

# Fabio Mohn

## List of Publications by Year in Descending Order

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**Version:** 2024-04-25

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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	The ChAHP Complex Counteracts Chromatin Looping at CTCF Sites that Emerged from SINE Expansions in Mouse. <i>Cell</i> , <b>2019</b> , 178, 1437-1451.e14	56.2	46
20	Inheritance of a Phenotypically Neutral Epimutation Evokes Gene Silencing in Later Generations. <i>Molecular Cell</i> , <b>2019</b> , 74, 534-541.e4	17.6	12
19	Distinctive features of lincRNA gene expression suggest widespread RNA-independent functions. <i>Life Science Alliance</i> , <b>2018</b> , 1, e201800124	5.8	21
18	Activity-dependent neuroprotective protein recruits HP1 and CHD4 to control lineage-specifying genes. <i>Nature</i> , <b>2018</b> , 557, 739-743	50.4	68
17	Genetic and mechanistic diversity of piRNA 3'end formation. <i>Nature</i> , <b>2016</b> , 539, 588-592	50.4	77
16	The RNA-induced transcriptional silencing complex targets chromatin exclusively via interacting with nascent transcripts. <i>Genes and Development</i> , <b>2016</b> , 30, 2571-2580	12.6	45
15	Noncoding RNA. piRNA-guided slicing specifies transcripts for Zucchini-dependent, phased piRNA biogenesis. <i>Science</i> , <b>2015</b> , 348, 812-817	33.3	221
14	The rhino-deadlock-cut-off complex licenses noncanonical transcription of dual-strand piRNA clusters in Drosophila. <i>Cell</i> , <b>2014</b> , 157, 1364-1379	56.2	217
13	Acetylation of histone H3 at lysine 64 regulates nucleosome dynamics and facilitates transcription. <i>ELife</i> , <b>2014</b> , 3, e01632	8.9	73
12	Identification of genetic elements that autonomously determine DNA methylation states. <i>Nature Genetics</i> , <b>2011</b> , 43, 1091-7	36.3	303
11	Genomic prevalence of heterochromatic H3K9me2 and transcription do not discriminate pluripotent from terminally differentiated cells. <i>PLoS Genetics</i> , <b>2011</b> , 7, e1002090	6	96
10	Genetics and epigenetics: stability and plasticity during cellular differentiation. <i>Trends in Genetics</i> , <b>2009</b> , 25, 129-36	8.5	232
9	H3K64 trimethylation marks heterochromatin and is dynamically remodeled during developmental reprogramming. <i>Nature Structural and Molecular Biology</i> , <b>2009</b> , 16, 777-81	17.6	118
8	Methylated DNA immunoprecipitation (MeDIP). <i>Methods in Molecular Biology</i> , <b>2009</b> , 507, 55-64	1.4	177
7	Relics of repeat-induced point mutation direct heterochromatin formation in <i>Neurospora crassa</i> . <i>Genome Research</i> , <b>2009</b> , 19, 427-37	9.7	113
6	DNA methylation in ES cells requires the lysine methyltransferase G9a but not its catalytic activity. <i>EMBO Journal</i> , <b>2008</b> , 27, 2691-701	13	189
5	MicroRNAs control de novo DNA methylation through regulation of transcriptional repressors in mouse embryonic stem cells. <i>Nature Structural and Molecular Biology</i> , <b>2008</b> , 15, 259-67	17.6	398

4	Lineage-specific polycomb targets and de novo DNA methylation define restriction and potential of neuronal progenitors. <i>Molecular Cell</i> , <b>2008</b> , 30, 755-66	17.6	694
3	EJC-independent degradation of nonsense immunoglobulin-mu mRNA depends on 3bUTR length. <i>Nature Structural and Molecular Biology</i> , <b>2006</b> , 13, 462-4	17.6	193
2	Transcriptional silencing of nonsense codon-containing immunoglobulin minigenes. <i>Molecular Cell</i> , <b>2005</b> , 18, 307-17	17.6	62
1	Nonsense-associated alternative splicing of T-cell receptor beta genes: no evidence for frame dependence. <i>Rna</i> , <b>2005</b> , 11, 147-56	5.8	18