

Fabio Mohn

List of Publications by Citations

Source: <https://exaly.com/author-pdf/2341599/fabio-mohn-publications-by-citations.pdf>

Version: 2024-04-25

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

21
papers

3,373
citations

19
h-index

24
g-index

24
ext. papers

3,882
ext. citations

21.1
avg, IF

5.11
L-index

#	Paper	IF	Citations
21	Lineage-specific polycomb targets and de novo DNA methylation define restriction and potential of neuronal progenitors. <i>Molecular Cell</i> , 2008 , 30, 755-66	17.6	694
20	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, 259-67	17.6	398
19	Identification of genetic elements that autonomously determine DNA methylation states. <i>Nature Genetics</i> , 2011 , 43, 1091-7	36.3	303
18	Genetics and epigenetics: stability and plasticity during cellular differentiation. <i>Trends in Genetics</i> , 2009 , 25, 129-36	8.5	232
17	Noncoding RNA. piRNA-guided slicing specifies transcripts for Zucchini-dependent, phased piRNA biogenesis. <i>Science</i> , 2015 , 348, 812-817	33.3	221
16	The rhino-deadlock-cut-off complex licenses noncanonical transcription of dual-strand piRNA clusters in <i>Drosophila</i> . <i>Cell</i> , 2014 , 157, 1364-1379	56.2	217
15	EJC-independent degradation of nonsense immunoglobulin-mu mRNA depends on 3'UTR length. <i>Nature Structural and Molecular Biology</i> , 2006 , 13, 462-4	17.6	193
14	DNA methylation in ES cells requires the lysine methyltransferase G9a but not its catalytic activity. <i>EMBO Journal</i> , 2008 , 27, 2691-701	13	189
13	Methylated DNA immunoprecipitation (MeDIP). <i>Methods in Molecular Biology</i> , 2009 , 507, 55-64	1.4	177
12	H3K64 trimethylation marks heterochromatin and is dynamically remodeled during developmental reprogramming. <i>Nature Structural and Molecular Biology</i> , 2009 , 16, 777-81	17.6	118
11	Relics of repeat-induced point mutation direct heterochromatin formation in <i>Neurospora crassa</i> . <i>Genome Research</i> , 2009 , 19, 427-37	9.7	113
10	Genomic prevalence of heterochromatic H3K9me2 and transcription do not discriminate pluripotent from terminally differentiated cells. <i>PLoS Genetics</i> , 2011 , 7, e1002090	6	96
9	Genetic and mechanistic diversity of piRNA 3'end formation. <i>Nature</i> , 2016 , 539, 588-592	50.4	77
8	Acetylation of histone H3 at lysine 64 regulates nucleosome dynamics and facilitates transcription. <i>ELife</i> , 2014 , 3, e01632	8.9	73
7	Activity-dependent neuroprotective protein recruits HP1 and CHD4 to control lineage-specifying genes. <i>Nature</i> , 2018 , 557, 739-743	50.4	68
6	Transcriptional silencing of nonsense codon-containing immunoglobulin minigenes. <i>Molecular Cell</i> , 2005 , 18, 307-17	17.6	62
5	The ChAHP Complex Counteracts Chromatin Looping at CTCF Sites that Emerged from SINE Expansions in Mouse. <i>Cell</i> , 2019 , 178, 1437-1451.e14	56.2	46

4	The RNA-induced transcriptional silencing complex targets chromatin exclusively via interacting with nascent transcripts. <i>Genes and Development</i> , 2016 , 30, 2571-2580	12.6	45
3	Distinctive features of lincRNA gene expression suggest widespread RNA-independent functions. <i>Life Science Alliance</i> , 2018 , 1, e201800124	5.8	21
2	Nonsense-associated alternative splicing of T-cell receptor beta genes: no evidence for frame dependence. <i>Rna</i> , 2005 , 11, 147-56	5.8	18
1	Inheritance of a Phenotypically Neutral Epimutation Evokes Gene Silencing in Later Generations. <i>Molecular Cell</i> , 2019 , 74, 534-541.e4	17.6	12