

# Daniel Zilberman

## List of Publications by Citations

**Source:** <https://exaly.com/author-pdf/2453745/daniel-zilberman-publications-by-citations.pdf>  
**Version:** 2024-04-10

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.  
The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

45 papers	11,061 citations	36 h-index	55 g-index
55 ext. papers	12,871 ext. citations	17.5 avg, IF	6.35 L-index

#	Paper	IF	Citations
45	Genome-wide evolutionary analysis of eukaryotic DNA methylation. <i>Science</i> , <b>2010</b> , 328, 916-9	33.3	1220
44	Genetic and functional diversification of small RNA pathways in plants. <i>PLoS Biology</i> , <b>2004</b> , 2, E104	9.7	1160
43	Genome-wide analysis of Arabidopsis thaliana DNA methylation uncovers an interdependence between methylation and transcription. <i>Nature Genetics</i> , <b>2007</b> , 39, 61-9	36.3	1056
42	ARGONAUTE4 control of locus-specific siRNA accumulation and DNA and histone methylation. <i>Science</i> , <b>2003</b> , 299, 716-9	33.3	860
41	Requirement of CHROMOMETHYLASE3 for maintenance of CpXpG methylation. <i>Science</i> , <b>2001</b> , 292, 2077-80	33.3	678
40	The Arabidopsis nucleosome remodeler DDM1 allows DNA methyltransferases to access H1-containing heterochromatin. <i>Cell</i> , <b>2013</b> , 153, 193-205	56.2	642
39	Genome-wide demethylation of Arabidopsis endosperm. <i>Science</i> , <b>2009</b> , 324, 1451-4	33.3	516
38	Histone H2A.Z and DNA methylation are mutually antagonistic chromatin marks. <i>Nature</i> , <b>2008</b> , 456, 125-9	50.4	432
37	RNA silencing genes control de novo DNA methylation. <i>Science</i> , <b>2004</b> , 303, 1336	33.3	424
36	Role of the DRM and CMT3 methyltransferases in RNA-directed DNA methylation. <i>Current Biology</i> , <b>2003</b> , 13, 2212-7	6.3	411
35	DNA demethylation in the Arabidopsis genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2007</b> , 104, 6752-7	11.5	376
34	Active DNA demethylation in plant companion cells reinforces transposon methylation in gametes. <i>Science</i> , <b>2012</b> , 337, 1360-1364	33.3	352
33	Local DNA hypomethylation activates genes in rice endosperm. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2010</b> , 107, 18729-34	11.5	281
32	Role of Arabidopsis ARGONAUTE4 in RNA-directed DNA methylation triggered by inverted repeats. <i>Current Biology</i> , <b>2004</b> , 14, 1214-20	6.3	263
31	Regulation of imprinted gene expression in Arabidopsis endosperm. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2011</b> , 108, 1755-62	11.5	250
30	Deposition of histone variant H2A.Z within gene bodies regulates responsive genes. <i>PLoS Genetics</i> , <b>2012</b> , 8, e1002988	6	249
29	Genome-wide analysis of DNA methylation patterns. <i>Development (Cambridge)</i> , <b>2007</b> , 134, 3959-65	6.6	205

28	DNA methylation profiling identifies CG methylation clusters in Arabidopsis genes. <i>Current Biology</i> , <b>2005</b> , 15, 154-9	6.3	170
27	DNA methylation as a system of plant genomic immunity. <i>Trends in Plant Science</i> , <b>2014</b> , 19, 320-6	13.1	132
26	Evolution of eukaryotic DNA methylation and the pursuit of safer sex. <i>Current Biology</i> , <b>2010</b> , 20, R780-5	6.3	125
25	Dnmt1-independent CG methylation contributes to nucleosome positioning in diverse eukaryotes. <i>Cell</i> , <b>2014</b> , 156, 1286-1297	56.2	111
24	DNA demethylation is initiated in the central cells of Arabidopsis and rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2016</b> , 113, 15138-15143	11.5	98
23	EMF1 and PRC2 cooperate to repress key regulators of Arabidopsis development. <i>PLoS Genetics</i> , <b>2012</b> , 8, e1002512	6	96
22	Chromatin and siRNA pathways cooperate to maintain DNA methylation of small transposable elements in Arabidopsis. <i>Genome Biology</i> , <b>2005</b> , 6, R90	18.3	92
21	Imprinted expression of genes and small RNA is associated with localized hypomethylation of the maternal genome in rice endosperm. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2013</b> , 110, 7934-9	11.5	89
20	An evolutionary case for functional gene body methylation in plants and animals. <i>Genome Biology</i> , <b>2017</b> , 18, 87	18.3	87
19	Evolution and function of genomic imprinting in plants. <i>Genes and Development</i> , <b>2015</b> , 29, 2517-31	12.6	86
18	The evolving functions of DNA methylation. <i>Current Opinion in Plant Biology</i> , <b>2008</b> , 11, 554-9	9.9	72
17	A conversation across generations: soma-germ cell crosstalk in plants. <i>Developmental Cell</i> , <b>2013</b> , 24, 215-222	12.5	56
16	DDM1 and Lsh remodelers allow methylation of DNA wrapped in nucleosomes. <i>ELife</i> , <b>2017</b> , 6,	8.9	56
15	DNA Methylation and Histone H1 Jointly Repress Transposable Elements and Aberrant Intragenic Transcripts. <i>Molecular Cell</i> , <b>2020</b> , 77, 310-323.e7	17.6	52
14	The AAA-ATPase molecular chaperone Cdc48/p97 disassembles sumoylated centromeres, decondenses heterochromatin, and activates ribosomal RNA genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2014</b> , 111, 16166-71	11.5	51
13	Arabidopsis male sexual lineage exhibits more robust maintenance of CG methylation than somatic tissues. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2016</b> , 113, 15132-15137	11.5	48
12	Mechanism for DNA transposons to generate introns on genomic scales. <i>Nature</i> , <b>2016</b> , 538, 533-536	50.4	47
11	Epigenetic inheritance in Arabidopsis: selective silence. <i>Current Opinion in Genetics and Development</i> , <b>2005</b> , 15, 557-62	4.9	41

10	Silencing of transposons in plant genomes: kick them when theyZe down. <i>Genome Biology</i> , <b>2004</b> , 5, 249	18.3	41
9	FACT complex is required for DNA demethylation at heterochromatin during reproduction in. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2018</b> , 115, E4720-E4729	11.5	31
8	DNA methylation is maintained with high fidelity in the honey bee germline and exhibits global non-functional fluctuations during somatic development. <i>Epigenetics and Chromatin</i> , <b>2019</b> , 12, 62	5.8	27
7	DNA demethylation by ROS1a in rice vegetative cells promotes methylation in sperm. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2019</b> , 116, 9652-9657	11.5	24
6	Regulation of biological accuracy, precision, and memory by plant chromatin organization. <i>Current Opinion in Genetics and Development</i> , <b>2012</b> , 22, 132-8	4.9	20
5	DNA methylation and histone H1 cooperatively repress transposable elements and aberrant intragenic transcripts		3
4	Gene body methylation mediates epigenetic inheritance of plant traits		3
3	Histone H1 prevents non-CG methylation-mediated small RNA biogenesis in heterochromatin. <i>ELife</i> , <b>2021</b> , 10,	8.9	2
2	Balancing parental contributions in plant embryonic gene activation. <i>Developmental Cell</i> , <b>2011</b> , 20, 735-6	10.2	1
1	Maximum DNA Methylation Fidelity in the Germline Tolerates Global Non-Functional Gene Body Methylation Dynamics During Development. <i>SSRN Electronic Journal</i> ,	1	1