

Conserved role of intragenic DNA methylation in regula

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Next generation sequencing based approaches to epigenomics. <i>Briefings in Functional Genomics</i> , 2010, 9, 455-465.	1.3	60
2	Mammalian methyl-binding proteins: What might they do?. <i>BioEssays</i> , 2010, 32, 1025-1032.	1.2	19
3	Haploinsufficiency of the autism-associated Shank3 gene leads to deficits in synaptic function, social interaction, and social communication. <i>Molecular Autism</i> , 2010, 1, 15.	2.6	521
4	Comparison of sequencing-based methods to profile DNA methylation and identification of monoallelic epigenetic modifications. <i>Nature Biotechnology</i> , 2010, 28, 1097-1105.	9.4	647
5	Looking beyond promoters. <i>Nature Reviews Genetics</i> , 2010, 11, 596-596.	7.7	4
7	Cytidine deaminases: Aiding DNA demethylation?. <i>Genes and Development</i> , 2010, 24, 2107-2114.	2.7	109
8	Season of Conception in Rural Gambia Affects DNA Methylation at Putative Human Metastable Epialleles. <i>PLoS Genetics</i> , 2010, 6, e1001252.	1.5	393
9	Epigenetics in mental illness: Hope or hype?. <i>Journal of Psychiatry and Neuroscience</i> , 2010, 35, 366-368.	1.4	13
10	Germline Epigenetic Regulation of <i>KILLIN</i> in Cowden and Cowden-like Syndrome. <i>JAMA - Journal of the American Medical Association</i> , 2010, 304, 2724.	3.8	138
11	Functional Conservation of DNA Methylation in the Pea Aphid and the Honeybee. <i>Genome Biology and Evolution</i> , 2010, 2, 719-728.	1.1	109
12	The epigenome as a therapeutic target in prostate cancer. <i>Nature Reviews Urology</i> , 2010, 7, 668-680.	1.9	118
13	Epigenome Mapping in Normal and Disease States. <i>Circulation Research</i> , 2010, 107, 327-339.	2.0	164
14	Importance of Shank3 Protein in Regulating Metabotropic Glutamate Receptor 5 (mGluR5) Expression and Signaling at Synapses. <i>Journal of Biological Chemistry</i> , 2011, 286, 34839-34850.	1.6	180
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16	Cell type-specific DNA methylation at intragenic CpG islands in the immune system. <i>Genome Research</i> , 2011, 21, 1074-1086.	2.4	256
17	Determining Coding CpG Islands by Identifying Regions Significant for Pattern Statistics on Markov Chains. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2011, 10, .	0.2	1
18	Dynamic CpG island methylation landscape in oocytes and preimplantation embryos. <i>Nature Genetics</i> , 2011, 43, 811-814.	9.4	579
19	Biological Functions of Methyl-CpG-Binding Proteins. <i>Progress in Molecular Biology and Translational Science</i> , 2011, 101, 377-398.	0.9	80

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20	Genome-Wide Distribution of DNA Methylation at Single-Nucleotide Resolution. <i>Progress in Molecular Biology and Translational Science</i> , 2011, 101, 459-477.	0.9	3
21	New concepts of old epigenetic phenomena and their implications for selecting specific cell populations for epigenomic research. <i>Epigenomics</i> , 2011, 3, 383-386.	1.0	10
22	DNA Methylation: A Timeline of Methods and Applications. <i>Frontiers in Genetics</i> , 2011, 2, 74.	1.1	85
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56	Changes in DNA Methylation and Gene Expression during 2,3,7,8-Tetrachlorodibenzo-p-dioxin-Induced Suppression of the Lipopolysaccharide-Stimulated IgM Response in Splenocytes. <i>Toxicological Sciences</i> , 2011, 120, 339-348.	1.4	24

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