

Blake C Meyers

List of Publications by Year in descending order

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128
papers

24,453
citations

10351

72
h-index

16127

124
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144
all docs

144
docs citations

144
times ranked

17797
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-Wide Analysis of NBS-LRR-Encoding Genes in Arabidopsis[W]. Plant Cell, 2003, 15, 809-834.	3.1	1,457
2	Genome sequence and analysis of the Irish potato famine pathogen Phytophthora infestans. Nature, 2009, 461, 393-398.	13.7	1,405
3	The Medicago genome provides insight into the evolution of rhizobial symbioses. Nature, 2011, 480, 520-524.	13.7	1,166
4	Criteria for Annotation of Plant MicroRNAs. Plant Cell, 2008, 20, 3186-3190.	3.1	1,158
5	Clusters of Resistance Genes in Plants Evolve by Divergent Selection and a Birth-and-Death Process. Genome Research, 1998, 8, 1113-1130.	2.4	942
6	Global identification of microRNA-target RNA pairs by parallel analysis of RNA ends. Nature Biotechnology, 2008, 26, 941-946.	9.4	793
7	The <i>Amborella</i> Genome and the Evolution of Flowering Plants. Science, 2013, 342, 1241089.	6.0	743
8	Plant disease resistance genes encode members of an ancient and diverse protein family within the nucleotide-binding superfamily. Plant Journal, 1999, 20, 317-332.	2.8	729
9	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.	2.7	668
10	Elucidation of the Small RNA Component of the Transcriptome. Science, 2005, 309, 1567-1569.	6.0	582
11	Dissecting Arabidopsis thaliana DICER function in small RNA processing, gene silencing and DNA methylation patterning. Nature Genetics, 2006, 38, 721-725.	9.4	561
12	Phased, Secondary, Small Interfering RNAs in Posttranscriptional Regulatory Networks. Plant Cell, 2013, 25, 2400-2415.	3.1	543
13	Genome Evolution Following Host Jumps in the Irish Potato Famine Pathogen Lineage. Science, 2010, 330, 1540-1543.	6.0	440
14	Revisiting Criteria for Plant MicroRNA Annotation in the Era of Big Data. Plant Cell, 2018, 30, 272-284.	3.1	406
15	Massive Analysis of Rice Small RNAs: Mechanistic Implications of Regulated MicroRNAs and Variants for Differential Target RNA Cleavage. Plant Cell, 2011, 23, 4185-4207.	3.1	341
16	miRNAs trigger widespread epigenetically activated siRNAs from transposons in Arabidopsis. Nature, 2014, 508, 411-415.	13.7	331
17	Evolution of plant genome architecture. Genome Biology, 2016, 17, 37.	3.8	331
18	Genome assembly with in vitro proximity ligation data and whole-genome triplication in lettuce. Nature Communications, 2017, 8, 14953.	5.8	330

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19	MicroRNAs and other small RNAs enriched in the Arabidopsis RNA-dependent RNA polymerase-2 mutant. <i>Genome Research</i> , 2006, 16, 1276-1288.	2.4	329
20	Evolving disease resistance genes. <i>Current Opinion in Plant Biology</i> , 2005, 8, 129-134.	3.5	325
21	Spatiotemporally dynamic, cell-type-dependent premeiotic and meiotic phasiRNAs in maize anthers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 3146-3151.	3.3	310
22	Construction of Parallel Analysis of RNA Ends (PARE) libraries for the study of cleaved miRNA targets and the RNA degradome. <i>Nature Protocols</i> , 2009, 4, 356-362.	5.5	301
23	The Major Resistance Gene Cluster in Lettuce Is Highly Duplicated and Spans Several Megabases. <i>Plant Cell</i> , 1998, 10, 1817-1832.	3.1	290
24	Roles of DCL4 and DCL3b in rice phased small RNA biogenesis. <i>Plant Journal</i> , 2012, 69, 462-474.	2.8	289
25	Receptor-like Genes in the Major Resistance Locus of Lettuce Are Subject to Divergent Selection. <i>Plant Cell</i> , 1998, 10, 1833-1846.	3.1	288
26	Multiple Genetic Processes Result in Heterogeneous Rates of Evolution within the Major Cluster Disease Resistance Genes in Lettuce[W]. <i>Plant Cell</i> , 2004, 16, 2870-2894.	3.1	276
27	Plant MPSS databases: signature-based transcriptional resources for analyses of mRNA and small RNA. <i>Nucleic Acids Research</i> , 2006, 34, D731-D735.	6.5	276
28	A One Precursor One siRNA Model for Pol IV-Dependent siRNA Biogenesis. <i>Cell</i> , 2015, 163, 445-455.	13.5	260
29	Genome-wide identification of NBS resistance genes in <i>Populus trichocarpa</i> . <i>Plant Molecular Biology</i> , 2008, 66, 619-636.	2.0	247
30	An expression atlas of rice mRNAs and small RNAs. <i>Nature Biotechnology</i> , 2007, 25, 473-477.	9.4	246
31	TIR-X and TIR-NBS proteins: two new families related to disease resistance TIR-NBS-LRR proteins encoded in Arabidopsis and other plant genomes. <i>Plant Journal</i> , 2002, 32, 77-92.	2.8	241
32	The asparagus genome sheds light on the origin and evolution of a young Y chromosome. <i>Nature Communications</i> , 2017, 8, 1279.	5.8	240
33	<i>PMS1T</i> , producing phased small-interfering RNAs, regulates photoperiod-sensitive male sterility in rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 15144-15149.	3.3	234
34	Sample sequencing of vascular plants demonstrates widespread conservation and divergence of microRNAs. <i>Nature Communications</i> , 2014, 5, 3722.	5.8	224
35	Genome-wide analysis for discovery of rice microRNAs reveals natural antisense microRNAs (nat-miRNAs). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 4951-4956.	3.3	218
36	Construction of small RNA cDNA libraries for deep sequencing. <i>Methods</i> , 2007, 43, 110-117.	1.9	216

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37	Resistance Gene Candidates Identified by PCR with Degenerate Oligonucleotide Primers Map to Clusters of Resistance Genes in Lettuce. <i>Molecular Plant-Microbe Interactions</i> , 1998, 11, 815-823.	1.4	213
38	Distinct size distribution of endogenous siRNAs in maize: Evidence from deep sequencing in the <i>mop1-1</i> mutant. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 14958-14963.	3.3	208
39	The Diversification of Plant NBS-LRR Defense Genes Directs the Evolution of MicroRNAs That Target Them. <i>Molecular Biology and Evolution</i> , 2016, 33, 2692-2705.	3.5	200
40	Tracing the origin and evolutionary history of plant nucleotide-binding site-leucine-rich repeat (NBS-LRR) genes. <i>New Phytologist</i> , 2012, 193, 1049-1063.	3.5	198
41	Marek's Disease Virus Encodes MicroRNAs That Map to meq and the Latency-Associated Transcript. <i>Journal of Virology</i> , 2006, 80, 8778-8786.	1.5	196
42	Dicer-like 3 produces transposable element-associated 24-nt siRNAs that control agricultural traits in rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 3877-3882.	3.3	181
43	The Use of MPSS for Whole-Genome Transcriptional Analysis in Arabidopsis. <i>Genome Research</i> , 2004, 14, 1641-1653.	2.4	171
44	Plant Extracellular Vesicles Contain Diverse Small RNA Species and Are Enriched in 10- to 17-Nucleotide siRNAs. <i>Plant Cell</i> , 2019, 31, 315-324.	3.1	171
45	Global expression analysis of nucleotide binding site-leucine rich repeat-encoding and related genes in Arabidopsis. <i>BMC Plant Biology</i> , 2007, 7, 56.	1.6	166
46	An Atlas of Soybean Small RNAs Identifies Phased siRNAs from Hundreds of Coding Genes. <i>Plant Cell</i> , 2014, 26, 4584-4601.	3.1	163
47	Threshold-dependent repression of SPL gene expression by miR156/miR157 controls vegetative phase change in Arabidopsis thaliana. <i>PLoS Genetics</i> , 2018, 14, e1007337.	1.5	161
48	MicroRNA Superfamilies Descended from miR390 and Their Roles in Secondary Small Interfering RNA Biogenesis in Eudicots. <i>Plant Cell</i> , 2013, 25, 1555-1572.	3.1	141
49	Extensive Families of miRNAs and PHAS Loci in Norway Spruce Demonstrate the Origins of Complex phasiRNA Networks in Seed Plants. <i>Molecular Biology and Evolution</i> , 2015, 32, 2905-2918.	3.5	141
50	PhasiRNAs in Plants: Their Biogenesis, Genic Sources, and Roles in Stress Responses, Development, and Reproduction. <i>Plant Cell</i> , 2020, 32, 3059-3080.	3.1	139
51	Small RNA-mediated epigenetic modifications in plants. <i>Current Opinion in Plant Biology</i> , 2011, 14, 148-155.	3.5	135
52	Distinct and Cooperative Activities of HESO1 and URT1 Nucleotidyl Transferases in MicroRNA Turnover in Arabidopsis. <i>PLoS Genetics</i> , 2015, 11, e1005119.	1.5	125
53	Roles of small siRNAs in soybean defense against <i>Phytophthora sojae</i> infection. <i>Plant Journal</i> , 2014, 79, 928-940.	2.8	122
54	Deep Sequencing of Chicken microRNAs. <i>BMC Genomics</i> , 2008, 9, 185.	1.2	118

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55	Short-Read Sequencing Technologies for Transcriptional Analyses. <i>Annual Review of Plant Biology</i> , 2009, 60, 305-333.	8.6	118
56	Transcriptome dynamics through alternative polyadenylation in developmental and environmental responses in plants revealed by deep sequencing. <i>Genome Research</i> , 2011, 21, 1478-1486.	2.4	117
57	Plant MicroRNAs Display Differential 3' Truncation and Tailing Modifications That Are ARGONAUTE1 Dependent and Conserved Across Species. <i>Plant Cell</i> , 2013, 25, 2417-2428.	3.1	113
58	Small RNA-Directed Epigenetic Natural Variation in <i>Arabidopsis thaliana</i> . <i>PLoS Genetics</i> , 2008, 4, e1000056.	1.5	112
59	Multiple RNA recognition patterns during microRNA biogenesis in plants. <i>Genome Research</i> , 2013, 23, 1675-1689.	2.4	110
60	Dynamic changes of small RNAs in rice spikelet development reveal specialized reproductive phasiRNA pathways. <i>Journal of Experimental Botany</i> , 2016, 67, 6037-6049.	2.4	109
61	Prediction of novel miRNAs and associated target genes in <i>Glycine max</i> . <i>BMC Bioinformatics</i> , 2010, 11, S14.	1.2	108
62	24-nt reproductive phasiRNAs are broadly present in angiosperms. <i>Nature Communications</i> , 2019, 10, 627.	5.8	106
63	Genomic and Genetic Characterization of Rice Cen3 Reveals Extensive Transcription and Evolutionary Implications of a Complex Centromere. <i>Plant Cell</i> , 2006, 18, 2123-2133.	3.1	95
64	Small RNAs Add Zing to the Zig-Zag-Zig Model of Plant Defenses. <i>Molecular Plant-Microbe Interactions</i> , 2016, 29, 165-169.	1.4	95
65	Distinct extremely abundant siRNAs associated with cosuppression in petunia. <i>Rna</i> , 2009, 15, 1965-1970.	1.6	93
66	Genomic and small RNA sequencing of <i>Miscanthus Ã— giganteus</i> shows the utility of sorghum as a reference genome sequence for Andropogoneae grasses. <i>Genome Biology</i> , 2010, 11, R12.	13.9	93
67	Rapid construction of parallel analysis of RNA end (PARE) libraries for Illumina sequencing. <i>Methods</i> , 2014, 67, 84-90.	1.9	89
68	Evolutionary Patterns and Coevolutionary Consequences of <i>MIRNA</i> Genes and MicroRNA Targets Triggered by Multiple Mechanisms of Genomic Duplications in Soybean. <i>Plant Cell</i> , 2015, 27, 546-562.	3.1	89
69	Biogenesis and function of rice small RNAs from non-coding RNA precursors. <i>Current Opinion in Plant Biology</i> , 2013, 16, 170-179.	3.5	83
70	Despacito: the slow evolutionary changes in plant microRNAs. <i>Current Opinion in Plant Biology</i> , 2018, 42, 16-22.	3.5	83
71	Experimental design, preprocessing, normalization and differential expression analysis of small RNA sequencing experiments. <i>Silence: A Journal of RNA Regulation</i> , 2011, 2, 2.	8.0	82
72	Identification of micro RNA s and their mRNA targets during soybean nodule development: functional analysis of the role of miR393 in soybean nodulation. <i>New Phytologist</i> , 2015, 207, 748-759.	3.5	82

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73	Novel and Recently Evolved MicroRNA Clusters Regulate Expansive <i>F-BOX</i> Gene Networks through Phased Small Interfering RNAs in Wild Diploid Strawberry. <i>Plant Physiology</i> , 2015, 169, 594-610.	2.3	73
74	miRVine: a microRNA expression atlas of grapevine based on small RNA sequencing. <i>BMC Genomics</i> , 2015, 16, 393.	1.2	73
75	RNA polymerase V-dependent small RNAs in Arabidopsis originate from small, intergenic loci including most SINE repeats. <i>Epigenetics</i> , 2012, 7, 781-795.	1.3	69
76	sPARTA: a parallelized pipeline for integrated analysis of plant miRNA and cleaved mRNA data sets, including new miRNA target-identification software. <i>Nucleic Acids Research</i> , 2014, 42, e139-e139.	6.5	69
77	Small RNA Functions Are Required for Growth and Development of <i>Magnaporthe oryzae</i> . <i>Molecular Plant-Microbe Interactions</i> , 2017, 30, 517-530.	1.4	68
78	Parallel analysis of RNA ends enhances global investigation of microRNAs and target RNAs of <i>Brachypodium distachyon</i> . <i>Genome Biology</i> , 2013, 14, R145.	13.9	67
79	Secondary siRNA from <i>Medicago sativa</i> LRRs modulated via miRNA target interactions and their abundances. <i>Plant Journal</i> , 2015, 83, 451-465.	2.8	67
80	Sweating the small stuff: microRNA discovery in plants. <i>Current Opinion in Biotechnology</i> , 2006, 17, 139-146.	3.3	63
81	MicroRNAs in the Rhizobia Legume Symbiosis. <i>Plant Physiology</i> , 2009, 151, 1002-1008.	2.3	63
82	sRNAanno—a database repository of uniformly annotated small RNAs in plants. <i>Horticulture Research</i> , 2021, 8, 45.	2.9	63
83	Comprehensive Investigation of MicroRNAs Enhanced by Analysis of Sequence Variants, Expression Patterns, ARGONAUTE Loading, and Target Cleavage. <i>Plant Physiology</i> , 2013, 162, 1225-1245.	2.3	61
84	siRNAs compete with miRNAs for methylation by HEN1 in Arabidopsis. <i>Nucleic Acids Research</i> , 2010, 38, 5844-5850.	6.5	59
85	MicroRNAs of Gallid and Meleagrid herpesviruses show generally conserved genomic locations and are virus-specific. <i>Virology</i> , 2009, 388, 128-136.	1.1	56
86	Physiological stressors and invasive plant infections alter the small RNA transcriptome of the rice blast fungus, <i>Magnaporthe oryzae</i> . <i>BMC Genomics</i> , 2013, 14, 326.	1.2	49
87	FASTmiR: an RNA-based sensor for in vitro quantification and live-cell localization of small RNAs. <i>Nucleic Acids Research</i> , 2017, 45, e130-e130.	6.5	49
88	Plant 24-nt reproductive phasiRNAs from intramolecular duplex mRNAs in diverse monocots. <i>Genome Research</i> , 2018, 28, 1333-1344.	2.4	49
89	Frequent sequence exchanges between homologs of <i>RPP8</i> in Arabidopsis are not necessarily associated with genomic proximity. <i>Plant Journal</i> , 2008, 54, 69-80.	2.8	47
90	Coupling of microRNA-directed phased small interfering RNA generation from long noncoding genes with alternative splicing and alternative polyadenylation in small RNA-mediated gene silencing. <i>New Phytologist</i> , 2018, 217, 1535-1550.	3.5	46

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91	Biogenesis of a 22-nt microRNA in Phaseoleae species by precursor-programmed uridylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 8037-8042.	3.3	46
92	The Influence of Genotype and Environment on Small RNA Profiles in Grapevine Berry. <i>Frontiers in Plant Science</i> , 2016, 7, 1459.	1.7	40
93	Identification and functional characterization of soybean root hair microRNA _s expressed in response to <i>Bacteroides</i> japonicum infection. <i>Plant Biotechnology Journal</i> , 2016, 14, 332-341.	4.1	40
94	5'-directed cleavage and nonstoichiometric abundances of 21-nucleotide reproductive phased small interfering RNA _s in grasses. <i>New Phytologist</i> , 2018, 220, 865-877.	3.5	38
95	Small RNA discovery in the interaction between barley and the powdery mildew pathogen. <i>BMC Genomics</i> , 2019, 20, 610.	1.2	37
96	RNA-Seq reveals infection-related global gene changes in <i>Phytophthora phaseoli</i> , the causal agent of lima bean downy mildew. <i>Molecular Plant Pathology</i> , 2012, 13, 454-466.	2.0	36
97	Composition and Expression of Conserved MicroRNA Genes in Diploid Cotton (<i>Gossypium</i>) Species. <i>Genome Biology and Evolution</i> , 2013, 5, 2449-2459.	1.1	35
98	Soybean DICER-LIKE2 Regulates Seed Coat Color via Production of Primary 22-Nucleotide Small Interfering RNAs from Long Inverted Repeats. <i>Plant Cell</i> , 2020, 32, 3662-3673.	3.1	35
99	Bioinformatics Analysis of Small RNAs in Plants Using Next Generation Sequencing Technologies. <i>Methods in Molecular Biology</i> , 2010, 592, 89-106.	0.4	35
100	Coordination of MicroRNAs, PhasiRNAs, and NLR Genes in Response to a Plant Pathogen: Insights from Analyses of a Set of Soybean Rps Gene Near-Isogenic Lines. <i>Plant Genome</i> , 2015, 8, eplantgenome2014.09.0044.	1.6	31
101	The Major Resistance Gene Cluster in Lettuce Is Highly Duplicated and Spans Several Megabases. <i>Plant Cell</i> , 1998, 10, 1817.	3.1	29
102	Characterization of Plant Small RNAs by Next Generation Sequencing. <i>Current Protocols in Plant Biology</i> , 2017, 2, 39-63.	2.8	29
103	MicroRNAs in Plants: Key Findings from the Early Years. <i>Plant Cell</i> , 2019, 31, 1206-1207.	3.1	29
104	Molecular mechanisms that limit the costs of NLR-mediated resistance in plants. <i>Molecular Plant Pathology</i> , 2018, 19, 2516-2523.	2.0	26
105	Distinct and concurrent pathways of PolII- and PolIV-dependent siRNA biogenesis at a repetitive trans-silencer locus in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2014, 79, 127-138.	2.8	25
106	A Transgenic Mutant of <i>Lactuca sativa</i> (Lettuce) with a T-DNA Tightly Linked to Loss of Downy Mildew Resistance. <i>Molecular Plant-Microbe Interactions</i> , 1997, 10, 970-977.	1.4	24
107	High-resolution identification and abundance profiling of cassava (<i>Manihot esculenta</i> Crantz) microRNAs. <i>BMC Genomics</i> , 2016, 17, 85.	1.2	22
108	Next-Generation Sequence Databases: RNA and Genomic Informatics Resources for Plants. <i>Plant Physiology</i> , 2020, 182, 136-146.	2.3	22

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109	Pre-meiotic 21-nucleotide reproductive phasiRNAs emerged in seed plants and diversified in flowering plants. <i>Nature Communications</i> , 2021, 12, 4941.	5.8	21
110	A microRNA of infectious laryngotracheitis virus can downregulate and direct cleavage of ICP4 mRNA. <i>Virology</i> , 2011, 411, 25-31.	1.1	20
111	Pre-meiotic, 24-nt reproductive phasiRNAs are abundant in anthers of wheat and barley but not rice and maize. <i>Plant Physiology</i> , 2020, 184, pp.00816.2020.	2.3	20
112	An Online Database for Exploring Over 2,000 Arabidopsis Small RNA Libraries. <i>Plant Physiology</i> , 2020, 182, 685-691.	2.3	19
113	<i>Aegilops tauschii</i> genome assembly Aet v5.0 features greater sequence contiguity and improved annotation. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	19
114	Reproductive phasiRNA loci and DICER-LIKE5, but not microRNA loci, diversified in monocotyledonous plants. <i>Plant Physiology</i> , 2021, 185, 1764-1782.	2.3	17
115	Heat-responsive microRNAs and phased small interfering RNAs in reproductive development of flax. <i>Plant Direct</i> , 2022, 6, e385.	0.8	16
116	Conserved and non-conserved triggers of 24-nucleotide reproductive phasiRNAs in eudicots. <i>Plant Journal</i> , 2021, 107, 1332-1345.	2.8	15
117	Quantitative, super-resolution localization of small RNAs with sRNA-PAINT. <i>Nucleic Acids Research</i> , 2020, 48, e96-e96.	6.5	14
118	A transposable element is domesticated for service in the plant immune system. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 14821-14822.	3.3	13
119	Evolution and diversification of reproductive phased small interfering RNAs in <i>Oryza</i> species. <i>New Phytologist</i> , 2021, 229, 2970-2983.	3.5	12
120	Methods for Analysis of Gene Expression in Plants Using MPSS. , 2007, 406, 387-407.		9
121	Computational Methods for Comparative Analysis of Plant Small RNAs. <i>Methods in Molecular Biology</i> , 2010, 592, 163-181.	0.4	8
122	The Cornucopia of Small RNAs in Plant Genomes. <i>Rice</i> , 2008, 1, 52-62.	1.7	7
123	The evolutionary history of small RNAs in Solanaceae. <i>Plant Physiology</i> , 0, , .	2.3	7
124	Transposable Element Regulation in Rice and Arabidopsis: Diverse Patterns of Active Expression and siRNA-mediated Silencing. <i>Tropical Plant Biology</i> , 2008, 1, 72-84.	1.0	6
125	<i>Pseudomonas</i> versus Arabidopsis: Models for Genomic Research into Plant Disease Resistance. <i>BioScience</i> , 2005, 55, 679.	2.2	4
126	Maize Small RNAs as Seeds of Change and Stability in Gene Expression and Genome Stability. <i>Compendium of Plant Genomes</i> , 2018, , 113-127.	0.3	1

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127	Sequencing-based Measurements of mRNA and Small RNA. <i>Biotechnology in Agriculture and Forestry</i> , 2008, , 23-36.	0.2	0
128	Characterizing Small RNAs in Filamentous Fungi Using the Rice Blast Fungus, <i>Magnaporthe oryzae</i> , as an Example. <i>Methods in Molecular Biology</i> , 2018, 1848, 53-66.	0.4	0