

Assaf Zemach

List of Publications by Year in descending order

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14
papers

4,486
citations

758635

12
h-index

996533

15
g-index

17
all docs

17
docs citations

17
times ranked

5511
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-Wide Evolutionary Analysis of Eukaryotic DNA Methylation. <i>Science</i> , 2010, 328, 916-919.	6.0	1,598
2	The Arabidopsis Nucleosome Remodeler DDM1 Allows DNA Methyltransferases to Access H1-Containing Heterochromatin. <i>Cell</i> , 2013, 153, 193-205.	13.5	914
3	Genome-Wide Demethylation of <i>Arabidopsis</i> Endosperm. <i>Science</i> , 2009, 324, 1451-1454.	6.0	628
4	Active DNA Demethylation in Plant Companion Cells Reinforces Transposon Methylation in Gametes. <i>Science</i> , 2012, 337, 1360-1364.	6.0	445
5	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, 18729-18734.	3.3	342
6	Evolution of Eukaryotic DNA Methylation and the Pursuit of Safer Sex. <i>Current Biology</i> , 2010, 20, R780-R785.	1.8	160
7	Mutation of a major CG methylase in rice causes genome-wide hypomethylation, dysregulated genome expression, and seedling lethality. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 10642-10647.	3.3	149
8	Methyl-CpG-binding domain proteins in plants: interpreters of DNA methylation. <i>Trends in Plant Science</i> , 2007, 12, 80-85.	4.3	100
9	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.	1.8	50
10	RdDM-independent de novo and heterochromatin DNA methylation by plant CMT and DNMT3 orthologs. <i>Nature Communications</i> , 2019, 10, 1613.	5.8	46
11	DNA methylation mutants in <i>Physcomitrella patens</i> elucidate individual roles of CG and non-CG methylation in genome regulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 33700-33710.	3.3	21
12	Contiguous and stochastic CHH methylation patterns of plant DRM2 and CMT2 revealed by single-read methylome analysis. <i>Genome Biology</i> , 2020, 21, 194.	3.8	15
13	The COP9 signalosome influences the epigenetic landscape of <i>Arabidopsis thaliana</i> . <i>Bioinformatics</i> , 2019, 35, 2718-2723.	1.8	9
14	CMT3 and SUVH4/KYP silence the exonic Eukneivel retroelement to allow for reconstitution of CMT1 mRNA. <i>Epigenetics and Chromatin</i> , 2018, 11, 69.	1.8	5