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List of Publications by Year
in descending order

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128 papers	24,453 citations	10389 72 h-index	16183 124 g-index
144 all docs	144 docs citations	144 times ranked	17797 citing authors

#	ARTICLE	IF	CITATIONS
1	Heatâ€•responsive microRNAs and phased small interfering RNAs in reproductive development of flax. Plant Direct, 2022, 6, e385.	1.9	16
2	Evolution and diversification of reproductive phased small interfering RNAs in Oryza species. New Phytologist, 2021, 229, 2970-2983.	7.3	12
3	sRNAannoâ€”a database repository of uniformly annotated small RNAs in plants. Horticulture Research, 2021, 8, 45.	6.3	63
4	Conserved and nonâ€•conserved triggers of 24â€•nucleotide reproductive phasiRNAs in eudicots. Plant Journal, 2021, 107, 1332-1345.	5.7	15
5	Pre-meiotic 21-nucleotide reproductive phasiRNAs emerged in seed plants and diversified in flowering plants. Nature Communications, 2021, 12, 4941.	12.8	21
6	<i>Aegilops tauschii</i> genome assembly Aet v5.0 features greater sequence contiguity and improved annotation. G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	19
7	Reproductive phasiRNA loci and DICER-LIKE5, but not microRNA loci, diversified in monocotyledonous plants. Plant Physiology, 2021, 185, 1764-1782.	4.8	17
8	Next-Generation Sequence Databases: RNA and Genomic Informatics Resources for Plants. Plant Physiology, 2020, 182, 136-146.	4.8	22
9	An Online Database for Exploring Over 2,000 Arabidopsis Small RNA Libraries. Plant Physiology, 2020, 182, 685-691.	4.8	19
10	Soybean DICER-LIKE2 Regulates Seed Coat Color via Production of Primary 22-Nucleotide Small Interfering RNAs from Long Inverted Repeats. Plant Cell, 2020, 32, 3662-3673.	6.6	35
11	Pre-meiotic, 24-nt reproductive phasiRNAs are abundant in anthers of wheat and barley but not rice and maize. Plant Physiology, 2020, 184, pp.00816.2020.	4.8	20
12	Quantitative, super-resolution localization of small RNAs with sRNA-PAINT. Nucleic Acids Research, 2020, 48, e96-e96.	14.5	14
13	PhasiRNAs in Plants: Their Biogenesis, Genic Sources, and Roles in Stress Responses, Development, and Reproduction. Plant Cell, 2020, 32, 3059-3080.	6.6	139
14	Small RNA discovery in the interaction between barley and the powdery mildew pathogen. BMC Genomics, 2019, 20, 610.	2.8	37
15	Plant Extracellular Vesicles Contain Diverse Small RNA Species and Are Enriched in 10- to 17-Nucleotide â€œTinyâ€•RNAs. Plant Cell, 2019, 31, 315-324.	6.6	171
16	MicroRNAs in Plants: Key Findings from the Early Years. Plant Cell, 2019, 31, 1206-1207.	6.6	29
17	24-nt reproductive phasiRNAs are broadly present in angiosperms. Nature Communications, 2019, 10, 627.	12.8	106
18	Despacito: the slow evolutionary changes in plant microRNAs. Current Opinion in Plant Biology, 2018, 42, 16-22.	7.1	83

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19	Revisiting Criteria for Plant MicroRNA Annotation in the Era of Big Data. Plant Cell, 2018, 30, 272-284.	6.6	406
20	<i>Cis</i>â€directed cleavage and nonstoichiometric abundances of 21â€nucleotide reproductive phased small interfering <scp>RNA</scp>s in grasses. New Phytologist, 2018, 220, 865-877.	7.3	38
21	Coupling of micro<scp>RNA</scp>â€directed phased small interfering <scp>RNA</scp> generation from long noncoding genes with alternative splicing and alternative polyadenylation in small <scp>RNA</scp>â€mediated gene silencing. New Phytologist, 2018, 217, 1535-1550.	7.3	46
22	Maize Small RNAs as Seeds of Change and Stability in Gene Expression and Genome Stability. Compendium of Plant Genomes, 2018, , 113-127.	0.5	1
23	Characterizing Small RNAs in Filamentous Fungi Using the Rice Blast Fungus, Magnaporthe oryzae, as an Example. Methods in Molecular Biology, 2018, 1848, 53-66.	0.9	0
24	Biogenesis of a 22-nt microRNA in Phaseoleae species by precursor-programmed uridylation. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 8037-8042.	7.1	46
25	Molecular mechanisms that limit the costs of NLRâ€mediated resistance in plants. Molecular Plant Pathology, 2018, 19, 2516-2523.	4.2	26
26	Plant 24-nt reproductive phasiRNAs from intramolecular duplex mRNAs in diverse monocots. Genome Research, 2018, 28, 1333-1344.	5.5	49
27	Threshold-dependent repression of SPL gene expression by miR156/miR157 controls vegetative phase change in Arabidopsis thaliana. PLoS Genetics, 2018, 14, e1007337.	3.5	161
28	Characterization of Plant Small RNAs by Next Generation Sequencing. Current Protocols in Plant Biology, 2017, 2, 39-63.	2.8	29
29	Genome assembly with in vitro proximity ligation data and whole-genome triplication in lettuce. Nature Communications, 2017, 8, 14953.	12.8	330
30	Small RNA Functions Are Required for Growth and Development of <i>Magnaporthe oryzae</i>. Molecular Plant-Microbe Interactions, 2017, 30, 517-530.	2.6	68
31	FASTmiR: an RNA-based sensor for in vitro quantification and live-cell localization of small RNAs. Nucleic Acids Research, 2017, 45, e130-e130.	14.5	49
32	The asparagus genome sheds light on the origin and evolution of a young Y chromosome. Nature Communications, 2017, 8, 1279.	12.8	240
33	The Influence of Genotype and Environment on Small RNA Profiles in Grapevine Berry. Frontiers in Plant Science, 2016, 7, 1459.	3.6	40
34	<i>PMS1T</i> , producing phased small-interfering RNAs, regulates photoperiod-sensitive male sterility in rice. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 15144-15149.	7.1	234
35	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.	8.3	40
36	Dynamic changes of small RNAs in rice spikelet development reveal specialized reproductive phasiRNA pathways. Journal of Experimental Botany, 2016, 67, 6037-6049.	4.8	109

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37	The Diversification of Plant<i>NBS-LRR</i>Defense Genes Directs the Evolution of MicroRNAs That Target Them. Molecular Biology and Evolution, 2016, 33, 2692-2705.	8.9	200
38	Small RNAs Add Zing to the Zig-Zag-Zig Model of Plant Defenses. Molecular Plant-Microbe Interactions, 2016, 29, 165-169.	2.6	95
39	Evolution of plant genome architecture. Genome Biology, 2016, 17, 37.	8.8	331
40	High-resolution identification and abundance profiling of cassava (Manihot esculenta Crantz) microRNAs. BMC Genomics, 2016, 17, 85.	2.8	22
41	Secondary si<scp>RNA</scp>s from <i>Medicago <scp>NB</scp>â€<scp>LRR</scp>s</i> modulated via mi<scp>RNA</scp>â€"target interactions and their abundances. Plant Journal, 2015, 83, 451-465.	5.7	67
42	Coordination of MicroRNAs, PhasiRNAs, and NBâ€LRR Genes in Response to a Plant Pathogen: Insights from Analyses of a Set of Soybean Rps Gene Nearâ€Isogenic Lines. Plant Genome, 2015, 8, eplantgenome2014.09.0044.	2.8	31
43	Spatiotemporally dynamic, cell-typeâ€"dependent premeiotic and meiotic phasiRNAs in maize anthers. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 3146-3151.	7.1	310
44	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.	4.8	73
45	Distinct and Cooperative Activities of HESO1 and URT1 Nucleotidyl Transferases in MicroRNA Turnover in Arabidopsis. PLoS Genetics, 2015, 11, e1005119.	3.5	125
46	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.	6.6	89
47	miRVine: a microRNA expression atlas of grapevine based on small RNA sequencing. BMC Genomics, 2015, 16, 393.	2.8	73
48	Identification of micro RNA s and their mRNA targets during soybean nodule development: functional analysis of the role of miR393jâ€3p in soybean nodulation. New Phytologist, 2015, 207, 748-759.	7.3	82
49	A One Precursor One siRNA Model for Pol IV-Dependent siRNA Biogenesis. Cell, 2015, 163, 445-455.	28.9	260
50	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.	8.9	141
51	Dicer-like 3 produces transposable element-associated 24-nt siRNAs that control agricultural traits in rice. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 3877-3882.	7.1	181
52	An Atlas of Soybean Small RNAs Identifies Phased siRNAs from Hundreds of Coding Genes. Plant Cell, 2014, 26, 4584-4601.	6.6	163
53	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.	14.5	69
54	miRNAs trigger widespread epigenetically activated siRNAs from transposons in Arabidopsis. Nature, 2014, 508, 411-415.	27.8	331

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55	Sample sequencing of vascular plants demonstrates widespread conservation and divergence of microRNAs. Nature Communications, 2014, 5, 3722.	12.8	224
56	Distinct and concurrent pathways of <scp>P</scp>olÂ<scp>II</scp>â€•and PolÂ<scp>IV</scp>â€dependent si<scp>RNA</scp> biogenesis at a repetitive <i>trans</i>â€silencer locus in <i><scp>A</scp>rabidopsis thaliana</i>. Plant Journal, 2014, 79, 127-138.	5.7	25
57	Rapid construction of parallel analysis of RNA end (PARE) libraries for Illumina sequencing. Methods, 2014, 67, 84-90.	3.8	89
58	Roles of small <scp>RNA</scp>s in soybean defense against <i><scp>P</scp>hytophthora sojae</i> infection. Plant Journal, 2014, 79, 928-940.	5.7	122
59	Physiological stressors and invasive plant infections alter the small RNA transcriptome of the rice blast fungus, Magnaporthe oryzae. BMC Genomics, 2013, 14, 326.	2.8	49
60	Multiple RNA recognition patterns during microRNA biogenesis in plants. Genome Research, 2013, 23, 1675-1689.	5.5	110
61	The <i>Amborella</i> Genome and the Evolution of Flowering Plants. Science, 2013, 342, 1241089.	12.6	743
62	Biogenesis and function of rice small RNAs from non-coding RNA precursors. Current Opinion in Plant Biology, 2013, 16, 170-179.	7.1	83
63	Comprehensive Investigation of MicroRNAs Enhanced by Analysis of Sequence Variants, Expression Patterns, ARGONAUTE Loading, and Target Cleavage. Plant Physiology, 2013, 162, 1225-1245.	4.8	61
64	Composition and Expression of Conserved MicroRNA Genes in Diploid Cotton (Gossypium) Species. Genome Biology and Evolution, 2013, 5, 2449-2459.	2.5	35
65	Phased, Secondary, Small Interfering RNAs in Posttranscriptional Regulatory Networks. Plant Cell, 2013, 25, 2400-2415.	6.6	543
66	A transposable element is domesticated for service in the plant immune system. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 14821-14822.	7.1	13
67	Plant MicroRNAs Display Differential 3' Truncation and Tailing Modifications That Are ARGONAUTE1 Dependent and Conserved Across Species. Plant Cell, 2013, 25, 2417-2428.	6.6	113
68	MicroRNA Superfamilies Descended from miR390 and Their Roles in Secondary Small Interfering RNA Biogenesis in Eudicots. Plant Cell, 2013, 25, 1555-1572.	6.6	141
69	Parallel analysis of RNA ends enhances global investigation of microRNAs and target RNAs of Brachypodium distachyon. Genome Biology, 2013, 14, R145.	9.6	67
70	RNA polymerase V-dependent small RNAs in Arabidopsis originate from small, intergenic loci including most SINE repeats. Epigenetics, 2012, 7, 781-795.	2.7	69
71	Tracing the origin and evolutionary history of plant nucleotideâ€binding siteâ€“leucineâ€rich repeat (<i>NBSâ€LRR</i>) genes. New Phytologist, 2012, 193, 1049-1063.	7.3	198
72	Roles of DCL4 and DCL3b in rice phased small RNA biogenesis. Plant Journal, 2012, 69, 462-474.	5.7	289

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73	RNAâ€Seq reveals infectionâ€related global gene changes in <i>Phytophthora phaseoli</i>, the causal agent of lima bean downy mildew. Molecular Plant Pathology, 2012, 13, 454-466.	4.2	36
74	The Medicago genome provides insight into the evolution of rhizobial symbioses. Nature, 2011, 480, 520-524.	27.8	1,166
75	Small RNA-mediated epigenetic modifications in plants. Current Opinion in Plant Biology, 2011, 14, 148-155.	7.1	135
76	A microRNA of infectious laryngotracheitis virus can downregulate and direct cleavage of ICP4 mRNA. Virology, 2011, 411, 25-31.	2.4	20
77	MicroRNAs as master regulators of the plant <i>NB-LRR</i> defense gene family via the production of phased, <i>trans</i>-acting siRNAs. Genes and Development, 2011, 25, 2540-2553.	5.9	668
78	Experimental design, preprocessing, normalization and differential expression analysis of small RNA sequencing experiments. Silence: A Journal of RNA Regulation, 2011, 2, 2.	8.1	82
79	Transcriptome dynamics through alternative polyadenylation in developmental and environmental responses in plants revealed by deep sequencing. Genome Research, 2011, 21, 1478-1486.	5.5	117
80	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.	6.6	341
81	Prediction of novel miRNAs and associated target genes in Glycine max. BMC Bioinformatics, 2010, 11, S14.	2.6	108
82	siRNAs compete with miRNAs for methylation by HEN1 in Arabidopsis. Nucleic Acids Research, 2010, 38, 5844-5850.	14.5	59
83	Computational Methods for Comparative Analysis of Plant Small RNAs. Methods in Molecular Biology, 2010, 592, 163-181.	0.9	8
84	Genome Evolution Following Host Jumps in the Irish Potato Famine Pathogen Lineage. Science, 2010, 330, 1540-1543.	12.6	440
85	Genomic and small RNA sequencing of Miscanthus Ã— giganteus shows the utility of sorghum as a reference genome sequence for Andropogoneae grasses. Genome Biology, 2010, 11, R12.	9.6	93
86	Bioinformatics Analysis of Small RNAs in Plants Using Next Generation Sequencing Technologies. Methods in Molecular Biology, 2010, 592, 89-106.	0.9	35
87	Distinct extremely abundant siRNAs associated with cosuppression in petunia. Rna, 2009, 15, 1965-1970.	3.5	93
88	MicroRNAs of Gallid and Meleagrid herpesviruses show generally conserved genomic locations and are virus-specific. Virology, 2009, 388, 128-136.	2.4	56
89	Genome sequence and analysis of the Irish potato famine pathogen Phytophthora infestans. Nature, 2009, 461, 393-398.	27.8	1,405
90	Construction of Parallel Analysis of RNA Ends (PARE) libraries for the study of cleaved miRNA targets and the RNA degradome. Nature Protocols, 2009, 4, 356-362.	12.0	301

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91	MicroRNAs in the Rhizobia Legume Symbiosis. Plant Physiology, 2009, 151, 1002-1008.	4.8	63
92	Short-Read Sequencing Technologies for Transcriptional Analyses. Annual Review of Plant Biology, 2009, 60, 305-333.	18.7	118
93	Genome-wide identification of NBS resistance genes in Populus trichocarpa. Plant Molecular Biology, 2008, 66, 619-636.	3.9	247
94	The Cornucopia of Small RNAs in Plant Genomes. Rice, 2008, 1, 52-62.	4.0	7
95	Transposable Element Regulation in Rice and Arabidopsis: Diverse Patterns of Active Expression and siRNA-mediated Silencing. Tropical Plant Biology, 2008, 1, 72-84.	1.9	6
96	Frequent sequence exchanges between homologs of <i>RPP8</i> in Arabidopsis are not necessarily associated with genomic proximity. Plant Journal, 2008, 54, 69-80.	5.7	47
97	Global identification of microRNAâ€"target RNA pairs by parallel analysis of RNA ends. Nature Biotechnology, 2008, 26, 941-946.	17.5	793
98	Deep Sequencing of Chicken microRNAs. BMC Genomics, 2008, 9, 185.	2.8	118
99	Criteria for Annotation of Plant MicroRNAs. Plant Cell, 2008, 20, 3186-3190.	6.6	1,158
100	Sequencing-based Measurements of mRNA and Small RNA. Biotechnology in Agriculture and Forestry, 2008, , 23-36.	0.2	0
101	Distinct size distribution of endogenous siRNAs in maize: Evidence from deep sequencing in the <i>mop1-1</i> mutant. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 14958-14963.	7.1	208
102	Genome-wide analysis for discovery of rice microRNAs reveals natural antisense microRNAs (nat-miRNAs). Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 4951-4956.	7.1	218
103	Small RNA-Directed Epigenetic Natural Variation in Arabidopsis thaliana. PLoS Genetics, 2008, 4, e1000056.	3.5	112
104	Construction of small RNA cDNA libraries for deep sequencing. Methods, 2007, 43, 110-117.	3.8	216
105	An expression atlas of rice mRNAs and small RNAs. Nature Biotechnology, 2007, 25, 473-477.	17.5	246
106	Global expression analysis of nucleotide binding site-leucine rich repeat-encoding and related genes in Arabidopsis. BMC Plant Biology, 2007, 7, 56.	3.6	166
107	Methods for Analysis of Gene Expression in Plants Using MPSS. , 2007, 406, 387-407.		9
108	Dissecting Arabidopsis thaliana DICER function in small RNA processing, gene silencing and DNA methylation patterning. Nature Genetics, 2006, 38, 721-725.	21.4	561

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109	Sweating the small stuff: microRNA discovery in plants. Current Opinion in Biotechnology, 2006, 17, 139-146.	6.6	63
110	Genomic and Genetic Characterization of Rice Cen3 Reveals Extensive Transcription and Evolutionary Implications of a Complex Centromere. Plant Cell, 2006, 18, 2123-2133.	6.6	95
111	Plant MPSS databases: signature-based transcriptional resources for analyses of mRNA and small RNA. Nucleic Acids Research, 2006, 34, D731-D735.	14.5	276
112	MicroRNAs and other small RNAs enriched in the Arabidopsis RNA-dependent RNA polymerase-2 mutant. Genome Research, 2006, 16, 1276-1288.	5.5	329
113	Marek's Disease Virus Encodes MicroRNAs That Map to <i>meq</i> and the Latency-Associated Transcript. Journal of Virology, 2006, 80, 8778-8786.	3.4	196
114	Evolving disease resistance genes. Current Opinion in Plant Biology, 2005, 8, 129-134.	7.1	325
115	Pseudomonas versus Arabidopsis: Models for Genomic Research into Plant Disease Resistance. BioScience, 2005, 55, 679.	4.9	4
116	Elucidation of the Small RNA Component of the Transcriptome. Science, 2005, 309, 1567-1569.	12.6	582
117	Multiple Genetic Processes Result in Heterogeneous Rates of Evolution within the Major Cluster Disease Resistance Genes in Lettuce[W]. Plant Cell, 2004, 16, 2870-2894.	6.6	276
118	The Use of MPSS for Whole-Genome Transcriptional Analysis in Arabidopsis. Genome Research, 2004, 14, 1641-1653.	5.5	171
119	Genome-Wide Analysis of NBS-LRRâ€“Encoding Genes in Arabidopsis[W]. Plant Cell, 2003, 15, 809-834.	6.6	1,457
120	TIR-X and TIR-NBS proteins: two new families related to disease resistance TIR-NBS-LRR proteins encoded in Arabidopsis and other plant genomes. Plant Journal, 2002, 32, 77-92.	5.7	241
121	Plant disease resistance genes encode members of an ancient and diverse protein family within the nucleotide-binding superfamily. Plant Journal, 1999, 20, 317-332.	5.7	729
122	The Major Resistance Gene Cluster in Lettuce Is Highly Duplicated and Spans Several Megabases. Plant Cell, 1998, 10, 1817-1832.	6.6	290
123	Clusters of Resistance Genes in Plants Evolve by Divergent Selection and a Birth-and-Death Process. Genome Research, 1998, 8, 1113-1130.	5.5	942
124	Resistance Gene Candidates Identified by PCR with Degenerate Oligonucleotide Primers Map to Clusters of Resistance Genes in Lettuce. Molecular Plant-Microbe Interactions, 1998, 11, 815-823.	2.6	213
125	Receptor-like Genes in the Major Resistance Locus of Lettuce Are Subject to Divergent Selection. Plant Cell, 1998, 10, 1833-1846.	6.6	288
126	The Major Resistance Gene Cluster in Lettuce Is Highly Duplicated and Spans Several Megabases. Plant Cell, 1998, 10, 1817.	6.6	29

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127	A Transgenic Mutant of Lactuca sativa (Lettuce) with a T-DNA Tightly Linked to Loss of Downy Mildew Resistance. Molecular Plant-Microbe Interactions, 1997, 10, 970-977.	2.6	24
128	The evolutionary history of small RNAs in Solanaceae. Plant Physiology, 0, , .	4.8	7