

# Robert J Schmitz

## List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

152 papers	12,330 citations	57 h-index	110 g-index
176 ext. papers	16,464 ext. citations	11.5 avg, IF	6.6 L-index

#	Paper	IF	Citations
152	Evidence for network evolution in an Arabidopsis interactome map. <i>Science</i> , <b>2011</b> , 333, 601-7	33.3	689
151	Widespread dynamic DNA methylation in response to biotic stress. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, E2183-91	11.5	640
150	1,135 Genomes Reveal the Global Pattern of Polymorphism in Arabidopsis thaliana. <i>Cell</i> , <b>2016</b> , 166, 481-491	40.1	620
149	The genome sequences of Arachis duranensis and Arachis ipaensis, the diploid ancestors of cultivated peanut. <i>Nature Genetics</i> , <b>2016</b> , 48, 438-46	36.3	498
148	Transgenerational epigenetic instability is a source of novel methylation variants. <i>Science</i> , <b>2011</b> , 334, 369-73	33.3	485
147	Patterns of population epigenomic diversity. <i>Nature</i> , <b>2013</b> , 495, 193-8	50.4	406
146	Epigenomic Diversity in a Global Collection of Arabidopsis thaliana Accessions. <i>Cell</i> , <b>2016</b> , 166, 492-505	56.2	353
145	Targeted genome modifications in soybean with CRISPR/Cas9. <i>BMC Biotechnology</i> , <b>2015</b> , 15, 16	3.5	338
144	Linking photoreceptor excitation to changes in plant architecture. <i>Genes and Development</i> , <b>2012</b> , 26, 785-90	12.6	334
143	Processing and subcellular trafficking of ER-tethered EIN2 control response to ethylene gas. <i>Science</i> , <b>2012</b> , 338, 390-3	33.3	333
142	Widespread natural variation of DNA methylation within angiosperms. <i>Genome Biology</i> , <b>2016</b> , 17, 194	18.3	289
141	Temporal transcriptional response to ethylene gas drives growth hormone cross-regulation in Arabidopsis. <i>ELife</i> , <b>2013</b> , 2, e00675	8.9	265
140	RF1 knockout allows ribosomal incorporation of unnatural amino acids at multiple sites. <i>Nature Chemical Biology</i> , <b>2011</b> , 7, 779-86	11.7	255
139	Integration of omic networks in a developmental atlas of maize. <i>Science</i> , <b>2016</b> , 353, 814-8	33.3	232
138	Circadian oscillations of protein-coding and regulatory RNAs in a highly dynamic mammalian liver epigenome. <i>Cell Metabolism</i> , <b>2012</b> , 16, 833-45	24.6	199
137	MethylC-seq library preparation for base-resolution whole-genome bisulfite sequencing. <i>Nature Protocols</i> , <b>2015</b> , 10, 475-83	18.8	190
136	On the origin and evolutionary consequences of gene body DNA methylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2016</b> , 113, 9111-6	11.5	189

135	Epigenome-wide inheritance of cytosine methylation variants in a recombinant inbred population. <i>Genome Research</i> , <b>2013</b> , 23, 1663-74	9.7	189
134	Gene body DNA methylation in plants. <i>Current Opinion in Plant Biology</i> , <b>2017</b> , 36, 103-110	9.9	186
133	Revealing the playing field for analyses of single-base resolution DNA methylomes. <i>Trends in Genetics</i> , <b>2012</b> , 28, 583-5	8.5	182
132	Widespread adenine N6-methylation of active genes in fungi. <i>Nature Genetics</i> , <b>2017</b> , 49, 964-968	36.3	181
131	Two putative BIN2 substrates are nuclear components of brassinosteroid signaling. <i>Plant Physiology</i> , <b>2002</b> , 130, 1221-9	6.6	168
130	Evolution of DNA Methylation across Insects. <i>Molecular Biology and Evolution</i> , <b>2017</b> , 34, 654-665	8.3	162
129	A PHD finger protein involved in both the vernalization and photoperiod pathways in Arabidopsis. <i>Genes and Development</i> , <b>2006</b> , 20, 3244-8	12.6	161
128	Genome-wide identification of CCA1 targets uncovers an expanded clock network in Arabidopsis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2015</b> , 112, E4802-10	11.5	156
127	Rate, spectrum, and evolutionary dynamics of spontaneous epimutations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2015</b> , 112, 6676-81	11.5	145
126	Arabidopsis brassinosteroid-insensitive dwarf12 mutants are semidominant and defective in a glycogen synthase kinase 3beta-like kinase. <i>Plant Physiology</i> , <b>2002</b> , 130, 1506-15	6.6	136
125	Combining ATAC-seq with nuclei sorting for discovery of cis-regulatory regions in plant genomes. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, e41	20.1	133
124	Widespread long-range cis-regulatory elements in the maize genome. <i>Nature Plants</i> , <b>2019</b> , 5, 1237-1249	11.5	127
123	RNA-directed DNA methylation enforces boundaries between heterochromatin and euchromatin in the maize genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2015</b> , 112, 14728-33	11.5	126
122	Unique cell-type-specific patterns of DNA methylation in the root meristem. <i>Nature Plants</i> , <b>2016</b> , 2, 16058	11.5	125
121	Exploiting induced and natural epigenetic variation for crop improvement. <i>Nature Reviews Genetics</i> , <b>2017</b> , 18, 563-575	30.1	121
120	Sigma factor-mediated plastid retrograde signals control nuclear gene expression. <i>Plant Journal</i> , <b>2013</b> , 73, 1-13	6.9	117
119	Subgenome Dominance in an Interspecific Hybrid, Synthetic Allopolyploid, and a 140-Year-Old Naturally Established Neo-Allopolyploid Monkeyflower. <i>Plant Cell</i> , <b>2017</b> , 29, 2150-2167	11.6	115
118	Evolutionary conservation of the FLOWERING LOCUS C-mediated vernalization response: evidence from the sugar beet ( <i>Beta vulgaris</i> ). <i>Genetics</i> , <b>2007</b> , 176, 295-307	4	110

117	Improving nanopore read accuracy with the R2C2 method enables the sequencing of highly multiplexed full-length single-cell cDNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2018</b> , 115, 9726-9731	11.5	109
116	Genomic distribution of H3K9me2 and DNA methylation in a maize genome. <i>PLoS ONE</i> , <b>2014</b> , 9, e105267	3.7	108
115	The prevalence, evolution and chromatin signatures of plant regulatory elements. <i>Nature Plants</i> , <b>2019</b> , 5, 1250-1259	11.5	107
114	Epigenetics: Beyond Chromatin Modifications and Complex Genetic Regulation. <i>Plant Physiology</i> , <b>2014</b> , 165, 933-947	6.6	101
113	Histone arginine methylation is required for vernalization-induced epigenetic silencing of FLC in winter-annual <i>Arabidopsis thaliana</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2008</b> , 105, 411-6	11.5	98
112	Photoperiodic control of the floral transition through a distinct polycomb repressive complex. <i>Developmental Cell</i> , <b>2014</b> , 28, 727-36	10.2	95
111	Vernalization: a model for investigating epigenetics and eukaryotic gene regulation in plants. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , <b>2007</b> , 1769, 269-75		94
110	Release factor one is nonessential in <i>Escherichia coli</i> . <i>ACS Chemical Biology</i> , <b>2012</b> , 7, 1337-44	4.9	85
109	Putting DNA methylation in context: from genomes to gene expression in plants. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , <b>2017</b> , 1860, 149-156	6	84
108	Maize death acids, 9-lipoxygenase-derived cyclopent(a)enones, display activity as cytotoxic phytoalexins and transcriptional mediators. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2015</b> , 112, 11407-12	11.5	83
107	The evolution of CHROMOMETHYLASES and gene body DNA methylation in plants. <i>Genome Biology</i> , <b>2017</b> , 18, 65	18.3	80
106	Histone H2B deubiquitination is required for transcriptional activation of FLOWERING LOCUS C and for proper control of flowering in <i>Arabidopsis</i> . <i>Plant Physiology</i> , <b>2009</b> , 149, 1196-204	6.6	80
105	Full-length autonomous transposable elements are preferentially targeted by expression-dependent forms of RNA-directed DNA methylation. <i>Genome Biology</i> , <b>2016</b> , 17, 170	18.3	77
104	Epigenetic and epigenomic variation in <i>Arabidopsis thaliana</i> . <i>Trends in Plant Science</i> , <b>2012</b> , 17, 149-54	13.1	76
103	FRIGIDA-ESSENTIAL 1 interacts genetically with FRIGIDA and FRIGIDA-LIKE 1 to promote the winter-annual habit of <i>Arabidopsis thaliana</i> . <i>Development (Cambridge)</i> , <b>2005</b> , 132, 5471-8	6.6	74
102	Stable inheritance of DNA methylation allows creation of epigenotype maps and the study of epiallele inheritance patterns in the absence of genetic variation. <i>Genome Biology</i> , <b>2017</b> , 18, 155	18.3	72
101	The DNA binding landscape of the maize AUXIN RESPONSE FACTOR family. <i>Nature Communications</i> , <b>2018</b> , 9, 4526	17.4	69
100	The Genome and Methylome of a Beetle with Complex Social Behavior, <i>Nicrophorus vespilloides</i> (Coleoptera: Silphidae). <i>Genome Biology and Evolution</i> , <b>2015</b> , 7, 3383-96	3.9	65

99	DNA Methylation: Shared and Divergent Features across Eukaryotes. <i>Trends in Genetics</i> , <b>2019</b> , 35, 818-827.5	64
98	Firefly genomes illuminate parallel origins of bioluminescence in beetles. <i>ELife</i> , <b>2018</b> , 7, 1-12.9	64
97	Covering your bases: inheritance of DNA methylation in plant genomes. <i>Molecular Plant</i> , <b>2014</b> , 7, 472-8014.4	61
96	Unexpected Diversity of Chloroplast Noncoding RNAs as Revealed by Deep Sequencing of the Arabidopsis Transcriptome. <i>G3: Genes, Genomes, Genetics</i> , <b>2011</b> , 1, 559-70	3.2 58
95	Genome-wide redistribution of H3K27me3 is linked to genotoxic stress and defective growth. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2015</b> , 112, E6339-48	11.5 57
94	Diversity of cytosine methylation across the fungal tree of life. <i>Nature Ecology and Evolution</i> , <b>2019</b> , 3, 479-490	12.3 57
93	Divergent cytosine DNA methylation patterns in single-cell, soybean root hairs. <i>New Phytologist</i> , <b>2017</b> , 214, 808-819	9.8 49
92	A Comparative Analysis of 5-Azacytidine- and Zebularine-Induced DNA Demethylation. <i>G3: Genes, Genomes, Genetics</i> , <b>2016</b> , 6, 2773-80	3.2 49
91	DICER-LIKE 1 and DICER-LIKE 3 redundantly act to promote flowering via repression of FLOWERING LOCUS C in Arabidopsis thaliana. <i>Genetics</i> , <b>2007</b> , 176, 1359-62	4 43
90	Spontaneous epimutations in plants. <i>New Phytologist</i> , <b>2019</b> , 221, 1253-1259	9.8 43
89	Methylated DNA is over-represented in whole-genome bisulfite sequencing data. <i>Frontiers in Genetics</i> , <b>2014</b> , 5, 341	4.5 42
88	Dnmt1 is essential for egg production and embryo viability in the large milkweed bug, <i>Oncopeltus fasciatus</i> . <i>Epigenetics and Chromatin</i> , <b>2019</b> , 12, 6	5.8 40
87	High-throughput approaches for plant epigenomic studies. <i>Current Opinion in Plant Biology</i> , <b>2011</b> , 14, 130-6	9.9 40
86	De novo assembly, annotation, and comparative analysis of 26 diverse maize genomes. <i>Science</i> , <b>2021</b> , 373, 655-662	33.3 40
85	Single-cell RNA sequencing of developing maize ears facilitates functional analysis and trait candidate gene discovery. <i>Developmental Cell</i> , <b>2021</b> , 56, 557-568.e6	10.2 39
84	Brahma is required for proper expression of the floral repressor FLC in Arabidopsis. <i>PLoS ONE</i> , <b>2011</b> , 6, e17997	3.7 38
83	A cis-regulatory atlas in maize at single-cell resolution. <i>Cell</i> , <b>2021</b> , 184, 3041-3055.e21	56.2 37
82	Base-resolution detection of N4-methylcytosine in genomic DNA using 4mC-Tet-assisted-bisulfite-sequencing. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, e148	20.1 36

81	Multiple genes recruited from hormone pathways partition maize diterpenoid defences. <i>Nature Plants</i> , <b>2019</b> , 5, 1043-1056	11.5	36
80	Crop Epigenomics: Identifying, Unlocking, and Harnessing Cryptic Variation in Crop Genomes. <i>Molecular Plant</i> , <b>2015</b> , 8, 860-70	14.4	34
79	Epimutations are associated with CHROMOMETHYLASE 3-induced de novo DNA methylation. <i>ELife</i> , <b>2019</b> , 8,	8.9	34
78	Surveillance of 3RNoncoding Transcripts Requires FIERY1 and XRN3 in Arabidopsis. <i>G3: Genes, Genomes, Genetics</i> , <b>2012</b> , 2, 487-98	3.2	33
77	Monitoring the interplay between transposable element families and DNA methylation in maize. <i>PLoS Genetics</i> , <b>2019</b> , 15, e1008291	6	32
76	Histone H3 Variant Regulates RNA Polymerase II Transcription Termination and Dual Strand Transcription of siRNA Loci in Trypanosoma brucei. <i>PLoS Genetics</i> , <b>2016</b> , 12, e1005758	6	32
75	Specifications of Targeting Heterochromatin Modifications in Plants. <i>Molecular Plant</i> , <b>2018</b> , 11, 381-387	14.4	31
74	A genome assembly and the somatic genetic and epigenetic mutation rate in a wild long-lived perennial Populus trichocarpa. <i>Genome Biology</i> , <b>2020</b> , 21, 259	18.3	31
73	TET-mediated epimutagenesis of the Arabidopsis thaliana methylome. <i>Nature Communications</i> , <b>2018</b> , 9, 895	17.4	30
72	pENCODE: a plant encyclopedia of DNA elements. <i>Annual Review of Genetics</i> , <b>2014</b> , 48, 49-70	14.5	28
71	The Dnmt3L ADD Domain Controls Cytosine Methylation Establishment during Spermatogenesis. <i>Cell Reports</i> , <b>2015</b> , 10, 944-956	10.6	27
70	Stable unmethylated DNA demarcates expressed genes and their cis-regulatory space in plant genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2020</b> , 117, 23991-24000	11.5	25
69	Genome-Wide Reinforcement of DNA Methylation Occurs during Somatic Embryogenesis in Soybean. <i>Plant Cell</i> , <b>2019</b> , 31, 2315-2331	11.6	24
68	Evolutionary and Experimental Loss of Gene Body Methylation and Its Consequence to Gene Expression. <i>G3: Genes, Genomes, Genetics</i> , <b>2019</b> , 9, 2441-2445	3.2	24
67	Natural variation in DNA methylation homeostasis and the emergence of epialleles. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2020</b> , 117, 4874-4884	11.5	24
66	Arabidopsis Protein Kinase D6PKL3 Is Involved in the Formation of Distinct Plasma Membrane Aperture Domains on the Pollen Surface. <i>Plant Cell</i> , <b>2018</b> , 30, 2038-2056	11.6	21
65	Pericentromeric hypomethylation elicits an interferon response in an animal model of ICF syndrome. <i>ELife</i> , <b>2018</b> , 7,	8.9	21
64	Chromatin accessibility profiling methods. <i>Nature Reviews Methods Primers</i> , <b>2021</b> , 1,		21

63	Epigenomic programming contributes to the genomic drift evolution of the F-Box protein superfamily in Arabidopsis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2013</b> , 110, 16927-32	11.5	20
62	Cell wall composition and digestibility alterations in Brachypodium distachyon achieved through reduced expression of the UDP-arabinopyranose mutase. <i>Frontiers in Plant Science</i> , <b>2015</b> , 6, 446	6.2	18
61	The Genome as a Resource for Cotton Breeding and Evolution. <i>G3: Genes, Genomes, Genetics</i> , <b>2020</b> , 10, 1457-1467	3.2	17
60	Identification of a novel base J binding protein complex involved in RNA polymerase II transcription termination in trypanosomes. <i>PLoS Genetics</i> , <b>2020</b> , 16, e1008390	6	17
59	Identification of cis-regulatory elements by chromatin structure. <i>Current Opinion in Plant Biology</i> , <b>2018</b> , 42, 90-94	9.9	17
58	Zebularine treatment is associated with deletion of FT-B1 leading to an increase in spikelet number in bread wheat. <i>Plant, Cell and Environment</i> , <b>2018</b> , 41, 1346-1360	8.4	17
57	Histone H1 Limits DNA Methylation in Neurospora crassa. <i>G3: Genes, Genomes, Genetics</i> , <b>2016</b> , 6, 1879-89	3.2	17
56	Intragenic suppression of a trafficking-defective brassinosteroid receptor mutant in Arabidopsis. <i>Genetics</i> , <b>2010</b> , 185, 1283-96	4	17
55	Directions for research and training in plant omics: Big Questions and Big Data. <i>Plant Direct</i> , <b>2019</b> , 3, e00133	3.3	16
54	Genetics. The secret garden--epigenetic alleles underlie complex traits. <i>Science</i> , <b>2014</b> , 343, 1082-3	33.3	16
53	DNA topoisomerase 1 promotes transcriptional silencing of transposable elements through DNA methylation and histone lysine 9 dimethylation in Arabidopsis. <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004446	6	16
52	Epigenetic silencing of a multifunctional plant stress regulator. <i>ELife</i> , <b>2019</b> , 8,	8.9	16
51	FASTmC: A Suite of Predictive Models for Nonreference-Based Estimations of DNA Methylation. <i>G3: Genes, Genomes, Genetics</i> , <b>2015</b> , 6, 447-52	3.2	13
50	Enhanced JBrowse plugins for epigenomics data visualization. <i>BMC Bioinformatics</i> , <b>2018</b> , 19, 159	3.6	12
49	Base J represses genes at the end of polycistronic gene clusters in Leishmania major by promoting RNAP II termination. <i>Molecular Microbiology</i> , <b>2016</b> , 101, 559-74	4.1	12
48	AlphaBeta: computational inference of epimutation rates and spectra from high-throughput DNA methylation data in plants. <i>Genome Biology</i> , <b>2020</b> , 21, 260	18.3	10
47	Rational development of transformation in Clostridium thermocellum ATCC 27405 via complete methylome analysis and evasion of native restriction-modification systems. <i>Journal of Industrial Microbiology and Biotechnology</i> , <b>2019</b> , 46, 1435-1443	4.2	9
46	Subsets of Visceral Adipose Tissue Nuclei with Distinct Levels of 5-Hydroxymethylcytosine. <i>PLoS ONE</i> , <b>2016</b> , 11, e0154949	3.7	9



45	The LSH/DDM1 Homolog MUS-30 Is Required for Genome Stability, but Not for DNA Methylation in <i>Neurospora crassa</i> . <i>PLoS Genetics</i> , <b>2016</b> , 12, e1005790	6	9
44	De novo assembly, annotation, and comparative analysis of 26 diverse maize genomes		9
43	Changes of gene expression but not cytosine methylation are associated with male parental care reflecting behavioural state, social context and individual flexibility. <i>Journal of Experimental Biology</i> , <b>2019</b> , 222,	3	8
42	EvoChromo: towards a synthesis of chromatin biology and evolution. <i>Development (Cambridge)</i> , <b>2019</b> , 146,	6.6	7
41	Epigenomic diversification within the genus <i>Lupinus</i> . <i>PLoS ONE</i> , <b>2017</b> , 12, e0179821	3.7	7
40	Widespread natural variation of DNA methylation within angiosperms		7
39	Subgenome dominance in an interspecific hybrid, synthetic allopolyploid, and a 140 year old naturally established neo-allopolyploid monkeyflower		7
38	Genotypic variation of gene expression during the soybean innate immunity response. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , <b>2014</b> , 12, S27-S30	1	6
37	Cis-regulatory sequences in plants: their importance, discovery, and future challenges.. <i>Plant Cell</i> , <b>2021</b> ,	11.6	6
36	A novel requirement for DROSHA in maintenance of mammalian CG methylation. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, 9398-9412	20.1	5
35	More Than DNA Methylation: Does Pleiotropy Drive the Complex Pattern of Evolution of Dnmt1?. <i>Frontiers in Ecology and Evolution</i> , <b>2020</b> , 8,	3.7	5
34	Decoding the Epigenomes of Herbaceous Plants. <i>Advances in Botanical Research</i> , <b>2014</b> , 69, 247-277	2.2	5
33	The Role of VIN3-LIKE Genes in Environmentally Induced Epigenetic Regulation of Flowering. <i>Plant Signaling and Behavior</i> , <b>2007</b> , 2, 127-8	2.5	5
32	Anno genominis XX: 20 years of Arabidopsis genomics. <i>Plant Cell</i> , <b>2021</b> , 33, 832-845	11.6	5
31	The evolution of CHROMOMETHYLASES and gene body DNA methylation in plants		5
30	Cis-regulatory elements within TEs can influence expression of nearby maize genes		5
29	A cis-regulatory atlas in maize at single-cell resolution		5
28	Response to perspective: "separation anxiety: an analysis of ethylene-induced cleavage of EIN2". <i>Plant Signaling and Behavior</i> , <b>2013</b> , 8,	2.5	4



27	Epigenetics in the wild. <i>ELife</i> , <b>2015</b> , 4, e07808	8.9	4
26	Assessing the regulatory potential of transposable elements using chromatin accessibility profiles of maize transposons. <i>Genetics</i> , <b>2021</b> , 217, 1-13	4	4
25	Gene-regulatory independent functions for insect DNA methylation		4
24	Current status of the multinational Arabidopsis community. <i>Plant Direct</i> , <b>2020</b> , 4, e00248	3.3	4
23	The essential role of Dnmt1 in in the large milkweed bug. <i>ELife</i> , <b>2021</b> , 10,	8.9	4
22	Leveraging histone modifications to improve genome annotations. <i>G3: Genes, Genomes, Genetics</i> , <b>2021</b> , 11,	3.2	4
21	DNA cytosine hydroxymethylation levels are distinct among non-overlapping classes of peripheral blood leukocytes. <i>Journal of Immunological Methods</i> , <b>2016</b> , 436, 1-15	2.5	4
20	IMITATION SWITCH is required for normal chromatin structure and gene repression in PRC2 target domains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2021</b> , 118,	11.5	4
19	Single-cell analysis of cis-regulatory elements. <i>Current Opinion in Plant Biology</i> , <b>2021</b> , 65, 102094	9.9	4
18	The shocking consequences of hybrid epigenomes. <i>Genome Biology</i> , <b>2016</b> , 17, 85	18.3	3
17	The evolution of DNA methylation and its relationship to sociality in insects		3
16	The somatic genetic and epigenetic mutation rate in a wild long-lived perennial <i>Populus trichocarpa</i>		3
15	A Qualitative Change in the Transcriptome Occurs after the First Cell Cycle and Coincides with Lumen Establishment during MDCKII Cystogenesis. <i>IScience</i> , <b>2020</b> , 23, 101629	6.1	3
14	Evolution of Conserved Noncoding Sequences in <i>Arabidopsis thaliana</i> . <i>Molecular Biology and Evolution</i> , <b>2021</b> , 38, 2692-2703	8.3	3
13	Epimutations Define a Fast-Ticking Molecular Clock in Plants. <i>Trends in Genetics</i> , <b>2021</b> , 37, 699-710	8.5	3
12	Loss of the FOXP1 Transcription Factor Leads to Deregulation of B Lymphocyte Development and Function at Multiple Stages. <i>ImmunoHorizons</i> , <b>2019</b> , 3, 447-462	2.7	2
11	AlphaBeta: Computational inference of epimutation rates and spectra from high-throughput DNA methylation data in plants		2
10	On the Origin and Evolutionary Consequences of Gene Body DNA Methylation		2

9	Stable unmethylated DNA demarcates expressed genes and their cis-regulatory space in plant genomes	2	
8	Chromatin accessibility profiling in <i>Neurospora crassa</i> reveals molecular features associated with accessible and inaccessible chromatin. <i>BMC Genomics</i> , <b>2021</b> , 22, 459	4.5	2
7	Multiplex genome editing in using Mb3Cas12a. <i>Plant Direct</i> , <b>2021</b> , 5, e344	3.3	2
6	Heterochromatin is a quantitative trait associated with spontaneous epiallele formation. <i>Nature Communications</i> , <b>2021</b> , 12, 6958	17.4	1
5	Evolution of conserved noncoding sequences in <i>Arabidopsis thaliana</i>		1
4	The essential role of Dnmt1 in gametogenesis in the large milkweed bug <i>Oncopeltus fasciatus</i>		1
3	Firefly genomes illuminate parallel origins of bioluminescence in beetles		1
2	Profiling single-cell chromatin accessibility in plants. <i>STAR Protocols</i> , <b>2021</b> , 2, 100737	1.4	0
1	A combinatorial indexing strategy for low-cost epigenomic profiling of plant single cells. <i>Plant Communications</i> , <b>2022</b> , 100308	9	0