric (Curcuma longa L.) responsive to infection with the pathogenic fungus Pythium aphanidermatum. Physiological and Molecular Plant Pathology, 2016, 93, 119-128.	1.3	11
592	Phylogenetic tree-informed microRNAome analysis uncovers conserved and lineage-specific miRNAs in <i>Camellia</i> during floral organ development. Journal of Experimental Botany, 2016, 67, 2641-2653.	2.4	33
593	Dehydration-responsive miRNAs in foxtail millet: genome-wide identification, characterization and expression profiling. Planta, 2016, 243, 749-766.	1.6	35
594	Identification and characterization of microRNAs in the plant parasitic root-knot nematode Meloidogyne incognita using deep sequencing. Functional and Integrative Genomics, 2016, 16, 127-142.	1.4	22
595	Profiling and Characterization of Small RNAs in the Liverwort, <i>Marchantia polymorpha</i> , Belonging to the First Diverged Land Plants. Plant and Cell Physiology, 2016, 57, 359-372.	1.5	68
596	Unravelling the complexity of microRNA-mediated gene regulation in black pepper (Piper nigrum L.) using high-throughput small RNA profiling. Plant Cell Reports, 2016, 35, 53-63.	2.8	30
597	Identification and bioinformatics analysis of microRNAs from the sporophyte and gametophyte of Pyropia haitanensis. Chinese Journal of Oceanology and Limnology, 2016, 34, 451-459.	0.7	0
598	Determination of the precise sequences of computationally predicted miRNAs in Citrus reticulata by miR-RACE and characterization of the related target genes using RLM-RACE. Gene, 2016, 575, 498-505.	1.0	3
599	Discovery of microRNAs and transcript targets related to witches' broom disease in Paulownia fortunei by high-throughput sequencing and degradome approach. Molecular Genetics and Genomics, 2016, 291, 181-191.	1.0	21
600	Characterization of drought- and heat-responsive microRNAs in switchgrass. Plant Science, 2016, 242, 214-223.	1.7	81
601	Growth-Regulating Factors, A Transcription Factor Family Regulating More than Just Plant Growth. , 2016, , 269-280.		8
602	Multiple garlic ( Allium sativum L.) microRNAs regulate the immunity against the basal rot fungus Fusarium oxysporum f. sp. Cepae. Plant Science, 2017, 257, 9-21.	1.7	31
603	MicroRNA annotation of plant genomes â^ Do it right or not at all. BioEssays, 2017, 39, 1600113.	1.2	50
604	miR393-Mediated Auxin Signaling Regulation is Involved in Root Elongation Inhibition in Response to Toxic Aluminum Stress in Barley. Plant and Cell Physiology, 2017, 58, pcw211.	1.5	57
605	Genome-wide analysis of miRNAs and Tasi-RNAs in Zea mays in response to phosphate deficiency. Functional and Integrative Genomics, 2017, 17, 335-351.	1.4	34
606	Identification and profiling of conserved and novel microRNAs involved in oil and oleic acid production during embryogenesis in Carya cathayensis Sarg. Functional and Integrative Genomics, 2017, 17, 365-373.	1.4	7

#ARTICLEIFCITATIONS607Identification and characterization of novel microRNAs for fruit development and quality in hot<br/>pepper (Capsicum annuum L). Gene 2017, 608, 66-72.1.058608Conservation and diversification of the miR166 family in soybean and potential roles of newly1.666

**CITATION REPORT** 

609 Expression of microRNAs during female inflorescence development in African oil palm (Elaeis) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 662

610	miRCat2: accurate prediction of plant and animal microRNAs from next-generation sequencing datasets. Bioinformatics, 2017, 33, 2446-2454.	1.8	49
611	Genome-wide identification of cucumber green mottle mosaic virus-responsive microRNAs in watermelon. Archives of Virology, 2017, 162, 2591-2602.	0.9	27
612	Genome of Paulownia (Paulownia fortunei) illuminates the related transcripts, miRNA and proteins for salt resistance. Scientific Reports, 2017, 7, 1285.	1.6	13
613	<i>Puccinia striiformis</i> f. sp. <i>tritici</i> mi <scp>croRNA</scp> â€like <scp>RNA</scp> 1 ( <i>Pst</i> â€milR1), an important pathogenicity factor of <i>Pst</i> , impairs wheat resistance to <i>Pst</i> by suppressing the wheat pathogenesisâ€related 2 gene. New Phytologist, 2017, 215, 338-350.	3.5	168
614	Growing Diversity of Plant MicroRNAs and MIR-Derived Small RNAs. RNA Technologies, 2017, , 49-67.	0.2	8
615	In silico prediction of miRNAs targeting ToLCV and their regulation in susceptible and resistant tomato plants. Australasian Plant Pathology, 2017, 46, 379-386.	0.5	9
616	The small RNA repertoire in phloem tissue of three Vitis vinifera cultivars. Plant Gene, 2017, 10, 60-73.	1.4	15
617	Evolutionary Footprints Reveal Insights into Plant MicroRNA Biogenesis. Plant Cell, 2017, 29, 1248-1261.	3.1	69
618	The miRNAome of Catharanthus roseus: identification, expression analysis, and potential roles of microRNAs in regulation of terpenoid indole alkaloid biosynthesis. Scientific Reports, 2017, 7, 43027.	1.6	39
620	Identification and characterization of durum wheat microRNAs in leaf and root tissues. Functional and Integrative Genomics, 2017, 17, 583-598.	1.4	28
621	Characterization of the polyphenol oxidase gene family reveals a novel microRNA involved in posttranscriptional regulation of PPOs in Salvia miltiorrhiza. Scientific Reports, 2017, 7, 44622.	1.6	33
622	Identification and dynamic expression profiling of microRNAs and target genes of Paulownia tomentosa in response to Paulownia witches' broom disease. Acta Physiologiae Plantarum, 2017, 39, 1.	1.0	10
623	Plant genome and transcriptome annotations: from misconceptions to simple solutions. Briefings in Bioinformatics, 2018, 19, bbw135.	3.2	62
624	Comparative analysis of cadmium responsive microRNAs in roots of two Ipomoea aquatica Forsk. cultivars with different cadmium accumulation capacities. Plant Physiology and Biochemistry, 2017, 111, 329-339.	2.8	28
625	Integrating transcriptome and microRNA analysis identifies genes and microRNAs for AHO-induced systemic acquired resistance in N. tabacum. Scientific Reports, 2017, 7, 12504.	1.6	36

# 626	ARTICLE Data on identification of conserved and novel miRNAs in Elettaria cardamomum. Data in Brief, 2017, 14, 789-792.	IF 0.5	Citations
627	Genome-wide Identification of microRNAs that Respond to Drought Stress in Seedlings of Tertiary Relict Ammopiptanthus mongolicus. Horticultural Plant Journal, 2017, 3, 209-218.	2.3	12
628	MicroRNAs Associated with Tuberous Root Development. Compendium of Plant Genomes, 2017, , 121-136.	0.3	0
629	Genome-wide identification of microRNAs responsive to Ectropis oblique feeding in tea plant (Camellia) Tj ETQq1	1 0.78431 1.6	4.rgBT /Ove 71
630	Detecting and characterizing microRNAs of diverse genomic origins via miRvial. Nucleic Acids Research, 2017, 45, e176-e176.	6.5	6
631	Comparative analysis between low- and high-cadmium-accumulating cultivars of Brassica parachinensis to identify difference of cadmium-induced microRNA and their targets. Plant and Soil, 2017, 420, 223-237.	1.8	28
632	Polyphenol Oxidases (PPOs) in Plants. , 2017, , .		21
633	Advances in Polyphenol Oxidase (PPO) Research. , 2017, , 107-131.		0
634	Small RNA profiles from Panax notoginseng roots differing in sizes reveal correlation between miR156 abundances and root biomass levels. Scientific Reports, 2017, 7, 9418.	1.6	21
635	mi <scp>RP</scp> ursuit—a pipeline for automated analyses of small <scp>RNA</scp> s in model and nonmodel plants. FEBS Letters, 2017, 591, 2261-2268.	1.3	9
636	Identification and Characterization of microRNAs from Saccharum officinarum L by Deep Sequencing. Tropical Plant Biology, 2017, 10, 134-150.	1.0	4
637	Functional Analysis of Differentially Expressed MicroRNAs Associated with Drought Stress in Diploid and Tetraploid Paulownia fortunei. Plant Molecular Biology Reporter, 2017, 35, 389-398.	1.0	3
638	Bioinformatic identification and expression analysis of new microRNAs from wheat (Triticum) Tj ETQq0 0 0 rgBT /C	Verlock 1 1.0	0 Tf 50 262 14
639	Characterization of miRNAs responsive to exogenous ethylene in grapevine berries at whole genome level. Functional and Integrative Genomics, 2017, 17, 213-235.	1.4	19
640	Genome-wide analysis of microRNA targeting impacted by SNPs in cucumber genome. BMC Genomics, 2017, 18, 275.	1.2	12
641	Profiling of microRNAs in wild type and early flowering transgenic Chrysanthemum morifolium by deep sequencing. Plant Cell, Tissue and Organ Culture, 2017, 128, 283-301.	1.2	8
642	Drought stress-induced changes of microRNAs in diploid and autotetraploid Paulownia tomentosa. Genes and Genomics, 2017, 39, 77-86.	0.5	17
643	Identification of anthocyanin biosynthesis related microRNAs in a distinctive Chinese radish (Raphanus sativus L.) by high-throughput sequencing. Molecular Genetics and Genomics, 2017, 292, 215-229.	1.0	35

#	Article	IF	CITATIONS
644	Uncovering leaf rust responsive miRNAs in wheat (Triticum aestivum L.) using high-throughput sequencing and prediction of their targets through degradome analysis. Planta, 2017, 245, 161-182.	1.6	48
645	microRNAs differentially modulated in response to heat and drought stress in durum wheat cultivars with contrasting water use efficiency. Functional and Integrative Genomics, 2017, 17, 293-309.	1.4	44
646	"Mirador―on the potential role of miRNAs in synergy of light and heat networks. Indian Journal of Plant Physiology, 2017, 22, 587-607.	0.8	10
647	A comparative survey of small RNA and their targets in grapevine embryogenic callus cultures and young leaves. Acta Horticulturae, 2017, , 329-336.	0.1	1
648	High throughput deep sequencing reveals the important roles of microRNAs during sweetpotato storage at chilling temperature. Scientific Reports, 2017, 7, 16578.	1.6	20
649	MicroRNAs: potential target for genome editing in plants for traits improvement. Indian Journal of Plant Physiology, 2017, 22, 530-548.	0.8	13
650	miRNA. , 2017, , 329-343.		2
651	Genome-wide expression analysis of transcripts, microRNAs, and the degradome in Paulownia tomentosa under drought stress. Tree Genetics and Genomes, 2017, 13, 1.	0.6	4
652	MicroRNA expression profiles in the emerging tillers and inflorescence of switchgrass, a major feedstock for biofuel production. Indian Journal of Plant Physiology, 2017, 22, 558-565.	0.8	4
653	In Silico Analysis of Small RNAs Suggest Roles for Novel and Conserved miRNAs in the Formation of Epigenetic Memory in Somatic Embryos of Norway Spruce. Frontiers in Physiology, 2017, 8, 674.	1.3	46
654	Artificial MicroRNA-Based Specific Gene Silencing of Grain Hardness Genes in Polyploid Cereals Appeared to Be Not Stable Over Transgenic Plant Generations. Frontiers in Plant Science, 2016, 7, 2017.	1.7	25
655	A Comprehensive Prescription for Plant miRNA Identification. Frontiers in Plant Science, 2016, 7, 2058.	1.7	46
656	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.	1.7	69
657	Identification of Submergence-Responsive MicroRNAs and Their Targets Reveals Complex MiRNA-Mediated Regulatory Networks in Lotus (Nelumbo nucifera Gaertn). Frontiers in Plant Science, 2017, 8, 6.	1.7	25
658	Development of Incompletely Fused Carpels in Maize Ovary Revealed by miRNA, Target Gene and Phytohormone Analysis. Frontiers in Plant Science, 2017, 8, 463.	1.7	12
659	Identification of MicroRNA Targets of Capsicum spp. Using MiRTrans—a Trans-Omics Approach. Frontiers in Plant Science, 2017, 8, 495.	1.7	5
660	Small RNA and Transcriptome Sequencing Reveal a Potential miRNA-Mediated Interaction Network That Functions during Somatic Embryogenesis in Lilium pumilum DC. Fisch Frontiers in Plant Science, 2017, 8, 566.	1.7	44
661	Transcriptome-Wide Analysis of Botrytis elliptica Responsive microRNAs and Their Targets in Lilium Regale Wilson by High-Throughput Sequencing and Degradome Analysis. Frontiers in Plant Science, 2017, 8, 753.	1.7	19

#	Article	IF	CITATIONS
662	Small RNA-Sequencing Links Physiological Changes and RdDM Process to Vegetative-to-Floral Transition in Apple. Frontiers in Plant Science, 2017, 8, 873.	1.7	27
663	Identification and Characterization of miRNA Transcriptome in Asiatic Cotton (Gossypium arboreum) Using High Throughput Sequencing. Frontiers in Plant Science, 2017, 8, 969.	1.7	15
664	Identification of Conserved and Novel MicroRNAs in Blueberry. Frontiers in Plant Science, 2017, 8, 1155.	1.7	26
665	Abiotic Stress Responsive miRNA-Target Network and Related Markers (SNP, SSR) in Brassica juncea. Frontiers in Plant Science, 2017, 8, 1943.	1.7	39
666	Salicylic Acid Perturbs sRNA-Gibberellin Regulatory Network in Immune Response of Potato to Potato virus Y Infection. Frontiers in Plant Science, 2017, 8, 2192.	1.7	41
667	miRNAs involved in the development and differentiation of fertile and sterile flowers in Viburnum macrocephalum f. keteleeri. BMC Genomics, 2017, 18, 783.	1.2	9
668	Genome-Wide Profiling of Small RNAs and Degradome Revealed Conserved Regulations of miRNAs on Auxin-Responsive Genes during Fruit Enlargement in Peaches. International Journal of Molecular Sciences, 2017, 18, 2599.	1.8	28
669	Roles of Non-Coding RNA in Sugarcane-Microbe Interaction. Non-coding RNA, 2017, 3, 25.	1.3	6
670	Combined Analysis of mRNAs and miRNAs to Identify Genes Related to Biological Characteristics of Autotetraploid Paulownia. Forests, 2017, 8, 501.	0.9	1
671	Detecting the Candidate Gender Determinants by Bioinformatic Prediction of miRNAs and Their Targets from Transcriptome Sequences of the Male and Female Flowers in <i> Salix suchowensis</i> . BioMed Research International, 2017, 2017, 1-9.	0.9	1
672	Discovery of MicroRNAs and Their Target Genes Related to Drought in <i>Paulownia</i> "Yuza 1―by High-Throughput Sequencing. International Journal of Genomics, 2017, 2017, 1-11.	0.8	4
673	Mapping the microRNA Expression Profiles in Glyoxalase Overexpressing Salinity Tolerant Rice. Current Genomics, 2017, 19, 21-35.	0.7	9
674	Identification and expression profiling of microRNAs involved in the stigma exsertion under high-temperature stress in tomato. BMC Genomics, 2017, 18, 843.	1.2	42
675	Identification of microRNAs in Response to Drought in Common Wild Rice (Oryza rufipogon Griff.) Shoots and Roots. PLoS ONE, 2017, 12, e0170330.	1.1	45
676	Durum wheat miRNAs in response to nitrogen starvation at the grain filling stage. PLoS ONE, 2017, 12, e0183253.	1.1	55
677	Identification of Viscum album L. miRNAs and prediction of their medicinal values. PLoS ONE, 2017, 12, e0187776.	1.1	18
678	Identification of drought-responsive miRNAs and physiological characterization of tea plant (Camellia) Tj ETQq0 (	0 0 rgBT /0 1.6	Overlock 10 T

679	Genome-wide analysis of miRNAs in Carya cathayensis. BMC Plant Biology, 2017, 17, 228.	1.6	11
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#	Article	IF	CITATIONS
680	Small RNA profiling for identification of miRNAs involved in regulation of saponins biosynthesis in Chlorophytum borivilianum. BMC Plant Biology, 2017, 17, 265.	1.6	20
681	Conservation and divergence of small RNA pathways and microRNAs in land plants. Genome Biology, 2017, 18, 158.	3.8	91
682	Identification and characterisation of a previously unknown drought toleranceâ€associated micro RNA in barley. Plant Journal, 2018, 95, 138-149.	2.8	19
683	Analysis of <i><scp>RDR</scp>1</i> / <i><scp>RDR</scp>2</i> / <i><scp>RDR</scp>6</i> â€independent small <scp>RNA</scp> s in <i>Arabidopsis thaliana</i> improves <i><scp>MIRNA</scp></i> annotations and reveals unexplained types of short interfering <scp>RNA</scp> loci. Plant Journal, 2018, 94, 1051-1063.	2.8	27
684	Computational identification and characterization of conserved miRNAs and their putative target genes in Eclipta prostrata. Gene Reports, 2018, 11, 213-219.	0.4	1
685	Exploration of miRNAs and target genes of cytoplasmic male sterility line in cotton during flower bud development. Functional and Integrative Genomics, 2018, 18, 457-476.	1.4	19
686	Identification of miRNAs and their targets in maize in response to Sugarcane mosaic virus infection. Plant Physiology and Biochemistry, 2018, 125, 143-152.	2.8	28
687	Revisiting Criteria for Plant MicroRNA Annotation in the Era of Big Data. Plant Cell, 2018, 30, 272-284.	3.1	406
688	Identification of microRNAs involved in drought stress responses in early-maturing cotton by high-throughput sequencing. Genes and Genomics, 2018, 40, 305-314.	0.5	14
689	Mining Ferula gummosa transcriptome to identify miRNAs involved in the regulation and biosynthesis of terpenes. Gene, 2018, 645, 41-47.	1.0	38
690	Identification and comparative analysis of microRNAs from tomato varieties showing contrasting response to ToLCV infections. Physiology and Molecular Biology of Plants, 2018, 24, 185-202.	1.4	26
691	Identification and Characterization of microRNA during Bemisia tabaci Infestations in Solanum lycopersicum and Solanum habrochaites. Horticultural Plant Journal, 2018, 4, 62-72.	2.3	18
692	Analysis of physiological and miRNA responses to Pi deficiency in alfalfa (Medicago sativa L.). Plant Molecular Biology, 2018, 96, 473-492.	2.0	24
693	Unique miRNome in heat tolerant indica rice var. HT54 seedlings. Ecological Genetics and Genomics, 2018, 7-8, 13-22.	0.3	2
694	Identification and characterization of microRNAs in tree peony during chilling induced dormancy release by high-throughput sequencing. Scientific Reports, 2018, 8, 4537.	1.6	48
695	Identification and comparative analysis of aluminum-induced microRNAs conferring plant tolerance to aluminum stress in soybean. Biologia Plantarum, 2018, 62, 97-108.	1.9	19
696	In Silico Identification of Novel microRNAs and Targets Using EST Analysis in Allium cepa L Interdisciplinary Sciences, Computational Life Sciences, 2018, 10, 771-780.	2.2	9
697	Sex-biased miRNAs of yellow catfish (Pelteobagrus fulvidraco) and their potential role in reproductive development. Aquaculture, 2018, 485, 73-80.	1.7	11

#	Article	IF	CITATIONS
698	Genomeâ€wide discovery of tissueâ€specific mi <scp>RNA</scp> s in clusterbean ( <i>Cyamopsis) Tj ETQq0 0 0 rg</i>	BT /Overlo 4.1	ock 10 Tf 50 2
.,.	Journal, 2018, 16, 1241-1257.		
699	An expression atlas of miRNAs in Arabidopsis thaliana. Science China Life Sciences, 2018, 61, 178-189.	2.3	38
700	Can-miRn37a mediated suppression of ethylene response factors enhances the resistance of chilli against anthracnose pathogen Colletotrichum truncatum L. Plant Science, 2018, 267, 135-147.	1.7	29
701	Functional regulation of Q by microRNA172 and transcriptional coâ€repressor TOPLESS in controlling bread wheat spikelet density. Plant Biotechnology Journal, 2018, 16, 495-506.	4.1	59
702	Bioinformatics prediction and annotation of cherry ( Prunus avium L.) microRNAs and their targeted proteins. Turkish Journal of Botany, 2018, 42, 382-399.	0.5	4
703	Regulation through MicroRNAs in Response to Low-Energy N+ Ion Irradiation in Oryza sativa. Radiation Research, 2018, 191, 189.	0.7	2
704	The miRNAome of ramie (Boehmeria nivea L.): identification, expression, and potential roles of novel microRNAs in regulation of cadmium stress response. BMC Plant Biology, 2018, 18, 369.	1.6	13
705	Identification of Arbuscular Mycorrhiza Fungi Responsive microRNAs and Their Regulatory Network in Maize. International Journal of Molecular Sciences, 2018, 19, 3201.	1.8	29
706	Identification of microRNAs and their targets in four Gossypium species using RNA sequencing. Current Plant Biology, 2018, 14, 30-40.	2.3	8
707	Identification of browning-related microRNAs and their targets reveals complex miRNA-mediated browning regulatory networks in Luffa cylindrica. Scientific Reports, 2018, 8, 16242.	1.6	11
708	Genome-Wide Identification of microRNAs in Response to Salt/Alkali Stress in Medicago truncatula through High-Throughput Sequencing. International Journal of Molecular Sciences, 2018, 19, 4076.	1.8	30
709	Progress Toward Deep Sequencing-Based Discovery of Stress-Related MicroRNA in Plants and Available Bioinformatics Tools. Progress in Botany Fortschritte Der Botanik, 2018, , 41-76.	0.1	3
711	MicroRNAs, tasiRNAs, phasiRNAs, and Their Potential Functions in Pineapple. Plant Genetics and Genomics: Crops and Models, 2018, , 167-182.	0.3	1
712	High-throughput sequencing revealed that microRNAs were involved in the development of superior and inferior grains in bread wheat. Scientific Reports, 2018, 8, 13854.	1.6	22
713	Identification of miRNAs Associated with Graft Union Development in Pecan [Carya illinoinensis (Wangenh.) K. Koch]. Forests, 2018, 9, 472.	0.9	14
714	Therapeutic applications of zebrafish (Danio rerio) miRNAs linked with human diseases: A prospective review. Gene, 2018, 679, 202-211.	1.0	9
715	Combined small RNA and gene expression analysis revealed roles of miRNAs in maize response to rice black-streaked dwarf virus infection. Scientific Reports, 2018, 8, 13502.	1.6	17
716	Identification and functional analyses of new sesame miRNAs (Sesamum indicum L.) and their targets. Molecular Biology Reports, 2018, 45, 2145-2155.	1.0	9

#	Article	IF	CITATIONS
717	miRVIT: A Novel miRNA Database and Its Application to Uncover Vitis Responses to Flavescence dorée Infection. Frontiers in Plant Science, 2018, 9, 1034.	1.7	26
718	Small RNA profiling reveals involvement of microRNA-mediated gene regulation in response to mycorrhizal symbiosis in Poncirus trifoliata L. Raf Tree Genetics and Genomes, 2018, 14, 1.	0.6	9
719	In silico identification and characterization of microRNAs based on EST and CSS in orphan legume crop, Lens culinaris medik. (Lentil). Agri Gene, 2018, 8, 45-56.	1.9	7
720	Salinity Responses and Tolerance in Plants, Volume 2. , 2018, , .		5
721	miRNAs: The Game Changer in Producing Salinity Stress-Tolerant Crops. , 2018, , 143-188.		3
722	Integrated microRNA and mRNA expression profiling reveals a complex network regulating pomegranate (Punica granatum L.) seed hardness. Scientific Reports, 2018, 8, 9292.	1.6	20
723	Maintenance of graftingâ€induced epigenetic variations in the asexual progeny of <i>Brassica oleracea</i> and <i>B. juncea</i> chimera. Plant Journal, 2018, 96, 22-38.	2.8	20
724	Small RNA and Degradome Deep Sequencing Reveals the Roles of microRNAs in Seed Expansion in Peanut (Arachis hypogaea L.). Frontiers in Plant Science, 2018, 9, 349.	1.7	27
725	miR-MaCiC improves quantification accuracy for small RNA-seq. BMC Research Notes, 2018, 11, 296.	0.6	9
726	Identification and expression analysis of a microRNA cluster derived from pre-ribosomal RNA in Papaver somniferum L. and Papaver bracteatum L PLoS ONE, 2018, 13, e0199673.	1.1	9
727	Genome-Wide Analysis of Gene and microRNA Expression in Diploid and Autotetraploid Paulownia fortunei (Seem) Hemsl. under Drought Stress by Transcriptome, microRNA, and Degradome Sequencing. Forests, 2018, 9, 88.	0.9	11
728	Genome-Wide Identification of MicroRNAs in Response to Cadmium Stress in Oilseed Rape (Brassica) Tj ETQq1 1 1431.	0.784314 1.8	rgBT /Overld 34
729	Identification and Expression of miRNAs Related to Female Flower Induction in Walnut (Juglans regia) Tj ETQq0 0	0 rgBT /Ov	verlock 10 Tf
730	Integration of proteomic and transcriptomic profiles reveals multiple levels of genetic regulation of salt tolerance in cotton. BMC Plant Biology, 2018, 18, 128.	1.6	42
731	Identification and characterization of known and novel microRNAs in strawberry fruits induced by Botrytis cinerea. Scientific Reports, 2018, 8, 10921.	1.6	14
732	Genome-wide identification and comprehensive analysis of microRNAs and phased small interfering RNAs in watermelon. BMC Genomics, 2018, 19, 111.	1.2	14
733	MicroRNA transcriptome analysis of porcine vital organ responses to immunosuppressive porcine cytomegalovirus infection. Virology Journal, 2018, 15, 16.	1.4	8
734	Deep sequencing of small RNAs reveals ribosomal origin of microRNAs in Oryza sativa and their regulatory role in high temperature. Gene Reports, 2018, 11, 270-278.	0.4	11

#	Article	IF	CITATIONS
735	Highly preserved roles of Brassica MIR172 in polyploid Brassicas: ectopic expression of variants of Brassica MIR172 accelerates floral transition. Molecular Genetics and Genomics, 2018, 293, 1121-1138.	1.0	16
736	Identification of Magnaporthe oryzae-elicited rice novel miRNAs and their targets by miRNA and degradome sequencing. European Journal of Plant Pathology, 2018, 151, 629-647.	0.8	10
737	Systematic analysis of DEMETER-like DNA glycosylase genes shows lineage-specific Smi-miR7972 involved in SmDML1 regulation in Salvia miltiorrhiza. Scientific Reports, 2018, 8, 7143.	1.6	10
738	Physiological studies and genome-wide microRNA profiling of cold-stressed Brassica napus. Plant Physiology and Biochemistry, 2018, 132, 1-17.	2.8	16
739	Identification of miRNAs involved in SO2 preservation in Vitis vinifera L. by deep sequencing. Environmental and Experimental Botany, 2018, 153, 218-228.	2.0	17
740	Comparative analysis of miRNA and mRNA abundance in determinate cucumber by high-throughput sequencing. PLoS ONE, 2018, 13, e0190691.	1.1	9
741	MicroRNAs in durum wheat seedlings under chronic and short-term nitrogen stress. Functional and Integrative Genomics, 2018, 18, 645-657.	1.4	27
742	MicroRNA and IncRNA Databases and Analysis. , 2019, , 165-170.		Ο
743	Deep sequencing identified potential mi RNA s involved in defence response, stress and plant growth characteristics of wild genotypes of cardamom. Plant Biology, 2019, 21, 3-14.	1.8	8
744	Characterization and expression profiles of miRNAs in the triploid hybrids of Brassica napus and Brassica rapa. BMC Genomics, 2019, 20, 649.	1.2	7
745	Identifying microRNAs and Their Editing Sites in Macaca mulatta. Cells, 2019, 8, 682.	1.8	10
746	Unravelling the MicroRNA-Mediated Gene Regulation in Developing Pongamia Seeds by High-Throughput Small RNA Profiling. International Journal of Molecular Sciences, 2019, 20, 3509.	1.8	7
747	Genome-Wide Identification of Putative MicroRNAs in Cassava (Manihot esculenta Crantz) and Their Functional Landscape in Cellular Regulation. BioMed Research International, 2019, 2019, 1-16.	0.9	11
748	miRBaseMiner, a tool for investigating miRBase content. RNA Biology, 2019, 16, 1534-1546.	1.5	19
749	miRkwood: a tool for the reliable identification of microRNAs in plant genomes. BMC Genomics, 2019, 20, 532.	1.2	14
751	Analysis of the MIR160 gene family and the role of MIR160a_A05 in regulating fiber length in cotton. Planta, 2019, 250, 2147-2158.	1.6	17
752	Multiomics analysis of tolerant interaction of potato with potato virus Y. Scientific Data, 2019, 6, 250.	2.4	11
753	Adipocyte metabolism is improved by TNF receptor-targeting small RNAs identified from dried nuts. Communications Biology, 2019, 2, 317.	2.0	59

#	Article	IF	CITATIONS
754	Long non-coding RNAs and their potential functions in Ligon-lintless-1 mutant cotton during fiber development. BMC Genomics, 2019, 20, 661.	1.2	18
755	Identification of Fusarium oxysporum f. sp. cubense tropical race 4 (Foc TR4) responsive miRNAs in banana root. Scientific Reports, 2019, 9, 13682.	1.6	23
756	Analysis of Small RNAs from Solanum torvum Swartz by Deep Sequencing. Tropical Plant Biology, 2019, 12, 44-54.	1.0	1
758	Detection of MicroRNA Processing Intermediates Through RNA Ligation Approaches. Methods in Molecular Biology, 2019, 1932, 261-283.	0.4	2
759	Identification and characterization of miRNAs during flag leaf senescence in rice by high-throughput sequencing. Plant Physiology Reports, 2019, 24, 1-14.	0.7	6
760	Identification and characterization of drought responsive miRNAs in a drought tolerant upland rice cultivar KMJ 1-12-3. Plant Physiology and Biochemistry, 2019, 137, 62-74.	2.8	21
761	Identification of microRNAs from transcriptome data in gurmar (Gymnema sylvestre). Horticulture Environment and Biotechnology, 2019, 60, 383-397.	0.7	3
762	Identification of microRNA-target modules from rice variety Pusa Basmati-1 under high temperature and salt stress. Functional and Integrative Genomics, 2019, 19, 867-888.	1.4	12
763	MicroRNA-guided regulation of heat stress response in wheat. BMC Genomics, 2019, 20, 488.	1.2	78
764	Identification and characterization of Populus microRNAs in response to plant growth-promoting endophytic Streptomyces sp. SSD49. World Journal of Microbiology and Biotechnology, 2019, 35, 97.	1.7	13
765	Genome-wide identification of drought-responsive microRNAs in two sets of Malus from interspecific hybrid progenies. Horticulture Research, 2019, 6, 75.	2.9	43
766	Transcriptome-wide identification and characterization of microRNAs responsive to phosphate starvation in Populus tomentosa. Functional and Integrative Genomics, 2019, 19, 953-972.	1.4	19
767	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.	1.6	43
768	Comprehensive transcriptome analysis reveals genes potentially involved in isoflavone biosynthesis in Pueraria thomsonii Benth. PLoS ONE, 2019, 14, e0217593.	1.1	25
769	Genome-Wide Analysis of the miRNA–mRNAs Network Involved in Cold Tolerance in Populus simonii × P. nigra. Genes, 2019, 10, 430.	1.0	17
770	Genomeâ€scale, singleâ€cellâ€type resolution of micro <scp>RNA</scp> activities within a whole plant organ. EMBO Journal, 2019, 38, e100754.	3.5	41
771	Computational identification of miRNA and their cross kingdom targets from expressed sequence tags of Ocimum basilicum. Molecular Biology Reports, 2019, 46, 2979-2995.	1.0	21
772	EgmiR5179 from the mesocarp of oil palm (Elaeis guineensis Jacq.) regulates oil accumulation by targeting NAD transporter 1. Industrial Crops and Products, 2019, 137, 126-136.	2.5	8

#	Article	IF	CITATIONS
773	Identification of miRNAs and Their Response to Cold Stress in Astragalus Membranaceus. Biomolecules, 2019, 9, 182.	1.8	51
774	Comparative profile analysis reveals differentially expressed microRNAs regulate anther and pollen development in kenaf cytoplasmic male sterility line. Genome, 2019, 62, 455-466.	0.9	5
775	A comparative analysis of small RNAs between two Upland cotton backcross inbred lines with different fiber length: Expression and distribution. Crop Journal, 2019, 7, 198-208.	2.3	7
776	Analysis of microRNAs, phased small interfering RNAs and their potential targets in Rosarugosa Thunb BMC Genomics, 2019, 19, 983.	1.2	13
777	MicroRNAs in Plants: Key Findings from the Early Years. Plant Cell, 2019, 31, 1206-1207.	3.1	29
778	Bioinformatic Exploration of the Targets of Xylem Sap miRNAs in Maize under Cadmium Stress. International Journal of Molecular Sciences, 2019, 20, 1474.	1.8	34
779	High-throughput sequencing reveals microRNAs and their targets in response to drought stress in wheat ( <i>Triticum aestivum</i> L.). Biotechnology and Biotechnological Equipment, 2019, 33, 465-471.	0.5	17
780	Multiple microRNAs Regulate the Floral Development and Sex Differentiation in the Dioecious Cucurbit Coccinia grandis (L.) Voigt. Plant Molecular Biology Reporter, 2019, 37, 111-128.	1.0	11
781	Identification and analysis of oxygen responsive microRNAs in the root of wild tomato (S.) Tj ETQq0 0 0 rgBT /Ov	erlock 10 1.	Tf 50 422 Td
782	Identifying High Confidence microRNAs in the Developing Seeds of Jatropha curcas. Scientific Reports, 2019, 9, 4510.	1.6	12
783	Genome-wide comprehensive analysis of transcriptomes and small RNAs offers insights into the molecular mechanism of alkaline stress tolerance in a citrus rootstock. Horticulture Research, 2019, 6, 33.	2.9	26
784	Identification and expression profiling of miRNAs in two color variants of carrot (Daucus carota L.) using deep sequencing. PLoS ONE, 2019, 14, e0212746.	1.1	19
785	Development of species specific putative miRNA and its target prediction tool in wheat (Triticum) Tj ETQq0 0 0 r	gBŢ ¦Overl	ock 10 Tf 50
786	Identification and Analysis of microRNAs in the SAM and Leaves of Populus tomentosa. Forests, 2019, 10, 130.	0.9	11
787	MicroRNA Target Identification. Methods in Molecular Biology, 2019, , .	0.4	2

788	The miRNA-Mediated Post-Transcriptional Regulation of Maize in Response to High Temperature. International Journal of Molecular Sciences, 2019, 20, 1754.	1.8	37
789	Protocols for miRNA Target Prediction in Plants. Methods in Molecular Biology, 2019, 1970, 65-73.	0.4	3
790	Stress-responsive miRNAome of Glycine max (L.) Merrill: molecular insights and way forward. Planta, 2019, 249, 1267-1284.	1.6	20

#	Article	IF	CITATIONS
791	miRNAs play important roles in aroma weakening during the shelf life of â€~Nanguo' pear after cold storage. Food Research International, 2019, 116, 942-952.	2.9	9
792	Expression profiling and regulatory network of cucumber microRNAs and their putative target genes in response to cucumber green mottle mosaic virus infection. Archives of Virology, 2019, 164, 1121-1134.	0.9	20
793	Identification of copper (Cu) stress-responsive grapevine microRNAs and their target genes by high-throughput sequencing. Royal Society Open Science, 2019, 6, 180735.	1.1	19
794	Computational methods for microRNA and PIWI-interacting RNA gene discovery and functional predictions. , 2019, , 35-53.		0
795	PmiRDiscVali: an integrated pipeline for plant microRNA discovery and validation. BMC Genomics, 2019, 20, 133.	1.2	9
796	High-throughput sequencing and differential expression analysis of miRNAs in response to Brassinosteroid treatment in Arabidopsis thaliana. Functional and Integrative Genomics, 2019, 19, 597-615.	1.4	3
797	Discovery and Profiling of microRNAs at the Critical Period of Sex Differentiation in Xanthoceras sorbifolium Bunge. Forests, 2019, 10, 1141.	0.9	10
798	Systematic Analysis of Alkaline/Neutral Invertase Genes Reveals the Involvement of Smi-miR399 in Regulation of SmNINV3 and SmNINV4 in Salvia miltiorrhiza. Plants, 2019, 8, 490.	1.6	9
799	A transcriptomic profile of topping responsive non-coding RNAs in tobacco roots (Nicotiana) Tj ETQq0 0 0 rgBT /O	verlock 10 1.2	0 Jf 50 422
800	The Role of Micrornas in Genome Response to Plant–Lepidoptera Interaction. Plants, 2019, 8, 529.	1.6	1
801	Transcriptional and post-transcriptional responses of diploid and autotetraploid Paulownia tomentosa × Paulownia fortunei under water-deficit condition. Revista Brasileira De Botanica, 2019, 42 623-641.	2,0.5	6
802	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.	1.4	28
803	Identification and expression profiles of putative leaf growth related microRNAs in maize (Zea mays L.) hybrid ADA313. Gene, 2019, 690, 57-67.	1.0	18
804	MicroR408 regulates defense response upon wounding in sweet potato. Journal of Experimental Botany, 2019, 70, 469-483.	2.4	28
805	Identification of microRNAs responding to salt stress in barley by high-throughput sequencing and degradome analysis. Environmental and Experimental Botany, 2019, 160, 59-70.	2.0	29
806	An emerging technique for reducing the response time in plant miRNA identification. Computational Biology and Chemistry, 2019, 78, 382-388.	1.1	1
807	OsDCL3b affects grain yield and quality in rice. Plant Molecular Biology, 2019, 99, 193-204.	2.0	14
808	Exploration of miRNA-mediated fertility regulation network of cytoplasmic male sterility during flower bud development in soybean. 3 Biotech, 2019, 9, 22.	1.1	12

#	Article	IF	CITATIONS
809	Small RNA sequencing reveals dynamic microRNA expression of important nutrient metabolism during development of <i>Camellia oleifera</i> fruit. International Journal of Biological Sciences, 2019, 15, 416-429.	2.6	21
810	Banana sRNAome and degradome identify microRNAs functioning in differential responses to temperature stress. BMC Genomics, 2019, 20, 33.	1.2	78
811	Integrated transcriptome, small <scp>RNA</scp> and degradome sequencing approaches provide insights into Ascochyta blight resistance in chickpea. Plant Biotechnology Journal, 2019, 17, 914-931.	4.1	66
812	Small RNA molecules and their role in plant disease. European Journal of Plant Pathology, 2019, 154, 115-128.	0.8	18
813	Identification and function analysis of drought-specific small RNAs in Gossypium hirsutum L Plant Science, 2019, 280, 187-196.	1.7	12
814	Introduction to Non-coding RNAs and High Throughput Sequencing. , 2019, , 3-31.		1
815	Identification of microRNAs From Small RNA Sequencing Profiles. , 2019, , 35-82.		1
817	Genome-wide profiling reveals extensive alterations in Pseudomonas putida-mediated miRNAs expression during drought stress in chickpea (Cicer arietinum L.). Environmental and Experimental Botany, 2019, 157, 217-227.	2.0	33
818	Computational tools for plant small RNA detection and categorization. Briefings in Bioinformatics, 2019, 20, 1181-1192.	3.2	22
819	Development and characterization of non-coding RNA based simple sequence repeat markers in Capsicum species. Genomics, 2020, 112, 1554-1564.	1.3	32
820	PmiREN: a comprehensive encyclopedia of plant miRNAs. Nucleic Acids Research, 2020, 48, D1114-D1121.	6.5	120
821	<i>In silico</i> determination of transposon-derived miRNAs and targets in <i>Aegilops</i> species. Journal of Biomolecular Structure and Dynamics, 2020, 38, 3098-3109.	2.0	1
822	Genome-wide identification of drought-responsive miRNAs in grass pea (Lathyrus sativus L.). Plant Gene, 2020, 21, 100210.	1.4	16
823	miRNA applications for engineering abiotic stress tolerance in plants. Biologia (Poland), 2020, 75, 1063-1081.	0.8	43
825	Understanding epigenomics based on the rice model. Theoretical and Applied Genetics, 2020, 133, 1345-1363.	1.8	17
826	Identification and evolutionary analysis of polycistronic miRNA clusters in domesticated and wild wheat. Genomics, 2020, 112, 2334-2348.	1.3	12
827	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.	0.9	1
828	Regulation of micoRNA2111 and its target IbFBK in sweet potato on wounding. Plant Science, 2020, 292, 110391.	1.7	5

#	Article	IF	Citations
831	Identification of milRNAs and their target genes in Ganoderma lucidum by high-throughput sequencing and degradome analysis. Fungal Genetics and Biology, 2020, 136, 103313.	0.9	18
832	Evolution of small RNA expression following hybridization and allopolyploidization: insights from Spartina species (Poaceae, Chloridoideae). Plant Molecular Biology, 2020, 102, 55-72.	2.0	14
833	Computational Identification and Comparative Analysis of Conserved miRNAs and Their Putative Target Genes in the Juglans regia and J. microcarpa Genomes. Plants, 2020, 9, 1330.	1.6	1
834	Spatiotemporal Resolved Leaf Angle Establishment Improves Rice Grain Yield via Controlling Population Density. IScience, 2020, 23, 101489.	1.9	9
835	In silico identification and validation of miRNA and their DIR specific targets in Oryza sativa Indica under abiotic stress. Non-coding RNA Research, 2020, 5, 167-177.	2.4	21
836	Integrated sRNAome and RNA-Seq analysis reveals miRNA effects on betalain biosynthesis in pitaya. BMC Plant Biology, 2020, 20, 437.	1.6	18
837	Small RNA and degradome sequencing reveal roles of miRNAs in strobilus development in masson pine (Pinus massoniana). Industrial Crops and Products, 2020, 154, 112724.	2.5	17
838	Epigenetic mechanisms leading to genetic flexibility during abiotic stress responses in microalgae: A review. Algal Research, 2020, 50, 101999.	2.4	13
839	MicroRNA transcriptomic analysis of the sixth leaf of maize (Zea mays L.) revealed a regulatory mechanism of jointing stage heterosis. BMC Plant Biology, 2020, 20, 541.	1.6	6
840	Genome-wide analysis of PHD finger gene family and identification of potential miRNA and their PHD finger gene specific targets in Oryza sativa indica. Non-coding RNA Research, 2020, 5, 191-200.	2.4	2
841	Genome-Wide Screening and Characterization of Non-Coding RNAs in Coffea canephora. Non-coding RNA, 2020, 6, 39.	1.3	5
842	Computational methods for annotation of plant regulatory non-coding RNAs using RNA-seq. Briefings in Bioinformatics, 2021, 22, .	3.2	18
843	Small RNA sequencing revealed various microRNAs involved in ethylene-triggered flowering process in Aechmea fasciata. Scientific Reports, 2020, 10, 7348.	1.6	4
844	Genetic interactions among Pto-miR319 family members and their targets influence growth and wood properties in Populus tomentosa. Molecular Genetics and Genomics, 2020, 295, 855-870.	1.0	2
845	Integrated Analysis of mRNA and microRNA Elucidates the Regulation of Glycyrrhizic Acid Biosynthesis in Glycyrrhiza uralensis Fisch. International Journal of Molecular Sciences, 2020, 21, 3101.	1.8	10
846	Integrated small RNA and mRNA expression profiles reveal miRNAs and their target genes in response to Aspergillus flavus growth in peanut seeds. BMC Plant Biology, 2020, 20, 215.	1.6	17
847	Identification of UV-B radiation responsive microRNAs and their target genes in chrysanthemum (Chrysanthemum morifolium Ramat) using high-throughput sequencing. Industrial Crops and Products, 2020, 151, 112484.	2.5	15
848	Plant isomiRs: origins, biogenesis, and biological functions. Genomics, 2020, 112, 3382-3395.	1.3	12

#	Article	IF	CITATIONS
849	Identification of Known and Novel MicroRNAs in Raspberry Organs Through High-Throughput Sequencing. Frontiers in Plant Science, 2020, 11, 728.	1.7	6
850	Identification and profiling of microRNAs and differentially expressed genes during anther development between a genetic male-sterile mutant and its wildtype cotton via high-throughput RNA sequencing. Molecular Genetics and Genomics, 2020, 295, 645-660.	1.0	8
851	Prediction and experimental confirmation of banana bract mosaic virus encoding miRNAs and their targets. ExRNA, 2020, 2, .	1.0	6
852	First Report of Aleurocanthus spiniferus on Ailanthus altissima: Profiling of the Insect Microbiome and MicroRNAs. Insects, 2020, 11, 161.	1.0	11
853	Dynamic changes in the expression pattern of miRNAs and associated target genes during coconut somatic embryogenesis. Planta, 2020, 251, 79.	1.6	21
854	The role of microRNAs in the legume–Rhizobium nitrogen-fixing symbiosis. Journal of Experimental Botany, 2020, 71, 1668-1680.	2.4	18
855	miRNA–mRNA Integrated Analysis Reveals Roles for miRNAs in a Typical Halophyte, Reaumuria soongorica, during Seed Germination under Salt Stress. Plants, 2020, 9, 351.	1.6	19
856	Integrated Analysis of Large-Scale Omics Data Revealed Relationship Between Tissue Specificity and Evolutionary Dynamics of Small RNAs in Maize (Zea mays). Frontiers in Genetics, 2020, 11, 51.	1.1	7
857	Comparative Analysis of miRNA Expression Profiles between Heat-Tolerant and Heat-Sensitive Genotypes of Flowering Chinese Cabbage Under Heat Stress Using High-Throughput Sequencing. Genes, 2020, 11, 264.	1.0	21
858	Characterization of microRNA genes from Pigeonpea (Cajanus cajan L.) and understanding their involvement in drought stress. Journal of Biotechnology, 2020, 321, 23-34.	1.9	10
859	Identification of small nonâ€coding RNAs responsive to <i>GUN1</i> and <i>GUN5</i> related retrograde signals in <i>Arabidopsis thaliana</i> . Plant Journal, 2020, 104, 138-155.	2.8	10
860	Characteristic Dissection of Xanthomonas oryzae pv. oryzae Responsive MicroRNAs in Rice. International Journal of Molecular Sciences, 2020, 21, 785.	1.8	17
861	Identification of microRNAs in developing wheat grain that are potentially involved in regulating grain characteristics and the response to nitrogen levels. BMC Plant Biology, 2020, 20, 87.	1.6	35
862	Transcriptome-wide identification and profiling of miRNAs in a stress-tolerant conifer Sabina chinensis. Journal of Biosciences, 2020, 45, 1.	0.5	2
863	Diversity and types of small RNA. , 2020, , 37-47.		0
864	Recent trends and advances in identification and functional characterization of plant miRNAs. Acta Physiologiae Plantarum, 2020, 42, 1.	1.0	22
865	A Bioinformatics Pipeline to Accurately and Efficiently Analyze the MicroRNA Transcriptomes in Plants. Journal of Visualized Experiments, 2020, , .	0.2	1
866	PAREameters: a tool for computational inference of plant miRNA–mRNA targeting rules using small RNA and degradome sequencing data. Nucleic Acids Research, 2020, 48, 2258-2270.	6.5	16

	CITATION RE	PORT	
#	ARTICLE Identification and in Silico Characterization of Novel and Conserved MicroRNAs in Methyl	IF	CITATIONS
867	Jasmonate-Stimulated Scots Pine (Pinus sylvestris L.) Needles. Forests, 2020, 11, 384.	0.9	6
868	Identification and expression analysis of miRNAs and elucidation of their role in salt tolerance in rice varieties susceptible and tolerant to salinity. PLoS ONE, 2020, 15, e0230958.	1.1	62
869	Future scope of small RNA technology in crop science. , 2020, , 567-585.		0
870	Evidence of the Regulatory Roles of Candidate miRNAs During Somatic Embryogenesis in Lilium davidii var. unicolor. Journal of Plant Growth Regulation, 2021, 40, 197-214.	2.8	3
871	Roles of miR319-regulated TCPs in plant development and response to abiotic stress. Crop Journal, 2021, 9, 17-28.	2.3	39
872	Expression of miRNAs and their target genes in roots of â€ <sup>~</sup> Sanhu' tangerine (Citrus reticulata blanco) Tj ETÇ Protection, 2021, 128, 407-420.	q1 1 0.78 1.6	4314 rgBT 2
873	Small RNA Sequencing in Sugar Beet Under Alkaline Stress. Sugar Tech, 2021, 23, 57-64.	0.9	5
874	Profiling of MicroRNAs and Their Targets in Roots and Shoots Reveals a Potential MiRNA-Mediated Interaction Network in Response to Phosphate Deficiency in the Forestry Tree Betula luminifera. Frontiers in Genetics, 2021, 12, 552454.	1.1	10
875	Degradome Assisted Plant MicroRNA Prediction under Alternative Annotation Criteria. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, PP, 1-1.	1.9	1
876	Integrated miRNA-mRNA analysis reveals the roles of miRNAs in the replanting benefit of Achyranthes bidentata roots. Scientific Reports, 2021, 11, 1628.	1.6	8
877	Methodologies for Discovery and Quantitative Profiling of sRNAs in Potato. Methods in Molecular Biology, 2021, 2354, 221-260.	0.4	1
878	A Malvaceae-specific miRNA targeting the newly duplicated GaZIP1L to regulate Zn2+ ion transporter capacity in cotton ovules. Science China Life Sciences, 2021, 64, 339-351.	2.3	9
879	Identification of miRNA targets in eggplant in response to Verticillium dahliae by degradome sequencing. European Journal of Plant Pathology, 2021, 160, 97-111.	0.8	2
880	Study of expressions of miRNAs in the spikelets based on their spatial location on panicle in rice cultivars provided insight into their influence on grain development. Plant Physiology and Biochemistry, 2021, 159, 244-256.	2.8	14
881	Azadirachta indica MicroRNAs: Genome-Wide Identification, Target Transcript Prediction, and Expression Analyses. Applied Biochemistry and Biotechnology, 2021, 193, 1924-1944.	1.4	1
882	Genome-wide identification and functional characterization of natural antisense transcripts in Salvia miltiorrhiza. Scientific Reports, 2021, 11, 4769.	1.6	19
883	sRNAanno—a database repository of uniformly annotated small RNAs in plants. Horticulture Research, 2021, 8, 45.	2.9	63
884	Novel approaches on identification of conserved miRNAs for broad-spectrum Potyvirus control measures. Molecular Biology Reports, 2021, 48, 2377-2388.	1.0	1

		CITATION R	EPORT	
#	Article		IF	CITATIONS
886	MicroRNA annotation in plants: current status and challenges. Briefings in Bioinformati	cs, 2021, 22, .	3.2	10
887	On the origin of the widespread self-compatible allotetraploid Capsella bursa-pastoris (I Heredity, 2021, 127, 124-134.	Brassicaceae).	1.2	12
888	Identification and characterization of heat-responsive microRNAs at the booting stage i varieties, 9311 and Nagina 22. Genome, 2021, 64, 969-984.	n two rice	0.9	3
889	An Atlas of Genomic Resources for Studying Rosaceae Fruits and Ornamentals. Frontier Science, 2021, 12, 644881.	rs in Plant	1.7	5
890	Genome-wide analysis of microRNA156 and its targets, the genes encoding SQUAMOS promoter-binding protein-like (SPL) transcription factors, in the grass family Poaceae. Jo Zhejiang University: Science B, 2021, 22, 366-382.	A ournal of	1.3	3
891	Genome-Wide Analysis of Coding and Non-coding RNA Reveals a Conserved miR164†Regulatory Pathway for Disease Defense in Populus. Frontiers in Genetics, 2021, 12, 66	'NAC–mRNA 8940.	1.1	8
892	Identification of miRNAs and Their Targets Involved in Flower and Fruit Development ac Domesticated and Wild Capsicum Species. International Journal of Molecular Sciences,	ross 2021, 22, 4866.	1.8	13
893	One vectorâ€based method to verify predicted plant miRNAs, target sequences, and fu Biotechnology and Bioengineering, 2021, 118, 3105-3116.	nction modes.	1.7	1
894	Identification of a cartilage specific novel miRNA which directly targets PRMT3 in rats. C and Cartilage Open, 2021, 3, 100161.	Dsteoarthritis	0.9	0
895	High-throughput sequencing analysis reveals effects of short-term low-temperature sto miRNA-mediated flavonoid accumulation in postharvest toon buds. Plant Gene, 2021, 2	rage on 26, 100291.	1.4	6
896	The Processing and Regulation of Intronic miRNAs Are Independent of Their Host Genes Plant Molecular Biology Reporter, 0, , 1.	; in Arabidopsis.	1.0	0
897	Comparative Analysis of miRNA Expression Profiles Provides Insight into Regulation of E Flavonoids and Terpenoids Between Two Varieties of Toona sinensis Sprouts. Journal of 2022, 65, 291-310.	Biosynthesis of Plant Biology,	0.9	6
898	Genome-Wide Expression Profiling of Small RNAs in Indian Strain of Rhizoctonia solani Differential Regulation of milRNAs during Pathogenesis and Crosstalk of Gene Regulatio Fungi (Basel, Switzerland), 2021, 7, 561.	AG1-1A Reveals on. Journal of	1.5	1
900	An updated overview and classification of bioinformatics tools for MicroRNA analysis, w choose?. Computers in Biology and Medicine, 2021, 134, 104544.	vhich one to	3.9	13
901	Interactive Web-Based Annotation of Plant MicroRNAs with iwa-miRNA. Genomics, Prot Bioinformatics, 2022, 20, 557-567.	eomics and	3.0	5
902	Knockdown of miR393 Promotes the Growth and Biomass Production in Poplar. Frontie Science, 2021, 12, 714907.	ers in Plant	1.7	13
903	High nitrate inhibited adventitious roots formation in apple rootstock by altering hormo contents and miRNAs expression profiles. Scientia Horticulturae, 2021, 286, 110230.	onal	1.7	14
905	Profiling of MicroRNAs in Midguts of Plutella xylostella Provides Novel Insights Into the thuringiensis Resistance. Frontiers in Genetics, 2021, 12, 739849.	Bacillus	1.1	3

#	Article	IF	CITATIONS
906	Genomeâ€wide <scp>miRNAs</scp> profiles of pearl millet under contrasting high vapor pressure deficit reveal their functional roles in drought stress adaptations. Physiologia Plantarum, 2022, 174, .	2.6	5
907	Deep Sequencing Discovery and Profiling of Known and Novel miRNAs Produced in Response to DNA Damage in Rice. International Journal of Molecular Sciences, 2021, 22, 9958.	1.8	2
908	Integrated Analysis of MicroRNA and Target Genes in Brachypodium distachyon Infected by Magnaporthe oryzae by Small RNA and Degradome Sequencing. Frontiers in Plant Science, 2021, 12, 742347.	1.7	7
909	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.	1.7	6
910	A miR169c-NFYA10 module confers tolerance to low-nitrogen stress to Betula luminifera. Industrial Crops and Products, 2021, 172, 113988.	2.5	2
911	MicroRNAs expression dynamics reveal post-transcriptional mechanisms regulating seed development in Phaseolus vulgaris L Horticulture Research, 2021, 8, 18.	2.9	9
912	Noncoding Regulatory RNAs. , 2013, , 145-160.		2
913	Methods for RNA Profiling of Gravi-Responding Plant Tissues. Methods in Molecular Biology, 2015, 1309, 91-117.	0.4	2
914	Abiotic Stress-Associated miRNAs: Detection and Functional Analysis. Methods in Molecular Biology, 2010, 592, 203-230.	0.4	31
915	RNA Silencing and Antiviral Defense in Plants. Methods in Molecular Biology, 2012, 894, 17-38.	0.4	29
916	Role of microRNAs in Plant–Fungus Interactions. Concepts and Strategies in Plant Sciences, 2020, , 199-220.	0.6	2
917	Plant miRNomics: Novel Insights in Gene Expression and Regulation. , 2015, , 181-211.		7
918	Plant-pathogen interactions: MicroRNA-mediated trans-kingdom gene regulation in fungi and their host plants. Genomics, 2020, 112, 3021-3035.	1.3	22
919	Regulatory protein genes and microRNAs in response to selenium stimuli in <i>Pueraria lobata</i> (Willd.) Ohwi. Metallomics, 2021, 13, .	1.0	5
923	High-throughput deep sequencing reveals the important role that microRNAs play in the salt response in sweet potato (Ipomoea batatas L.). BMC Genomics, 2020, 21, 164.	1.2	46
925	Phosphorylation of CBP20 Links MicroRNA to Root Growth in the Ethylene Response. PLoS Genetics, 2016, 12, e1006437.	1.5	34
926	Identification of Novel miRNAs and miRNA Dependent Developmental Shifts of Gene Expression in Arabidopsis thaliana. PLoS ONE, 2010, 5, e10157.	1.1	22
927	MiR-RACE, a New Efficient Approach to Determine the Precise Sequences of Computationally Identified Trifoliate Orange (Poncirus trifoliata) MicroRNAs. PLoS ONE, 2010, 5, e10861.	1.1	55

		CITATION R	EPORT	
#	Article		IF	CITATIONS
928	Domestication of Transposable Elements into MicroRNA Genes in Plants. PLoS ONE, 201	1, 6, e19212.	1.1	96
929	First Survey of the Wheat Chromosome 5A Composition through a Next Generation Seq Approach. PLoS ONE, 2011, 6, e26421.	uencing	1.1	57
930	Sorting the Wheat from the Chaff: Identifying miRNAs in Genomic Survey Sequences of Taestivum Chromosome 1AL. PLoS ONE, 2012, 7, e40859.	riticum	1.1	64
931	Deep Sequencing and Microarray Hybridization Identify Conserved and Species-Specific I during Somatic Embryogenesis in Hybrid Yellow Poplar. PLoS ONE, 2012, 7, e43451.	MicroRNAs	1.1	66
932	Identification of Novel Oryza sativa miRNAs in Deep Sequencing-Based Small RNA Librarie Infected with Rice Stripe Virus. PLoS ONE, 2012, 7, e46443.	es of Rice	1.1	45
933	Characterization and Expression Patterns of microRNAs Involved in Rice Grain Filling. PLo 8, e54148.	S ONE, 2013,	1.1	71
934	Deep Sequencing of Maize Small RNAs Reveals a Diverse Set of MicroRNA in Dry and Imb ONE, 2013, 8, e55107.	ibed Seeds. PLoS	1.1	73
935	Identification and Characterization of miRNA Transcriptome in Potato by High-Throughpu Sequencing. PLoS ONE, 2013, 8, e57233.	ıt	1.1	119
936	Identification and Analysis of Red Sea Mangrove (Avicennia marina) microRNAs by High-T Sequencing and Their Association with Stress Responses. PLoS ONE, 2013, 8, e60774.	hroughput	1.1	33
937	Integrative Analysis of miRNA and mRNA Profiles in Response to Ethylene in Rose Petals o Opening. PLoS ONE, 2013, 8, e64290.	luring Flower	1.1	70
938	Elucidation of miRNAs-Mediated Responses to Low Nitrogen Stress by Deep Sequencing Genotypes. PLoS ONE, 2013, 8, e67423.	of Two Soybean	1.1	46
939	Transcriptome-Wide Identification and Characterization of MicroRNAs from Castor Bean	(Ricinus) Tj ETQq1 1 0.7	784314 rg[ 1.1	3T/Qverlock
940	High-Throughput Sequencing of Small RNAs from Pollen and Silk and Characterization of Candidate Factors Involved in Pollen-Silk Interactions in Maize. PLoS ONE, 2013, 8, e728	miRNAs as 52.	1.1	20
941	Systems and Evolutionary Characterization of MicroRNAs and Their Underlying Regulator in Soybean Cotyledons. PLoS ONE, 2014, 9, e86153.	ry Networks	1.1	37
942	Analysis of miRNAs and Their Targets during Adventitious Shoot Organogenesis of Acacia PLoS ONE, 2014, 9, e93438.	a crassicarpa.	1.1	20
943	Transcriptome/Degradome-Wide Discovery of MicroRNAs and Transcript Targets in Two I australis Genotypes. PLoS ONE, 2014, 9, e106736.	Paulownia	1.1	18
944	Genome-Wide Identification of Different Dormant Medicago sativa L. MicroRNAs in Resp Dormancy. PLoS ONE, 2014, 9, e114612.	onse to Fall	1.1	17
945	Bioinformatics Analysis of Small RNAs in Pima (Gossypium barbadense L.). PLoS ONE, 20	15, 10, e0116826.	1.1	7

#	Article	IF	CITATIONS
946	Identification and Characterization of MicroRNAs from Tree Peony (Paeonia ostii) and Their Response to Copper Stress. PLoS ONE, 2015, 10, e0117584.	1.1	30
947	Identification and Characterization of MicroRNAs in Ginkgo biloba var. epiphylla Mak. PLoS ONE, 2015, 10, e0127184.	1.1	37
948	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.	1.1	11
949	Transcripts and MicroRNAs Responding to Salt Stress in Musa acuminata Colla (AAA Group) cv. Berangan Roots. PLoS ONE, 2015, 10, e0127526.	1.1	47
950	Identification of MicroRNAs in Response to Different Day Lengths in Soybean Using High-Throughput Sequencing and qRT-PCR. PLoS ONE, 2015, 10, e0132621.	1.1	16
951	Identification of microRNAs in the Toxigenic Dinoflagellate Alexandrium catenella by High-Throughput Illumina Sequencing and Bioinformatic Analysis. PLoS ONE, 2015, 10, e0138709.	1.1	14
952	Identification of Novel and Conserved microRNAs in Homalodisca vitripennis, the Glassy-Winged Sharpshooter by Expression Profiling. PLoS ONE, 2015, 10, e0139771.	1.1	4
953	Plant–Pathogen Interaction-Related MicroRNAs and Their Targets Provide Indicators of Phytoplasma Infection in Paulownia tomentosa × Paulownia fortunei. PLoS ONE, 2015, 10, e0140590.	1.1	14
954	Genome-Wide Identification of MicroRNAs in Leaves and the Developing Head of Four Durum Genotypes during Water Deficit Stress. PLoS ONE, 2015, 10, e0142799.	1.1	43
955	Comparative Analysis and Identification of miRNAs and Their Target Genes Responsive to Salt Stress in Diploid and Tetraploid Paulownia fortunei Seedlings. PLoS ONE, 2016, 11, e0149617.	1.1	24
956	DsTRD: Danshen Transcriptional Resource Database. PLoS ONE, 2016, 11, e0149747.	1.1	23
957	Characterization of the Small RNA Transcriptome of the Marine Coccolithophorid, Emiliania huxleyi. PLoS ONE, 2016, 11, e0154279.	1.1	12
958	The Small-RNA Profiles of Almond (Prunus dulcis Mill.) Reproductive Tissues in Response to Cold Stress. PLoS ONE, 2016, 11, e0156519.	1.1	31
959	Transcriptome and Degradome of microRNAs and Their Targets in Response to Drought Stress in the Plants of a Diploid and Its Autotetraploid Paulownia australis. PLoS ONE, 2016, 11, e0158750.	1.1	9
960	Identification of Known and Novel microRNAs and Their Targets in Peach (Prunus persica) Fruit by High-Throughput Sequencing. PLoS ONE, 2016, 11, e0159253.	1.1	17
961	Identification and Characterization of Salvia miltiorrhizain miRNAs in Response to Replanting Disease. PLoS ONE, 2016, 11, e0159905.	1.1	18
962	Genome-Wide Identification and Characterization of MicroRNAs and Target Genes in Lonicera japonica. PLoS ONE, 2016, 11, e0164140.	1.1	18
963	Genome-Wide Identification and Analysis of MicroRNAs Involved in Witches'-Broom Phytoplasma Response in Ziziphus jujuba. PLoS ONE, 2016, 11, e0166099.	1.1	33

#	Article	IF	CITATIONS
964	Genome-wide identification and characterization of miRNAome from tomato (Solanum lycopersicum) roots and root-knot nematode (Meloidogyne incognita) during susceptible interaction. PLoS ONE, 2017, 12, e0175178.	1.1	42
965	Genome-wide identification and characterization of microRNAs differentially expressed in fibers in a cotton phytochrome A1 RNAi line. PLoS ONE, 2017, 12, e0179381.	1.1	9
966	The use of high-throughput small RNA sequencing reveals differentially expressed microRNAs in response to aster yellows phytoplasma-infection in Vitis vinifera cv. â€~Chardonnay'. PLoS ONE, 2017, 12, e0182629.	1.1	40
967	Identification of protoplast-isolation responsive microRNAs in Citrus reticulata Blanco by high-throughput sequencing. PLoS ONE, 2017, 12, e0183524.	1.1	3
968	Small RNA Transcriptome of Hibiscus Syriacus Provides Insights into the Potential Influence of microRNAs in Flower Development and Terpene Synthesis. Molecules and Cells, 2017, 40, 587-597.	1.0	6
969	Cold stress responsive microRNAs and their targets in Musa balbisiana. Frontiers of Agricultural Science and Engineering, 2016, 3, 335.	0.9	4
970	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.	0.5	5
971	In Silico Identification of Conserved MiRNAs from Physcomitrella patens ESTs and their Target Characterization. Current Bioinformatics, 2018, 14, 33-42.	0.7	9
972	Differential Expression of Hyperhydricity Responsive Peach miRNAs. Journal of Integrative Bioinformatics, 2016, 13, 308.	1.0	5
973	Identification of microRNAs in ecological model plant <i>Mimulus</i> . Journal of Biophysical Chemistry, 2011, 02, 322-331.	0.1	15
974	Comparative miRNAome Analysis Revealed Numerous Conserved and Novel Drought Responsive miRNAs in Cotton ( <i>Gossypium spp.</i> ). Cotton Genomics and Genetics, 0, , .	0.0	1
975	Abiotic Stress Response in Plants - Physiological, Biochemical and Genetic Perspectives. , 2011, , .		23
976	Facing the Environment: Small RNAs and the Regulation of Gene Expression Under Abiotic Stress in Plants. , O, , .		4
977	Analysis of microRNAs and their targets from onion (Allium cepa) using genome survey sequences (GSS) and expressed sequence tags (ESTs). Bioinformation, 2019, 15, 907-917.	0.2	6
978	Analysis of the laccase gene family and miR397-/miR408-mediated posttranscriptional regulation in <i>Salvia miltiorrhiza</i> . PeerJ, 2019, 7, e7605.	0.9	18
979	Analysis of small RNA changes in different <i> Brassica napus</i> synthetic allopolyploids. PeerJ, 2019, 7, e7621.	0.9	7
980	Distinct Evolutionary Profiles and Functions of microRNA156 and microRNA529 in Land Plants. International Journal of Molecular Sciences, 2021, 22, 11100.	1.8	8
982	The Non-coding Landscape of the Genome of Arabidopsis thaliana. , 2011, , 67-121.		0

#	Article	IF	CITATIONS
983	Antisense Transcription Associated with microRNA Target mRNAs. , 2011, , 35-58.		0
984	Small RNA in Legumes. , 2011, , 121-138.		0
986	GENOMIC DATABASES FOR CROP IMPROVEMENT. , 2014, , 219-234.		0
987	miR-RACE: An Effective Approach to Accurately Determine the Sequence of Computationally Identified miRNAs. Methods in Molecular Biology, 2015, 1296, 109-118.	0.4	0
988	Identification of Novel MicroRNAs and their Target Prediction in Stevia rebaudiana. Transcriptomics: Open Access, 2015, 03, .	0.2	0
989	Mungbean Yellow Mosaic India Virus (MYMIV)-infection, Small RNA Library Construction and Deep Sequencing for MicroRNA Identification in Vigna mungo. Bio-protocol, 2016, 6, .	0.2	0
990	Advances in Computational Tools for Plant microRNA Identification. , 2017, , 1-16.		0
996	COMPUTATIONAL IDENTIFICATION OF MICRORNA IN FIVE WOODY OIL TREE CROPS AND THEIR miRNA TARGET SEQUENCES. Journal of Oil Palm Research, 0, , .	2.1	0
998	Salvia miltiorrhiza Epigenetics. Compendium of Plant Genomes, 2019, , 69-81.	0.3	0
1000	MirLibSpark. , 2019, , .		0
1002	Computational methods for the ab initio identification of novel microRNA in plants: a systematic review. PeerJ Computer Science, 2019, 5, e233.	2.7	3
1004	Identification and Characterization of Known and Novel MicroRNAs in Five Tissues of Wax Gourd (Benincasa hispida) Based on High-Throughput Sequencing. Applied Sciences (Switzerland), 2021, 11, 10068.	1.3	4
1005	Plant and animal small RNA communications between cells and organisms. Nature Reviews Molecular Cell Biology, 2022, 23, 185-203.	16.1	72
1006	MirCure: a tool for quality control, filter and curation of microRNAs of animals and plants. Bioinformatics, 2020, 36, i618-i624.	1.8	4
1008	The Pliable Genome: Epigenomics of Norway Spruce. Compendium of Plant Genomes, 2020, , 65-95.	0.3	2
1009	Small RNAs in Duckweeds. Compendium of Plant Genomes, 2020, , 157-164.	0.3	0
1010	Genome-Wide Analysis of Alternative Splicing and Non-Coding RNAs Reveal Complicated Transcriptional Regulation in Cannabis sativa L International Journal of Molecular Sciences, 2021, 22, 11989.	1.8	7
1011	Identification of miRNAs and their target genes in genic male sterility lines in Brassica napus by small RNA sequencing. BMC Plant Biology, 2021, 21, 520.	1.6	11

		CITATION R	EPORT	
#	Article		IF	CITATIONS
1012	Discovery of Conserved and Novel MicroRNAs in. Iranian Journal of Biotechnology, 2021	., 19, e2671.	0.3	0
1013	MicroRNA profiles in Sorghum exposed to individual drought or heat or their combination of Plant Biochemistry and Biotechnology, 2021, 30, 848-861.	bn. Journal	0.9	4
1014	Combined Stress Conditions in Melon Induce Non-additive Effects in the Core miRNA Re Network. Frontiers in Plant Science, 2021, 12, 769093.	gulatory	1.7	3
1015	Integrated analysis of small RNA, transcriptome and degradome sequencing reveals that regulate anther development in CMS cotton. Industrial Crops and Products, 2022, 176,	t micro-RNAs 114422.	2.5	3
1016	Comprehensive Identification and Profiling of miRNAs Involved in Terpenoid Synthesis o sinensis Lam Forests, 2022, 13, 108.	f Cleditsia	0.9	8
1017	Small RNA populations reflect the complex dialogue established between heterograft pagrapevine. Horticulture Research, 2022, 9, .	artners in	2.9	8
1018	Creating and maintaining a high-confidence microRNA repository for crop research: A br and re-examination of the current crop microRNA registries. Journal of Plant Physiology, 153636.	ief review 2022, 270,	1.6	1
1019	MicroRNA and cDNA-Microarray as Potential Targets against Abiotic Stress Response in Advances and Prospects. Agronomy, 2022, 12, 11.	Plants:	1.3	6
1020	Transcriptome-wide identification and profiling of miRNAs in a stress-tolerant conifer. Jo Biosciences, 2020, 45, .	urnal of	0.5	1
1021	Non-Coding RNA Analyses of Seasonal Cambium Activity in Populus tomentosa. Cells, 2	022, 11, 640.	1.8	10
1022	Small RNA and Degradome Sequencing Reveal Important MicroRNA Function in Nicotian Response to Bemisia tabaci. Genes, 2022, 13, 361.	na tabacum	1.0	5
1023	Understanding the Molecular Mechanisms of Betel miRNAs on Human Health. MicroRN/	A (Shariqah,) Tj ETQq1 1	0.784314 ı 0.6	rgBT /Overlo
1024	Micro RNA mediated regulation of nutrient response in plants: the case of nitrogen. Plan Reports, 2022, 27, 345-357.	nt Physiology	0.7	5
1025	In silico identification of candidate miRNA-encoded Peptides in four Fabaceae species. C Biology and Chemistry, 2022, 97, 107644.	Computational	1.1	2
1026	MicroRNA and Degradome Profiling Uncover Defense Response of Fraxinus velutina Tor Stress. Frontiers in Plant Science, 2022, 13, 847853.	r. to Salt	1.7	5
1027	Sequencing and de novo transcriptome assembly for discovering regulators of gene exp (Artocarpus heterophyllus). Genomics, 2022, 114, 110356.	ression in Jack	1.3	1
1100	Deciphering comparative and structural variation that regulates abiotic stress response. 561-586.	.,2022,,		0
1101	The Construction and Exploration of a Comprehensive MicroRNA Centered Regulatory N Foxtail Millet (Setaria italica L.). Frontiers in Plant Science, 2022, 13, .	Network in	1.7	2

#	Article	IF	CITATIONS
1102	Integrated small RNA profiling and degradome analysis of Anthurium andraeanum cultivars with different-colored spathes. Journal of Plant Research, 2022, 135, 609-626.	1.2	1
1103	Analysis of miRNAs responsive to longâ€ŧerm calcium deficiency in tef ( <scp><i>Eragrostis tef</i></scp> ) Tj ETQ	q1_1_0.78	4314 rgBT /(
1104	Key regulatory pathways, microRNAs, and target genes participate in adventitious root formation of Acer rubrum L. Scientific Reports, 2022, 12, .	1.6	4
1105	Comparative Analysis of Salt Responsive MicroRNAs in Two Sweetpotato [Ipomoea batatas (L.) Lam.] Cultivars With Different Salt Stress Resistance. Frontiers in Plant Science, 0, 13, .	1.7	3
1106	Evolutionary conservation of nested MIR159 structural microRNA genes and their promoter characterization in Arabidopsis thaliana. Frontiers in Plant Science, 0, 13, .	1.7	1
1107	Roles of microRNAs in abiotic stress response and characteristics regulation of plant. Frontiers in Plant Science, 0, 13, .	1.7	28
1108	Integrated transcriptome and regulatory network analyses identify candidate genes and pathways modulating ewe fertility. Gene Reports, 2022, 28, 101659.	0.4	2
1109	<scp>Pmâ€miR</scp> â€29b is involved in nacre formation by regulating tyrosinaseâ€like protein in <i>Pinctada martensii</i> . Aquaculture Research, 0, , .	0.9	0
1110	The role of phytohormones and their related miRNAs in sex differentiation of Xanthoceras sorbifolium Bunge. Scientia Horticulturae, 2023, 307, 111498.	1.7	2
1111	Small RNA-omics: Decoding the regulatory networks associated with horticultural traits. , 2022, , 15-25.		0
1112	Integrated miRNA, target mRNA, and metabolome profiling of Tinospora cordifolia with reference to berberine biosynthesis. 3 Biotech, 2022, 12, .	1.1	0
1113	BrumiR: A toolkit for <i>de novo</i> discovery of microRNAs from sRNA-seq data. GigaScience, 2022, 11,	3.3	3
1114	Integrated transcriptomics and miRNAomics provide insights into the complex multi-tiered regulatory networks associated with coleoptile senescence in rice. Frontiers in Plant Science, 0, 13, .	1.7	2
1115	Miniature Inverted-repeat Transposable Elements Drive Rapid MicroRNA Diversification in Angiosperms. Molecular Biology and Evolution, 2022, 39, .	3.5	10
1116	Analysis of the <scp><i>MIR396</i></scp> gene family and the role of <scp><i>MIR396b</i></scp> in regulating fiber length in cotton. Physiologia Plantarum, 2022, 174, .	2.6	2
1117	MicroRNA sequencing reveals the salt responses in four Tartary buckwheat cultivars. Theoretical and Experimental Plant Physiology, 0, , .	1.1	0
1118	Further Mining and Characterization of miRNA Resource in Chinese Fir (Cunninghamia lanceolata). Genes, 2022, 13, 2137.	1.0	1
1119	miRNA and other noncoding RNAs. , 2023, , 351-374.		0

			-
#	ARTICLE	IF	CITATIONS
1120	Genome-wide comprehensive analysis of miRNAs and their target genes expressed in resistant and susceptible Capsicum annuum genotypes during Phytophthora capsici infection. Molecular Genetics and Genomics, 2023, 298, 273-292.	1.0	4
1121	miRador: a fast and precise tool for the prediction of plant miRNAs. Plant Physiology, 2023, 191, 894-903.	2.3	4
1122	High-Throughput Sequencing Reveals Novel microRNAs Involved in the Continuous Flowering Trait of Longan (Dimocarpus longan Lour.). International Journal of Molecular Sciences, 2022, 23, 15565.	1.8	3
1123	Fungal Secondary Metabolites and Small RNAs Enhance Pathogenicity during Plant-Fungal Pathogen Interactions. Journal of Fungi (Basel, Switzerland), 2023, 9, 4.	1.5	5
1124	Comprehensive re-analysis of hairpin small RNAs in fungi reveals loci with conserved links. ELife, 0, 11,	2.8	4
1125	A tissue-specific profile of miRNAs and their targets related to paeoniaflorin and monoterpenoids biosynthesis in Paeonia lactiflora Pall. by transcriptome, small RNAs and degradome sequencing. PLoS ONE, 2023, 18, e0279992.	1.1	2
1126	miRNA transcriptome reveals key miRNAs and their targets contributing to the difference in Cd tolerance of two contrasting maize genotypes. Ecotoxicology and Environmental Safety, 2023, 256, 114881.	2.9	4
1128	Novel microRNAs associated with the immune response to cucumber mosaic virus in hot pepper (Capsicum annuum L.). Physiological and Molecular Plant Pathology, 2023, 124, 101963.	1.3	2
1129	Exploring conserved and novel MicroRNA-like small RNAs from stress tolerant Trichoderma fusants and parental strains during interaction with fungal phytopathogen Sclerotium rolfsii Sacc Pesticide Biochemistry and Physiology, 2023, 191, 105368.	1.6	4
1130	Small RNA and Degradome Sequencing in Floral Bud Reveal Roles of miRNAs in Dormancy Release of Chimonanthus praecox. International Journal of Molecular Sciences, 2023, 24, 4210.	1.8	2
1131	Genome-Wide Analysis of microRNAs and Their Target Genes in Dongxiang Wild Rice (Oryza rufipogon) Tj ETQq0	0.0 rgBT / 1.8	Oyerlock 10
1132	High throughput sRNA sequencing revealed gene regulatory role mediated by pathogen-derived small RNAs during Sri Lankan Cassava Mosaic Virus infection in Cassava. 3 Biotech, 2023, 13, .	1.1	0
1133	Analysis of Small Non-coding RNAs as Signaling Intermediates of Environmentally Integrated Responses to Abiotic Stress. Methods in Molecular Biology, 2023, , 403-427.	0.4	0
1134	Prediction of novel putative miRNAs and their targets in buffalo. Indian Journal of Animal Sciences, 2017, 87, .	0.1	1
1135	Intracellular metabolomics and microRNAomics unveil new insight into the regulatory network for potential biocontrol mechanism of stressâ€tolerant <i>Trichoâ€</i> fusants interacting with phytopathogen <i>Sclerotium rolfsii</i> Sacc. Journal of Cellular Physiology, 2023, 238, 1288-1307.	2.0	4
1136	Identification of miRNAs Involved in Male Fertility and Pollen Development in Brassica oleracea var. capitata L. by High-Throughput Sequencing. Horticulturae, 2023, 9, 515.	1.2	1

Role of miRNAs in the cross-talk of phytohormone signaling pathways. , 2023, , 373-422.

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