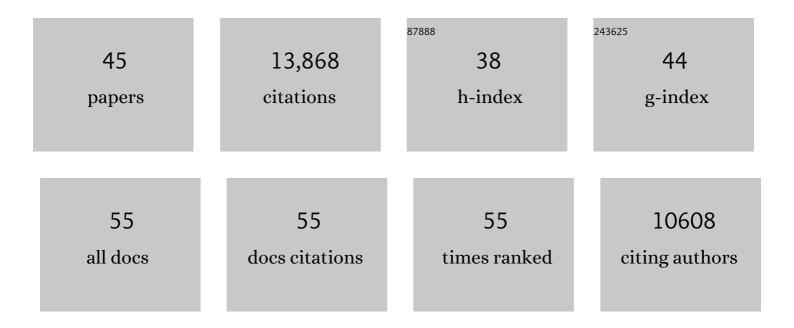
Daniel Zilberman

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Divergence among rice cultivars reveals roles for transposition and epimutation in ongoing evolution of genomic imprinting. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	11
2	Histone H1 prevents non-CG methylation-mediated small RNA biogenesis in Arabidopsis heterochromatin. ELife, 2021, 10, .	6.0	23
3	DNA Methylation and Histone H1 Jointly Repress Transposable Elements and Aberrant Intragenic Transcripts. Molecular Cell, 2020, 77, 310-323.e7.	9.7	99
4	DNA methylation is maintained with high fidelity in the honey bee germline and exhibits global non-functional fluctuations during somatic development. Epigenetics and Chromatin, 2019, 12, 62.	3.9	50
5	DNA demethylation by ROS1a in rice vegetative cells promotes methylation in sperm. Proceedings of the United States of America, 2019, 116, 9652-9657.	7.1	56
6	FACT complex is required for DNA demethylation at heterochromatin during reproduction in <i>Arabidopsis</i> . Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E4720-E4729.	7.1	54
7	An evolutionary case for functional gene body methylation in plants and animals. Genome Biology, 2017, 18, 87.	8.8	135
8	DDM1 and Lsh remodelers allow methylation of DNA wrapped in nucleosomes. ELife, 2017, 6, .	6.0	98
9	DNA demethylation is initiated in the central cells of <i>Arabidopsis</i> and rice. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 15138-15143.	7.1	157
10	<i>Arabidopsis</i> male sexual lineage exhibits more robust maintenance of CG methylation than somatic tissues. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 15132-15137.	7.1	75
11	Mechanism for DNA transposons to generate introns on genomic scales. Nature, 2016, 538, 533-536.	27.8	83
12	Evolution and function of genomic imprinting in plants. Genes and Development, 2015, 29, 2517-2531.	5.9	133
13	The AAA-ATPase molecular chaperone Cdc48/p97 disassembles sumoylated centromeres, decondenses heterochromatin, and activates ribosomal RNA genes. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 16166-16171.	7.1	74
14	DNA methylation as a system of plant genomic immunity. Trends in Plant Science, 2014, 19, 320-326.	8.8	197
15	Dnmt1-Independent CG Methylation Contributes to Nucleosome Positioning in Diverse Eukaryotes. Cell, 2014, 156, 1286-1297.	28.9	188
16	The Arabidopsis Nucleosome Remodeler DDM1 Allows DNA Methyltransferases to Access H1-Containing Heterochromatin. Cell, 2013, 153, 193-205.	28.9	914
17	A Conversation across Generations: Soma-Germ Cell Crosstalk in Plants. Developmental Cell, 2013, 24, 215-225.	7.0	65
18	Imprinted expression of genes and small RNA is associated with localized hypomethylation of the maternal genome in rice endosperm. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 7934-7939.	7.1	125

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19	EMF1 and PRC2 Cooperate to Repress Key Regulators of Arabidopsis Development. PLoS Genetics, 2012, 8, e1002512.	3.5	114
20	Deposition of Histone Variant H2A.Z within Gene Bodies Regulates Responsive Genes. PLoS Genetics, 2012, 8, e1002988.	3.5	329
21	Active DNA Demethylation in Plant Companion Cells Reinforces Transposon Methylation in Gametes. Science, 2012, 337, 1360-1364.	12.6	445
22	Regulation of biological accuracy, precision, and memory by plant chromatin organization. Current Opinion in Genetics and Development, 2012, 22, 132-138.	3.3	29
23	Balancing Parental Contributions in Plant Embryonic Gene Activation. Developmental Cell, 2011, 20, 735-736.	7.0	1
24	Regulation of imprinted gene expression in <i>Arabidopsis</i> endosperm. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 1755-1762.	7.1	317
25	Genome-Wide Evolutionary Analysis of Eukaryotic DNA Methylation. Science, 2010, 328, 916-919.	12.6	1,598
26	Evolution of Eukaryotic DNA Methylation and the Pursuit of Safer Sex. Current Biology, 2010, 20, R780-R785.	3.9	160
27	Local DNA hypomethylation activates genes in rice endosperm. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 18729-18734.	7.1	342
28	Genome-Wide Demethylation of <i>Arabidopsis</i> Endosperm. Science, 2009, 324, 1451-1454.	12.6	628
29	Histone H2A.Z and DNA methylation are mutually antagonistic chromatin marks. Nature, 2008, 456, 125-129.	27.8	508
30	The evolving functions of DNA methylation. Current Opinion in Plant Biology, 2008, 11, 554-559.	7.1	83
31	DNA demethylation in the Arabidopsis genome. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 6752-6757.	7.1	470
32	Genome-wide analysis of DNA methylation patterns. Development (Cambridge), 2007, 134, 3959-3965.	2.5	224
33	The human promoter methylome. Nature Genetics, 2007, 39, 442-443.	21.4	26
34	Genome-wide analysis of Arabidopsis thaliana DNA methylation uncovers an interdependence between methylation and transcription. Nature Genetics, 2007, 39, 61-69.	21.4	1,257
35	DNA Methylation Profiling Identifies CG Methylation Clusters in Arabidopsis Genes. Current Biology, 2005, 15, 154-159.	3.9	212
36	Epigenetic inheritance in Arabidopsis: selective silence. Current Opinion in Genetics and Development, 2005, 15, 557-562.	3.3	44

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#	Article	IF	CITATIONS
37	Chromatin and siRNA pathways cooperate to maintain DNA methylation of small transposable elements in Arabidopsis. Genome Biology, 2005, 6, R90.	9.6	107
38	Role of Arabidopsis ARGONAUTE4 in RNA-Directed DNA Methylation Triggered by Inverted Repeats. Current Biology, 2004, 14, 1214-1220.	3.9	285
39	RNA Silencing Genes Control de Novo DNA Methylation. Science, 2004, 303, 1336-1336.	12.6	484
40	Silencing of transposons in plant genomes: kick them when they're down. Genome Biology, 2004, 5, 249.	9.6	46
41	Genetic and Functional Diversification of Small RNA Pathways in Plants. PLoS Biology, 2004, 2, e104.	5.6	1,347
42	Role of the DRM and CMT3 Methyltransferases in RNA-Directed DNA Methylation. Current Biology, 2003, 13, 2212-2217.	3.9	462
43	<i>ARGONAUTE4</i> Control of Locus-Specific siRNA Accumulation and DNA and Histone Methylation. Science, 2003, 299, 716-719.	12.6	966
44	Requirement of CHROMOMETHYLASE3 for Maintenance of CpXpG Methylation. Science, 2001, 292, 2077-2080.	12.6	820
45	Maximum DNA Methylation Fidelity in the Germline Tolerates Global Non-Functional Gene Body Methylation Dynamics During Development, SSRN Electronic Journal, 0,	0.4	1