

Daniel Zilberman

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.

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	Histone H1 prevents non-CG methylation-mediated small RNA biogenesis in heterochromatin. <i>ELife</i> , 2021 , 10,	8.9	2
44	DNA Methylation and Histone H1 Jointly Repress Transposable Elements and Aberrant Intragenic Transcripts. <i>Molecular Cell</i> , 2020 , 77, 310-323.e7	17.6	52
43	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> , 2019 , 116, 9652-9657	11.5	24
42	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> , 2019 , 12, 62	5.8	27
41	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> , 2018 , 115, E4720-E4729	11.5	31
40	An evolutionary case for functional gene body methylation in plants and animals. <i>Genome Biology</i> , 2017 , 18, 87	18.3	87
39	DDM1 and Lsh remodelers allow methylation of DNA wrapped in nucleosomes. <i>ELife</i> , 2017 , 6,	8.9	56
38	Mechanism for DNA transposons to generate introns on genomic scales. <i>Nature</i> , 2016 , 538, 533-536	50.4	47
37	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> , 2016 , 113, 15138-15143	11.5	98
36	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> , 2016 , 113, 15132-15137	11.5	48
35	Evolution and function of genomic imprinting in plants. <i>Genes and Development</i> , 2015 , 29, 2517-31	12.6	86
34	Dnmt1-independent CG methylation contributes to nucleosome positioning in diverse eukaryotes. <i>Cell</i> , 2014 , 156, 1286-1297	56.2	111
33	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> , 2014 , 111, 16166-71	11.5	51
32	DNA methylation as a system of plant genomic immunity. <i>Trends in Plant Science</i> , 2014 , 19, 320-6	13.1	132
31	The Arabidopsis nucleosome remodeler DDM1 allows DNA methyltransferases to access H1-containing heterochromatin. <i>Cell</i> , 2013 , 153, 193-205	56.2	642
30	A conversation across generations: soma-germ cell crosstalk in plants. <i>Developmental Cell</i> , 2013 , 24, 215-225	15.2	56
29	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> , 2013 , 110, 7934-9	11.5	89

28	Regulation of biological accuracy, precision, and memory by plant chromatin organization. <i>Current Opinion in Genetics and Development</i> , 2012 , 22, 132-8	4.9	20
27	EMF1 and PRC2 cooperate to repress key regulators of Arabidopsis development. <i>PLoS Genetics</i> , 2012 , 8, e1002512	6	96
26	Deposition of histone variant H2A.Z within gene bodies regulates responsive genes. <i>PLoS Genetics</i> , 2012 , 8, e1002988	6	249
25	Active DNA demethylation in plant companion cells reinforces transposon methylation in gametes. <i>Science</i> , 2012 , 337, 1360-1364	33.3	352
24	Balancing parental contributions in plant embryonic gene activation. <i>Developmental Cell</i> , 2011 , 20, 735-610.2	1	
23	Regulation of imprinted gene expression in Arabidopsis endosperm. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 1755-62	11.5	250
22	Local DNA hypomethylation activates genes in rice endosperm. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 18729-34	11.5	281
21	Genome-wide evolutionary analysis of eukaryotic DNA methylation. <i>Science</i> , 2010 , 328, 916-9	33.3	1220
20	Evolution of eukaryotic DNA methylation and the pursuit of safer sex. <i>Current Biology</i> , 2010 , 20, R780-5	6.3	125
19	Genome-wide demethylation of Arabidopsis endosperm. <i>Science</i> , 2009 , 324, 1451-4	33.3	516
18	Histone H2A.Z and DNA methylation are mutually antagonistic chromatin marks. <i>Nature</i> , 2008 , 456, 125-90.4	30.4	432
17	The evolving functions of DNA methylation. <i>Current Opinion in Plant Biology</i> , 2008 , 11, 554-9	9.9	72
16	Genome-wide analysis of DNA methylation patterns. <i>Development (Cambridge)</i> , 2007 , 134, 3959-65	6.6	205
15	Genome-wide analysis of Arabidopsis thaliana DNA methylation uncovers an interdependence between methylation and transcription. <i>Nature Genetics</i> , 2007 , 39, 61-9	36.3	1056
14	DNA demethylation in the Arabidopsis genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 6752-7	11.5	376
13	Epigenetic inheritance in Arabidopsis: selective silence. <i>Current Opinion in Genetics and Development</i> , 2005 , 15, 557-62	4.9	41
12	Chromatin and siRNA pathways cooperate to maintain DNA methylation of small transposable elements in Arabidopsis. <i>Genome Biology</i> , 2005 , 6, R90	18.3	92
11	DNA methylation profiling identifies CG methylation clusters in Arabidopsis genes. <i>Current Biology</i> , 2005 , 15, 154-9	6.3	170

10	Role of Arabidopsis ARGONAUTE4 in RNA-directed DNA methylation triggered by inverted repeats. <i>Current Biology</i> , 2004 , 14, 1214-20	6.3	263
9	RNA silencing genes control de novo DNA methylation. <i>Science</i> , 2004 , 303, 1336	33.3	424
8	Silencing of transposons in plant genomes: kick them when theyZe down. <i>Genome Biology</i> , 2004 , 5, 249	18.3	41
7	Genetic and functional diversification of small RNA pathways in plants. <i>PLoS Biology</i> , 2004 , 2, E104	9.7	1160
6	Role of the DRM and CMT3 methyltransferases in RNA-directed DNA methylation. <i>Current Biology</i> , 2003 , 13, 2212-7	6.3	411
5	ARGONAUTE4 control of locus-specific siRNA accumulation and DNA and histone methylation. <i>Science</i> , 2003 , 299, 716-9	33.3	860
4	Requirement of CHROMOMETHYLASE3 for maintenance of CpXpG methylation. <i>Science</i> , 2001 , 292, 2077-80	33.3	678
3	Maximum DNA Methylation Fidelity in the Germline Tolerates Global Non-Functional Gene Body Methylation Dynamics During Development. <i>SSRN Electronic Journal</i> ,	1	1
2	DNA methylation and histone H1 cooperatively repress transposable elements and aberrant intragenic transcripts		3
1	Gene body methylation mediates epigenetic inheritance of plant traits		3