

Detlef Weigel

List of Publications by Year in descending order

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420
papers

87,382
citations

333

137
h-index

407

277
g-index

584
all docs

584
docs citations

584
times ranked

47540
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-Wide Insertional Mutagenesis of <i>Arabidopsis thaliana</i> . <i>Science</i> , 2003, 301, 653-657.	6.0	4,667
2	A gene expression map of <i>Arabidopsis thaliana</i> development. <i>Nature Genetics</i> , 2005, 37, 501-506.	9.4	2,293
3	Target mimicry provides a new mechanism for regulation of microRNA activity. <i>Nature Genetics</i> , 2007, 39, 1033-1037.	9.4	1,845
4	Control of leaf morphogenesis by microRNAs. <i>Nature</i> , 2003, 425, 257-263.	13.7	1,676
5	Genome-wide association study of 107 phenotypes in <i>Arabidopsis thaliana</i> inbred lines. <i>Nature</i> , 2010, 465, 627-631.	13.7	1,651
6	LEAFY controls floral meristem identity in <i>Arabidopsis</i> . <i>Cell</i> , 1992, 69, 843-859.	13.5	1,442
7	The Sequential Action of miR156 and miR172 Regulates Developmental Timing in <i>Arabidopsis</i> . <i>Cell</i> , 2009, 138, 750-759.	13.5	1,405
8	Specific Effects of MicroRNAs on the Plant Transcriptome. <i>Developmental Cell</i> , 2005, 8, 517-527.	3.1	1,345
9	Activation Tagging of the Floral Inducer FT. <i>Science</i> , 1999, 286, 1962-1965.	6.0	1,311
10	miR156-Regulated SPL Transcription Factors Define an Endogenous Flowering Pathway in <i>Arabidopsis thaliana</i> . <i>Cell</i> , 2009, 138, 738-749.	13.5	1,255
11	Integration of Spatial and Temporal Information During Floral Induction in <i>Arabidopsis</i> . <i>Science</i> , 2005, 309, 1056-1059.	6.0	1,230
12	Highly Specific Gene Silencing by Artificial MicroRNAs in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2006, 18, 1121-1133.	3.1	1,207
13	Criteria for Annotation of Plant MicroRNAs. <i>Plant Cell</i> , 2008, 20, 3186-3190.	3.1	1,158
14	1,135 Genomes Reveal the Global Pattern of Polymorphism in <i>Arabidopsis thaliana</i> . <i>Cell</i> , 2016, 166, 481-491.	13.5	1,107
15	A Role for Flavin Monooxygenase-Like Enzymes in Auxin Biosynthesis. <i>Science</i> , 2001, 291, 306-309.	6.0	1,075
16	Microbial Hub Taxa Link Host and Abiotic Factors to Plant Microbiome Variation. <i>PLoS Biology</i> , 2016, 14, e1002352.	2.6	1,065
17	The Rate and Molecular Spectrum of Spontaneous Mutations in <i>Arabidopsis thaliana</i> . <i>Science</i> , 2010, 327, 92-94.	6.0	1,004
18	The ABCs of floral homeotic genes. <i>Cell</i> , 1994, 78, 203-209.	13.5	999

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19	Targeted mutagenesis in the model plant <i>Nicotiana benthamiana</i> using Cas9 RNA-guided endonuclease. <i>Nature Biotechnology</i> , 2013, 31, 691-693.	9.4	951
20	Whole-genome sequencing of multiple <i>Arabidopsis thaliana</i> populations. <i>Nature Genetics</i> , 2011, 43, 956-963.	9.4	910
21	Activation Tagging in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2000, 122, 1003-1014.	2.3	896
22	The <i>Drosophila</i> homology of the mouse mammary oncogene <i>int-1</i> is identical to the segment polarity gene <i>wingless</i> . <i>Cell</i> , 1987, 50, 649-657.	13.5	883
23	The <i>Arabidopsis lyrata</i> genome sequence and the basis of rapid genome size change. <i>Nature Genetics</i> , 2011, 43, 476-481.	9.4	814
24	Negative Regulation of Anthocyanin Biosynthesis in <i>Arabidopsis</i> by a miR156-Targeted SPL Transcription Factor. <i>Plant Cell</i> , 2011, 23, 1512-1522.	3.1	804
25	Control of Jasmonate Biosynthesis and Senescence by miR319 Targets. <i>PLoS Biology</i> , 2008, 6, e230.	2.6	803
26	A developmental switch sufficient for flower initiation in diverse plants. <i>Nature</i> , 1995, 377, 495-500.	13.7	787
27	The homeotic gene <i>fork head</i> encodes a nuclear protein and is expressed in the terminal regions of the <i>Drosophila</i> embryo. <i>Cell</i> , 1989, 57, 645-658.	13.5	739
28	Evolution of metal hyperaccumulation required cis-regulatory changes and triplication of HMA4. <i>Nature</i> , 2008, 453, 391-395.	13.7	739
29	High-quality de novo assembly of the apple genome and methylome dynamics of early fruit development. <i>Nature Genetics</i> , 2017, 49, 1099-1106.	9.4	693
30	Common Sequence Polymorphisms Shaping Genetic Diversity in <i>Arabidopsis thaliana</i> . <i>Science</i> , 2007, 317, 338-342.	6.0	689
31	Spontaneous epigenetic variation in the <i>Arabidopsis thaliana</i> methylome. <i>Nature</i> , 2011, 480, 245-249.	13.7	681
32	A Molecular Link between Stem Cell Regulation and Floral Patterning in <i>Arabidopsis</i> . <i>Cell</i> , 2001, 105, 793-803.	13.5	650
33	Gene silencing in plants using artificial microRNAs and other small RNAs. <i>Plant Journal</i> , 2008, 53, 674-690.	2.8	622
34	Epigenomic Diversity in a Global Collection of <i>Arabidopsis thaliana</i> Accessions. <i>Cell</i> , 2016, 166, 492-505.	13.5	594
35	Antagonistic Regulation of PIN Phosphorylation by PP2A and PINOID Directs Auxin Flux. <i>Cell</i> , 2007, 130, 1044-1056.	13.5	590
36	Genomewide SNP variation reveals relationships among landraces and modern varieties of rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 12273-12278.	3.3	581

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37	SHOREmap: simultaneous mapping and mutation identification by deep sequencing. <i>Nature Methods</i> , 2009, 6, 550-551.	9.0	558
38	Comprehensive Interaction Map of the Arabidopsis MADS Box Transcription Factors. <i>Plant Cell</i> , 2005, 17, 1424-1433.	3.1	528
39	A genetic framework for floral patterning. <i>Nature</i> , 1998, 395, 561-566.	13.7	525
40	Rapid generation of a transgene-free powdery mildew resistant tomato by genome deletion. <i>Scientific Reports</i> , 2017, 7, 482.	1.6	525
41	Gibberellins Promote Flowering of Arabidopsis by Activating the LEAFY Promoter. <i>Plant Cell</i> , 1998, 10, 791-800.	3.1	519
42	Dual Effects of miR156-Targeted <i>SPL</i> Genes and <i>CYP78A5/KLUH</i> on Plastochron Length and Organ Size in <i>Arabidopsis thaliana</i> . <i>Plant Cell</i> , 2008, 20, 1231-1243.	3.1	514
43	Potent Induction of Arabidopsis thaliana Flowering by Elevated Growth Temperature. <i>PLoS Genetics</i> , 2006, 2, e106.	1.5	502
44	Recombination and linkage disequilibrium in Arabidopsis thaliana. <i>Nature Genetics</i> , 2007, 39, 1151-1155.	9.4	497
45	Autoimmune Response as a Mechanism for a Dobzhansky-Muller-Type Incompatibility Syndrome in Plants. <i>PLoS Biology</i> , 2007, 5, e236.	2.6	489
46	Control of cell proliferation in <i>Arabidopsis thaliana</i> by microRNA miR396. <i>Development (Cambridge)</i> , 2010, 137, 103-112.	1.2	476
47	Regulation of Auxin Response by the Protein Kinase PINOID. <i>Cell</i> , 2000, 100, 469-478.	13.5	464
48	Integration of floral inductive signals in Arabidopsis. <i>Nature</i> , 2000, 404, 889-892.	13.7	458
49	The fork head domain: A novel DNA binding motif of eukaryotic transcription factors?. <i>Cell</i> , 1990, 63, 455-456.	13.5	456
50	A divergent external loop confers antagonistic activity on floral regulators FT and TFL1. <i>EMBO Journal</i> , 2006, 25, 605-614.	3.5	445
51	Sequencing of natural strains of <i>Arabidopsis thaliana</i> with short reads. <i>Genome Research</i> , 2008, 18, 2024-2033.	2.4	442
52	Transcriptional Control of Gene Expression by MicroRNAs. <i>Cell</i> , 2010, 140, 111-122.	13.5	431
53	The extent of linkage disequilibrium in Arabidopsis thaliana. <i>Nature Genetics</i> , 2002, 30, 190-193.	9.4	425
54	A thermosensory pathway controlling flowering time in Arabidopsis thaliana. <i>Nature Genetics</i> , 2003, 33, 168-171.	9.4	420

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55	The 1001 Genomes Project for <i>Arabidopsis thaliana</i> . <i>Genome Biology</i> , 2009, 10, 107.	13.9	420
56	Dissection of floral induction pathways using global expression analysis. <i>Development (Cambridge)</i> , 2003, 130, 6001-6012.	1.2	418
57	Genomes of 13 domesticated and wild rice relatives highlight genetic conservation, turnover and innovation across the genus <i>Oryza</i> . <i>Nature Genetics</i> , 2018, 50, 285-296.	9.4	413
58	Next-generation genetics in plants. <i>Nature</i> , 2008, 456, 720-723.	13.7	409
59	Move on up, it's time for change" mobile signals controlling photoperiod-dependent flowering. <i>Genes and Development</i> , 2007, 21, 2371-2384.	2.7	404
60	Sequence and Expression Differences Underlie Functional Specialization of <i>Arabidopsis</i> MicroRNAs miR159 and miR319. <i>Developmental Cell</i> , 2007, 13, 115-125.	3.1	399
61	The genome of the stress-tolerant wild tomato species <i>Solanum pennellii</i> . <i>Nature Genetics</i> , 2014, 46, 1034-1038.	9.4	391
62	Hybrid necrosis: autoimmunity as a potential gene-flow barrier in plant species. <i>Nature Reviews Genetics</i> , 2007, 8, 382-393.	7.7	382
63	Dual roles of the nuclear cap-binding complex and SERRATE in pre-mRNA splicing and microRNA processing in <i>Arabidopsis thaliana</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 8795-8800.	3.3	378
64	Natural allelic variation underlying a major fitness trade-off in <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2010, 465, 632-636.	13.7	378
65	MIRNA Control of Vegetative Phase Change in Trees. <i>PLoS Genetics</i> , 2011, 7, e1002012.	1.5	374
66	The <i>Capsella rubella</i> genome and the genomic consequences of rapid mating system evolution. <i>Nature Genetics</i> , 2013, 45, 831-835.	9.4	374
67	Convergent Targeting of a Common Host Protein-Network by Pathogen Effectors from Three Kingdoms of Life. <i>Cell Host and Microbe</i> , 2014, 16, 364-375.	5.1	367
68	Activation of a Floral Homeotic Gene in <i>Arabidopsis</i> . <i>Science</i> , 1999, 285, 585-587.	6.0	364
69	Large-Scale Identification of Single-Feature Polymorphisms in Complex Genomes. <i>Genome Research</i> , 2003, 13, 513-523.	2.4	345
70	A Collection of Target Mimics for Comprehensive Analysis of MicroRNA Function in <i>Arabidopsis thaliana</i> . <i>PLoS Genetics</i> , 2010, 6, e1001031.	1.5	339
71	The rise and fall of the <i>Phytophthora infestans</i> lineage that triggered the Irish potato famine. <i>ELife</i> , 2013, 2, e00731.	2.8	339
72	The Scale of Population Structure in <i>Arabidopsis thaliana</i> . <i>PLoS Genetics</i> , 2010, 6, e1000843.	1.5	338

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73	MicroRNA networks and developmental plasticity in plants. <i>Trends in Plant Science</i> , 2011, 16, 258-264.	4.3	337
74	Natural Variation in Arabidopsis: From Molecular Genetics to Ecological Genomics. <i>Plant Physiology</i> , 2012, 158, 2-22.	2.3	330
75	Comparative transcriptomics reveals patterns of selection in domesticated and wild tomato. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E2655-62.	3.3	325
76	Highly specific gene silencing by artificial microRNAs in the unicellular alga <i>Chlamydomonas reinhardtii</i> . <i>Plant Journal</i> , 2009, 58, 165-174.	2.8	317
77	Selective epigenetic control of retrotransposition in Arabidopsis. <i>Nature</i> , 2009, 461, 427-430.	13.7	315
78	Transposable elements and small RNAs contribute to gene expression divergence between <i>Arabidopsis thaliana</i> and <i>Arabidopsis lyrata</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 2322-2327.	3.3	308
79	Diversity of Flowering Responses in Wild Arabidopsis thaliana Strains. <i>PLoS Genetics</i> , 2005, 1, e6.	1.5	303
80	Cell-Cell Signaling and Movement by the Floral Transcription Factors LEAFY and APETALA1. <i>Science</i> , 2000, 289, 779-781.	6.0	300
81	Highly Specific Gene Silencing by Artificial miRNAs in Rice. <i>PLoS ONE</i> , 2008, 3, e1829.	1.1	295
82	<i>GAMYB-like</i> Genes, Flowering, and Gibberellin Signaling in Arabidopsis. <i>Plant Physiology</i> , 2001, 127, 1682-1693.	2.3	291
83	Activation of Floral Homeotic Genes in Arabidopsis. <i>Science</i> , 1993, 261, 1723-1726.	6.0	284
84	Stem cells that make stems. <i>Nature</i> , 2002, 415, 751-754.	13.7	282
85	Hyperosmotic stress memory in Arabidopsis is mediated by distinct epigenetically labile sites in the genome and is restricted in the male germline by DNA glycosylase activity. <i>ELife</i> , 2016, 5, .	2.8	282
86	The role of JAGGED in shaping lateral organs. <i>Development (Cambridge)</i> , 2004, 131, 1101-1110.	1.2	277
87	Stress-induced changes in the <i>Arabidopsis thaliana</i> transcriptome analyzed using whole-genome tiling arrays. <i>Plant Journal</i> , 2009, 58, 1068-1082.	2.8	273
88	A LEAFY co-regulator encoded by UNUSUAL FLORAL ORGANS. <i>Current Biology</i> , 1997, 7, 95-104.	1.8	271
89	The Arabidopsis thaliana MERISTEM LAYER 1 promoter specifies epidermal expression in meristems and young primordia. <i>Plant Journal</i> , 1999, 20, 259-263.	2.8	269
90	A Species-Wide Inventory of NLR Genes and Alleles in Arabidopsis thaliana. <i>Cell</i> , 2019, 178, 1260-1272.e14.	13.5	265

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91	Natural variation in light sensitivity of Arabidopsis. <i>Nature Genetics</i> , 2001, 29, 441-446.	9.4	261
92	Genome-wide analysis of local chromatin packing in <i>Arabidopsis thaliana</i> . <i>Genome Research</i> , 2015, 25, 246-256.	2.4	254
93	Species-wide Genetic Incompatibility Analysis Identifies Immune Genes as Hot Spots of Deleterious Epistasis. <i>Cell</i> , 2014, 159, 1341-1351.	13.5	247
94	High contiguity Arabidopsis thaliana genome assembly with a single nanopore flow cell. <i>Nature Communications</i> , 2018, 9, 541.	5.8	243
95	Reference-guided assembly of four diverse <i>Arabidopsis thaliana</i> genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 10249-10254.	3.3	237
96	MicroRNA Gene Evolution in <i>Arabidopsis lyrata</i> and <i>Arabidopsis thaliana</i> . <i>Plant Cell</i> , 2010, 22, 1074-1089.	3.1	234
97	Transformation of <i>Medicago truncatula</i> via infiltration of seedlings or flowering plants with <i>Agrobacterium</i> . <i>Plant Journal</i> , 2000, 22, 531-541.	2.8	233
98	The EDS1-PAD4-ADR1 node mediates Arabidopsis pattern-triggered immunity. <i>Nature</i> , 2021, 598, 495-499.	13.7	223
99	Increased Leaf Size: Different Means to an End. <i>Plant Physiology</i> , 2010, 153, 1261-1279.	2.3	222
100	Requirement of Homeobox Gene STIMPY/WOX9 for Arabidopsis Meristem Growth and Maintenance. <i>Current Biology</i> , 2005, 15, 436-440.	1.8	219
101	Fast-Forward Genetics Identifies Plant CPL Phosphatases as Regulators of miRNA Processing Factor HYL1. <i>Cell</i> , 2012, 151, 859-870.	13.5	219
102	Two gap genes mediate maternal terminal pattern information in <i>Drosophila</i> . <i>Science</i> , 1990, 248, 495-498.	6.0	218
103	Fast-forward genetics enabled by new sequencing technologies. <i>Trends in Plant Science</i> , 2011, 16, 282-288.	4.3	216
104	Simultaneous alignment of short reads against multiple genomes. <i>Genome Biology</i> , 2009, 10, R98.	13.9	215
105	Plant secondary siRNA production determined by microRNA-duplex structure. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 2461-2466.	3.3	215
106	On reconciling the interactions between <i>APETALA2</i> , miR172 and <i>AGAMOUS</i> with the ABC model of flower development. <i>Development (Cambridge)</i> , 2010, 137, 3633-3642.	1.2	214
107	Building Beauty. <i>Developmental Cell</i> , 2002, 2, 135-142.	3.1	212
108	Double-strand break repair processes drive evolution of the mitochondrial genome in Arabidopsis. <i>BMC Biology</i> , 2011, 9, 64.	1.7	209

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109	Mutation bias reflects natural selection in <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2022, 602, 101-105.	13.7	206
110	Modes of intercellular transcription factor movement in the <i>Arabidopsis</i> apex. <i>Development (Cambridge)</i> , 2003, 130, 3735-3745.	1.2	204
111	Recent speciation of <i>Capsella rubella</i> from <i>Capsella grandiflora</i> , associated with loss of self-incompatibility and an extreme bottleneck. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 5246-5251.	3.3	204
112	Regulatory Elements of the Floral Homeotic Gene <i>AGAMOUS</i> Identified by Phylogenetic Footprinting and Shadowing [W]. <i>Plant Cell</i> , 2003, 15, 1296-1309.	3.1	200
113	Improved white spruce (<i>Picea glauca</i>) genome assemblies and annotation of large gene families of conifer terpenoid and phenolic defense metabolism. <i>Plant Journal</i> , 2015, 83, 189-212.	2.8	200
114	Prominent topologically associated domains differentiate global chromatin packing in rice from <i>Arabidopsis</i> . <i>Nature Plants</i> , 2017, 3, 742-748.	4.7	200
115	Sequencing of the genus <i>Arabidopsis</i> identifies a complex history of nonbifurcating speciation and abundant trans-specific polymorphism. <i>Nature Genetics</i> , 2016, 48, 1077-1082.	9.4	198
116	The genomic landscape of meiotic crossovers and gene conversions in <i>Arabidopsis thaliana</i> . <i>ELife</i> , 2013, 2, e01426.	2.8	197
117	Structural Features Determining Flower-Promoting Activity of <i>Arabidopsis</i> FLOWERING LOCUS T. <i>Plant Cell</i> , 2014, 26, 552-564.	3.1	196
118	<i>Arabidopsis</i> FLL2 promotes liquid-liquid phase separation of polyadenylation complexes. <i>Nature</i> , 2019, 569, 265-269.	13.7	196
119	The Floral Regulator <i>LEAFY</i> Evolves by Substitutions in the DNA Binding Domain. <i>Science</i> , 2005, 308, 260-263.	6.0	195
120	The <i>PHYTOCHROME C</i> photoreceptor gene mediates natural variation in flowering and growth responses of <i>Arabidopsis thaliana</i> . <i>Nature Genetics</i> , 2006, 38, 711-715.	9.4	191
121	Genome-wide analysis of chromatin packing in <i>Arabidopsis thaliana</i> at single-gene resolution. <i>Genome Research</i> , 2016, 26, 1057-1068.	2.4	187
122	Evolution of DNA Methylation Patterns in the Brassicaceae is Driven by Differences in Genome Organization. <i>PLoS Genetics</i> , 2014, 10, e1004785.	1.5	184
123	A proposed regulatory framework for genome-edited crops. <i>Nature Genetics</i> , 2016, 48, 109-111.	9.4	184
124	The Genetics of Flower Development: From Floral Induction to Ovule Morphogenesis. <i>Annual Review of Genetics</i> , 1995, 29, 19-39.	3.2	179
125	Identification of plant microRNA homologs. <i>Bioinformatics</i> , 2006, 22, 359-360.	1.8	178
126	Genome-Wide Comparison of Nucleotide-Binding Site-Leucine-Rich Repeat-Encoding Genes in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2011, 157, 757-769.	2.3	175

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127	Quantitative trait locus mapping and DNA array hybridization identify an FLM deletion as a cause for natural flowering-time variation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 2460-2465.	3.3	174
128	Local-Scale Patterns of Genetic Variability, Outcrossing, and Spatial Structure in Natural Stands of <i>Arabidopsis thaliana</i> . <i>PLoS Genetics</i> , 2010, 6, e1000890.	1.5	172
129	Ubiquitin facilitates a quality-control pathway that removes damaged chloroplasts. <i>Science</i> , 2015, 350, 450-454.	6.0	171
130	Genomic estimation of complex traits reveals ancient maize adaptation to temperate North America. <i>Science</i> , 2017, 357, 512-515.	6.0	169
131	The Evolution of Selfing in <i>Arabidopsis thaliana</i> . <i>Science</i> , 2007, 317, 1070-1072.	6.0	160
132	Genetic Architecture of Flowering-Time Variation in <i>Arabidopsis thaliana</i> . <i>Genetics</i> , 2011, 188, 421-433.	1.2	160
133	Genome-wide patterns of single-feature polymorphism in <i>Arabidopsis thaliana</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 12057-12062.	3.3	157
134	Temporal Control of Leaf Complexity by miRNA-Regulated Licensing of Protein Complexes. <i>Current Biology</i> , 2014, 24, 2714-2719.	1.8	157
135	Genomic basis and evolutionary potential for extreme drought adaptation in <i>Arabidopsis thaliana</i> . <i>Nature Ecology and Evolution</i> , 2018, 2, 352-358.	3.4	157
136	Genome expansion of <i>Arabis alpina</i> linked with retrotransposition and reduced symmetric DNA methylation. <i>Nature Plants</i> , 2015, 1, 14023.	4.7	156
137	The Role of the <i>Arabidopsis</i> Morning Loop Components CCA1, LHY, PRR7, and PRR9 in Temperature Compensation. <i>Plant Cell</i> , 2010, 22, 3650-3661.	3.1	155
138	The recombination landscape in <i>Arabidopsis thaliana</i> F2 populations. <i>Heredity</i> , 2012, 108, 447-455.	1.2	155
139	<i>LNK</i> genes integrate light and clock signaling networks at the core of the <i>Arabidopsis</i> oscillator. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 12120-12125.	3.3	154
140	Flowering-Time Genes Modulate the Response to LEAFY Activity. <i>Genetics</i> , 1998, 150, 403-410.	1.2	151
141	Prediction of Regulatory Interactions from Genome Sequences Using a Biophysical Model for the <i>Arabidopsis</i> LEAFY Transcription Factor. <i>Plant Cell</i> , 2011, 23, 1293-1306.	3.1	148
142	Century-scale Methylome Stability in a Recently Diverged <i>Arabidopsis thaliana</i> Lineage. <i>PLoS Genetics</i> , 2015, 11, e1004920.	1.5	148
143	Natural selection on the <i>Arabidopsis thaliana</i> genome in present and future climates. <i>Nature</i> , 2019, 573, 126-129.	13.7	148
144	Combinations of WOX activities regulate tissue proliferation during <i>Arabidopsis</i> embryonic development. <i>Developmental Biology</i> , 2007, 309, 306-316.	0.9	147

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145	Structure Determinants for Accurate Processing of miR172a in <i>Arabidopsis thaliana</i> . <i>Current Biology</i> , 2010, 20, 42-48.	1.8	146
146	<i>Arabidopsis thaliana</i> and <i>Pseudomonas</i> Pathogens Exhibit Stable Associations over Evolutionary Timescales. <i>Cell Host and Microbe</i> , 2018, 24, 168-179.e4.	5.1	145
147	The 35S promoter used in a selectable marker gene of a plant transformation vector affects the expression of the transgene. <i>Planta</i> , 2005, 221, 523-530.	1.6	144
148	Climate Change and the Integrity of Science. <i>Science</i> , 2010, 328, 689-690.	6.0	143
149	Epialleles in plant evolution. <i>Genome Biology</i> , 2012, 13, 249.	13.9	142
150	A genetic framework for fruit patterning in <i>Arabidopsis thaliana</i> . <i>Development (Cambridge)</i> , 2005, 132, 4687-4696.	1.2	141
151	High-resolution experimental and computational profiling of tissue-specific known and novel miRNAs in <i>Arabidopsis</i> . <i>Genome Research</i> , 2012, 22, 163-176.	2.4	140
152	FRIGIDA-Independent Variation in Flowering Time of Natural <i>Arabidopsis thaliana</i> Accessions. <i>Genetics</i> , 2005, 170, 1197-1207.	1.2	138
153	User guide for mapping-by-sequencing in <i>Arabidopsis</i> . <i>Genome Biology</i> , 2013, 14, R61.	3.8	138
154	Probing the Reproducibility of Leaf Growth and Molecular Phenotypes: A Comparison of Three <i>Arabidopsis</i> Accessions Cultivated in Ten Laboratories. <i>Plant Physiology</i> , 2010, 152, 2142-2157.	2.3	137
155	A genetic and molecular model for flower development in <i>Arabidopsis thaliana</i> . <i>Development (Cambridge)</i> , 1991, 113, 157-167.	1.2	136
156	The <i>NGATHA</i> Genes Direct Style Development in the <i>Arabidopsis</i> Gynoecium. <i>Plant Cell</i> , 2009, 21, 1394-1409.	3.1	135
157	Evolution of Floral Meristem Identity Genes. Analysis of <i>Lolium temulentum</i> Genes Related to <i>APETALA1</i> and <i>LEAFY</i> of <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2001, 125, 1788-1801.	2.3	134
158	Evolution of <i>Arabidopsis thaliana</i> microRNAs from random sequences. <i>Rna</i> , 2008, 14, 2455-2459.	1.6	133
159	Genome-wide single nucleotide polymorphisms reveal population history and adaptive divergence in wild guppies. <i>Molecular Ecology</i> , 2010, 19, 968-984.	2.0	133
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