

Fabio Mohn

List of Publications by Year in descending order

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Version: 2024-02-01

21
papers

4,238
citations

361045

20
h-index

713013

21
g-index

24
all docs

24
docs citations

24
times ranked

6738
citing authors

#	ARTICLE	IF	CITATIONS
1	Lineage-Specific Polycomb Targets and De Novo DNA Methylation Define Restriction and Potential of Neuronal Progenitors. <i>Molecular Cell</i> , 2008, 30, 755-766.	4.5	802
2	MicroRNAs control de novo DNA methylation through regulation of transcriptional repressors in mouse embryonic stem cells. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 259-267.	3.6	451
3	Identification of genetic elements that autonomously determine DNA methylation states. <i>Nature Genetics</i> , 2011, 43, 1091-1097.	9.4	351
4	The Rhino-Deadlock-Cutoff Complex Licenses Noncanonical Transcription of Dual-Strand piRNA Clusters in <i>Drosophila</i> . <i>Cell</i> , 2014, 157, 1364-1379.	13.5	339
5	piRNA-guided slicing specifies transcripts for Zucchini-dependent, phased piRNA biogenesis. <i>Science</i> , 2015, 348, 812-817.	6.0	304
6	Genetics and epigenetics: stability and plasticity during cellular differentiation. <i>Trends in Genetics</i> , 2009, 25, 129-136.	2.9	271
7	EJC-independent degradation of nonsense immunoglobulin- μ mRNA depends on 3' UTR length. <i>Nature Structural and Molecular Biology</i> , 2006, 13, 462-464.	3.6	225
8	DNA methylation in ES cells requires the lysine methyltransferase G9a but not its catalytic activity. <i>EMBO Journal</i> , 2008, 27, 2691-2701.	3.5	207
9	Methylated DNA Immunoprecipitation (MeDIP). <i>Methods in Molecular Biology</i> , 2009, 507, 55-64.	0.4	203
10	Activity-dependent neuroprotective protein recruits HP1 and CHD4 to control lineage-specifying genes. <i>Nature</i> , 2018, 557, 739-743.	13.7	169
11	Relics of repeat-induced point mutation direct heterochromatin formation in <i>Neurospora crassa</i> . <i>Genome Research</i> , 2009, 19, 427-437.	2.4	137
12	H3K64 trimethylation marks heterochromatin and is dynamically remodeled during developmental reprogramming. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 777-781.	3.6	125
13	Genomic Prevalence of Heterochromatic H3K9me2 and Transcription Do Not Discriminate Pluripotent from Terminally Differentiated Cells. <i>PLoS Genetics</i> , 2011, 7, e1002090.	1.5	119
14	The ChAHP Complex Counteracts Chromatin Looping at CTCF Sites that Emerged from SINE Expansions in Mouse. <i>Cell</i> , 2019, 178, 1437-1451.e14.	13.5	118
15	Genetic and mechanistic diversity of piRNA 3'-end formation. <i>Nature</i> , 2016, 539, 588-592.	13.7	115
16	Acetylation of histone H3 at lysine 64 regulates nucleosome dynamics and facilitates transcription. <i>ELife</i> , 2014, 3, e01632.	2.8	99
17	Transcriptional Silencing of Nonsense Codon-Containing Immunoglobulin Minigenes. <i>Molecular Cell</i> , 2005, 18, 307-317.	4.5	64
18	The RNA-induced transcriptional silencing complex targets chromatin exclusively via interacting with nascent transcripts. <i>Genes and Development</i> , 2016, 30, 2571-2580.	2.7	60

#	ARTICLE	IF	CITATIONS
19	Distinctive features of lincRNA gene expression suggest widespread RNA-independent functions. <i>Life Science Alliance</i> , 2018, 1, e201800124.	1.3	32
20	Inheritance of a Phenotypically Neutral Epimutation Evokes Gene Silencing in Later Generations. <i>Molecular Cell</i> , 2019, 74, 534-541.e4.	4.5	23
21	Nonsense-associated alternative splicing of T-cell receptor \hat{A} genes: No evidence for frame dependence. <i>Rna</i> , 2005, 11, 147-156.	1.6	20