

Robert J Schmitz

List of Publications by Year in Descending Order

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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	A combinatorial indexing strategy for low-cost epigenomic profiling of plant single cells. <i>Plant Communications</i> , 2022 , 100308	9	0
151	Cis-regulatory sequences in plants: their importance, discovery, and future challenges.. <i>Plant Cell</i> , 2021 ,	11.6	6
150	Heterochromatin is a quantitative trait associated with spontaneous epiallele formation. <i>Nature Communications</i> , 2021 , 12, 6958	17.4	1
149	Assessing the regulatory potential of transposable elements using chromatin accessibility profiles of maize transposons. <i>Genetics</i> , 2021 , 217, 1-13	4	4
148	Anno genominis XX: 20 years of Arabidopsis genomics. <i>Plant Cell</i> , 2021 , 33, 832-845	11.6	5
147	The essential role of Dnmt1 in in the large milkweed bug. <i>ELife</i> , 2021 , 10,	8.9	4
146	A cis-regulatory atlas in maize at single-cell resolution. <i>Cell</i> , 2021 , 184, 3041-3055.e21	56.2	37
145	Chromatin accessibility profiling in <i>Neurospora crassa</i> reveals molecular features associated with accessible and inaccessible chromatin. <i>BMC Genomics</i> , 2021 , 22, 459	4.5	2
144	Leveraging histone modifications to improve genome annotations. <i>G3: Genes, Genomes, Genetics</i> , 2021 , 11,	3.2	4
143	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> , 2021 , 118,	11.5	4
142	Evolution of Conserved Noncoding Sequences in <i>Arabidopsis thaliana</i> . <i>Molecular Biology and Evolution</i> , 2021 , 38, 2692-2703	8.3	3
141	Single-cell RNA sequencing of developing maize ears facilitates functional analysis and trait candidate gene discovery. <i>Developmental Cell</i> , 2021 , 56, 557-568.e6	10.2	39
140	Epimutations Define a Fast-Ticking Molecular Clock in Plants. <i>Trends in Genetics</i> , 2021 , 37, 699-710	8.5	3
139	De novo assembly, annotation, and comparative analysis of 26 diverse maize genomes. <i>Science</i> , 2021 , 373, 655-662	33.3	40
138	Multiplex genome editing in using Mb3Cas12a. <i>Plant Direct</i> , 2021 , 5, e344	3.3	2
137	Profiling single-cell chromatin accessibility in plants. <i>STAR Protocols</i> , 2021 , 2, 100737	1.4	0
136	Single-cell analysis of cis-regulatory elements. <i>Current Opinion in Plant Biology</i> , 2021 , 65, 102094	9.9	4

135	Chromatin accessibility profiling methods. <i>Nature Reviews Methods Primers</i> , 2021 , 1,		21
134	The Genome as a Resource for Cotton Breeding and Evolution. <i>G3: Genes, Genomes, Genetics</i> , 2020 , 10, 1457-1467	3.2	17
133	Identification of a novel base J binding protein complex involved in RNA polymerase II transcription termination in trypanosomes. <i>PLoS Genetics</i> , 2020 , 16, e1008390	6	17
132	More Than DNA Methylation: Does Pleiotropy Drive the Complex Pattern of Evolution of Dnmt1?. <i>Frontiers in Ecology and Evolution</i> , 2020 , 8,	3.7	5
131	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> , 2020 , 117, 4874-4884	11.5	24
130	A genome assembly and the somatic genetic and epigenetic mutation rate in a wild long-lived perennial <i>Populus trichocarpa</i> . <i>Genome Biology</i> , 2020 , 21, 259	18.3	31
129	Current status of the multinational Arabidopsis community. <i>Plant Direct</i> , 2020 , 4, e00248	3.3	4
128	AlphaBeta: computational inference of epimutation rates and spectra from high-throughput DNA methylation data in plants. <i>Genome Biology</i> , 2020 , 21, 260	18.3	10
127	A Qualitative Change in the Transcriptome Occurs after the First Cell Cycle and Coincides with Lumen Establishment during MDCKII Cystogenesis. <i>IScience</i> , 2020 , 23, 101629	6.1	3
126	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> , 2020 , 117, 23991-24000	11.5	25
125	Genome-Wide Reinforcement of DNA Methylation Occurs during Somatic Embryogenesis in Soybean. <i>Plant Cell</i> , 2019 , 31, 2315-2331	11.6	24
124	Monitoring the interplay between transposable element families and DNA methylation in maize. <i>PLoS Genetics</i> , 2019 , 15, e1008291	6	32
123	EvoChromo: towards a synthesis of chromatin biology and evolution. <i>Development (Cambridge)</i> , 2019 , 146,	6.6	7
122	Dnmt1 is essential for egg production and embryo viability in the large milkweed bug, <i>Oncopeltus fasciatus</i> . <i>Epigenetics and Chromatin</i> , 2019 , 12, 6	5.8	40
121	Evolutionary and Experimental Loss of Gene Body Methylation and Its Consequence to Gene Expression. <i>G3: Genes, Genomes, Genetics</i> , 2019 , 9, 2441-2445	3.2	24
120	Directions for research and training in plant omics: Big Questions and Big Data. <i>Plant Direct</i> , 2019 , 3, e00133	3.3	16
119	DNA Methylation: Shared and Divergent Features across Eukaryotes. <i>Trends in Genetics</i> , 2019 , 35, 818-827	27.5	64
118	Rational development of transformation in <i>Clostridium thermocellum</i> ATCC 27405 via complete methylome analysis and evasion of native restriction-modification systems. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2019 , 46, 1435-1443	4.2	9

117	Loss of the FOXP1 Transcription Factor Leads to Deregulation of B Lymphocyte Development and Function at Multiple Stages. <i>ImmunoHorizons</i> , 2019 , 3, 447-462	2.7	2
116	Epigenetic silencing of a multifunctional plant stress regulator. <i>ELife</i> , 2019 , 8,	8.9	16
115	Epimutations are associated with CHROMOMETHYLASE 3-induced de novo DNA methylation. <i>ELife</i> , 2019 , 8,	8.9	34
114	Diversity of cytosine methylation across the fungal tree of life. <i>Nature Ecology and Evolution</i> , 2019 , 3, 479-490	12.3	57
113	Widespread long-range cis-regulatory elements in the maize genome. <i>Nature Plants</i> , 2019 , 5, 1237-1249	11.5	127
112	The prevalence, evolution and chromatin signatures of plant regulatory elements. <i>Nature Plants</i> , 2019 , 5, 1250-1259	11.5	107
111	Multiple genes recruited from hormone pathways partition maize diterpenoid defences. <i>Nature Plants</i> , 2019 , 5, 1043-1056	11.5	36
110	Spontaneous epimutations in plants. <i>New Phytologist</i> , 2019 , 221, 1253-1259	9.8	43
109	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> , 2019 , 222,	3	8
108	TET-mediated epimutagenesis of the Arabidopsis thaliana methylome. <i>Nature Communications</i> , 2018 , 9, 895	17.4	30
107	Identification of cis-regulatory elements by chromatin structure. <i>Current Opinion in Plant Biology</i> , 2018 , 42, 90-94	9.9	17
106	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> , 2018 , 41, 1346-1360	8.4	17
105	Enhanced JBrowse plugins for epigenomics data visualization. <i>BMC Bioinformatics</i> , 2018 , 19, 159	3.6	12
104	Specifications of Targeting Heterochromatin Modifications in Plants. <i>Molecular Plant</i> , 2018 , 11, 381-387	14.4	31
103	Arabidopsis Protein Kinase D6PKL3 Is Involved in the Formation of Distinct Plasma Membrane Aperture Domains on the Pollen Surface. <i>Plant Cell</i> , 2018 , 30, 2038-2056	11.6	21
102	Pericentromeric hypomethylation elicits an interferon response in an animal model of ICF syndrome. <i>ELife</i> , 2018 , 7,	8.9	21
101	Firefly genomes illuminate parallel origins of bioluminescence in beetles. <i>ELife</i> , 2018 , 7,	8.9	64
100	The DNA binding landscape of the maize AUXIN RESPONSE FACTOR family. <i>Nature Communications</i> , 2018 , 9, 4526	17.4	69

99	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> , 2018 , 115, 9726-9731	11.5	109
98	Divergent cytosine DNA methylation patterns in single-cell, soybean root hairs. <i>New Phytologist</i> , 2017 , 214, 808-819	9.8	49
97	Gene body DNA methylation in plants. <i>Current Opinion in Plant Biology</i> , 2017 , 36, 103-110	9.9	186
96	Widespread adenine N6-methylation of active genes in fungi. <i>Nature Genetics</i> , 2017 , 49, 964-968	36.3	181
95	A novel requirement for DROSHA in maintenance of mammalian CG methylation. <i>Nucleic Acids Research</i> , 2017 , 45, 9398-9412	20.1	5
94	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> , 2017 , 18, 155	18.3	72
93	Subgenome Dominance in an Interspecific Hybrid, Synthetic Allopolyploid, and a 140-Year-Old Naturally Established Neo-Allopolyploid Monkeyflower. <i>Plant Cell</i> , 2017 , 29, 2150-2167	11.6	115
92	The evolution of CHROMOMETHYLASES and gene body DNA methylation in plants. <i>Genome Biology</i> , 2017 , 18, 65	18.3	80
91	Exploiting induced and natural epigenetic variation for crop improvement. <i>Nature Reviews Genetics</i> , 2017 , 18, 563-575	30.1	121
90	Putting DNA methylation in context: from genomes to gene expression in plants. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2017 , 1860, 149-156	6	84
89	Combining ATAC-seq with nuclei sorting for discovery of cis-regulatory regions in plant genomes. <i>Nucleic Acids Research</i> , 2017 , 45, e41	20.1	133
88	Epigenomic diversification within the genus <i>Lupinus</i> . <i>PLoS ONE</i> , 2017 , 12, e0179821	3.7	7
87	Evolution of DNA Methylation across Insects. <i>Molecular Biology and Evolution</i> , 2017 , 34, 654-665	8.3	162
86	Histone H1 Limits DNA Methylation in <i>Neurospora crassa</i> . <i>G3: Genes, Genomes, Genetics</i> , 2016 , 6, 1879-89	3.2	17
85	Integration of omic networks in a developmental atlas of maize. <i>Science</i> , 2016 , 353, 814-8	33.3	232
84	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> , 2016 , 113, 9111-6	11.5	189
83	Epigenomic Diversity in a Global Collection of <i>Arabidopsis thaliana</i> Accessions. <i>Cell</i> , 2016 , 166, 492-505	56.2	353
82	Unique cell-type-specific patterns of DNA methylation in the root meristem. <i>Nature Plants</i> , 2016 , 2, 16058	11.5	125

81	The shocking consequences of hybrid epigenomes. <i>Genome Biology</i> , 2016 , 17, 85	18.3	3
80	1,135 Genomes Reveal the Global Pattern of Polymorphism in <i>Arabidopsis thaliana</i> . <i>Cell</i> , 2016 , 166, 481-491	40.1	620
79	Base J represses genes at the end of polycistronic gene clusters in <i>Leishmania major</i> by promoting RNAP II termination. <i>Molecular Microbiology</i> , 2016 , 101, 559-74	4.1	12
78	The genome sequences of <i>Arachis duranensis</i> and <i>Arachis ipaensis</i> , the diploid ancestors of cultivated peanut. <i>Nature Genetics</i> , 2016 , 48, 438-46	36.3	498
77	Subsets of Visceral Adipose Tissue Nuclei with Distinct Levels of 5-Hydroxymethylcytosine. <i>PLoS ONE</i> , 2016 , 11, e0154949	3.7	9
76	Histone H3 Variant Regulates RNA Polymerase II Transcription Termination and Dual Strand Transcription of siRNA Loci in <i>Trypanosoma brucei</i> . <i>PLoS Genetics</i> , 2016 , 12, e1005758	6	32
75	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> , 2016 , 12, e1005790	6	9
74	A Comparative Analysis of 5-Azacytidine- and Zebularine-Induced DNA Demethylation. <i>G3: Genes, Genomes, Genetics</i> , 2016 , 6, 2773-80	3.2	49
73	DNA cytosine hydroxymethylation levels are distinct among non-overlapping classes of peripheral blood leukocytes. <i>Journal of Immunological Methods</i> , 2016 , 436, 1-15	2.5	4
72	Full-length autonomous transposable elements are preferentially targeted by expression-dependent forms of RNA-directed DNA methylation. <i>Genome Biology</i> , 2016 , 17, 170	18.3	77
71	Widespread natural variation of DNA methylation within angiosperms. <i>Genome Biology</i> , 2016 , 17, 194	18.3	289
70	Targeted genome modifications in soybean with CRISPR/Cas9. <i>BMC Biotechnology</i> , 2015 , 15, 16	3.5	338
69	Rate, spectrum, and evolutionary dynamics of spontaneous epimutations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 6676-81	11.5	145
68	Crop Epigenomics: Identifying, Unlocking, and Harnessing Cryptic Variation in Crop Genomes. <i>Molecular Plant</i> , 2015 , 8, 860-70	14.4	34
67	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> , 2015 , 112, E6339-48	11.5	57
66	The Genome and Methylome of a Beetle with Complex Social Behavior, <i>Nicrophorus vespilloides</i> (Coleoptera: Silphidae). <i>Genome Biology and Evolution</i> , 2015 , 7, 3383-96	3.9	65
65	Genome-wide identification of CCA1 targets uncovers an expanded clock network in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, E4802-10	11.5	156
64	Maize death acids, 9-lipoxygenase-derived cyclopentane(a)nones, display activity as cytotoxic phytoalexins and transcriptional mediators. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 11407-12	11.5	83

63	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> , 2015 , 112, 14728-33	11.5	126
62	Cell wall composition and digestibility alterations in <i>Brachypodium distachyon</i> achieved through reduced expression of the UDP-arabinopyranose mutase. <i>Frontiers in Plant Science</i> , 2015 , 6, 446	6.2	18
61	Base-resolution detection of N4-methylcytosine in genomic DNA using 4mC-Tet-assisted-bisulfite-sequencing. <i>Nucleic Acids Research</i> , 2015 , 43, e148	20.1	36
60	The Dnmt3L ADD Domain Controls Cytosine Methylation Establishment during Spermatogenesis. <i>Cell Reports</i> , 2015 , 10, 944-956	10.6	27
59	MethylC-seq library preparation for base-resolution whole-genome bisulfite sequencing. <i>Nature Protocols</i> , 2015 , 10, 475-83	18.8	190
58	Epigenetics in the wild. <i>ELife</i> , 2015 , 4, e07808	8.9	4
57	FASTmC: A Suite of Predictive Models for Nonreference-Based Estimations of DNA Methylation. <i>G3: Genes, Genomes, Genetics</i> , 2015 , 6, 447-52	3.2	13
56	Genetics. The secret garden--epigenetic alleles underlie complex traits. <i>Science</i> , 2014 , 343, 1082-3	33.3	16
55	Epigenetics: Beyond Chromatin Modifications and Complex Genetic Regulation. <i>Plant Physiology</i> , 2014 , 165, 933-947	6.6	101
54	Covering your bases: inheritance of DNA methylation in plant genomes. <i>Molecular Plant</i> , 2014 , 7, 472-80	14.4	61
53	pENCODE: a plant encyclopedia of DNA elements. <i>Annual Review of Genetics</i> , 2014 , 48, 49-70	14.5	28
52	Photoperiodic control of the floral transition through a distinct polycomb repressive complex. <i>Developmental Cell</i> , 2014 , 28, 727-36	10.2	95
51	Genomic distribution of H3K9me2 and DNA methylation in a maize genome. <i>PLoS ONE</i> , 2014 , 9, e105267	3.7	108
50	DNA topoisomerase 1 promotes transcriptional silencing of transposable elements through DNA methylation and histone lysine 9 dimethylation in <i>Arabidopsis</i> . <i>PLoS Genetics</i> , 2014 , 10, e1004446	6	16
49	Decoding the Epigenomes of Herbaceous Plants. <i>Advances in Botanical Research</i> , 2014 , 69, 247-277	2.2	5
48	Genotypic variation of gene expression during the soybean innate immunity response. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2014 , 12, S27-S30	1	6
47	Methylated DNA is over-represented in whole-genome bisulfite sequencing data. <i>Frontiers in Genetics</i> , 2014 , 5, 341	4.5	42
46	Sigma factor-mediated plastid retrograde signals control nuclear gene expression. <i>Plant Journal</i> , 2013 , 73, 1-13	6.9	117

45	Patterns of population epigenomic diversity. <i>Nature</i> , 2013 , 495, 193-8	50.4	406
44	Response to perspective: "separation anxiety: an analysis of ethylene-induced cleavage of EIN2". <i>Plant Signaling and Behavior</i> , 2013 , 8,	2.5	4
43	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> , 2013 , 110, 16927-32	11.5	20
42	Epigenome-wide inheritance of cytosine methylation variants in a recombinant inbred population. <i>Genome Research</i> , 2013 , 23, 1663-74	9.7	189
41	Temporal transcriptional response to ethylene gas drives growth hormone cross-regulation in Arabidopsis. <i>ELife</i> , 2013 , 2, e00675	8.9	265
40	Circadian oscillations of protein-coding and regulatory RNAs in a highly dynamic mammalian liver epigenome. <i>Cell Metabolism</i> , 2012 , 16, 833-45	24.6	199
39	Linking photoreceptor excitation to changes in plant architecture. <i>Genes and Development</i> , 2012 , 26, 785-90	12.6	334
38	Release factor one is nonessential in Escherichia coli. <i>ACS Chemical Biology</i> , 2012 , 7, 1337-44	4.9	85
37	Epigenetic and epigenomic variation in Arabidopsis thaliana. <i>Trends in Plant Science</i> , 2012 , 17, 149-54	13.1	76
36	Processing and subcellular trafficking of ER-tethered EIN2 control response to ethylene gas. <i>Science</i> , 2012 , 338, 390-3	33.3	333
35	Revealing the playing field for analyses of single-base resolution DNA methylomes. <i>Trends in Genetics</i> , 2012 , 28, 583-5	8.5	182
34	Widespread dynamic DNA methylation in response to biotic stress. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, E2183-91	11.5	640
33	Surveillance of 3RNoncoding Transcripts Requires FIERY1 and XRN3 in Arabidopsis. <i>G3: Genes, Genomes, Genetics</i> , 2012 , 2, 487-98	3.2	33
32	RF1 knockout allows ribosomal incorporation of unnatural amino acids at multiple sites. <i>Nature Chemical Biology</i> , 2011 , 7, 779-86	11.7	255
31	Transgenerational epigenetic instability is a source of novel methylation variants. <i>Science</i> , 2011 , 334, 369-73	33.3	485
30	Brahma is required for proper expression of the floral repressor FLC in Arabidopsis. <i>PLoS ONE</i> , 2011 , 6, e17997	3.7	38
29	High-throughput approaches for plant epigenomic studies. <i>Current Opinion in Plant Biology</i> , 2011 , 14, 130-6	9.9	40
28	Evidence for network evolution in an Arabidopsis interactome map. <i>Science</i> , 2011 , 333, 601-7	33.3	689

27	Unexpected Diversity of Chloroplast Noncoding RNAs as Revealed by Deep Sequencing of the Arabidopsis Transcriptome. <i>G3: Genes, Genomes, Genetics</i> , 2011 , 1, 559-70	3.2	58
26	Intragenic suppression of a trafficking-defective brassinosteroid receptor mutant in Arabidopsis. <i>Genetics</i> , 2010 , 185, 1283-96	4	17
25	Histone H2B deubiquitination is required for transcriptional activation of FLOWERING LOCUS C and for proper control of flowering in Arabidopsis. <i>Plant Physiology</i> , 2009 , 149, 1196-204	6.6	80
24	Histone arginine methylation is required for vernalization-induced epigenetic silencing of FLC in winter-annual Arabidopsis thaliana. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 411-6	11.5	98
23	Vernalization: a model for investigating epigenetics and eukaryotic gene regulation in plants. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 2007 , 1769, 269-75		94
22	The Role of VIN3-LIKE Genes in Environmentally Induced Epigenetic Regulation of Flowering. <i>Plant Signaling and Behavior</i> , 2007 , 2, 127-8	2.5	5
21	Evolutionary conservation of the FLOWERING LOCUS C-mediated vernalization response: evidence from the sugar beet (<i>Beta vulgaris</i>). <i>Genetics</i> , 2007 , 176, 295-307	4	110
20	DICER-LIKE 1 and DICER-LIKE 3 redundantly act to promote flowering via repression of FLOWERING LOCUS C in Arabidopsis thaliana. <i>Genetics</i> , 2007 , 176, 1359-62	4	43
19	A PHD finger protein involved in both the vernalization and photoperiod pathways in Arabidopsis. <i>Genes and Development</i> , 2006 , 20, 3244-8	12.6	161
18	FRIGIDA-ESSENTIAL 1 interacts genetically with FRIGIDA and FRIGIDA-LIKE 1 to promote the winter-annual habit of Arabidopsis thaliana. <i>Development (Cambridge)</i> , 2005 , 132, 5471-8	6.6	74
17	Two putative BIN2 substrates are nuclear components of brassinosteroid signaling. <i>Plant Physiology</i> , 2002 , 130, 1221-9	6.6	168
16	Arabidopsis brassinosteroid-insensitive dwarf12 mutants are semidominant and defective in a glycogen synthase kinase 3beta-like kinase. <i>Plant Physiology</i> , 2002 , 130, 1506-15	6.6	136
15	Evolution of conserved noncoding sequences in Arabidopsis thaliana		1
14	AlphaBeta: Computational inference of epimutation rates and spectra from high-throughput DNA methylation data in plants		2
13	On the Origin and Evolutionary Consequences of Gene Body DNA Methylation		2
12	Widespread natural variation of DNA methylation within angiosperms		7
11	The evolution of CHROMOMETHYLASES and gene body DNA methylation in plants		5
10	The evolution of DNA methylation and its relationship to sociality in insects		3

9	Subgenome dominance in an interspecific hybrid, synthetic allopolyploid, and a 140 year old naturally established neo-allopolyploid monkeyflower	7
8	Cis-regulatory elements within TEs can influence expression of nearby maize genes	5
7	Stable unmethylated DNA demarcates expressed genes and their cis-regulatory space in plant genomes	2
6	The essential role of Dnmt1 in gametogenesis in the large milkweed bug <i>Oncopeltus fasciatus</i>	1
5	A cis-regulatory atlas in maize at single-cell resolution	5
4	Firefly genomes illuminate parallel origins of bioluminescence in beetles	1
3	Gene-regulatory independent functions for insect DNA methylation	4
2	The somatic genetic and epigenetic mutation rate in a wild long-lived perennial <i>Populus trichocarpa</i>	3
1	De novo assembly, annotation, and comparative analysis of 26 diverse maize genomes	9