Fabio Mohn

List of Publications by Year in descending order

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Ελβίο ΜομΝ

#	Article	IF	CITATIONS
1	Lineage-Specific Polycomb Targets and De Novo DNA Methylation Define Restriction and Potential of Neuronal Progenitors. Molecular Cell, 2008, 30, 755-766.	9.7	802
2	MicroRNAs control de novo DNA methylation through regulation of transcriptional repressors in mouse embryonic stem cells. Nature Structural and Molecular Biology, 2008, 15, 259-267.	8.2	451
3	Identification of genetic elements that autonomously determine DNA methylation states. Nature Genetics, 2011, 43, 1091-1097.	21.4	351
4	The Rhino-Deadlock-Cutoff Complex Licenses Noncanonical Transcription of Dual-Strand piRNA Clusters in Drosophila. Cell, 2014, 157, 1364-1379.	28.9	339
5	piRNA-guided slicing specifies transcripts for Zucchini-dependent, phased piRNA biogenesis. Science, 2015, 348, 812-817.	12.6	304
6	Genetics and epigenetics: stability and plasticity during cellular differentiation. Trends in Genetics, 2009, 25, 129-136.	6.7	271
7	EJC-independent degradation of nonsense immunoglobulin-μ mRNA depends on 3′ UTR length. Nature Structural and Molecular Biology, 2006, 13, 462-464.	8.2	225
8	DNA methylation in ES cells requires the lysine methyltransferase G9a but not its catalytic activity. EMBO Journal, 2008, 27, 2691-2701.	7.8	207
9	Methylated DNA Immunoprecipitation (MeDIP). Methods in Molecular Biology, 2009, 507, 55-64.	0.9	203
10	Activity-dependent neuroprotective protein recruits HP1 and CHD4 to control lineage-specifying genes. Nature, 2018, 557, 739-743.	27.8	169
11	Relics of repeat-induced point mutation direct heterochromatin formation in <i>Neurospora crassa</i> . Genome Research, 2009, 19, 427-437.	5.5	137
12	H3K64 trimethylation marks heterochromatin and is dynamically remodeled during developmental reprogramming. Nature Structural and Molecular Biology, 2009, 16, 777-781.	8.2	125
13	Genomic Prevalence of Heterochromatic H3K9me2 and Transcription Do Not Discriminate Pluripotent from Terminally Differentiated Cells. PLoS Genetics, 2011, 7, e1002090.	3.5	119
14	The ChAHP Complex Counteracts Chromatin Looping at CTCF Sites that Emerged from SINE Expansions in Mouse. Cell, 2019, 178, 1437-1451.e14.	28.9	118
15	Genetic and mechanistic diversity of piRNA $3\hat{a}\in^2$ -end formation. Nature, 2016, 539, 588-592.	27.8	115
16	Acetylation of histone H3 at lysine 64 regulates nucleosome dynamics and facilitates transcription. ELife, 2014, 3, e01632.	6.0	99
17	Transcriptional Silencing of Nonsense Codon-Containing Immunoglobulin Minigenes. Molecular Cell, 2005, 18, 307-317.	9.7	64
18	The RNA-induced transcriptional silencing complex targets chromatin exclusively via interacting with nascent transcripts. Genes and Development, 2016, 30, 2571-2580.	5.9	60

ΓΑΒΙΟ ΜΟΗΝ

#	Article	IF	CITATIONS
19	Distinctive features of lincRNA gene expression suggest widespread RNA-independent functions. Life Science Alliance, 2018, 1, e201800124.	2.8	32
20	Inheritance of a Phenotypically Neutral Epimutation Evokes Gene Silencing in Later Generations. Molecular Cell, 2019, 74, 534-541.e4.	9.7	23
21	Nonsense-associated alternative splicing of T-cell receptor genes: No evidence for frame dependence. Rna, 2005, 11, 147-156.	3.5	20