

Reprogramming of DNA Methylation in Pollen Guides E

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Reprogramming the Epigenome in Arabidopsis Pollen. Cold Spring Harbor Symposia on Quantitative Biology, 2012, 77, 1-5.	2.0	20
2	Plant & Cell Physiology Research Highlights. Plant and Cell Physiology, 2012, 53, 1985-1988.	1.5	1
3	What Triggers Differential DNA Methylation of Genes and TEs: Contribution of Body Methylation?. Cold Spring Harbor Symposia on Quantitative Biology, 2012, 77, 155-160.	2.0	27
4	Hypothesis: Selection of Imprinted Genes Is Driven by Silencing Deleterious Gene Activity in Somatic Tissues. Cold Spring Harbor Symposia on Quantitative Biology, 2012, 77, 23-29.	2.0	19
5	Imprinting: DNA Methyltransferases Illuminate Reprogramming. Current Biology, 2012, 22, R929-R931.	1.8	4
7	Long-Distance Systemic Signaling and Communication in Plants. Signaling and Communication in Plants, 2013, , .	0.5	16
8	De Novo Methyltransferase, OsDRM2, Interacts with the ATP-Dependent RNA Helicase, OsEIF4A, in Rice. Journal of Molecular Biology, 2013, 425, 2853-2866.	2.0	22
9	Early steps of active DNA demethylation initiated by ROS1 glycosylase require three putative helix-invading residues. Nucleic Acids Research, 2013, 41, 8654-8664.	6.5	15
10	Kin Conflict in Seed Development: An Interdependent but Fractious Collective. Annual Review of Cell and Developmental Biology, 2013, 29, 189-211.	4.0	86
11	Small RNAs, big impact: small RNA pathways in transposon control and their effect on the host stress response. Chromosome Research, 2013, 21, 587-600.	1.0	45
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18	Classification and Comparison of Small RNAs from Plants. Annual Review of Plant Biology, 2013, 64, 137-159.	8.6	832
19	The impact of climate change on plant epigenomes. Trends in Genetics, 2013, 29, 503-505.	2.9	20

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20	Patterns of population epigenomic diversity. <i>Nature</i> , 2013, 495, 193-198.	13.7	543
21	Microgenomics: Genome-Scale, Cell-Specific Monitoring of Multiple Gene Regulation Tiers. <i>Annual Review of Plant Biology</i> , 2013, 64, 293-325.	8.6	46
22	Establishing epigenetic variation during genome reprogramming. <i>RNA Biology</i> , 2013, 10, 490-494.	1.5	23
23	Epigenetics and Development in Plants. <i>Current Topics in Developmental Biology</i> , 2013, 104, 189-222.	1.0	24
24	Epigenetic trigger for tomato ripening. <i>Nature Biotechnology</i> , 2013, 31, 119-120.	9.4	21
25	Widespread, abundant, and diverse TE-associated siRNAs in developing wheat grain. <i>Gene</i> , 2013, 522, 1-7.	1.0	23
26	Small RNAs, RNAi and the Inheritance of Gene Silencing in <i>Caenorhabditis elegans</i> . <i>Journal of Genetics and Genomics</i> , 2013, 40, 153-160.	1.7	36
27	RNA-directed DNA methylation regulates parental genomic imprinting at several loci in <i>Arabidopsis</i> . <i>Development (Cambridge)</i> , 2013, 140, 2953-2960.	1.2	80
28	Conceptual links between DNA methylation reprogramming in the early embryo and primordial germ cells. <i>Current Opinion in Cell Biology</i> , 2013, 25, 281-288.	2.6	103
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34	The Initiation of Epigenetic Silencing of Active Transposable Elements Is Triggered by RDR6 and 21-22 Nucleotide Small Interfering RNAs. <i>Plant Physiology</i> , 2013, 162, 116-131.	2.3	267
35	Perspectives on deciphering mechanisms underlying plant heat stress response and thermotolerance. <i>Frontiers in Plant Science</i> , 2013, 4, 315.	1.7	323
36	Silicon Era of Carbon-Based Life: Application of Genomics and Bioinformatics in Crop Stress Research. <i>International Journal of Molecular Sciences</i> , 2013, 14, 11444-11483.	1.8	8
37	Pollen-Specific, but Not Sperm-Specific, Genes Show Stronger Purifying Selection and Higher Rates of Positive Selection Than Sporophytic Genes in <i>Capsella grandiflora</i> . <i>Molecular Biology and Evolution</i> , 2013, 30, 2475-2486.	3.5	90

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39	Warm temperatures induce transgenerational epigenetic release of RNA silencing by inhibiting siRNA biogenesis in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 9171-9176.	3.3	104
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41	Epigenomic programming contributes to the genomic drift evolution of the F-Box protein superfamily in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 16927-16932.	3.3	25
42	Epigenome-wide inheritance of cytosine methylation variants in a recombinant inbred population. <i>Genome Research</i> , 2013, 23, 1663-1674.	2.4	227
43	Small RNAs and regulation of transposons in plants. <i>Genes and Genetic Systems</i> , 2013, 88, 3-7.	0.2	34
44	Parental origin control of transgenerational retrotransposon proliferation in <i>Arabidopsis</i> . <i>EMBO Reports</i> , 2013, 14, 823-828.	2.0	22
45	The study of a barley epigenetic regulator, HvDME, in seed development and under drought. <i>BMC Plant Biology</i> , 2013, 13, 172.	1.6	44
46	Epigenetic Repression of Male Gametophyte-Specific Genes in the <i>Arabidopsis</i> Sporophyte. <i>Molecular Plant</i> , 2013, 6, 1176-1186.	3.9	13
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53	Chromatin dynamics during plant sexual reproduction. <i>Frontiers in Plant Science</i> , 2014, 5, 354.	1.7	33
54	Decoding the Epigenomes of Herbaceous Plants. <i>Advances in Botanical Research</i> , 2014, 69, 247-277.	0.5	5
55	Three Groups of Transposable Elements with Contrasting Copy Number Dynamics and Host Responses in the Maize (<i>Zea mays</i> ssp. <i>mays</i>) Genome. <i>PLoS Genetics</i> , 2014, 10, e1004298.	1.5	52

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57	Regulation of meiotic gene expression in plants. <i>Frontiers in Plant Science</i> , 2014, 5, 413.	1.7	35
58	Maize germinal cell initials accommodate hypoxia and precociously express meiotic genes. <i>Plant Journal</i> , 2014, 77, 639-652.	2.8	47
59	Pollen grain development is highly sensitive to temperature stress in <i>Vitis vinifera</i> . <i>Australian Journal of Grape and Wine Research</i> , 2014, 20, 474-484.	1.0	22
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65	The convergence of autophagy, small RNA and the stress response – implications for transgenerational epigenetic inheritance in plants. <i>Biomolecular Concepts</i> , 2014, 5, 1-8.	1.0	5
66	Hypomethylated Pollen Bypasses the Interploidy Hybridization Barrier in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2014, 26, 3556-3568.	3.1	49
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94	Overproduction of stomatal lineage cells in <i>Arabidopsis</i> mutants defective in active DNA demethylation. <i>Nature Communications</i> , 2014, 5, 4062.	5.8	90
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96	Heterosis and inbreeding depression of epigenetic <i>Arabidopsis</i> hybrids. <i>Nature Plants</i> , 2015, 1, 15092.	4.7	91
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132	Crop Epigenomics: Identifying, Unlocking, and Harnessing Cryptic Variation in Crop Genomes. <i>Molecular Plant</i> , 2015, 8, 860-870.	3.9	44
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134	Impact of repetitive DNA on sex chromosome evolution in plants. <i>Chromosome Research</i> , 2015, 23, 561-570.	1.0	43
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145	Emerging links between iron-sulfur clusters and 5-methylcytosine base excision repair in plants. <i>Genes and Genetic Systems</i> , 2016, 91, 51-62.	0.2	16
146	DNA demethylation is initiated in the central cells of <i>Arabidopsis</i> and rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 15138-15143.	3.3	157
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165	Unique cell-type-specific patterns of DNA methylation in the root meristem. <i>Nature Plants</i> , 2016, 2, 16058.	4.7	159
166	DISMISS: detection of stranded methylation in MeDIP-Seq data. <i>BMC Bioinformatics</i> , 2016, 17, 295.	1.2	16

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168	Epigenetic events in plant male germ cell heat stress responses. <i>Plant Reproduction</i> , 2016, 29, 21-29.	1.3	32
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