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List of Publications by Year in Descending Order

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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.

63 papers	5,023 citations	34 h-index	70 g-index
71 ext. papers	6,117 ext. citations	15.9 avg, IF	5.46 L-index

#	Paper	IF	Citations
63	Profiling Histone Methylation in Low Numbers of Cells. <i>Methods in Molecular Biology</i> , 2022 , 229-251	1.4	
62	Repression of germline genes by PRC1.6 and SETDB1 in the early embryo precedes DNA methylation-mediated silencing. <i>Nature Communications</i> , 2021 , 12, 7020	17.4	4
61	Interplay between chromatin marks in development and disease. <i>Nature Reviews Genetics</i> , 2021 ,	30.1	8
60	Histone H3 lysine 4 trimethylation in sperm is transmitted to the embryo and associated with diet-induced phenotypes in the offspring. <i>Developmental Cell</i> , 2021 , 56, 671-686.e6	10.2	22
59	Paternal MTHFR deficiency leads to hypomethylation of young retrotransposons and reproductive decline across two successive generations. <i>Development (Cambridge)</i> , 2021 , 148,	6.6	2
58	Transcription shapes genome-wide histone acetylation patterns. <i>Nature Communications</i> , 2021 , 12, 210	17.4	16
57	Vertebrate diapause preserves organisms long term through Polycomb complex members. <i>Science</i> , 2020 , 367, 870-874	33.3	41
56	Setting the chromatin stage in oocytes. <i>Nature Cell Biology</i> , 2020 , 22, 355-357	23.4	
55	Inter-Strain Epigenomic Profiling Reveals a Candidate IAP Master Copy in C3H Mice. <i>Viruses</i> , 2020 , 12,	6.2	4
54	Maternal DNMT3A-dependent de novo methylation of the paternal genome inhibits gene expression in the early embryo. <i>Nature Communications</i> , 2020 , 11, 5417	17.4	4
53	NSD1-deposited H3K36me2 directs de novo methylation in the mouse male germline and counteracts Polycomb-associated silencing. <i>Nature Genetics</i> , 2020 , 52, 1088-1098	36.3	39
52	SETD2 regulates the maternal epigenome, genomic imprinting and embryonic development. <i>Nature Genetics</i> , 2019 , 51, 844-856	36.3	101
51	Histone H3K9 Methyltransferase G9a in Oocytes Is Essential for Preimplantation Development but Dispensable for CG Methylation Protection. <i>Cell Reports</i> , 2019 , 27, 282-293.e4	10.6	38
50	ZFP57 regulation of transposable elements and gene expression within and beyond imprinted domains. <i>Epigenetics and Chromatin</i> , 2019 , 12, 49	5.8	23
49	Evolution of imprinting via lineage-specific insertion of retroviral promoters. <i>Nature Communications</i> , 2019 , 10, 5674	17.4	22
48	Development and application of an integrated allele-specific pipeline for methylomic and epigenomic analysis (MEA). <i>BMC Genomics</i> , 2018 , 19, 463	4.5	9
47	LTR retrotransposons transcribed in oocytes drive species-specific and heritable changes in DNA methylation. <i>Nature Communications</i> , 2018 , 9, 3331	17.4	43

46	H3S10ph broadly marks early-replicating domains in interphase ESCs and shows reciprocal antagonism with H3K9me2. <i>Genome Research</i> , 2018 , 28, 37-51	9.7	27
45	On the role of H3.3 in retroviral silencing. <i>Nature</i> , 2017 , 548, E1-E3	50.4	13
44	Evidence for Converging DNA Methylation Pathways in Placenta and Cancer. <i>Developmental Cell</i> , 2017 , 43, 257-258	10.2	18
43	Epigenetic modifier drugs trigger widespread transcription of endogenous retroviruses. <i>Nature Genetics</i> , 2017 , 49, 974-975	36.3	7
42	Long Terminal Repeats: From Parasitic Elements to Building Blocks of the Transcriptional Regulatory Repertoire. <i>Molecular Cell</i> , 2016 , 62, 766-76	17.6	144
41	ChAsE: chromatin analysis and exploration tool. <i>Bioinformatics</i> , 2016 , 32, 3324-3326	7.2	23
40	Dynamic and flexible H3K9me3 bridging via HP1 dimerization establishes a plastic state of condensed chromatin. <i>Nature Communications</i> , 2016 , 7, 11310	17.4	83
39	Activation of Endogenous Retroviruses in Dnmt1(-/-) ESCs Involves Disruption of SETDB1-Mediated Repression by NP95 Binding to Hemimethylated DNA. <i>Cell Stem Cell</i> , 2016 , 19, 81-94	18	53
38	An ultra-low-input native ChIP-seq protocol for genome-wide profiling of rare cell populations. <i>Nature Communications</i> , 2015 , 6, 6033	17.4	214
37	hnRNP K coordinates transcriptional silencing by SETDB1 in embryonic stem cells. <i>PLoS Genetics</i> , 2015 , 11, e1004933	6	45
36	Systematic identification of factors for provirus silencing in embryonic stem cells. <i>Cell</i> , 2015 , 163, 230-45	56.2	117
35	VisRseq: R-based visual framework for analysis of sequencing data. <i>BMC Bioinformatics</i> , 2015 , 16 Suppl 11, S2	3.6	37
34	Regulation of DNA methylation turnover at LTR retrotransposons and imprinted loci by the histone methyltransferase Setdb1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 6690-5	11.5	68
33	Setdb1 is required for germline development and silencing of H3K9me3-marked endogenous retroviruses in primordial germ cells. <i>Genes and Development</i> , 2014 , 28, 2041-55	12.6	154
32	Primate-specific endogenous retrovirus-driven transcription defines naive-like stem cells. <i>Nature</i> , 2014 , 516, 405-9	50.4	272
31	ALEA: a toolbox for allele-specific epigenomics analysis. <i>Bioinformatics</i> , 2014 , 30, 1172-1174	7.2	17
30	Genome-wide mapping of chromatin marks from 1,000 cells to study epigenetic reprogramming in primordial germ cells. <i>Epigenetics and Chromatin</i> , 2013 , 6,	5.8	1
29	Distinct roles of KAP1, HP1 and G9a/GLP in silencing of the two-cell-specific retrotransposon MERVL in mouse ES cells. <i>Epigenetics and Chromatin</i> , 2013 , 6, 15	5.8	107

28	Kinetics and epigenetics of retroviral silencing in mouse embryonic stem cells defined by deletion of the D4Z4 element. <i>Molecular Therapy</i> , 2013 , 21, 1536-50	11.7	18
27	An Interactive Analysis and Exploration Tool for Epigenomic Data. <i>Computer Graphics Forum</i> , 2013 , 32, 91-100	2.4	9
26	Vitamin C induces Tet-dependent DNA demethylation and a blastocyst-like state in ES cells. <i>Nature</i> , 2013 , 500, 222-6	50.4	562
25	Silencing of endogenous retroviruses: when and why do histone marks predominate?. <i>Trends in Biochemical Sciences</i> , 2012 , 37, 127-33	10.3	95
24	Histone H3K4 demethylation is negatively regulated by histone H3 acetylation in <i>Saccharomyces cerevisiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 18505-10	11.5	41
23	DNA methylation and SETDB1/H3K9me3 regulate predominantly distinct sets of genes, retroelements, and chimeric transcripts in mESCs. <i>Cell Stem Cell</i> , 2011 , 8, 676-87	18	309
22	H3K9me3-binding proteins are dispensable for SETDB1/H3K9me3-dependent retroviral silencing. <i>Epigenetics and Chromatin</i> , 2011 , 4, 12	5.8	33
21	Lysine methyltransferase G9a is required for de novo DNA methylation and the establishment, but not the maintenance, of proviral silencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 5718-23	11.5	94
20	Retrotransposon-induced heterochromatin spreading in the mouse revealed by insertional polymorphisms. <i>PLoS Genetics</i> , 2011 , 7, e1002301	6	104
19	Proviral silencing in embryonic stem cells requires the histone methyltransferase ESET. <i>Nature</i> , 2010 , 464, 927-31	50.4	513
18	Targeting of EZH2 to a defined genomic site is sufficient for recruitment of Dnmt3a but not de novo DNA methylation. <i>Epigenetics</i> , 2009 , 4, 404-14	5.7	66
17	H2A.Z and DNA methylation: irreconcilable differences. <i>Trends in Biochemical Sciences</i> , 2009 , 34, 158-61	10.3	14
16	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
15	An unmethylated 3Vpromoter-proximal region is required for efficient transcription initiation. <i>PLoS Genetics</i> , 2007 , 3, e27	6	51
14	RNA polymerase II: just stopping by. <i>Cell</i> , 2007 , 130, 16-8	56.2	12
13	Dynamics, stability and inheritance of somatic DNA methylation imprints. <i>Journal of Theoretical Biology</i> , 2006 , 242, 890-9	2.3	63
12	Intragenic DNA methylation alters chromatin structure and elongation efficiency in mammalian cells. <i>Nature Structural and Molecular Biology</i> , 2004 , 11, 1068-75	17.6	372
11	DNA methylation density influences the stability of an epigenetic imprint and Dnmt3a/b-independent de novo methylation. <i>Molecular and Cellular Biology</i> , 2002 , 22, 7572-80	4.8	103

10	Methylation-mediated proviral silencing is associated with MeCP2 recruitment and localized histone H3 deacetylation. <i>Molecular and Cellular Biology</i> , 2001 , 21, 7913-22	4.8	92
9	C(m)C(a/t)GG methylation: a new epigenetic mark in mammalian DNA?. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001 , 98, 10034-6	11.5	31
8	Position effects are influenced by the orientation of a transgene with respect to flanking chromatin. <i>Molecular and Cellular Biology</i> , 2001 , 21, 298-309	4.8	64
7	Dynamic analysis of proviral induction and De Novo methylation: implications for a histone deacetylase-independent, methylation density-dependent mechanism of transcriptional repression. <i>Molecular and Cellular Biology</i> , 2000 , 20, 842-50	4.8	118
6	Genomic targeting of methylated DNA: influence of methylation on transcription, replication, chromatin structure, and histone acetylation. <i>Molecular and Cellular Biology</i> , 2000 , 20, 9103-12	4.8	135
5	Single cell analysis and selection of living retrovirus vector-corrected mucopolysaccharidosis VII cells using a fluorescence-activated cell sorting-based assay for mammalian beta-glucuronidase enzymatic activity. <i>Journal of Biological Chemistry</i> , 1999 , 274, 657-65	5.4	11
4	Detection and Isolation of Gene-Corrected Cells in Gaucher Disease Via a Fluorescence-Activated Cell Sorter Assay for Lysosomal Glucocerebrosidase Activity. <i>Blood</i> , 1997 , 89, 3412-3420	2.2	29
3	Simultaneous fluorescence-activated cell sorter analysis of two distinct transcriptional elements within a single cell using engineered green fluorescent proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1996 , 93, 8508-11	11.5	95
2	Enzyme-generated intracellular fluorescence for single-cell reporter gene analysis utilizing <i>Escherichia coli</i> beta-glucuronidase. <i>Cytometry</i> , 1996 , 24, 321-9		16
1	The majority of histone acetylation is a consequence of transcription		3